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Abstracts

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Technical Session 1

Harnessing Genetic Diversity: Conservation, Evaluation and Utilization



Genome-Wide Dissection of Root and Physiological Traits

Underpinning Drought Tolerance in Maize

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Abstract: Drought stress remains a major constraint to maize productivity under increasingly erratic climatic conditions, necessitating the development of resilient cultivars. However, the complex and polygenic nature of drought tolerance limits the efficiency of conventional selection approaches. In this study, a genome-wide association analysis was conducted to identify simple sequence repeat (SSR) markers associated with key root and physiological traits conferring drought tolerance in maize. A diverse panel of 100 maize inbred lines was genotyped using 235 SSR markers distributed across all ten chromosomes. Genomic DNA was extracted following a modified CTAB protocol and subjected to PCR-based SSR analysis. Population structure was assessed using STRUCTURE, principal component analysis, and kinship matrices, revealing three distinct subpopulations with varying degrees of admixture. Marker-trait associations were evaluated using both general linear (GLM) and mixed linear models (MLM), incorporating population structure and kinship to minimize spurious associations. The analysis identified eight significant marker–trait associations linked to critical drought-responsive root and physiological traits. These loci were distributed across chromosomes 1, 2, 4, 7, 9, and 10, confirming the polygenic architecture of drought tolerance in maize. Quantile-quantile (QQ) plots demonstrated strong model fitness and effective control of false positives. The identified SSR markers represent valuable genomic resources for marker-assisted breeding. Their validation across diverse genetic backgrounds and environments will facilitate the development of drought-resilient maize cultivars through accelerated and precise selection strategies.

Key words: Maize, Drought, SSR markers, Genome-wide association study, Marker

Elite Suitable Hybrid Maize Varieties for Post-rice Cultivation in Upper Northern of Thailand: UP242 and UP227

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Abstract: [Objective] To develop maize hybrids suited for post-rice paddy cultivation in upper northern Thailand. [Method] A seven-year evaluation trial was conducted in standard environments to develop hybrid maize varieties for post-rice cultivation in the upper northern region. This research phase focused on producing single-cross hybrids and evaluated their yield performance, stability and adaptability through multi-location on-farm trials across the target provinces. [Result] The evaluation trials initially commenced with 439 crosses, which were subsequently narrowed down to 253 promising hybrids. On-farm trials were then conducted to validate their performance under actual farming conditions. Moreover, yield stability was using regression coefficients and deviations. On-farm trials, yield trials across four provinces showed that four elite hybrids (UP227, UP242, UP319 and UP342) produced comparable mean yields ranging from 8,887-10,293 kg ha⁻¹. These elite hybrids outperformed both government check varieties (8,431-9,843 kg ha⁻¹) and private sector counterparts (8,456-9,825 kg ha⁻¹). An analysis of variance revealed that the top-performing hybrids, particularly UP227 and UP242, produced the highest mean yield of 9,156 kg ha⁻¹, outperforming commercial varieties (9,043 kg ha⁻¹) and government cultivars (8,862 kg ha⁻¹). Consequently, two potential elite hybrids, UP227 and UP242, were released. Their first parents, UP27 and UP42, were developed through nine generations of selfing (*S*₉), while the second parent utilized the elite inbred line Ki60. [Conclusion] UP227 and UP242 were high yields and good adaptability 9,256 and 9,918 kg ha⁻¹, respectively. Both hybrids are ready for promotion as recommended varieties uniquely suited for post-rice cultivation in the upper north region. They aim to be distributed to farmers and relevant stakeholders for further commercial utilization.

Key words: Post-rice paddy cultivation, Hybrid maize, Upper northern of Thailand

Funding acknowledgment: This study was supported by Agricultural Research Development Agency (Public Organization).

Characterization of Mating Types, Genetic Diversity, Pathogenicity, and Sensitivity to Tebuconazole in *Bipolaris Maydis* Isolates from Henan Province, China

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Abstract:[Objective] The present study was performed to characterize the mating type distribution, population genetic structure, and tebuconazole susceptibility of *Bipolaris maydis* isolates from Henan Province. [Method] Multiplex PCR was used to detect mating types in 146 isolates. The genetic diversity of these 146 isolates was analyzed using ISSR markers. Pathogenicity of 107 isolates on resistant and susceptible maize cultivars was evaluated through field inoculation assay. The sensitivity of 167 isolates to tebuconazole was determined using the mycelial growth rate method. [Result] The ratio of MAT1-1 to MAT1-2 isolates was approximately 1.15 : 1, which conformed to the theoretical 1 : 1 expectation ($\chi^2 = 0.6849$, $P = 0.4079$) with no significant deviation. Both mating types were found in all regions, indicating the potential for sexual reproduction under natural conditions. These populations exhibited a high level of genetic diversity (polymorphic loci, PPL = 98.68%). Central Henan exhibited the richest diversity. Genetic variation existed within populations (89.28%), while differentiation among populations was low (genetic differentiation coefficient, $G_{ST} = 0.1072$) with considerable gene flow ($N_m = 2.8690$). All geographical populations were closely related (genetic similarity coefficient, $GS > 0.94$) but displayed discernible phylogenetic differences; northern Henan and eastern Henan populations were the most closely related, whereas the Jiangsu and Shandong populations were the most distantly related. All tested isolates were pathogenic to both resistant and susceptible cultivars, with average disease indices ranging from 33.33 to 100.00. Pathogenicity varied significantly among isolates from different regions and among different isolates on the same cultivar. The EC_{50} values of tebuconazole for the 167 isolates ranged from 0.0191 to 1.0411 $\mu\text{g}\cdot\text{mL}^{-1}$, with a mean of $0.3665 \pm 0.2254 \mu\text{g}\cdot\text{mL}^{-1}$. The frequency distribution of sensitivity showed a unimodal curve, establishing a baseline sensitivity of *B. maydis* to tebuconazole. [Conclusion] This study elucidates the population genetic structure and pathogenic differentiation of *B. maydis* and provides a baseline sensitivity to tebuconazole, which provides a theoretical basis for integrated disease management.

Key words: *Bipolaris maydis*, Mating type, ISSR, Genetic diversity, Pathogenicity, Tebuconazole

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Exploring Genetic Diversity of Thai Waxy Corn Landraces Through MassARRAY Genotyping

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Abstract: [Objective] Modern maize breeding has primarily focused on increasing grain yield through the development of hybrid cultivars. However, the continuous use of elite germplasm may narrow the genetic base of maize and reduce its adaptability to emerging biotic and abiotic stresses. Thai waxy maize landraces represent valuable genetic resources that may contribute to broadening genetic diversity in breeding programs. Therefore, this study aimed to collect and evaluate the genetic diversity of Thai waxy maize landraces using molecular markers. [Method] A total of 187 waxy maize landrace accessions from four regions of Thailand and five commercial cultivars were evaluated. Genetic diversity was assessed using MassARRAY genotyping, while population structure and genetic relationships were analyzed using STRUCTURE and Neighbor-Joining analyses. [Result] The average gene diversity across all accessions was 0.21, indicating the presence of substantial genetic variation within the germplasm collection. Both Neighbor-Joining and STRUCTURE analyses produced consistent results and classified all accessions into five genetic groups. Most commercial cultivars were assigned to Group 1, whereas the remaining groups consisted predominantly of landrace accessions. [Conclusion] Thai waxy maize landraces possess considerable genetic diversity and are genetically distinct from most commercial cultivars. These landraces represent valuable germplasm resources that can be utilized in future maize breeding programs to broaden the genetic base and enhance resilience to changing environmental conditions.

Key words: Waxy maize, Landrace, Genetic diversity, MassARRAY

Funding acknowledgement: Department of Agronomy, Faculty of Agriculture at Kamphaeng Saen, Kasetsart University, Kamphaeng Saen Campus, Nakhon Pathom, Thailand

Diverse and Stable Male Sterile Tropical Asian Maize Inbred Lines Provide Strategic Opportunity for Hybrid Development

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Abstract: Cytoplasmic Male Sterility (CMS), a maternally inherited trait which suppresses the production of viable pollen, eliminates the need for detasseling of females in hybrid maize seed production. A set of 88 diverse elite CIMMYT Asia maize inbred lines converted to CMS-C using LP1 CMS HT- a temperate donor, were evaluated for stable per se performance for grain yield, male sterility and *Turcicum* Leaf Blight resistance. Performances of CMS maize hybrids of varied genetic backgrounds across diverse environments -- seasons, years, agroecologies, countries, abiotic- and biotic stresses -- established a stable and robust diversification process which included the identification of potential maintainers and restorers that will benefit researchers, the seed industry and farmers. While multiple CMS hybrids showed a range of yield performances comparable to non-CMS checks, we report on a distinct 9.9% yield advantage of a CMS hybrid CSMH13 compared to its isogenic non-CMS counterpart through a head-to-head analysis. From implications in enhancing global genetic gains to directly addressing issues of labour availability and rising operational wages, the technology offers opportunities for intellectual property protection strictly to the legal owner and region-wide taming of tropical Asian maize germplasm diversity by imposing a heterotic discipline.

Key words: Cytoplasmic Male Sterility (CMS), Maintainer, Restorer, Genetic Gain, Seed Production

Funding acknowledgement: International Maize Improvement Consortium for Asia (IMIC-Asia), the CGIAR Research Program (CRP) MAIZE and the CGIAR Accelerated Breeding Initiative.

Development of MTP-Maize Introgression Lines with Salt Tolerance and Dissection of the Genetic and Physiological Basis

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Abstract: [Objective] *Tripsacum* and *Teosinte* are valuable wild germplasm resources for maize improvement due to their remarkable tolerance to salinity, cold, and pests. This study aimed to develop salt-tolerant introgression lines from an MTP genetic bridge (incorporating genomes of maize, *Tripsacum*, and *Zea perennis*) and to elucidate the genetic and physiological mechanisms underlying salt tolerance. [Method] We generated a population of 169 MTP-maize introgression lines through successive introgressive hybridization, evaluated their genetic diversity and salt tolerance, and identified a highly tolerant line, STIL-44. Physiological and anatomical analyses were performed under 200 mM NaCl stress, including measurements of Na⁺ content and root apoplastic barrier deposition. Genetic analysis was conducted using F₂ segregation populations derived from crosses between STIL-44 and sensitive lines (B73 and Mo17), followed by BSA-based mapping and fine-mapping with polymorphic markers. [Result] STIL-44 exhibited significantly lower Na⁺ accumulation in both roots and leaves than the recurrent parent B73 under salt stress. Root anatomical observations revealed substantially increased suberin and lignin deposition in the cortex and endodermis of STIL-44, suggesting that enhanced apoplastic barriers restrict Na⁺ influx. Chi-square tests in both F₂ populations fitted a 1:2:1 segregation ratio (sensitive:intermediate:tolerant), indicating control by a single major dominant gene. BSA-associated analysis localized the candidate gene to a 25.69 Mb interval on chromosome 3 (167–204 Mb) at 99% confidence level. GO enrichment highlighted lignin metabolism pathways within this region. Subsequent fine-mapping narrowed the interval to 40 kb. [Conclusion] Our findings provide both a valuable salt-tolerant line and a fine-mapped candidate locus for cloning the underlying gene and for marker-assisted breeding of salt-tolerant maize.

Key words: Maize, Salt tolerance, Introgression lines, Genetic mechanism, BSA, Fine-mapping

From Genebank to Field: Allele Mining Unlocks Novel Diversity for Climate-resilient Maize Breeding

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Abstract: [Objective] To identify and deploy novel adaptive alleles from maize landraces for improving heat and drought tolerance in elite breeding germplasm and to broaden the genetic base available for climate-resilient maize improvement. [Method] An environmental genome-wide association study (envGWAS) leveraging environmental and genomic information from approximately 17,300 maize landraces was conducted to identify alleles associated with adaptation to diverse climatic conditions. These adaptive alleles were subsequently used to screen more than 26,000 accessions conserved in the CIMMYT germplasm bank. Around 1,000 donor landraces representing diverse geographic origins and environmental adaptations were selected and crossed with elite germplasm. Derived populations were advanced and evaluated in managed-stress field trials in Mexico under heat and drought conditions. Early-generation materials and introgression-derived populations were assessed for grain yield, adaptation, and stress tolerance traits. [Results] Introgressed materials exhibited improved performance under heat and drought stress relative to adapted checks, demonstrating that landrace-derived variation can contribute positively to quantitative traits. Significant diversity for yield stability, adaptation, and stress resilience was observed across the evaluated populations. These findings confirm that underutilized genetic resources contain valuable alleles capable of enhancing breeding progress in challenging production environments. The results also support the effectiveness of combining environmental association analysis with targeted introgression to identify and deploy beneficial diversity from genebank collections. [Conclusion] Integrating allele mining, envGWAS, and strategic use of landrace diversity accelerates the development of climate-resilient maize germplasm. Ongoing molecular validation studies will further elucidate the genetic basis of adaptive alleles and support their efficient deployment in future maize breeding program

Key words: Maize landraces, Allele mining, EnvGWAS, Climate resilience, Abiotic stress, Germplasm

Funding acknowledgement: Gates Foundation; Foundation for Food and Agriculture Research (FFAR).

Multivariate Characterization of Agronomic and Yield-related Traits in Maize Hybrids Under Rainfed Conditions

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Abstract: Rainfed maize production systems are characterized by high yield variability due to fluctuating climatic conditions and complex stress interactions, necessitating efficient hybrid evaluation strategies that account for multi-trait performance. The present study aimed to characterize phenotypic diversity among maize hybrids evaluated under rainfed kharif conditions and to identify distinct ideotype-based groups using multivariate analysis. A total of 74 maize hybrids were evaluated over two kharif seasons (2022–23 and 2023–24) at the research farm of Rani Lakshmi Bai Central Agricultural University, Jhansi, India. Hybrid-wise mean values of agronomic, phenological, and yield-related traits were subjected to descriptive statistics, correlation analysis, principal component analysis (PCA), and cluster analysis. Substantial phenotypic variation was observed across traits, with higher coefficients of variation for ear height and cob weight, indicating scope for diversity-based selection. Correlation analysis revealed strong associations among plant architecture, stand establishment, and yield-related traits. PCA identified three principal components explaining 70.22% of the total phenotypic variation, representing plant architecture and stand establishment, phenological timing, and yield-related traits, respectively. Cluster analysis based on principal component scores classified hybrids into four distinct phenotypic groups, each characterized by specific trait combinations corresponding to different ideotypes. Based on multi-trait performance, three hybrids (Hybrid maize 1, Hybrid maize 2, and Hybrid maize 3) were identified as promising candidates under rainfed conditions. Overall, the study demonstrates that multivariate phenotypic analysis is an effective approach for characterizing diversity, identifying ideotypes, and supporting hybrid selection in rainfed maize production environments.

Key words: Multivariate characterization, Principal component analysis, Rainfed condition and hybrid maize

Enhancing Tropical Maize Productivity Through Temperate Ex-PVP Introgression: Yield and Combining Ability Under Contrasting Moisture Regimes

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Abstract: [Objective] Low grain yield and recurrent drought remain major constraints to maize production in sub-Saharan Africa (SSA), highlighting the need to develop climate-resilient, high-yielding hybrids. This study aimed to assess the breeding value of temperate expired Plant Variety Protection (ex-PVP) maize lines introgressed into tropical germplasm and to determine the genetic basis of grain yield and related agronomic traits under well-watered (WW) and drought-stressed (DS) environments. [Method] Fifteen temperate introgressed (TI) lines and six tropical lines were crossed with eight single-cross testers to generate 168 testcross hybrids. The hybrids were evaluated across eight environments in Kenya, comprising WW and two managed DS sites. [Result] Highly significant genotypic, environmental, and genotype $\times$ environment interaction effects were observed for grain yield and most agronomic traits, particularly under DS. Both general combining ability (GCA) and specific combining ability (SCA) contributed significantly to trait expression, although additive genetic variance predominated under both WW and DS conditions. Temperate introgression substantially improved grain yield in most tropical backgrounds, with TI-derived hybrids producing 1.20–2.04 t ha⁻¹ higher yield than tropical hybrids under WW conditions, while maintaining comparable performance under DS (TI: 1.88 t ha⁻¹; tropical: 1.89 t ha⁻¹). DS reduced grain yield by up to 74%, plant height by 22%, and ear height by 18%, while increasing the anthesis–silking interval by 72% relative to WW conditions. Lines L2, L10, and L16, together with testers T1, T2, T3, T4, and T7, exhibited consistently favorable GCA effects for grain yield and shorter anthesis–silking interval, identifying them as valuable parental resources for drought-tolerant hybrid development. [Conclusion] These findings demonstrate that temperate ex-PVP germplasm is an effective source of favorable alleles for enhancing yield potential while maintaining drought adaptation in tropical maize. The predominance of additive genetic effects, together with the significant contribution of non-additive effects, suggests that integrating pedigree-based selection and genomic selection with strategic exploitation of heterosis can accelerate the development of high-yielding, climate-resilient maize hybrids for drought-prone regions of SSA.

Key words: Ex-PVP germplasm, Temperate introgression, Drought stress, GCA, Grain yield

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From Microstructure Characteristics to Macroscopic Properties: A Multi-scale Study on the Characteristics of 271 Maize (*Zea mays* L.) Germplasm Resources

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Abstract: [Objective] The comprehensive characterization of maize (*Zea mays* L.) germplasm diversity in China is crucial for targeted breeding and end-use applications. [Method] In this study, 271 maize germplasms from 21 provinces in four regions (Huang-Huai-Hai, Northwest, Northeast and South) were evaluated, and their water content, 1000-grain weight and bulk density were measured, and their water distribution was evaluated by low field nuclear magnetic resonance. [Result] It was observed that the overall moisture concentration was between 5.6% and 12.7%, with the minimum value of HN-WK702 (5.60%) and the maximum value of GXNN-QH509 (12.70%). The bulk density was mostly in the range of 700 ~ 900 g/L. The bulk density of SH-SKT811 was significantly lower, while the bulk density of XJWLMQ-DF20 was the highest (921.33 g/L). The thousand-grain weight varied greatly, from less than 100 g (sweet corn) to nearly 500 g (some horse-tooth varieties), reflecting the huge difference in grain size between varieties. The results of low field nuclear magnetic resonance showed a variety of water distribution. [Conclusion] In summary, the germplasm resources in the main maize producing areas in China showed extensive variation in physical quality traits. These findings have deepened the understanding of the diversity of different maize germplasms and laid the foundation for the utilization and breeding of germplasm resources to achieve customized principal component characteristics such as starch and protein.

Key words: Corn (*Zea mays* L.), Germplasm, Moisture content, Thousand seed weight, Volumetric weight

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The Transcription Factor ZmbZIP75 Promotes Both Grain Filling and Kernel Dehydration in Maize

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Abstract:[Objective] The selection of both high-yield and low-kernel-moisture varieties is essential for modern maize production; however, such breeding efforts are constrained by the limited availability of valuable regulatory genes. [Method] By integrating reverse genetics with comprehensive analyses of hormonal dynamics, gene expression profiles, transcription factor screening, and candidate gene association assays during kernel development we identified ZmbZIP75, a kernel-preferential, ABA-dependent basic leucine zipper (bZIP) transcription factor, as a putative regulator of maize kernel development. Furthermore, using CRISPR-Cas9-mediated mutagenesis, multi-omics profiling, biochemical assays, physiological measurements, and transgenic experiments, we systematically elucidated the functional mechanisms of ZmbZIP75 in maize. [Result] Knockout of ZmbZIP75 results in defective grain filling and kernel dehydration, whereas ZmbZIP75 overexpression confers increased grain yield per plant and decreased kernel moisture without altering plant architecture. Mechanistically, during the grain filling stage, ZmbZIP75 is transcriptionally induced by maternal-derived basal abscisic acid (ABA) and directly activates multiple core starch synthesis-related genes and key TFs, thereby promoting grain filling and final yield. In the late stage of kernel development, high concentrations of zygotic ABA enhance ZmbZIP75 phosphorylation through SnRK2.10. The phosphorylated ZmbZIP75 subsequently transactivates and interacts with TF VP1 to synergistically promote kernel dehydration. [Conclusion] Our findings demonstrate that ZmbZIP75 promotes grain yield and reduces kernel moisture in maize. Collectively, this study underscores the potential of ZmbZIP75 for engineering both high-yield and low-kernel-moisture varieties to meet the demands of high-efficiency maize production.

Key words: ZmbZIP75, Grain filling, Grain dehydration, ABA

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A G-type Lectin Receptor-Like Kinase Confers Seed Low-temperature Germination Ability via Promoting ABA Mediated Germination Speed in Maize

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Abstract: [Objective] Low-temperature germination ability (LTGA) is a critical determinant for stable stand establishment and high crop productivity of maize in temperate regions. However, very few causal genes have been isolated for this trait, and the underlying molecular mechanisms remain poorly understood, partially due to its complex quantitative genetic architecture. This study aimed to clone the major quantitative trait locus (QTL) qLTG1 controlling maize LTGA, uncover its functional variations and molecular mechanism. [Method] Map-based cloning was executed using large backcross populations (>10,000 individuals) generated from a cold-tolerant donor line (L220) and a cold-sensitive recurrent parent (PH4CV). Candidate genes were validated through Mu insertion mutants, CRISPR/Cas9-mediated knockouts, and transgenic overexpression lines. Functional variations were analyzed using dual-luciferase reporter assays in maize protoplasts, tissue-specific RT-qPCR, and in situ hybridization. Downstream molecular networks were analyzed using RNA-seq and quantitative phosphoproteomics on germinating embryos. Finally, marker-assisted selection was employed to evaluate field emergence and yield performance of qLTG1 introgressed lines under low-temperature conditions. [Result] qLTG1 was fine-mapped to a 23.7-kb interval, and genetic validation confirmed that Zm00001d031230, which encodes a plant-specific plasma membrane-localized G-type Lectin Receptor-Like Kinase (named ZmLTGA1), is the causal gene. A 2,112-bp Gypsy-LTR transposon insertion at the -600 bp position in the promoter of the sensitive line (PH4CV) significantly suppressed promoter activity and abolished the expression of ZmLTGA1, resulting in a dramatic drop in germination speed. Transcriptomic and phosphoproteomic profiling revealed that loss of function of ZmLTGA1 significantly upregulated the expression and phosphorylation levels of key abscisic acid (ABA) biosynthetic and signaling components (including PYLs, PP2Cs, SnRKs, and ABFs et al.). Exogenous ABA treatments confirmed that *zmltga1* mutants displayed hypersensitivity to ABA, whereas overexpression lines exhibited reduced sensitivity, demonstrating that ZmLTGA1 acts as a negative regulator of the ABA pathway. Field evaluations showed that introgressing the favorable ZmLTGA1 allele into PH4CV significantly boosted field emergence speed, emergence index, and grain yield under cold early-spring conditions. [Conclusion] This study demonstrates that ZmLTGA1 is a novel G-type lectin receptor-like kinase that actively promotes seed germination speed and low-temperature seedling establishment by negatively regulating ABA accumulation and signal transduction. These findings fill a crucial gap regarding RLK functions in seed biology and provide an exceptional genetic resource for breeding elite, cold-resilient maize hybrids.

Key words: Seed, Germination, Low temperature, Lectin Receptor-Like Kinase, Maize

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Identification of Stable Cytoplasmic Male Sterile Lines and Fertility Restorers for Efficient Hybrid Seed Production in Maize (*Zea mays* L.)

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Abstract: [Objective] The objectives of the investigation were to identify stable C-CMS lines and reliable fertility restorers for efficient hybrid seed production in maize. [Method] Three CMS lines developed at the University and four CMS lines received from CIMMYT, Hyderabad were evaluated during rabi (post-rainy) 2023-24 and kharif (rainy) 2024 to assess the stability of male sterility expression. Further, 25 diverse maize inbred lines were crossed with three CMS lines (CAL1514A, CAL1426A and ZL153493A) and the resulting 75 single cross hybrids and checks were evaluated during kharif 2024 to identify the restorer lines. [Result] All seven CMS lines consistently exhibited complete absence of anther exertion and pollen shedding across the environments confirming stable male sterility. While, four testers viz., VL184899, VL19978, VL161566 and CML451 consistently restored fertility across all CMS lines indicating their potential as reliable restorers. [Conclusion] The stable CMS lines and fertility restorers could serve as an excellent source for developing CMS based high yielding maize hybrids of high genetic purity at reduced cost of hybrid seed production.

Key words: C-CMS, Fertility restorer, Maize

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Evaluation and Screening of 115 Maize Germplasms under High-temperature Conditions during Flowering

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Abstract: [Objective] High-temperature stress during the flowering period has become a frequent abiotic constraint in the Huang-Huai-Hai summer maize planting region in recent years, severely threatening regional maize yield stability. To mitigate its adverse impacts on maize production, this study carried out systematic heat tolerance evaluation and targeted screening on 115 collected maize germplasm accessions. [Method] Under consistent natural field high-temperature stress conditions, 16 agronomic traits closely related to heat tolerance, including tassel main axis length and silk length, were accurately measured. A series of statistical methods including genetic diversity analysis, correlation analysis, principal component analysis, multiple linear regression analysis and cluster analysis were comprehensively applied, and the screening and identification of heat-tolerant maize germplasm was completed with the germplasm comprehensive evaluation system constructed based on F-values. [Result] The results showed that the tested materials had abundant phenotypic variations, with the coefficient of variation ranging from 13.46% to 97.76% and the diversity index from 1.7% to 2.07%. Correlation analysis revealed different degrees of significant or non-significant correlations among the 16 measured traits. Principal component analysis reduced the original 16 traits into 4 independent principal components, which cumulatively explained 73.067% of the total phenotypic variation. The four principal components corresponded to four core indicators: yield-related traits, plant morphology and tassel characteristics, barren stalk rate, and 100-kernel weight. Multiple linear regression analysis confirmed that both 100-kernel weight and kernels per row had significant positive effects on plot yield, and kernels per row exerted a relatively stronger effect on yield formation. Cluster analysis classified all tested materials into three groups: Group I represented high-yielding elite heat-tolerant germplasm; Group II had moderate yield performance and the shortest anthesis-silking interval (ASI); Group III showed low yield, prolonged ASI and higher barren stalk rate. [Conclusion] Through F-value comprehensive scoring and screening, 10 elite heat-tolerant maize germplasm accessions with stable performance were finally obtained, which can provide important practical references for subsequent targeted identification of heat-tolerant germplasm and breeding utilization of heat-tolerant summer maize varieties in the Huang-Huai-Hai region.

Key words: Maize, Flowering stage, High temperature stress, Germplasm, Heat tolerance

Progress, Challenges, and Future Prospects through DAR-CIMMYT Collaboration

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Abstract: A long-term hybrid maize research initiative was established in 1974–1975 at the Department of Agricultural Research (DAR), Yezin, Myanmar, utilizing introduced genetic materials from CIMMYT. Systematic selection and selfing for six to seven generations led to the release of early commercial varieties—Yezin Hybrid-2, Yezin Hybrid-3, and Yezin Hybrid-4—between 1990 and 1994, which significantly expanded hybrid seed distribution across the country. However, after 2006, the influx of high-yielding imported commercial hybrids (such as CP-888) and a reduction in introduced trials created major competitive challenges, resulting in declining adoption of DAR-released hybrids. To address these constraints, DAR re-established access to CIMMYT's elite germplasm resources in 2019. Furthermore, integrating advanced Doubled Haploid (DH) technology into DAR's breeding framework has modernized national research capabilities. This strategic collaboration accelerates the development of elite, stress-resilient inbred lines and high-yielding competitive hybrid cultivars tailored to local agro-ecological conditions. Ultimately, the renewed DAR-CIMMYT partnership plays a vital role in enhancing national food security, improving farmer livelihoods, strengthening seed sector competitiveness, and driving sustainable agricultural development in Myanmar.

Key words: Hybrid maize, DAR, CIMMYT, Double haploid technology, Myanmar

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Utilizing Tropical Maize Germplasm to Address Genetic Homogenization in Chinese Maize Breeding

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Abstract: Maize underwent severe genetic bottlenecks during domestication and its northward spread from tropical origins, resulting in substantial loss of disease resistance and stress tolerance in modern temperate varieties. In China, commercial hybrids have become increasingly dependent on a narrow set of elite inbred lines, most notably derivatives of Zheng58 and Chang7-2, creating a genetic uniformity problem that elevates vulnerability to emerging diseases. Recent outbreaks of southern rust (2021) and the rapid spread of maize white spot disease—now affecting over 15 million mu across multiple provinces—illustrate the biosecurity risks associated with this narrow genetic base. This study presents a systematic strategy to broaden the genetic diversity of Chinese temperate maize breeding through the targeted use of tropical germplasm, particularly Suwan1 and Cateto populations. Key findings include: identification of the molecular mechanisms controlling photoperiod sensitivity in tropical germplasm, with JA and ROS signaling pathways shown to regulate flowering time in a 541-RIL multi-parent population; development of a “triangular” heterotic pattern incorporating Suwan1 alongside Reid and non-Reid temperate groups, which improved breeding efficiency by 21%; development of a tropical doubled haploid inducer line (Yunyou No. 2) adapted to subtropical conditions; and construction of a 52-genome pan-genome and a nested association mapping (NAM) population to identify favorable alleles lost during temperate adaptation. GWAS analysis of the NAM population identified five candidate genes associated with white spot resistance, including Zmhsftf25 (PVE = 6.05%). To date, over 20 hybrids have been released under this breeding framework. An optimal tropical germplasm introgression proportion of 6.25–12.5% was identified as effective for enhancing genetic diversity without compromising agronomic performance. These results provide practical guidance for addressing genetic uniformity in Chinese maize breeding and offer broader implications for sustainable global maize improvement.

Key words: Tropical maize germplasm, Genetic diversity, Heterotic pattern, Suwan1, Doubled haploid, Pan-genome, Maize white spot disease

Deciphering the Contributions of Hybridization and Genome Dosage to Vegetative Vigor in Perennial Forage Maize

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Abstract: [Objective] Heterosis and genomic dosage each enhance plant vigor, yet their manifestation and underlying mechanisms in vegetative growth, particularly within polyploid systems, remain unclear. [Method] We synthesized and analyzed a series of *Zea-Tripsacum* allopolyploid trihybrids (MTPs) with varying genomic compositions, to dissect the synergistic contributions of hybridization and polyploidy/aneuploidy effects to vegetative vigor. [Result] We demonstrate that increased *Z. perennis* genome dosage directly enhances fresh weight (FW) and photosynthetic capacity, whereas interspecific hybridization triggered extensive transcriptome reprogramming. Heterotic hybrids exhibited transcriptional signatures of improved energy-use efficiency, characterized by the downregulation of energy-costly protein quality control systems and upregulation of energy metabolism and carbon fixation pathways. Co-expression network analysis linked modules of fructose metabolism and glycolysis positively to FW heterosis, while protein folding modules were negatively correlated. Field trials confirmed the agronomic superiority of elite MTP-derived perennial forage cultivars, Yucao 6 and Yucao 9919, which achieved high yields (127.68-142.61 t ha⁻¹) across diverse ecological zones, 156.28%-186.25% higher than conventional silage maize. These perennial forage cultivars can be harvested for many years after a single planting, substantially lowering production costs and providing a practical option for utilizing sloping and abandoned lands in southern China. [Conclusion] Our findings clarify how hybridization and genomic dosage, via transcriptional remodeling, jointly boost plant vigor, offering both a mechanistic framework and a practical breeding roadmap for integrating heterosis and genomic-dosage strategies in crop improvement.

Key words: Allopolyploidization, Heterosis, Genome dosage, *Zea*, *Tripsacum*; Perennial forage maize

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Dynamic Responses of Maize Root Morphology and Turnover Characteristics to Nitrogen Supply Based on an in situ Root-window Approach

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Abstract: [Objective] Rational nitrogen management is essential for improving crop productivity and nitrogen use efficiency (NUE), while root system traits play a critical role in regulating nutrient acquisition and plant growth. However, the dynamic responses of maize roots to different nitrogen supplies remain difficult to characterize due to limitations of conventional destructive sampling methods. This study aimed to establish an in situ root-window observation approach and investigate the effects of nitrogen supply on maize root morphology, turnover dynamics, root–shoot coordination, and nitrogen utilization. [Method] A field experiment was conducted during 2023–2024 at the Gongzhuling Experimental Station, Jilin Province, China, using two representative maize hybrids, Xianyu 335 and Weike 702. Five nitrogen application rates (0, 100, 200, 300, and 400 kg N ha⁻¹) were established. Root growth dynamics within the 0–60 cm soil layer were continuously monitored using an inter-row in situ root-window system throughout the growing season. Root morphology, root production, mortality, lifespan, root exudates, plant nitrogen accumulation, nitrogen use efficiency, and grain yield were measured. [Result] The developed root-window system enabled low-cost, large-scale, and continuous observation of maize root growth under field conditions. Root traits obtained using this approach showed significant correlations with traditional measurements. Optimal nitrogen application (N200–N300) significantly promoted root elongation, surface area development, and root volume expansion, increasing root length, surface area, and volume by 11.84%, 14.00%, and 13.98%, respectively. Excessive nitrogen supply inhibited root elongation, whereas nitrogen deficiency stimulated deeper root exploration but disrupted carbon–nitrogen balance. Root production followed a Logistic growth model ($R^2 > 0.9786$), and suitable nitrogen supply increased maximum root production rate while shortening the time required to reach peak production. Nitrogen application also regulated root mortality dynamics and enhanced root turnover through increased root exudate activity. Furthermore, optimized root biomass improved leaf photosynthetic capacity and root–shoot coordination, resulting in increased nitrogen accumulation, nitrogen harvest index, and grain yield. [Conclusion] In situ root-window observations revealed that appropriate nitrogen supply improves maize root morphology and turnover characteristics, establishes a coordinated root–shoot relationship, and enhances nitrogen utilization and yield formation. These findings provide a physiological basis for optimizing nitrogen management and improving nitrogen-efficient maize production.

Key words: Maize, In situ root window, Root morphology, Root turnover, Nitrogen use efficiency

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Integrated Phenotyping and Genomic Dissection of Saline-Alkaline Tolerance in Maize Germplasm

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Abstract: Soil salinization and alkalization are major abiotic stresses threatening global maize production. The development of tolerant varieties is crucial for utilizing affected lands, yet progress is hindered by a lack of precise and standardized phenotyping methods. This study aimed to systematically evaluate saline-alkaline tolerance in a diverse panel of 461 maize inbred lines and dissect the underlying genetic architecture. We employed a novel, high-throughput sand-bed germination protocol that enables the independent and concurrent assessment of salt (NaCl) and alkali (NaHCO₃/Na₂CO₃) stress at the seedling stage. This was complemented by a two-year field evaluation in natural saline-alkaline soil. A comprehensive multi-trait scoring system, based on a membership function analysis (D-value), was used to rank germplasm for tolerance. Our results revealed substantial phenotypic variation, with coefficients of variation for stress-related traits ranging from 10.46% to 27.80% in seedling assays and 11.31% to 45.03% in the field. Based on the integrated D-values, we identified 39 highly salt-tolerant and 35 highly alkali-tolerant lines. Notably, 17 lines, including Jian1495b and HYS, exhibited dual tolerance to both stresses, while 7 lines, such as 4019 and M03, were highly sensitive. GWAS analysis identified 152 significant SNP loci corresponding to 33 candidate genes with diverse functions. These include ion transporters (e.g., plasma membrane ATPase), signaling components transcriptional regulators and genes involved in cellular homeostasis and stress mitigation, such as Aquaporin for water transport, Glycosyltransferase and Alpha-galactosidase for cell wall modification and osmoprotection. This study offers a robust screening protocol, identifies elite tolerant germplasm, and reveals key candidate genes and natural alleles. These findings provide a strong theoretical foundation and valuable genetic resources for marker-assisted selection and the genetic improvement of saline-alkaline tolerance in maize.

Key words: Maize, Saline-alkaline tolerance, GWAS, Phenotyping, Candidate genes, Germplasm evaluation

Evaluation of Improvement Effects of TSPT Germplasm Using Early-Maturing Germplasm

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Abstract: [Objective] Tangsipingtou (TSPT) represents a vital maize germplasm resource in China and has exerted a profound influence on maize breeding in the Huang-Huai-Hai region. However, the practical utilization of TSPT germplasm is constrained by several undesirable traits, including excessive vegetative growth and pronounced susceptibility to lodging. Early-maturing germplasms, which typically possess ideotype plant architecture and robust lodging resistance, hold promise as potential donors for the genetic improvement of TSPT. Nevertheless, systematic studies exploring this strategy remain scarce. [Method] In this study, four elite early-maturing inbred lines (CAVA104, CAVB110, K523, and QF252) and four representative TSPT inbred lines (C116A, C7-2, CALB169, and J2416) were selected to construct a multi-reference nested-association mapping (MR-NAM) population following the NCII design, comprising 16 subpopulations. From each subpopulation, six superior lines were chosen, resulting in a panel of 96 inbred lines. These lines were crossed with five testers using a complete diallel mating scheme, generating 480 hybrids. The hybrids were evaluated across seven environments, and 4 phenotypic traits—including days to anthesis (DTA), days to silking (DTS), grain moisture content (GMC), and grain yield (GY)—were systematically assessed. [Result] Relative to the controls, the MR-NAM hybrid population exhibited an average reduction of 2 days in both DTA and DTS. The population mean for GMC was approximately 1.69% lower than that of the controls, with 334 hybrids showing reduced moisture content. For GY, the population average was 1.3 kg below the control mean, although five hybrids outperformed the controls. Among the early-maturing donors, hybrids derived from CAVB110 displayed the lowest GMC, while those from QF252 showed the earliest DTA and DTS. Hybrids involving C116A achieved higher grain yields in spring-sowing regions, whereas those from CALB169 performed better in summer-sowing environments. Notably, 14 lines derived from the cross J2416 × CAVA104 exhibited superior comprehensive performance, characterized by higher GY and lower GMC, accounting for 16.7% of the total lines tested. [Conclusion] Introducing early-maturing germplasm into TSPT effectively accelerates flowering and reduces grain moisture without sacrificing yield, especially derived from the cross J2416 × CAVA104. The MR-NAM population provides a robust platform for genetic dissection and marker-assisted improvement of key traits. Environment-specific performance differences highlight the need for tailored breeding strategies, and genomic selection will facilitate the development of high-yielding, low-moisture, lodging-resistant cultivars for the Huang-Huai-Hai region.

Key words: Tangsipingtou, Early-maturing inbred lines, MR-NAM, GMC, GY

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Regulation of Maize Grain Yield and Quality Through Selection of Varieties and Densities Adapted to Environmental Factors

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Abstract: [Objective] The intensification of global climate change has consistently posed a severe threat to agricultural production, and elucidating the relationships between climatic factors and crop yield and quality is crucial for addressing climate change and ensuring human food security. [Method] This study was conducted in eight representative regions of the Songnen Plain in Northeast China during 2024-2025 to identify the major environmental factors influencing maize yield and quality and to match these factors with agronomic practices, including cultivar and planting density, for improving maize yield and quality. A large-plot experimental design was adopted with two planting densities (6×10^4 plants ha⁻¹ and 7.5×10^4 plants ha⁻¹) and 20 historically high-yielding cultivars across each region, resulting in a total of 320 treatments. [Result] The results showed that genotype and environment were the primary sources of variation in maize yield and quality. Increasing planting density did not lead to significant yield differences, but grain protein content significantly decreased by 2.43% on average while starch content increased by 0.18% on average. Diurnal temperature range (DTR), growing degree days (GDD), precipitation (PR), and cumulative photosynthetically active radiation (CPAR) were identified as the key environmental factors driving the variation in maize yield and quality across different treatments. Overall, a 0.1°C increase in GDD within the corresponding window increased yield by 59.6 kg ha⁻¹, a 0.1°C increase in DTR increased yield by 116.7 kg ha⁻¹, a 0.1 mL increase in PR decreased yield by 66.8 kg ha⁻¹, and a 0.1 unit increase in CPAR decreased yield by 268.0 kg ha⁻¹. The corresponding windows also exhibited significant linear relationships with grain protein and starch contents. The correlation coefficients between yield and quality of the 20 cultivars and the key environmental factor windows were 0.46 and 0.42 at planting densities of 6×10^4 plants ha⁻¹ and 7.5×10^4 plants ha⁻¹, with corresponding coefficients of variation of 0.38 and 0.45, respectively. Multiple linear regression models constructed using the four key environmental factors explained 66.2%, 71.90%, 44.2%, and 70.6% of the variation in grain yield, protein content, fat content, and starch content, respectively. DTR and CPAR together contributed 82.75% to yield variation, CPAR contributed 77.25% to protein content variation, DTR and PR together contributed 73.29% to fat content variation, and PR and CPAR together contributed 80.46% to starch content variation. [Conclusion] This study quantified the relationships between critical environmental factor windows and maize yield and

quality, proposed a theoretical framework for aligning agronomic practices, including cultivar and planting density, with environmental factors to synergistically improve yield and quality, and aimed to establish an environment-matching maize production system to achieve the coordinated goals of yield enhancement and quality optimization.

Key words: Maize, Grain yield and quality, Environmental factors, Correlation analysis, Quantitative analysis

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Discovery of Salt-Tolerant Maize Resources and Genes and Their Application in Breeding

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Abstract: [Objective] To develop high-yield maize varieties with improved saline-alkali adaptability, this study carried out systematic research on saline-alkali tolerant maize, including germplasm identification, mining of tolerance-related genes and breeding utilization. [Method] A stable laboratory evaluation system was established to assess saline-alkali tolerance of maize at germination and seedling stages, with 150 mM NaCl treatment for 7 days set as the optimal assay conditions. Population resequencing, GWAS and transcriptome profiling were combined to excavate salt-tolerant regulatory genes. Field trials were conducted on saline-alkali land across Northeast China and the Huanghuaihai Plain, with real-time monitoring of soil salinity, pH value and standardized plot management. [Result] A total of 346 maize inbred lines were phenotyped and graded for saline-alkali tolerance, and three core candidate genes responsible for salt tolerance were identified. More than 60 elite salt-tolerant inbred lines and 26 new breeding materials were screened out. The heterosis characteristics of grain yield and stress resistance in spring and summer maize populations were clarified, and multiple superior hybrid combinations were bred. Notably, Zhongdan 1112 and Zhongdan 1130, which feature outstanding saline-alkali tolerance and high yield potential, were granted national variety certification in China in 2024; an additional three tolerant lines are currently undergoing regional adaptability trials. [Conclusion] This study supplies valuable germplasm resources and technical references for the genetic improvement and high-yield breeding of saline-alkali tolerant maize.

Key words: Maize, Saline-alkali tolerance, Germplasm, Salt-tolerant regulatory genes, High-yield breeding

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Construction of Maize Genomic Selection Breeding Platform

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Abstract: [Objective] To accelerate plant breeding, shorten cycle times, and reduce fieldtrial costs, genomic selection (GS) should be widely adopted. This study therefore aimed to develop a onestop online analysis platform that enables efficient prediction and evaluation of genomic breeding values, lowers the barrier for data analysis, and supports rapid computations under multiple models and breeding scenarios. [Method] The platform integrates multi-population field data, including both genotypic and phenotypic records. For algorithmic flexibility, we implemented a suite of predictive models—linear mixed models, Bayesian regressions, and machine-learning algorithms—and embedded an automated model-selection routine to identify the best-performing method for each input dataset. To facilitate user interaction, we fine-tuned an open-source conversational AI agent to provide real-time guidance on data formatting, workflow navigation, and parameter settings. Prior to analysis, a built-in data-filtering pipeline performs quality control (missing rate, minor allele frequency, Hardy–Weinberg equilibrium), linkage disequilibrium-based SNP pruning, and association mapping to pinpoint SNP markers linked to QTL regions for target traits. [Result] The resulting web interface offers: (i) straightforward upload of individuallevel genotype and phenotype files; (ii) a selection of diverse analytical models with oneclick execution; (iii) optional pedigree data import, enabling full pedigree tracing and relationship inference; (iv) integrated GWAS and GS modules that output trait–marker association networks and progeny performance predictions; (v) heterosis forecasting and in silico crossdesign recommendations for optimal hybrid combinations; and (vi) access to several preloaded public population databases, allowing users to train models using existing trait data and then predict phenotypes for newly uploaded genotypes alone. Additionally, the embedded AI conversational assistant supports users throughout the analysis—from correcting file formats to interpreting output results. Algorithmic optimizations, including parallel computing and hyperparameter tuning, have substantially improved both computation speed and prediction accuracy. [Conclusion] This platform provides a comprehensive, user-friendly solution for genomic-assisted breeding, effectively bridging the gap between complex statistical genetics and practical breeding decisions. By combining multi-model inference, interactive AI support, and flexible data resources, it empowers breeders with diverse expertise to efficiently evaluate germplasm, design crosses, and accelerate genetic gains. Future work will focus on expanding the database with more crop species, incorporating real-time environmental covariates, and refining the AI agent for automated report generation.

Key words: Genome selection, Plant breeding, Online analysis platform

Polymerization of Drought-Tolerant Genes in Maize and Creation of Germplasm Resources

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Abstract: [Objective] This study aimed to explore and conserve maize genetic resources, expand the genetic basis of maize breeding via exogenous excellent alleles, and establish a technical system for polygenic aggregation and drought-tolerant germplasm improvement through integrating phenotypic identification, genetic analysis and molecular breeding technologies. [Method] A total of 172 genetically diverse maize inbred lines were used as materials. Their agronomic traits were evaluated under normal irrigation and drought stress conditions, and the selection index (SI) was adopted for comprehensive drought tolerance evaluation. Based on 20K liquid-phase chip high-density SNP data, the population genetic structure and kinship of the materials were analyzed. Precise genotyping was conducted using seven core maize drought-tolerant genes, and an additive effect model was applied to clarify the influence of drought-tolerant allelic variations on SI. Excellent recipient and donor materials were screened, with haploid induction and marker-assisted backcross breeding adopted for drought tolerance improvement. [Result] The resulting web interface offers: (i) Totally 13 extremely drought-tolerant and 44 highly drought-tolerant inbred lines were screened out. The tested materials were classified into SS, NSS and CML populations, with SS and NSS further divided into six groups; (ii) The superior alleles of seven drought-tolerant genes all exerted positive effects on SI, and the number of superior alleles was significantly positively correlated with maize drought tolerance; (iii) 17 elite drought-tolerant donor materials with target alleles and high genetic similarity to recipients were selected, and 28 improved F1 combinations were developed by introducing tropical CML germplasm; (iv) 688 new accessions were obtained via haploid induction, and 28 BC2F1 improved lines were generated through marker-assisted backcrossing; [Conclusion] LAN, PA and PB germplasm subgroups showed superior comprehensive drought tolerance and application potential. The accumulation of multiple superior allelic variants is verified as an efficient strategy to improve maize drought tolerance, and the performance of improved F1 combinations further confirmed the effectiveness of this polygenic aggregation improvement method.

Key words: Genetic diversity, Genetic improvement for drought tolerance, Gene aggregation, Germplasm development

Integrated Transcriptomic and Proteomic Analyses Provide Insights into Potential Molecular Mechanisms Underlying Globulin Content Variation in Maize Embryos

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Abstract: [Objective] Maize kernel globulin is a high-quality storage protein primarily accumulated in maize embryos. At present, the molecular regulatory mechanism governing globulin synthesis in maize embryos has not been fully elucidated, which restricts the genetic improvement of maize protein quality. This study aimed to explore the key genes and core pathways mediating maize globulin synthesis, so as to provide a theoretical basis for the breeding of high-protein maize varieties. [Method] Two maize inbred lines with significantly different globulin contents, low-globulin line B73 and high-globulin line HP434, were used as test materials. Transcriptomic and proteomic integrated analysis was performed to screen and annotate differentially expressed genes (DEGs) and differentially expressed proteins (DEPs), and further identify the key regulatory pathways and candidate genes related to globulin synthesis. [Result] Two maize inbred lines were selected for this study, including B73 (low globulin content) and HP434 (high globulin content). Integrated transcriptomic and proteomic analyses revealed that DEGs and DEPs were predominantly enriched in the endoplasmic reticulum (ER) protein processing pathway. Significantly, most of these DEGs and DEPs belonged to the heat shock protein (HSP) family. This indicates that globulin synthesis is closely related to the genes of this family, especially the small molecule heat shock proteins. [Conclusion] The high expression of HSP family genes in HP434 might alleviate the increased ER processing pressure caused by the aggregation of misfolded proteins during the high-abundance synthesis of globulin, thereby contributing to the synthesis of globulin in the ER.

Key words: Maize; Globulin, Protein processing, Transcriptome, Proteome

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High-Resolution Multi-Omics Profiling Reveals the Transcriptional Regulatory Basis of Heterosis During Early Ear Development in Maize

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Abstract: [Objective] To clarify how developmental reprogramming and temporal reorganization of regulatory programs contribute to heterosis during maize ear development, beyond the static transcriptional differences traditionally used to interpret hybrid vigor. [Method] We generated high-resolution time-series transcriptomic and chromatin accessibility profiles of early ear development in the maize hybrid WY111 and its parental inbred lines VK22-4 and M51, and integrated these datasets with morphological staging and developmental trajectory alignment to characterize genotype-specific developmental dynamics and regulatory changes. [Result] WY111 did not exhibit a uniformly accelerated developmental program, but instead followed a heterochronic developmental trajectory characterized by an extended early inflorescence-patterning phase and relatively rapid subsequent reproductive differentiation. This temporal reconfiguration was accompanied by stage-specific remodeling of transcriptional programs, including enhanced cell-cycle and inflorescence-patterning activities during early development and relative attenuation of selected defense- and stress-responsive programs. In addition, parental expression complementation, dynamic allele-specific expression, chromatin accessibility remodeling, and extensive gene regulatory network rewiring collectively contributed to the establishment of hybrid-specific transcriptional and regulatory states. [Conclusion] Developmental time reconfiguration represents a central organizational principle underlying maize ear heterosis. Rather than simply accelerating development, hybridization redistributes the timing and duration of developmental programs, thereby coordinating stage-specific transcriptional and regulatory activities to promote hybrid vigor.

Key words: Maize, Ear development, Heterosis, Time-series multi-omics

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Activities and Achievements of the Collaboration Between Myanmar and CIMMYT in Maize Research and Development

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Abstract: [Objective] This study summarizes the major activities and achievements of the long-term collaboration between the Department of Agricultural Research (DAR), Myanmar, and the International Maize and Wheat Improvement Center (CIMMYT) in strengthening maize research, breeding, and sustainable production. [Method] Collaborative activities, including germplasm exchange, multi-location variety evaluation, hybrid breeding, climate-resilient germplasm screening, capacity building, and technology transfer, were reviewed based on DAR research records and joint research programs. [Result] The collaboration enriched Myanmar's maize genetic resources through the introduction of elite inbred lines, breeding populations, and improved germplasm. It strengthened hybrid maize breeding, enhanced researchers' technical capacity through training, and promoted the development of high-yielding, climate-resilient maize varieties adapted to diverse agro-ecological conditions. [Conclusion] The DAR–CIMMYT partnership has significantly contributed to maize research and agricultural development in Myanmar. Continued collaboration will accelerate climate-resilient variety development, sustainable seed systems, and improved food security while strengthening national and regional research cooperation.

Key words: Myanmar, Cimmyt, Maize breeding, Germplasm exchange, Climate resilience, Capacity building

Development, Innovation, and Exploration of Highly Adaptable Superior Maize Germplasm Resources

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Abstract: [Objective] Maize is a crucial dual-purpose crop for both food and animal feed in China; factors such as diseases and drought pose major obstacles to the development of the maize industry. Developing new varieties with disease resistance, drought tolerance, and stress tolerance represents the most economical and effective approach to addressing this issue, while strengthening the exploration and innovation of germplasm resources serves as the fundamental basis for breeding such new varieties and driving the advancement of the seed industry. [Method] Innovation in maize germplasm resources is a long-term, systematic endeavor. It is essential to fully utilize local germplasm, introduced resources, and wild relatives. Furthermore, appropriate population improvement methods and biotechnological techniques should be employed to facilitate the innovation and utilization of maize germplasm. This can be achieved through various approaches—including germplasm amplification, improvement, and innovation—such as optimizing hybrid vigor models, implementing population improvement strategies, tapping into the potential of local germplasm resources, introducing and utilizing superior germplasm from tropical and subtropical regions, domesticating wild maize, and applying biotechnology. [Result] By utilizing gene editing technology, it is possible to improve maize traits such as drought resistance, disease resistance, moisture tolerance, high-temperature tolerance, and salt tolerance, thereby enhancing its adaptability and yield. Freshly harvested corn should undergo scientific evaluation based on its germplasm resource characteristics, origin, genetic functions, distribution, and value, to facilitate germplasm utilization and innovation. In the tropical regions of southern China, efforts should be intensified to explore and innovate maize varieties with disease resistance, high-temperature tolerance, and high-moisture tolerance. In northern and northwestern China, focus should be placed on developing germplasm resources with drought resistance, disease resistance, and tolerance to poor soil conditions. [Conclusion] By addressing the key challenges in the maize industry across different regions and aiming for "high yield, stress tolerance, poor-soil adaptability, and suitability for mechanical grain harvesting," breakthrough new germplasm varieties suitable for regional needs can be cultivated.

Key words: Corn, Broad adaptability, High-quality germplasm resources, Breeding, Innovation

Technical Session 2

Decoding the Maize Genome: From Basic Mechanisms to Frontier Technologies



RNA N⁶-methyladenosine Methyltransferase Regulates Drought Tolerance in Maize by Mediating U6 snRNA

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Abstract: [Objective] This study aimed to identify the key m⁶A methyltransferase governing drought tolerance in maize and elucidate its underlying regulatory mechanism.[Method] The candidate gene *METTL* was identified through QTL mapping and genome-wide association analysis (GWAS). *METTL* knockout mutants and overexpression lines were generated via CRISPR/Cas9 and transgenic approaches. In vitro methyltransferase activity assays, RNA-EMSA, SELECT-qPCR, and third-generation direct RNA nanopore sequencing were employed to characterize the enzymatic activity, substrate binding, and m⁶A regulatory function of *METTL* on U6 snRNA. Actinomycin D-mediated transcription inhibition, chromatin-associated RNA (caRNA) isolation, 5-ethynyl-uridine (5-EU) labeling of nascent RNA, DNase I-TUNEL assays, and histone modification detection were performed to dissect the molecular mechanism. Additionally, dCas13-based m⁶A editing system was applied to generate U6 snRNA hypermethylated and demethylated transgenic lines. [Result] Under drought stress, *METTL* mutants displayed robust root architecture and mitigated yield penalty, whereas *METTL*-overexpressing lines exhibited opposite phenotypes. Mechanistically, *METTL* directly binds to U6 snRNA and mediates its m⁶A methylation. Reduced m⁶A modification enhanced U6 snRNA stability, thereby increasing U6 snRNA abundance. Both U6 snRNA overexpression and site-specific m⁶A-edited plants recapitulated the phenotypes of *METTL* mutants and overexpression lines, respectively. Moreover, *METTL* mutants exhibited elevated chromatin accessibility, increased enrichment of U6 in caRNA, and higher levels of nascent U6 snRNA. [Conclusion] Collectively, our findings reveal that *METTL*-mediated m⁶A modification on U6 snRNA modulates root development and drought tolerance in maize, providing a promising target for genetic improvement of drought resistance in maize breeding.

Key words: Maize, RNA m⁶A Modification, Methyltransferase, Drought, U6 snRNA.

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ZmMETTL3 Phase Separation Coordinates m⁶A-dependent R-loop

Dynamics and Transcription Termination for Maize miRNA Biogenesis

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Abstract: [Objective] RNA N6-methyladenosine (m⁶A) modifications are well-characterized in post-transcriptional regulation, but their co-transcriptional functions in plant microRNA (miRNA) biogenesis remain poorly understood. Here, we demonstrate that ZmMETTL3, the maize ortholog of the m⁶A writer Methyltransferase-like, acts as a central coordinator of transcription termination and miRNA biogenesis. [Method] In this study we biochemical validation via glutathione S-transferase (GST) pull-down, split-luciferase (split-LUC), and co-immunoprecipitation (co-IP) assays confirmed METTL3-Pol II binding, which was disrupted upon mutation, particularly in the intrinsically disordered region (IDR) of ZmMETTL3. Disruption of the IDR abolishes phase separation and impairs the METTL3-Pol II interaction, as evidenced by impaired binding upon treatment with the phase separation inhibitor 1,6-hexanediol. Mechanistically, ZmMETTL3 depletion reduced the m⁶A modification levels in nascent RNAs, leading to destabilized R-loop formation. [Result] In maize, Zmmettl3 knockout mutants exhibit severe developmental defects and a global depletion of both precursor and mature miRNAs. Mechanistically, ZmMETTL3 interacts directly with RNA polymerase II (Pol II) to facilitate transcription. This interaction is driven by liquid-liquid phase separation (LLPS), which is dependent on the intrinsically disordered region 3 (IDR3) of ZmMETTL3 and on local RNA concentrations. Disruption of ZmMETTL3 condensates abolishes its association with Pol II. Importantly, ZmMETTL3-mediated m⁶A deposition on nascent transcripts stabilizes chromatin-associated R-loops, a structural prerequisite for proper transcription termination. Loss of ZmMETTL3 destabilizes these R-loops, leading to impaired Pol II pausing, reduced Ser2 phosphorylation, and widespread transcriptional readthrough at MIR loci. Consequently, the depletion of mature miRNAs including miR528, underlies the dwarf phenotype of zmmettl3 mutants. [Conclusion] Our findings demonstrate that ZmMETTL3 integrat m⁶A-dependent R-loop regulation with phase separation-mediated Pol II compartmentalization, thereby acting as a central coordinator of transcriptional fidelity, ensuring precise termination and robust miRNA biogenesis in plants. These findings bridge the critical knowledge gap in plant epitranscriptomics and miRNA biogenesis.

Key words: Maize, Liquid-liquid phase separation, ZmMETTL3, MicroRNA biogenesis, m⁶A, R-loop

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Genome-Wide Association Mapping of Seedling Root Architecture Identifies QTL Hotspots and Candidate Genes for Aluminium Tolerance in Tropical Maize

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Abstract [Objective] This study aimed to elucidate the genetic basis of seedling-stage root architectural traits associated with aluminium (Al) tolerance in tropical maize, a key adaptation trait for improving productivity in the acidic soils prevalent across hilly and mountain production systems. [Method] A hydroponic phenotyping protocol was optimized and applied to 250 diverse maize inbred lines exposed to 300 μM AlCl_3 . Root traits were measured and genome-wide association analysis was performed using 60,227 SNP markers. [Result] Al stress significantly reduced root growth and branching traits. GWAS identified 44 significant SNPs on eight chromosomes, explaining 9.68–18.43% of phenotypic variation, and revealed eight QTL clusters, including major hotspots on chromosomes 8 and 3. Candidate gene analysis identified 33 stress-responsive genes involved in detoxification, transport, and transcriptional regulation. [Conclusion] The identified QTL hotspots and candidate genes provide valuable genomic resources for marker-assisted breeding and genomic prediction to improve aluminium tolerance in tropical maize.

Key words: Aluminium toxicity, Tropical maize, Root architecture, QTL hotspots, Candidate genes

ZmCDPK40 Negatively Regulates Seedling Drought Tolerance in Maize and Interacts with Transcription Factor ZmMYBR17: A Preliminary Study

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Abstract: [Objective] Maize (*Zea mays* L.) is a globally cultivated cereal crop used for both food and feed. In Xinjiang, it has become the second most important grain crop after wheat and a characteristic crop of the oasis agricultural system. However, the harsh environment—characterized by water scarcity and the combined stress of atmospheric and soil drought—severely constrains stable and high yields of maize in Xinjiang. Therefore, identifying key drought-tolerance genes and creating novel drought-tolerant germplasm are critical strategies for improving maize drought resistance. [Method] In this study, we analyzed the expression profiles of the maize *ZmCDPK* gene family members under drought stress and identified a candidate gene, *ZmCDPK40* (*Zm00001d044185*), that responds to drought. We generated knockout mutants using CRISPR/Cas9 technology and evaluated their drought tolerance at the seedling stage through drought-rewatering experiments; overexpression lines were also produced for phenotypic comparison. Protein–protein interactions were verified by yeast two-hybrid, Pull-down, co-immunoprecipitation (Co-IP), and bimolecular fluorescence complementation (BiFC) assays, and phosphorylation activity was examined by in vitro phosphorylation tests. [Result] Under drought stress, the *zmcdpk40* knockout mutants exhibited significantly reduced water loss rates, increased relative water content and antioxidant enzyme activities, and decreased stomatal aperture. Moreover, after exogenous ABA treatment, the stomatal aperture of the mutants was also significantly smaller than that of the wild type. In contrast, plants overexpressing *ZmCDPK40* were more sensitive to drought. Protein interaction experiments demonstrated that *ZmCDPK40* directly interacts with the transcription factor *ZmMYBR17* both in vitro and in vivo, and that *ZmCDPK40* can phosphorylate *ZmMYBR17*. [Conclusion] In summary, this study preliminarily reveals a regulatory pathway involving the “*ZmCDPK40*–*ZmMYBR17*” module that mediates calcium signaling perception and transcriptional reprogramming, providing new targets and a theoretical basis for molecular breeding of drought-tolerant maize.

Key words: Maize, Drought tolerance, *ZmCDPK40*, *ZmMYBR17*, CRISPR/Cas9, Stomatal regulation

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Genetic Diversity and Population Structure Analysis by SNP Markers in Sweet Maize Inbred Line

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Abstract: [Objective] Sweet corn (*Zea mays* var. *saccharata*) originated in the American continent and is a mutant endosperm variety of common corn, belonging to a sweet-quality corn subspecies of the maize genus. Sweet corn is rich in nutrients, has a unique flavor, is easy to cultivate, and has significant economic benefits, thus being highly popular among growers and consumers. It has high economic value. Sweet corn has the genetic trait of inhibiting the conversion of sugar into starch, with less starch accumulation and a higher sugar content in the grains during the milk stage. To understand the genetic basis of sweet corn varieties, to improve the efficiency of selecting superior sweet corn varieties, and to provide theoretical basis for the improvement and breeding of sweet corn varieties. [Method] In this experiment, 167 sweet corn inbred lines were provided by the Corn Center of the Crop Research Institute of Shanghai Academy of Agricultural Sciences. Using 20,648 high-quality SNP loci for genotype typing based on resequencing methods, genetic diversity and population structure of these 167 sweet corn inbred lines were analyzed. [Result] The results showed that the expected heterozygosity of 167 sweet corn inbred lines ranged from 0.095 to 0.5, with an average value of 0.2277. The observed heterozygosity ranged from 0.01325 to 0.9521, with an average value of 0.2495. The variation range of the major allele frequency was 0.5 to 0.95, with an average value of 0.8548. The variation range of polymorphism information content was 0.095 to 0.5, with an average value of 0.2277. The population genetic structure analysis indicated that when $K = 3$, the cross-validation error rate was the lowest. Combined with the phylogenetic tree, the 167 sweet corn inbred lines were classified into three subgroups. This subgroup classification result was basically consistent with the classification based on the origin of the germplasm (tropical, subtropical and temperate). [Conclusion] This study conducted a genetic diversity and population structure analysis of 167 sweet corn inbred lines based on SNP molecular markers. The research results will be helpful for the selection of parents in hybrid breeding and the prediction of hybrid superiority, providing a scientific basis for the selection of excellent new sweet corn varieties. At the same time, the cluster analysis indicated that the relationship between the temperate group and the subtropical group was relatively distant. Increasing the mating intensity between these two groups may lead to better hybrid combinations.

Key words: Sweet maize, SNP marker, Genetic diversity, Population structure

Genetic Basis of Flavor Complexity in Sweet Corn

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Abstract: [Objective] Sweet corn is an important vegetable crop consumed globally. However, the genetic differentiation between field corn and sweet corn, and the impact of breeding on the metabolite composition and flavor (other than sweetness) of sweet corn, remain poorly understood. [Method] Here we assembled a cultivated sweet-corn genome de novo and re-sequenced 295 diverse sweet-corn inbred lines. We examined the genetic architecture of sweet-corn kernel quality by combining genetic, metabolite and expression profiling methodologies. [Result] New genes (for example, ZmAPS1, ZmSK1 and ZmCRR5) and metabolites associated with flavor and consumer preference were identified, highlighting important target flavor metabolites, including sugars, acids and volatiles. [Conclusion] These findings provide valuable knowledge and targets for future genetic breeding of sweet-corn flavor, and to balance grain yield and quality and contribute to our broader understanding of crop diversification.

Key words: Sweet corn, Flavor, Genome, Metabolite, Yield

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Genome-Wide Identification of ZmGT14 Family Uncovers ZmGT14-36 as a Drought Tolerance Gene Interacting with UGT85A2

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Abstract: [Objective] Drought stress disrupts maize cell wall integrity and reduces grain yield. Glycosyltransferase 14 (GT14) regulates cell wall formation, yet its drought regulatory mechanism in maize remains unclear. Part of this research has been published in *Plants* (DOI:10.3390/plants15030512). [Method] Genome-wide identification, phylogenetic, gene structure and promoter element analyses were conducted. Transcriptome combined with RT-qPCR screened drought-induced genes, and yeast two-hybrid (Y2H) was used to verify protein interaction of key candidate *ZmGT14-36*. [Result] A total of 42 *ZmGT14* members were mapped on 10 maize chromosomes, with high intra-subfamily conservation. Their promoters contain abundant ABRE, DRE and MBS drought-responsive cis-elements. *ZmGT14-36* expression rose nearly 30-fold at 36 h under drought stress. Y2H assay confirmed *ZmGT14-36* physically interacts UGT85A2, a redox homeostasis-related protein. [Conclusion] *ZmGT14-36* positively participates in maize drought response. This work clarifies evolutionary features of *ZmGT14* family and provides a promising candidate gene for drought-resistant maize molecular breeding.

Key words: Zea mays, ZmGT14, Drought stress, Glycosyltransferase, UGT85A2

Funding acknowledgement: Supported by National Key Agricultural Biological Breeding Special Project (2022ZD0400504), China Agriculture Research System (CARS-02-07) and China Postdoctoral Science Foundation (2025MD774089).

Natural Variations of *ZmMADS31* Regulates Husk Number in Maize

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Abstract: [Objective] Mechanical kernel harvesting is an important strategy for modern maize production. Rapid kernel dehydration during the late grain-filling stage is essential for improving harvesting efficiency and reducing grain moisture content at harvest. Husk number is a key trait of kernel dehydration during maize maturation and is positively correlated with grain moisture content at harvest. However, the genetic basis and molecular mechanisms regulating husk number remain largely unknown. This study aimed to identify the key gene controlling husk number and characterize its biological function, natural variation, regulatory network, and breeding potential for improving kernel dehydration in maize. [Method] Genome-wide association analysis (GWAS) was performed using 1,604 maize accessions to identify candidate genes controlling husk number across ten environments. The identified gene, *ZmMADS31*, was subsequently characterized through gene editing, overexpression, and molecular analyses. Its natural variation, regulatory network, and breeding value were further investigated through haplotype analysis, promoter activity assays, RNA-seq, DAP-seq, protein interaction assays, and hybrid evaluation. [Result] A GWAS identified a significant association between the natural variation of *ZmMADS31* and the husk number. *ZmMADS31*, which encodes a MADS-box transcription factor, negatively regulates husk number. Loss-of-function mutants of *ZmMADS31* showed remarkably increased husk number and delayed kernel dehydration at maturity. In contrast, transgenic maize with enhanced *ZmMADS31* expression exhibited reduced husk number and accelerated kernel dehydration. Candidate gene association analysis based on re-sequencing identified a functional 196-base pair promoter InDel as the key natural variation affecting promoter activity and gene expression. The deletion allele reduces expression and consequently decreases husk number. A yeast two-hybrid screen identified *ZmPHYB1* as an interacting protein of *ZmMADS31*. Transgenic lines expressing the hyperactive *ZmPHYB1* variants (*ZmPHYB1*^{Y98F} and *ZmPHYB1*^{Y359F}) exhibited fewer husks than the wild type. Interestingly, we found that the interaction between *ZmPHYB1* and *ZmMADS31* was temperature dependent. Integrative DAP-seq and RNA-seq analyses identified *ZmWAT1*, an auxin transport facilitator, as a potential downstream target of *ZmMADS31*. Finally, hybrid combinations carrying the *ZmMADS31* knockout allele consistently exhibited increased husk number, delayed kernel dehydration, and higher grain moisture content at harvest across multiple genetic backgrounds, while showing no obvious yield penalty. [Conclusion] This study identified *ZmMADS31* as a key negative regulator of husk number that contributes to kernel dehydration at maize maturity. A functional 196-bp promoter InDel was identified as the major natural variation controlling husk number, and a preliminary *ZmPHYB1*–*ZmMADS31*–*WAT1* regulatory module was proposed. This

work provides both genetic resources and a mechanistic framework for molecular breeding toward faster kernel dehydration in maize.

Key words: Maize, *ZmMADS31*, Husk number, Natural variation, Kernel dehydration, Mechanical kernel harvesting

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Molecular Mechanism of the *ZmPHR1-ZmG6PE* Module Regulating Phosphorus Use Efficiency and Grain Yield in Maize

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Abstract: [Objective] Although the application of phosphate fertilizers has enhanced crop yields, their excessive use reduces phosphorus use efficiency (PUE) and triggers severe environmental concerns. Therefore, improving crop PUE is an urgent necessity for sustainable agricultural development. [Method] In this study, through genome-wide association analysis (GWAS) and multi-omics approaches, we identified a low-phosphate-responsive gene in maize (*Zea mays* L.), named *ZmG6PE* (Glucose-6-phosphate epimerase 1). [Result] *ZmG6PE* encodes an aldose epimerase involved in carbohydrate metabolism that catalyzes the anomeric interconversion of glucose-6-phosphate. It possesses a highly conserved catalytic domain, Aldose_epim, spanning an active region from amino acids 41 to 308 (41aa–308aa). The transcript levels of *ZmG6PE* are significantly upregulated under low-phosphate stress, a process directly modulated by *ZmPHR1*, a central regulatory factor in phosphate signaling. Functional analyses demonstrated that *ZmG6PE* positively regulates maize adaptation to low-phosphorus stress: *ZmG6PE*-overexpressing lines exhibited significantly superior growth performance compared to wild-type (WT) controls under low-phosphorus conditions, whereas *zmG6pe* knockout lines showed the opposite phenotype. Furthermore, *ZmG6PE* was found to be tightly correlated with yield-component traits. The *zmG6pe* mutants displayed significant reductions in ear length and the number of kernels per row, resulting in a further decline in grain yield under field-based low-phosphorus stress. Subsequent spatial expression analysis revealed that *ZmG6PE* is predominantly expressed in the inflorescence meristem (IM) of the immature ear. In *zmG6pe* knockout lines, the development of the ear tip was highly abnormal, accompanied by increased floret abortion. [Conclusion] Collectively, our findings uncover a crucial genetic module that simultaneously coordinates grain yield and phosphorus efficiency in maize, offering a promising target for molecular breeding.

Key words: Maize (*Zea mays* L.), Low-phosphate stress, Phosphorus use efficiency (PUE), *ZmG6PE*, Inflorescence meristem, Grain yield

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Maize Seedling Establishment under Hydrogel-Altered Seed Microenvironment with Different Water Dynamics in Sand

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Abstract: [Objective] To assess the potential of hydrogel-based seed coating technology to regulate seed microenvironment and alleviate drought stress at maize seedling stage. [Method] This study examined the physiological and molecular responses of maize seeds coated with two hydrogel formulations (SA1 and SA5) compared to non-coated seed during seed imbibition (SI) and seedling establishment stage under two initial water-holding capacity (IW) levels (IW1 = 30% and IW2 = 60% IW) in sand medium. [Result] Hydrogel seed coating significantly enhanced SI within 48 hours after imbibition (HAI). At 36 HAI, non-coated seed exhibited the highest expression levels of *ZmSOD4* and *ZmCAT2*, irrespective of IW level while reduced malondialdehyde content was detected in non- and SA1-coated seed under IW2 level. At 48 HAI, radicle emergence (RE) of non-coated and SA1-coated seed did not differ under IW1; in contrast, under IW2, non-coated seed showed significantly higher RE than SA1-coated and SA5-coated seed. At 96 and 168 HAI, only SA5-coated seed exhibited a lower germination percentage compared with non-coated seed under IW2. At 168 HAI, SA1-coated seed displayed higher seed vigor index II, root conversion rate and total conversion rate than non-coated seed under IW1, indicating enhanced root development. In contrast, seedlings establishment of non-coated seed was greater than that of hydrogel-coated seed under IW2. [Conclusion] These results highlight the importance of hydrogel formulations, particularly their interaction with water availability dynamics in surrounding medium which are critical factors in regulating seed microenvironment and driving the distinct seed responses.

Key words: Hydrogel, Drought, Seed microenvironment, Seed coating, Gene expression

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Fine Mapping of Major QTL for Low-Temperature Emergence Tolerance in MTP-Maize Introgression Lines

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Abstract: [Objective] Maize is tropical in origin, and most existing germplasm performs poorly under low-temperature germination. In contrast, wild relatives like *Tripsacum* and tetraploid *Zea perennis* are highly cold-tolerant, yet these resources remain largely untapped. We previously constructed a maize–*Zea perennis*–*Tripsacum* allohexaploid (MTP) as a bridging material to break distant-crossing barriers, and from it derived cold-tolerant introgression lines. Here we aimed to pinpoint major QTLs and likely candidate genes underlying low-temperature emergence using these lines. [Method] F2:3 and F2 populations were generated by crossing the tolerant line IB030 with the sensitive line IB021 and with Mo17, respectively, and joint QTL analysis across both populations placed two major loci, qLTRL1-1 and qLTRL10-1, on chromosomes 1 and 10. For each locus, we built BC3F2 populations from IB030 and the sensitive parent B73, then used marker-assisted selection to obtain near-isogenic lines. Fine mapping of qLTRL1-1 employed 1056 F2 individuals, narrowing it to a 254-kb interval. Transcriptome profiling of IB030 versus B73, coupled with qRT-PCR validation, was used to filter and verify candidate genes. The same 1056 F2 plants also allowed us to delimit qLTRL10-1 to a 125-kb region, followed by GO enrichment and qRT-PCR analysis of its candidates. [Result] For qLTRL1-1, the 254-kb interval contained 13 predicted genes, but only three showed differential expression between the parental lines, and qRT-PCR confirmed their significant expression changes, pointing to them as strong candidates. For qLTRL10-1, the 125-kb interval harbored seven genes; three were significantly enriched in the GO term “response to stimulus” (GO:0050896) and also exhibited clear expression differences by qRT-PCR, suggesting their involvement in low-temperature emergence. [Conclusion] By combining two-population QTL mapping with transcriptomic screening in large backcross populations, we successfully fine-mapped these major QTLs and identified several credible candidate genes. These results provide useful gene resources for cold-tolerance breeding in maize.

Key words: Maize, Low-temperature emergence, QTL fine mapping

ZmALKBH2-mediated m⁶A Femethylation Regulates Maize Flowering Time by Stabilizing AP2 and FKF1 Transcripts

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Abstract: [Objective] RNA N⁶-methyladenosine (m⁶A) is a prevalent post-transcriptional modification that plays critical roles in plant development. However, the biological functions of individual m⁶A demethylases in regulating reproductive transition in crops remain largely unexplored. This study aimed to determine how the maize m⁶A demethylase ZmALKBH2 regulates flowering time, identify its direct RNA targets, and elucidate the molecular mechanism by which m⁶A demethylation modulates flowering. [Method] CRISPR/Cas9-mediated knockout and transgenic overexpression lines of ZmALKBH2 were generated in the maize inbred line KN5585. Flowering-related traits, including tasseling, silking, pollen shedding, and ear architecture, were evaluated under field conditions. The subcellular localization of ZmALKBH2 was examined in maize protoplasts and *Nicotiana benthamiana* leaves. Global m⁶A abundance was quantified by LC-MS/MS, and demethylase activity was validated through in vitro enzymatic assays. Transcriptome-wide targets of ZmALKBH2 were identified by MeRIP-seq, and direct RNA binding was confirmed by RIP-qPCR. Target transcript m⁶A levels, transcript abundance, and decay rates following transcriptional inhibition were analyzed to investigate the underlying mechanism of mRNA stability regulation. [Result] Compared with the wild type, *zmalkbh2* mutants exhibited a nearly 5-day delay in both pollen shedding and silking and displayed reduced ear length, ear diameter, and ear weight. ZmALKBH2 was highly expressed in silks and ear rachises during the silking stage and was localized predominantly in the nucleus. LC-MS/MS analysis revealed a significant increase in global m⁶A levels in *zmalkbh2* mutants, and in vitro assays confirmed that ZmALKBH2 possesses m⁶A demethylase activity. MeRIP-seq identified AP2, FKF1, and genes encoding PRC2 subunits as direct targets of ZmALKBH2. In *zmalkbh2* mutants, AP2 transcripts exhibited increased m⁶A enrichment, elevated steady-state abundance, and accelerated degradation following transcriptional inhibition, indicating that ZmALKBH2-mediated demethylation is required to maintain AP2 mRNA stability. RIP-qPCR further confirmed the direct association between ZmALKBH2 and AP2 transcripts. Similar m⁶A-dependent alterations in transcript stability were observed for FKF1 and PRC2 subunit genes, suggesting that ZmALKBH2 coordinates a post-transcriptional regulatory network controlling flowering time. [Conclusion] ZmALKBH2 regulates maize flowering by removing m⁶A modifications from AP2 and other flowering-related transcripts, thereby maintaining their stability. Loss of ZmALKBH2-mediated demethylation disrupts transcript stability, delays flowering, and compromises ear development. These findings establish m⁶A-dependent regulation of mRNA stability as a key post-transcriptional mechanism controlling flowering time and reproductive development in maize.

Key words: Maize, Flowering time, m⁶A RNA demethylase, ZmALKBH2, AP2, mRNA stability

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Cloning QTLs for Developmental and Adaptive Traits in Maize: Lessons Learned and Impact on Breeding

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Abstract: [Objective] Understanding the molecular basis of quantitative traits is essential for identifying the genes and the biochemical, developmental, and regulatory pathways controlling agronomic traits, thereby enabling targeted genetic engineering and genome editing. Molecular insights into quantitative variation also improve genomic prediction in breeding programs and facilitate the characterization and exploitation of genetic diversity. In our group, we have focused on the molecular dissection of QTLs controlling flowering time (e.g., *Vegetative to generative transition1* (*Vgt1*), *Vgt3*, and others) and root architecture (e.g., *Root-yield-1.06* and others). Our findings will be presented and discussed within the broader context of the molecular dissection of quantitative traits in crop species. [Method] Major QTLs controlling flowering time and root architecture were identified through biparental mapping populations and association analyses in diverse germplasm collections. Causal genes were identified using the now well-established strategy of positional cloning following QTL isogenization, and subsequently validated through transgenic approaches, genome editing, or other reverse genetics tools. [Results] Our work, together with that of the broader scientific community, has revealed a molecular landscape far more complex than initially anticipated, encompassing coding and regulatory variation, copy number variation, structural rearrangements, and epigenetic modifications that underlie quantitative trait variation. Moreover, the integration of QTL cloning with ecological and population genetics is providing new insights into the frequency, evolutionary history, and phenotypic effects of causal alleles in cultivated germplasm. A critical assessment of the broader significance of QTL cloning for understanding quantitative trait variation will also be presented. [Conclusions] QTL cloning has redefined the role of quantitative genetics in crop improvement. By linking naturally occurring genetic variation to biological function, it is revealing the molecular basis of crop adaptation and phenotypic diversity. This knowledge provides the foundation for next-generation breeding strategies that integrate genomic prediction, allele mining, and precision genome editing to accelerate the development of high-yielding, climate-resilient crop varieties.

Key words: Flowering time, Gene editing, QTL cloning, Root system architecture

Epigenetic Regulation of epiMAP Locus Confers Drought Tolerance via Modulating Natural Antisense Transcript of MAP65 in Maize

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Abstract: [Objective] DNA methylation is a key epigenetic mechanism underlying plant adaptation to abiotic stresses. Previous genome-wide association studies have confirmed that the DNA methylation on the natural antisense transcript region of maize microtubule-associated protein (NATMAP65) is significantly associated with maize survival rate and root traits under drought stress. However, the regulatory relationship between the epiMAP locus and NATMAP65, as well as its functional mechanism in maize drought tolerance, remains unclear. [Method] In this study, we developed a CRISPR/dCas9-based locus-specific DNA methylation editing system and generated transgenic maize lines carrying epiMAP demethylation (dCas9-TET1), hypermethylation (dCas9-DRM), and NATMAP65 overexpression constructs. Bisulfite sequencing PCR (BSP) was used to quantify methylation at the target locus in transgenic lines. Drought tolerance was evaluated at seedling and adult stages. Pol II CUT&Tag-qPCR and 5-EU-qPCR were used to verify the regulatory relationship between epiMAP methylation and NATMAP65 transcription. The interacting proteins of the NATMAP65-encoded small peptide and the downstream drought-response pathway were further characterized. [Result] BSP confirmed that DNA methylation at the epiMAP locus was significantly reduced in dCas9-TET1 transgenic lines. Demethylated lines showed markedly improved drought resistance at both seedling and adult stages. At the hypermethylated epiMAP locus, RNA Pol II was significantly enriched and nascent NATMAP65 RNA synthesis was promoted, indicating a positive correlation between epiMAP methylation and NATMAP65 expression. The small peptide translated from NATMAP65 interacted with ATP synthase. By altering ATP synthase activity, the peptide regulated H⁺ transmembrane transport and modulated ROS levels in guard cells, thereby affecting stomatal movement and mediating maize drought response. [Conclusion] This study defines the molecular mechanism by which the epiMAP DNA methylation locus epigenetically regulates NATMAP65 expression to confer maize drought tolerance. The findings establish the biological function of the epiMAP locus in environmental stress adaptation and provide a theoretical basis and epigenetic locus resources for drought tolerant molecular breeding in maize.

Key words: Maize, DNA methylation, EpiMAP locus, Drought tolerance, Epigenetic regulation

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Genetic Analysis and Candidate Gene Mining for Plasticity in Maize Plant Height and Ear Height

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Abstract: [Objective] Plant height is an important agronomic trait influences grain yield, lodging resistance, and adaptability to diverse environments. Nevertheless, the genetic architecture governing its phenotypic plasticity and molecular mechanisms underlying adaptation of tropical germplasm to temperate environments, remain poorly understood. This research aims to elucidate the genetic architecture of plant height plasticity and pinpoint pivotal genes that underpin environmental adaptation. In this context, a total of 1,015 maize inbred lines comprised of CIMMYT tropical population and a domestic temperate–tropical mixed population, were phenotyped across multiple years and locations in representative environments in China and Mexico. Plant height and ear height were recorded across all test environments, and the resulting phenotypic data were combined with whole-genome resequencing data. Environmental effects were corrected using mixed linear models, while the Critical Environmental Regressor through Informed Search (CERIS) algorithm identified key environmental factors and critical developmental stages. Reaction norm models were employed to estimate environmental plasticity, followed by genome-wide association studies (GWAS) for ear height (EH), plant height (PH) and EH/PH ratio. This study discovered candidate genes playing key roles in cell division, including putative cyclin-A3-1 (*Zm00001d033365*) and FtsZ homolog 2-2 chloroplastic (*Zm00001d026669*). These findings will enhance our understanding of the genetic mechanisms governing plant height plasticity and tropical maize adaptation, while also furnishing valuable genetic resources and theoretical foundation for the molecular breeding of environmentally adaptable maize.

Key words: Tropical maize, Plant height, Ear height, Environmental plasticity, Genome-wide association study, Candidate genes

A Graph-based Pangenome Reveals Structural Variations Underlying Tropical Versus Temperate Maize Adaptation

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Abstract: [Objective] Maize is cultivated across a broad latitudinal range from 40°S to 45°N, encompassing diverse tropical and temperate agroecologies. However, the structural variants (SVs) underlying this remarkable adaptation remain poorly resolved by linear reference genomes, which fail to capture non-reference sequence content. Graph-based pangenomes address this limitation by representing SVs and non-reference sequences absent from single linear assemblies, thereby facilitating marker discovery that bridges tropical and temperate germplasm pools and accelerates climate-resilient breeding. We constructed a graph-based pangenome using the Minigraph-Cactus pipeline from 11 chromosome-level genome assemblies, comprising eight tropical and temperate maize lines (B73, Mo17, Zheng58, CIMBL55, CML228, CML69, CML52, and CML333) and three wild teosinte accessions (Ames21814, TIL01, and TIL11), with the telomere-to-telomere (T2T) Mo17 assembly as the backbone reference. The resulting GFA-format graph was converted to VG format using vg view, and structural variants were called against the backbone using vg deconstruct to generate VCF files. Ecotype-specific SNPs, InDels, and SVs were identified and filtered using custom Python scripts. Presence-absence variation (PAV) regions ranging from 50 to 1,500 bp were used to design PCR markers with Primer3, which were subsequently validated across tropical and temperate maize panels by gel electrophoresis. The resulting pangenome graph spans 5.2 Gb and comprises 159 million nodes, 214 million edges, and 21.77 million variants, including 14.79 million SNPs, 6.41 million InDels, and 0.57 million SVs. Small variants (SNPs and InDels) accounted for 97.4% of total variation, while SVs accounted for 2.6%. Within 42 photoperiod-adaptation genes, we identified 6,842 variants (4,913 SNPs, 1,840 InDels, and 89 SVs), with small variants comprising 98.7% and SVs 1.3% of this subset. *ZmPRR37* carried the highest variant load (1,018 variants), followed by *ZMM4* (660) and *ZMM15* (635). Within the corresponding 2-kb upstream promoter regions, we detected 2,586 variants (1,657 SNPs, 847 InDels, and 82 SVs), with small variants comprising 96.8% and SVs 3.2%. The promoters of *ZmCCT10*, *ZmELF3.1*, and *ZmELF4.2* harbored the highest variant loads, with 161, 135, and 126 variants, respectively. From the identified PAV regions, we designed 55,427 PCR markers (50–1,500 bp), of which 21.8% were genic (2.9% exonic and 18.9% intronic) and 78.2% intergenic. Marker density was highest on chromosome 1 (9,052 markers), followed by chromosomes 2 (6,305), 3 (6,194), and 5 (6,246), with the lowest density on chromosome 10 (3,787 markers). A subset of markers validated by gel electrophoresis across tropical and temperate panels showed clear, discrete presence-absence patterns. This graph-based

pangenome captures the full spectrum of genetic variation (SNPs, InDels, SVs) and non-reference sequences inaccessible to linear references, providing a robust resource for read mapping, GWAS, and PAV marker-based breeding. By resolving variation underlying photoperiod adaptation, it will accelerate bridging of tropical–temperate germplasm and development of climate-resilient maize cultivars.

Key words: Maize, Graph based pangenome, SVs and PAVs

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Genomic Selection for Grain Yield in a Southwest China Maize Population

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Abstract: [Objective] Genome-wide selection (GS) has emerged as a powerful tool for the breeding of elite inbred lines and efficiently screening of hybrids. [Method] Here, we crossed 160 inbred lines following a "temperate x tropical" pattern using an incomplete diallel cross design (NCII), generating 511 hybrids that were evaluated in field trials at four ecological sites in Southwest China. [Result] Five-fold cross-validation was performed to compare the prediction accuracies of five GS models, which revealed that rrBLUP was the best overall predictive model across multiple environments. Incorporating associated SNPs identified from genome-wide association analysis (GWAS) into the rrBLUP model further improved precision accuracy, and cross-year independent validation demonstrated relatively higher precision of yield per plant. Three predicted superior hybrids have been entered into the 2026 regional comparison trial for spring maize. [Conclusion] This study indicates that GS can effectively accelerate breeding process in maize.

Key words: Maize, Genomic selection, Southwest China

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Identification of a New Genomic Regions Associated with Leaf Angle and Internode Length in Maize

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Abstract: [Objective] The present study aimed to identify a novel quantitative trait loci (QTLs) associated with the architectural traits for developing a compact plant genotype. It addresses the climate smart maize for High Density System by facilitating maximize light interception, minimize interplant competition and improving resource-use efficiency. [Method Two contrasting maize inbred lines, UMID-23 and UMIT-23. UMID-23 is evaluated from diverse germplasm, one for short stature, shorter internodes and drooping leaves, the other UMIT-23 for tall stature, elongated internodes and erect leaves. A total of 210 F₂ plants were genotyped using 90 polymorphic molecular markers and the corresponding F₃ families were evaluated for leaf angle and internode length. [Result] QTL analysis identified two novel QTLs (qLA-8-1, qLA-8-2) for leaf angle on chromosome 8 with explained phenotypic variation of 23.44% to 26.61% of which new kind of QTL regions identified, similarly four (qIL- 2-1, qIL-3 -1, qIL- 3-2, qIL- 3-3) QTLs for internode length on chromosomes 3, 4 and 9 with explained phenotypic variation ranging from 6.53 to 10.88% also new kind of QTLs.[Conclusion] These QTLs facilitate with the existing QTLs for fine mapping and candidate gene identification from diverse germplasm using marker-assisted breeding and enhancing the approaches for the development of superior compact cultivars and also for development of hybrids adapted to high density planting system. These identified QTLs provide new insights into the plant genetic architecture representing valuable genomic resources for marker assisted breeding in the development of desired plant architecture. The new kind of QTLs obtained in the molecular mapping for the leaf angle and will be presented in detail in oral presentation.

Key words: Plant architecture, Leaf angle, Internode length, Novel QTL, Germplasm utilization

Comprehensive Characterization of the Mildew Resistance Locus O (MLO) Gene Family in Maize Highlights Potential Roles in Stress Responses and Calcium Signaling

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Abstract: [Objective] The *MLO* gene family encodes plant-specific membrane proteins originally identified as powdery mildew susceptibility factors but now recognized to participate in diverse biological processes. However, a systematic investigation of *MLO* genes in maize (*Zea mays* L.) remains limited. This study aimed to conduct a genome-wide characterization of the maize *MLO* gene family, including member identification, evolutionary classification, structural and regulatory feature analysis, expression profiling under multiple stress conditions, and functional domain prediction, to establish a framework for understanding *MLO* gene evolution and potential functions in maize. [Method] *MLO* gene family members were identified from the B73 reference genome using hidden Markov model profile searches and BLAST analysis. Phylogenetic analysis was performed to classify the identified genes into evolutionary clades. Gene structure, conserved motifs, and transmembrane topology were analyzed to characterize structural diversity. Promoter cis-regulatory elements and miRNA target sites were predicted to explore transcriptional and post-transcriptional regulatory mechanisms. Expression profiling was conducted under methyl jasmonate treatment, insect feeding, fungal infection, and cold stress. Co-expression analysis between *ZmMLO* genes and calmodulin genes was performed, and structural modeling of conserved C-terminal regions was carried out to predict calmodulin-binding domains. [Result] A total of 18 *ZmMLO* genes producing 53 transcript isoforms were identified and classified into four evolutionary clades. Analyses of gene structure, conserved motifs, and transmembrane topology revealed substantial structural diversity among family members. Promoter cis-element and miRNA target analyses suggested that *ZmMLO* genes are regulated by complex transcriptional and post-transcriptional mechanisms associated with phytohormones and stress responses. Expression profiling revealed dynamic, gene-specific patterns under methyl jasmonate treatment, insect feeding, fungal infection, and cold stress. Notably, *ZmMLO16* and *ZmMLO18* consistently responded to multiple biotic and abiotic stresses, suggesting their roles as central regulators in stress adaptation. Co-expression analysis revealed significant correlations between several *ZmMLO* genes and calmodulin genes under stress. Structural modeling identified putative calmodulin-binding domains in conserved C-terminal regions characterized by amphipathic α -helices, indicating potential associations with Ca^{2+} -related signaling. [Conclusion] This study provides a comprehensive framework for understanding the evolution, structural diversity, and potential functions of the *MLO* gene family in maize. The identification of *ZmMLO16* and *ZmMLO18* as multi-stress responsive genes, together with the prediction of calmodulin-binding domains, offers insights into MLO-mediated stress adaptation mechanisms in maize and lays a foundation for future functional characterization and molecular breeding.

Key words: *MLO* gene family, calmodulin, stress response, genome-wide analysis

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Genome-wide Identification and Expression Pattern Analysis of

ZmDIR Gene Family in Maize

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Abstract: [Objective] Dirigent (DIR) genes play important roles in plant growth, development and environmental adaptation. The objectives of this study are to identify the *ZmDIR* gene family in maize (*Zea mays* L.) and to preliminarily reveal its potential role in stress defense, thereby providing a theoretical basis for further research. [Method] Bioinformatics were used to identify the members of the *ZmDIR* family and systematically analyzed their conserved motifs, conserved domains, chromosomal distribution, gene duplication events, cisregulatory elements in promoter regions and phylogenetic relationships. Transcriptome data were further employed to elucidate the expression patterns of these genes across different tissues and under both abiotic and biotic stresses. [Result] A total of 41 *ZmDIR* genes were identified in the maize genome and distributed across all 10 chromosomes and contain zero to four introns, 78% of them shared the core conserved motif 1, motif 2 and motif 4. Phylogenetic analysis indicated that DIR proteins in maize can be classified into six subgroups. Gene duplication analysis revealed that segmental and tandem duplications were the main driving forces for the expansion of this family. Gene duplication event analysis suggested that segmental duplication and tandem duplication were the primary drivers for *DIR* genes' evolution in maize. Promoter analysis revealed that *ZmDIR* genes were enriched with cis-acting elements involved in plant growth and development, phytohormone response, environmental stress and light response. Tissue-specific expression profiles revealed that *ZmDIRs* were differentially expressed in the roots, stems, leaves, leaf tip, leaf base, embryo, endosperm, anther, tassel and ear. The expression pattern of these genes appeared to be diverse in the different developmental tissues. Transcriptome data confirmed the differential expression of *ZmDIR* under abiotic (heat, salt, UV, cold, drought and WS) and biotic stress (*Colletotrichum graminicola*). qRT-PCR analysis validated the specific dynamic changes in selected *ZmDIR* genes under salt (NaCl), cold (4°C), drought (PEG) and *Colletotrichum graminicola* stresses. [Conclusion] This study identifies 41 *ZmDIR* genes in the maize genome. Stress-related transcriptome analysis reveals that this gene family responds extensively to both biotic and abiotic stresses. RT-qPCR verification further identifies six candidate genes with significantly induced expression, providing targets for elucidating the stress resistance mechanisms of key members and for molecular breeding.

Key words: *Zea mays*, *DIR* gene family, Bioinformatics analysis, Adversity stress, Expression analysis

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Integrated BSA-Seq and RNA-Seq Reveal Genes Associated with the Defective Ear of Maize

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Abstract: [Objective] Maize ear architecture is the core determinant of grain yield, and defective ear mutants serve as ideal materials to dissect the genetic regulatory mechanisms underlying female inflorescence development. This study aimed to identify candidate genes responsible for the defective ear phenotype of maize mutant *Zmdea2*, and reveal the molecular regulatory basis of abnormal ear development via integrated BSA-Seq and RNA-Seq strategies. [Method] The defective ear mutant *Zmdea2* originating from the DH population of CML451/CML282 was used as experimental material. Phenotypic traits including ear morphology, kernel row number, kernels per row, hundred-kernel weight and single ear weight were statistically compared, and scanning electron microscopy (SEM) was applied to observe the early developmental ear primordia. The mutant was crossed with the reference inbred line B73 to construct F₂ and F₃ segregating populations, and BSA-Seq was performed on two extreme phenotype DNA pools of each generation. RNA-Seq was conducted on young ear primordia of B73 and *Zmdea2* to screen differentially expressed genes (DEGs), followed by GO and KEGG functional enrichment analysis of DEGs. The overlapping genes within the mapping intervals and DEGs were selected as candidate genes, and qRT-PCR was utilized to verify their expression patterns. [Result] 1) Phenotypic identification: Compared with DH-A, *Zmdea2* displayed severely disordered ear development; its kernel row number and single ear weight were significantly decreased at $P < 0.01$, while kernels per row and hundred-kernel weight had no significant difference. SEM observation showed abnormal differentiation of inflorescence meristems in early ear primordia of *Zmdea2*. 2) BSA-Seq mapping: Combined Δ SNP-index and ED analysis of F₂ and F₃ populations narrowed the candidate regions to multiple fragments on maize chromosome 2. 3) Transcriptome analysis: A total of 6367 DEGs were identified between B73 and *Zmdea2*. These DEGs were significantly enriched in carbon metabolism, photosynthesis, amino acid metabolism and lipid metabolism pathways. 4) Candidate gene validation: Eight candidate genes located in the chromosome 2 target intervals were screened, and qRT-PCR results confirmed that all eight genes exhibited significant differential expression between B73 and *Zmdea2*, consistent with RNA-Seq data. [Conclusion] This study successfully mapped the genetic intervals controlling the defective ear trait of *Zmdea2* on maize chromosome 2 by integrating BSA-Seq and RNA-Seq, and verified eight key candidate genes related to abnormal ear development. The disordered primary metabolic pathways in young ear primordia are speculated to be the core factor triggering defective ear formation. The findings provide valuable gene resources and theoretical basis for elucidating the molecular regulatory network of maize ear development and facilitating high-yield molecular breeding of maize.

Key words: Maize, Defective ear, BSA-Seq, RNA-Seq, Candidate gene

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Genome-wide Association Analysis and Genomic Selection for Maize Yield

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Abstract: [Objective] Maize (*Zea mays* L.) is a key cereal crop and industrial raw material, playing a crucial role in food security. Developing high-yield, high-quality hybrids and germplasm remains a primary goal in maize breeding. [Method] This study conducted a comprehensive genome-wide association study using the F1 hybrid populations derived from Shaan A and Shaan B breeding groups, which dedicated to cultivating new varieties of drought resistant, dense tolerant, and suitable mechanized in northwest China, in 2019 and 2020. [Result] The results identified 48 significant SNPs and 68 pairs of epistatic SNPs, which collectively explained 19.03% to 45.53% of phenotypic variation. Meanwhile, 172 candidate genes with additive or dominant effects and 369 with epistatic effects were identified, including Zm00001d027957 (MADS68), Zm00001d045596 (BAG7), and Zm00001d052948 (CCT8). Furthermore, we explored the practical application of genomic selection methods in breeding and found that a "culling" strategy based on predicted hybrid yields could increase population means by up to 0.58–0.77 t/ha, with selection efficiencies ranging from 3.23% to 16.56%. Moreover, a similar strategy targeting parental inbred lines could increase the mean population by 0.68–0.95 t/ha, with selection efficiencies ranging from 5.70% to 25.50%. [Conclusion] Our study provides insights into the genetic basis of hybrid yield and offers a scientific basis for integrating genomic selection method into the breeding systems of Shaan A and Shaan B groups, thereby improving breeding efficiency.

Key words: Maize, Hybrid population, Grain yield, Genome-wide association study, Genomic selection

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The Molecular Mechanism Underlying ZmERF4-Mediated Regulation of Saline-Alkali Stress Tolerance in Maize

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Abstract: [Objective] Soil salinization and alkalization, which lead to land degradation and crop yield reduction, have emerged as severe ecological challenges threatening global agriculture and food security. The western Songnen Plain in China is one of the three major soda saline-alkali regions worldwide, where salts predominantly composed of NaHCO₃ and Na₂CO₃ impose severe alkaline stress. Therefore, elucidating the molecular mechanisms underlying maize responses to soda alkaline stress and identifying key tolerance genes are essential for improving maize production in these regions and safeguarding national food security. This study aims to identify key genes conferring Na₂CO₃ tolerance in maize and elucidate their regulatory networks, providing promising genetic targets for molecular breeding of alkaline-tolerant maize varieties. [Method] Transcriptome sequencing (RNA-seq) was performed on maize roots subjected to Na₂CO₃, NaCl, and NaOH treatments to identify candidate genes specifically responsive to Na₂CO₃ stress. ZmERF4-overexpressing and knockout lines were generated and subjected to phenotypic evaluation. Chromatin immunoprecipitation sequencing (ChIP-seq) and RNA-seq were combined to analyze the downstream regulatory network of this gene. Yeast one-hybrid (Y1H) and dual-luciferase (Dual-LUC) assays were employed to verify the regulatory relationships between ZmERF4 and candidate target genes. [Result] ZmERF4 was strongly induced by Na₂CO₃ stress and encodes a nucleus-localized AP2/ERF transcription factor. Phenotypic evaluation confirmed that the overexpression of ZmERF4 significantly enhanced maize tolerance to Na₂CO₃ stress, whereas the knockout mutants exhibited increased sensitivity to this stress. Reactive oxygen species (ROS) scavenging assays revealed that under alkaline stress, the activities of CAT, SOD, and APX were significantly increased, while the accumulation of H₂O₂ and O₂⁻ was significantly reduced in the overexpression lines; the knockout lines displayed the opposite physiological trend. The combined analysis of ChIP-seq and RNA-seq revealed that ZmERF4 regulates a broad set of genes involved in ROS homeostasis. Furthermore, Y1H and Dual-LUC assays demonstrated that ZmERF4 directly binds to and activates the promoters of ZmGST12 and ZmMIPS2. [Conclusion] The transcriptional regulatory module consisting of ZmERF4 and its downstream target genes plays a crucial positive regulatory role in the maize response to Na₂CO₃ alkaline stress. This study elucidates the molecular mechanism by which ZmERF4 mediates ROS homeostasis to enhance alkaline tolerance in maize, providing promising genetic targets and a foundation for the development and molecular breeding of saline-alkali-tolerant maize germplasm.

Key words: Maize (*Zea mays* L.), AP2/ERF, Salt-alkali stress

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Fine Mapping of Maize Low Ear Height Gene ZmEH3

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Abstract: [Objective] Higher planting densities have driven maize yield gains in recent decades but increased lodging susceptibility. Modifying plant architecture effectively improves lodging resistance. Ear height (EH) is a vital component of maize plant architecture; however, its regulatory functional network remains poorly understood. [Method] In this study, we identified a mutant line Leh8787 with significantly reduced ear height yet no notable variation in plant height (PH) from progenies of commercial maize hybrids. A panel consisted of 257 recombinant inbred lines (RILs) and 275 F₂ progeny from Leh8787×B73 was constructed and genotyped via a 20K SNP array. All RILs were cultivated across three locations with two replications per site under a complete block design, and phenotypic data for EH and PH were recorded. QTL mapping was performed with the software QTL IciMapping for genes controlling low ear height. [Result] Field survey results showed that for B73 plant height was 212.18 cm, ear height was 81.75 cm, and the ear-to-plant height ratio was 0.38. In contrast, the mutant displayed 206.2 cm in plant height and only 31.72 cm in ear height, with a corresponding ear-to-plant height ratio of 0.15. B73 developed 17.7 internodes on average, and its ear node at the 12.4th internode; the mutant had 15.5 internodes in total, with the ear node shift down to the 8.4th internode. QTL mapping identified two quantitative trait loci (QTLs) on chromosome 3 and 6, respectively. and the major QTL on chromosome 3, with a LOD score of 7.61, PVE of 7.41, and add of -5.21 (The adverse effects stem from the mutant). Further fine mapping narrowed the maize low ear height gene ZmEH3 to a 2.06 Mb interval. There are 15 candidate genes within this region, 9 of which are involved in female ear development. [Conclusion] In summary, This study characterized the Leh8787 with stable plant height but sharply reduced ear position, which drastically lowered the ear-to-plant height ratio and altered internode numbers and ear-node distribution. Two EH-associated QTLs were identified and the major locus ZmEH3 were fine-mapping to a 2.06 Mb genomic interval on chromosome 3 containing 15 candidate genes. The mutant germplasm and major-effect QTL identified here can serve as promising genetic resources for breeding lodging-resistant maize varieties suitable for high-density cultivation

Key words: Maize, Ear height, QTL, ZmEH3.

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***ZmMs21A* Determines Cell Fate Specification and Differentiation During Early Anther Development in Maize**

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Abstract: [Objective] Maize depends on elaborate, precisely orchestrated somatic and germinal cell proliferation and differentiation processes within floral tissues. Here, we perform the characterization of *ZmMs21A*, which encodes an LRR-RLK and plays a vital role in maize germinal cell development. [Result] *ZmMs21A* is highly expressed in pre-meiotic anthers. The *ms21a* mutant displays complete male sterility, with no pollen grains in the anther. Cytological analysis showed that *ms21a* produced an excessive number of archesporial cells and failed to form the tapetum layer cells at the anther somatic cell differentiation stage. Several megaspores were observed in *ms21a* ovules, which led to reduced seed setting. *ZmMs21A* is the ortholog of rice OsMsp1, and maize contains another closely related homolog designated Msp2. CRISPR/Cas9 knockout mutants of *ZmMs21A* exhibited a male-sterility phenotype with no pollen grains. By contrast, partial fertility occurred in the *Msp2* knockout mutant, with 22.44%–41.99% of pollen grains aborted. The phenotype of the *ms21a/msp2* double mutant was comparable to *ms21a*, with the anther lacking pollen grains and complete male sterility. RNA sequencing showed that most differentially expressed genes in the plant hormone signal transduction pathway, including auxin response factors, protein kinases, and transcription factors, were downregulated in *ms21a* anthers. [Conclusion] These findings imply that *ZmMs21A* serves a pivotal function in modulating the signals that govern reproductive cell fate in maize.

Key words: Maize, *ZmMs21A*, Leucine-rich repeat receptor-like kinase, Anther development

Technical Session 3

Biotechnology Innovations and Precision Germplasm Enhancement



Genetic Segregation Analysis in F₂ Maize Seed Population Derived from Insee 2 × T7-1 Cross

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Abstract: [Objective] While doubled haploid technology is essential for accelerating sweet corn breeding, selecting haploid kernels in a shrunken background is often hindered by physiological masking effects on marker gene expression. This study aimed to investigate the inheritance of endosperm texture, kernel color, and anthocyanin pigmentation in an F₂ population derived from the cross between the sweet corn hybrid “Insee 2” and the haploid inducer “T7-1”, and to provide a genetic basis for developing sweet corn-specific haploid inducers. [Method] A total of 392 F₂ kernels were phenotypically classified based on endosperm texture (starchy/ shrunken), background endosperm color (yellow/white), and anthocyanin pigmentation in the endosperm and embryo. Genetic segregation was validated using the Chi-square (χ^2) test, and the haploid induction rate (HIR) was computed based on the Navajo marker (*RI- η j*) phenotype. [Result] Endosperm texture (293 starchy: 99 shrunken) and among the 167 non-anthocyanin kernels, background endosperm color (114 yellow: 53 white) segregated in accordance with Mendel’s 3:1 ratio. Anthocyanin pigmentation segregated according to a complementary gene interaction model 9: 7 (225 purple: 167 non-purple; $\chi^2 = 0.21$), indicating a complementary interaction between two dominant loci controlling anthocyanin pigmentation. The haploid induction rate (HIR) in this F₂ population was 0.00% (0 seeds), consistent with genetic expectations, as the recessive induction locus (*mtl*) was masked in the heterozygous state of the F₁ parent. Additionally, the recessive shrunken endosperm (*sh2/sh2*) exhibited a pleiotropic masking effect, hindering anthocyanin accumulation on the endosperm crown. [Conclusion] The F₂ segregation patterns conform to Mendelian and epistasis models, and the 0.00% HIR validates the recessive nature of the induction trait. Developing stable sweet corn-specific haploid inducers in subsequent generations requires recovering the homozygous recessive state (*mtl/mtl*) using marker-assisted selection (MAS), integrated with alternative physiological markers such as root color (*P1I*) and liguleless leaf (*lg1*) to overcome the shrunken endosperm limitation.

Key words: Sweet corn, Haploid inducer, Haploid induction rate (HIR), Complementary gene action, Navajo marker (*RI- η j*)

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Harnessing Maize Genetic Diversity Through Doubled Haploid Technology to Accelerate Genetic Gain in Pakistan's Maize Breeding Program

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Abstract: Pakistan's maize sector relies heavily on imported hybrid seed, while climate change and a narrow genetic base constrain breeding progress. To accelerate genetic gain, a PARC–ALP project (CS-1138) established the country's first doubled haploid (DH) breeding platform using CIMMYT tropicalized haploid inducers (TAILs). Diverse locally adapted populations will be converted into homozygous DH lines through haploid induction and chromosome doubling. The initiative established a functional DH facility, broadened the genetic base, accelerated elite line development, and strengthened Pakistan's capacity to develop climate-resilient hybrids while reducing dependence on imported seed. The platform integrates haploid induction, identification, chromosome doubling, and advancement of locally adapted maize germplasm within a systematic breeding pipeline. CIMMYT-derived inducer lines were introduced, acclimatized, maintained, and utilized for induction crosses with diverse local breeding populations, including commercial hybrids and open-pollinated varieties. This approach enables the development of completely homozygous inbred lines within a substantially shorter breeding cycle and facilitates rapid fixation of desirable alleles and development of parental lines for hybrid breeding. Integration of DH technology with the existing maize breeding program will support the incorporation of tolerance to heat, drought, cold, and other emerging climatic stresses into locally adapted genetic backgrounds. Furthermore, establishment of indigenous infrastructure and technical expertise enhances national capacity for advanced maize breeding and strengthens collaboration with national and international research partners. The DH platform represents an important step toward an efficient, sustainable, and locally driven maize improvement system capable of delivering productive, climate-resilient hybrids for Pakistan's diverse maize-growing environments.

Key words: Doubled haploid technology, Maize diversity, Climate resilience, Hybrid breeding, Pakistan

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Prime Editing for Trait Improvement in Maize: Disease Resistance and promoter engineering for Nutritional Biofortification

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Prime editing enables precise nucleotide substitutions without inducing double-strand breaks or requiring donor DNA, hence offers a versatile strategy for improving elite maize germplasm. CIMMYT is applying this technology to two priority areas: resistance to Maize Lethal Necrosis (MLN) and nutritional biofortification. For MLN resistance, prime editing was used to recreate a naturally occurring sequence variant of a peroxisomal peptidase gene associated with resistance in the donor line KS23-6 from Thailand. This approach introduces the beneficial allele directly into adapted germplasm without lengthy introgression, demonstrating the potential of prime editing to accelerate trait deployment. For biofortification, we applied prime editing to modify cis-regulatory elements in selected promoters and transcription factors to enhance endogenous gene expression in maize endosperm. One target involves phytase, which hydrolyzes phytic acid, a major inhibitor of iron bioavailability. By engineering native regulatory regions, this strategy aims to improve mineral bioavailability while retaining a potentially non-transgenic product profile. Together, these applications illustrate the versatility of prime editing for both precise recreation of beneficial alleles and quantitative modulation of native gene expression. The work complements CIMMYT's broader genome-editing portfolio, including MLN-resistance materials already advancing toward field evaluation, as well as projects targeting plant architecture and Striga resistance. These efforts are supported by capacity building, training of students and visiting scientists, and sustained engagement with regulatory stakeholders. Collectively, this work lays the foundation for scaling and deploying genome-edited maize products for smallholder farmers in Africa and Asia under diverse production and market environments globally.

Key words: Prime editing, Maize Lethal Necrosis, Biofortification, CRISPR/Cas9

AMF Alter Root-Shoot Scaling Trajectories in the Presence of Phosphorus but Impose a Photochemical Penalty in Phosphorus-Deficient Early Vegetative Maize

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Abstract: [Objective] This study aimed to: (i) quantify the effects of arbuscular mycorrhiza fungi (AMF) on biomass distribution in zinc and phosphorus deficiency, and (ii) determine the impact of AMF on electron transport rate (ETR) and quantum yield of photosystem II (Φ PSII) under zinc and phosphorus deficiency conditions. [Method] Maize seeds were grown in sand culture under five nutrient regimes (+Zn+P, -Zn-P, +Zn-P, -Zn+P, and deionized water) with and without AMF in RCBD split-plot for 22 days. [Result] Phosphorus deficiency resulted in a 2–4-fold reduction in dry weights. Leaf, stem, and roots biomass were reduced by 8.6%, 19.0%, and 47.5% in +Zn+P, respectively, due to mycorrhiza-induced growth depression. Notably, root-shoot scaling slopes derived from linear-mixed model revealed a negative scaling trajectory in -Zn+P, an effect that was reversed by AMF in the presence of phosphorus, outlining a previously unexplored role of AMF. Crucially, AMF reduced Φ PSII and ETR by approximately 30% in phosphorus deficient treatments, an effect attributed to the cost of symbiosis to an already strained system. -Zn-P treatment revealed anomalously high stomatal conductance despite reduced Φ PSII and ETR. [Conclusion] Findings highlight nutrient specific AMF-mediated growth and physiology in early vegetative stage.

Key words: Arbuscular mycorrhiza fungi, Mycorrhiza-induced growth depression, Root shoot scaling trajectory, Photosystem II, Electron transport rate

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Haploid Induction Rate Evaluation and Identification Methods in Three Maize Types for Doubled Haploid Breeding

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Abstract: [Objective] Doubled haploid (DH) breeding has become a powerful tool for accelerating maize inbred line development, significantly reducing the time required compared to conventional selfing methods. The haploid induction rate (HIR) and the accuracy of haploid identification are critical determinants of the overall efficiency of a DH program. This study aimed to (1) evaluate HIR across three maize types — field corn, sweet corn, and waxy corn — and different varieties using a haploid inducer population, and (2) assess the effectiveness of R1-nj anthocyanin marker-based kernel selection and stomatal size measurement as sequential haploid identification methods.

[Method] Three maize types comprising six varieties were crossed with a haploid inducer population at the National Corn and Sorghum Research Center, Faculty of Agriculture, Kasetsart University, Thailand. Each variety was planted in three replications. Following pollination, kernels were scored using the R1-nj anthocyanin marker to identify putative haploid seeds based on the absence of anthocyanin coloration in the embryo region. Fifty putative haploid seeds per variety were germinated in trays with four replications. To confirm haploid status, stomatal guard cells of the resulting seedlings were examined and measured microscopically, as haploid plants characteristically exhibit smaller guard cells than diploids. [Result] The proportion of putative haploid seeds identified by the R1-nj anthocyanin marker was relatively high across most varieties, ranging from 7.98% to 19.92%, with lower rates observed in field corn S7328 (3.80%) and sweet corn Hi-Brix 72 (5.96%). However, stomatal size analysis revealed that the actual proportion of true haploid plants was considerably lower than the putative rates suggested, with a high number of false positives recorded among putative haploid seedlings. Confirmed HIR varied among corn types and varieties, ranging from 0.40% to 0.72% in field corn, 0.62% to 1.39% in sweet corn, and 0.90% to 0.96% in waxy corn. [Conclusion] These findings demonstrate that HIR differs among maize types and genotypes. While the R1-nj anthocyanin marker serves as a practical initial screening tool, its use alone results in a substantial false-positive rate. Stomatal size measurement is therefore essential as a secondary confirmation step for accurate haploid identification in maize DH breeding programs.

Key words: Doubled haploid, Haploid induction rate, R1-nj anthocyanin marker, Stomatal size, Maize

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Mainstreaming Novel Breeding Tools and Technologies to Enhance Genetic Gains in CIMMYT Maize Breeding Pipelines.

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Abstract: Rapid genetic gain and resource-efficient breeding are critical for resilient maize in tropical rainfed systems. This review aims to explore the progress and accomplishments in the adoption of new breeding tools and technologies in CIMMYT's Africa maize breeding pipelines. We reviewed operational reports and trial outcomes addressing doubled haploidy (DH), marker-assisted screening and molecular QA/QC, genomic selection (GS) with genomic estimated breeding values (GEBVs), and operational approaches including sparse phenotyping, incomplete testcrossing, and modified tricot designs. DH reduced line-development generations markedly, accelerating advancement to multi-location testing. Marker-assisted early screening effectively removed susceptible material pre-phenotyping and, together with QA/QC markers, preserved genetic identity and seed purity, reducing downstream costs and risks. GS/GEBV implementation yielded higher predicted and realized genetic gains than phenotypic selection for complex traits with evidence shorten breeding cycles. The use of sparse phenotyping, incomplete testcrossing, and farmer-managed tricot trials expanded environmental sampling of the target population while maintain phenotyping costs and improving on-farm relevance. Overall, integration of molecular and operational innovations has enhanced breeding efficiency and genetic gain and genetic-gain, supporting scalable impact for smallholder farmers in the region

Key words: Maize, Genomic selection, Doubled haploidy, GEBVs

Funding acknowledgment: The research was supported by the Bill and Melinda Gates Foundation (B&MGF) and the United States Agency for International Development (USAID) through various projects.

ZmCPK6/ZmbZIP107/ZmSAUR15 Module Underlying the Natural Variation of Embryonic Callus Induction Capability in Maize

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Abstract: [Objective] The ability of immature maize (*Zea mays* L.) embryos to produce embryogenic callus (EC) is highly genotype dependent, which remains a major bottleneck for maize genetic transformation and transgenic breeding. This study aimed to identify the genetic determinants underlying natural variation in EC induction and to clarify the regulatory mechanism controlling this trait. [Method] A panel of 309 maize inbred lines with contrasting EC-forming capacities was used for association analysis, gene cloning, expression and haplotype analyses, transgenic validation, physiological assays of indole-3-acetic acid (IAA) biosynthesis and cell division, and protein-DNA/protein-protein interaction and phosphorylation assays. [Result] *ZmSAUR15*, encoding a small auxin-up RNA (SAUR) protein, was identified as a negative regulator of EC induction from immature embryos. Genetic variation in the *ZmSAUR15* promoter altered transcript abundance and thereby modulated EC-induction capacity. Functional analyses showed that *ZmSAUR15* affects IAA biosynthesis and cell division in immature embryo-derived callus. Upstream of *ZmSAUR15*, the transcription factor *ZmbZIP107* bound both promoter haplotypes but exerted haplotype-dependent effects: it suppressed the activity of the favorable haplotype and activated the unfavorable haplotype. Consistently, in the favorable-haplotype inbred line KN5585, overexpression and knockout of *ZmbZIP107* significantly increased and decreased EC formation, respectively, whereas knockout of *ZmbZIP107* in the unfavorable-haplotype line B73 significantly enhanced EC formation. The calcium-dependent protein kinase *ZmCPK6* physically interacted with *ZmbZIP107* and phosphorylated it mainly at Ser258 and Ser266, reducing its DNA-binding activity and weakening *ZmbZIP107*-dependent repression of *ZmSAUR15*. Overexpression and knockout of *ZmCPK6* decreased and increased EC-forming capacity, respectively. [Conclusion] These findings reveal a previously unrecognized *ZmCPK6/ZmbZIP107/ZmSAUR15* regulatory module that underlies natural variation in maize EC induction. By connecting protein phosphorylation with transcriptional regulation of a key auxin-responsive gene, this study advances mechanistic understanding of maize tissue culture and provides promising molecular targets for improving genetic transformation efficiency.

Key words: Genetic transformation, Embryogenic callus, *ZmSAUR15*, *ZmbZIP107*, *ZmCPK6*

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Synergizing Genome Editing and Artificial Intelligence for Predictive Maize Design

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Abstract: [Objective] The convergence of genome editing (GE) and artificial intelligence (AI) is shifting maize improvement from empirical optimization toward predictive design. [Method] In this Perspective, we propose that GE and AI are linked by a reciprocal innovation cycle. AI improves GE by enabling more accurate guide RNA design, editing outcome and off-target prediction, and data-driven development of next-generation editing systems. In turn, GE provides a powerful experimental platform to validate AI predictions, dissect causal genotype-to-phenotype relationships, and generate high-resolution perturbation datasets for iterative model refinement. [Result] This bidirectional interplay is beginning to accelerate the engineering of complex agronomic traits, including trait stacking, metabolic rewiring, climate resilience, stress tolerance, nutritional enhancement, and de novo domestication. Here, we argue that this synergy is emerging most clearly in predictive editing design and iterative model validation, although robust breeding-scale evidence remains limited. We also discuss emerging opportunities for AI-guided closed-loop editing platforms and generative biological design, together with key bottlenecks, including limited training data, biological complexity across scales, model interpretability, and heterogeneous regulatory landscapes. [Conclusion] We argue that integrating AI with GE can establish a practical framework for predictive maize design and enable more efficient and sustainable maize engineering.

Key words: Genome editing, Artificial intelligence, Bidirectional reinforcement, Maize improvement, Crop design, Foundational framework

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Genomic Prediction of GCA with Sparse Testcrossing for DH Lines in Early Stage Maize Breeding

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Abstract: [Objective] General combining ability (GCA) is an essential criterion to evaluate inbred lines. Traditional GCA estimation demands testcrossing with multi testers, leading to high cost of time, labor and resources, particularly given the rapidly growing quantities of doubled haploid (DH) lines. The integration of genomic selection (GS) with DH technology holds great potential to accelerate genetic gain in maize hybrid breeding, yet the optimization of tester selection and testcross design for early stage GCA prediction remains unclear. [Method] In this study, 385 DH lines were crossed with 4 testers in an Line×Tester design, generating 1,505 F₁ hybrids evaluated across 5 environments for grain yield (Yield), grain dry matter content at harvest (GDMC), ear height (EH) and days to silking (DTS). Materials were subjected to 1× resequencing to obtain genotype data. Different factors affecting prediction accuracy were explored, such as prediction models, prediction algorithms, the proportion of training sets and different tester sparse schemes. The accuracy of GCA estimation for tested and untested DH lines under different sparse strategies was evaluated under conditions of fixed testers (CV0) and random testers (CV1-3). GCA is calculated after predicting the phenotypes of all potential hybrids. [Result] The results indicate that there are significant differences in prediction accuracy (Pearson correlation coefficient) across different traits, models and algorithms. EH and GDMC have higher prediction accuracy compared to DTS and Yield. In the comparison of algorithms, methods based on linear or Bayesian frameworks, such as GBLUP, Bayes B, and Bayes LASSO, show high consistency and stability; while in tree-based ensemble machine learning algorithms such as Random Forest, XGBoost, and Light GBM, prediction accuracy is more sensitive to the choice of prediction model. For testers used in GCA estimation, all traits showed a significant and continuous increasing trend with the increase of the number of testers. For sparse strategies influence on the accuracy of GCA estimation, the CV3 sparse design outperforms CV1, CV2 and CV0. Conversely, when predicting the GCA value of untested DH lines, the CV1 and CV2 are significantly higher than CV3. The prediction accuracy of untested DH lines increases as the ratio of tested to untested rises, and the rate of increase diminishes when the ratio reaches 0.5. [Conclusion] The GBLUP algorithm combined with the GCA+SCA model demonstrates higher predictive accuracy and stability compared with other algorithms including machine learning. Given identical tester number per DH line, random sparse scheme performs better than a fixed testcross scheme. DH GCA can be accurately estimated by crossed two or more testers in traditional calculation methods. For single-tester scenarios, the CV3 sparse approach yields the best GP prediction performance.

Key words: Maize, DH, GS, Sparse tester design, GCA, Hybrid breeding

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Harnessing Haploid-Inducer Mediated Genome Editing for Accelerated Maize Variety Development

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Abstract: [Objective] This study characterizes the technical framework of haploid-inducer mediated genome editing (HI-Edit/IMGE) and evaluates its feasibility for accelerating targeted trait integration in maize, aiming to circumvent constraints of conventional transformation-based delivery. [Method] Three HI-Edit/IMGE maize lines (Edit^{Wx}, Edit^{Sh}, Edit^{Wx&Sh}) were developed by stacking the haploid inducer line CHO13 with CRISPR-Cas9 constructs targeting *Waxy1* (*Wx1*) and/or *Shrunken2* (*Sh2*). Using B73 and six other elite commercial inbred lines as recipients, maternal haploid induction rates (HIR) and targeted mutation efficiency were systematically assessed. Key techniques included flow cytometry for ploidy confirmation, Maize 60K SNP array for genomic background analysis, Sanger sequencing for mutation profiling, and phenotypic evaluations through iodine staining, starch composition assays, and agronomic trait assessments. [Result] The HI-Edit/IMGE system achieved maternal HIR ranging from 8.55% to 20.89% and targeted mutation efficiencies between 0.38% and 1.46%. The Edit^{Wx&Sh} line successfully induced simultaneous mutations in both *Wx1* and *Sh2* in one haploid individual among 1980 screened. ddPCR confirmed homozygous integration of all components including dual fluorescence protein (DFP) and Cas9. Flow cytometry and SNP array analyses validated high haploid genome purity. However, rare instances of somatic chimerism and limited introgressed segments from the inducer were also detected. The somatic chimerism was attributed to incomplete paternal chromosome elimination. Doubled haploid mutants exhibited expected phenotypic alterations: *Wx1* edits conferred modified starch composition, *Sh2* mutants displayed shrunken kernel phenotypes, and no significant adverse effects on key agronomic traits were observed. [Conclusion] HI-Edit/IMGE provides an efficient and scalable platform for generating targeted mutations through pollination in maize, circumventing the need for stable transformation and extensive backcrossing. Precise characterization of CRISPR-Cas9 copy number is critical to system performance. The technology demonstrates strong potential for industrial application, and further optimizations, such as enhancing editing efficiency and minimizing chimerism, will strengthen its utility in accelerating the development of improved maize varieties.

Key words: Genome editing, Haploid induction, HI-Edit/IMGE, Maize, Seed industrial application

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Pollen Self-Elimination CRISPR-Cas9 Prevents Transgenic Pollen Dispersal in Maize

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Abstract: [Objective] To develop a CRISPR-Cas system that prevents transgenic pollen dispersal while retaining heritable genome-editing activity in maize. [Method] A pollen self-elimination CRISPR-Cas9 (PSEC) construct was created by linking a pollen-specific suicide cassette, *ZmPG47pro:ZmAA1*, with Cas9 and sgRNAs targeting *ZmGRF1*, *ZmGRF5*, and *ZmGRF6*. The PSEC construct was introduced into maize through Agrobacterium-mediated transformation, and pollen viability, transgene inheritance patterns, and genome-editing efficiency were analyzed in transformed plants and their progeny. [Result] In PSEC plants, pollen grains carrying the transgene were selectively eliminated due to the activation of the pollen-specific suicide cassette, while viable pollen was confirmed to be free of the PSEC transgene. Genetic analyses demonstrated that PSEC was unable to transmit through the male gametophyte but could be inherited through the female gametophyte. Importantly, the inherited PSEC cassette maintained strong *in vivo* Cas9 editing activity across generations and efficiently generated targeted mutations, including single, double, and triple mutants of *ZmGRF1*, *ZmGRF5*, and *ZmGRF6*, through selfing and crossing experiments. [Conclusion] The PSEC system effectively prevents transgenic pollen dispersal while preserving active genome-editing capability in subsequent generations. This strategy provides a practical biosafety solution for maintaining CRISPR/Cas components in maize breeding programs and may be broadly applicable to other outcrossing crop species.

Key words: Maize, CRISPR-Cas9, Pollen self-elimination, Transgene containment, Genome editing

Funding acknowledgment: Supported by the National Key Research and Development Program of China (2020YFE0202300), Henan Provincial Department of Agriculture and Rural Affairs (2022010201), CARS-Maize (CARS-02-06), and Hainan Yazhou Bay Seed Laboratory (B21HJ0215).

CRISPR/Cas9 Editing of *ZmTms5* Creates Thermosensitive Male-Sterile Maize for Two-Line Hybrid Seed Production

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Abstract: [Objective] To develop stable and applicable thermosensitive genic male-sterile (TGMS) maize germplasm resources for two-line hybrid breeding and characterize their temperature-dependent fertility transition, agronomic performance, and regional adaptability. [Method] CRISPR/Cas9-mediated genome editing was used to disrupt the maize *ZmTms5* gene. Homozygous mutant lines without the transgenic cassette were identified and evaluated under controlled temperature regimes and multi-environment field conditions. Fertility transition, agronomic traits, and reproductive performance were systematically assessed, and regional adaptability was evaluated across 14 representative maize-growing locations in China. [Result] The *ZmTms5*-edited mutants maintained male fertility under moderate temperatures, with a daily average temperature of approximately 23 °C, but exhibited stable male sterility under high-temperature conditions, with daily average temperatures of 28–29 °C, during the critical stages from tetrad formation to pollen maturation. This temperature-dependent fertility transition was highly reproducible. The mutants showed no significant differences from the wild type in major agronomic traits, including plant height and ear height, indicating limited effects of *ZmTms5* disruption on vegetative growth. Multi-location trials identified environmental conditions favorable for sterile-line multiplication and hybrid seed production and demonstrated the potential of these TGMS lines for regional deployment. [Conclusion] CRISPR/Cas9-mediated modification of *ZmTms5* provides an effective strategy for generating TGMS maize germplasm. The developed lines exhibit stable fertility transition, favorable agronomic performance, and broad application potential, providing valuable genetic resources for establishing flexible two-line hybrid breeding systems in maize.

Key words: Maize, CRISPR/Cas9, *ZmTms5*, Thermosensitive male sterility, Two-line hybrid breeding

Funding acknowledgment: Supported by the National Key Research and Development Program of China (2022YFF1003504-003).

Adaptive Maize Development to Overcome Agro-ecological Challenges and Climate Change in Indonesia

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Abstract: Maize development in Indonesia is critical for national food security but faces significant agro-ecological challenges, including cultivation on suboptimal lands (acidic, saline, and dry), climate anomalies such as El Niño, and severe biotic pressures from downy mildew and false army worm. Historically national maize research was led by the Indonesian Agency for Agricultural Research and Development under Ministry of Agriculture, and since the issuance of new regulation, national research has transitioned to the National Research and Innovation Agency (BRIN) completely in 2022. This current era prioritizes precision breeding to develop high-yielding and stable hybrids of maize varieties across Indonesia's diverse regions. High-yielding maize varieties have been released by Ministry of Agriculture including parental lines such as Arjuna and Abimanyu, followed by the high-yielding Bima series, the prolific NASA-29. Recently the legacy is continuing by BRIN with releasing hybrids like HJBRIN101 and HJBRIN103, which boast potential yields up to 12.9 t/ha and high resistance to fungal pathogens. Importantly, climate adaptation research currently focuses on multi-stress resilience. Research into low-nitrogen (N) tolerance, specifically identifying hybrids aims to maintain productivity with a 50% reduction in fertilizer, while the other promising hybrids address shade tolerance for inter-cropping system, and water logging tolerance. Advanced technological integration supports these efforts which employ Marker-Assisted Selection (MAS) for selecting population that resistant to downy mildew gene PR-1, molecular identification of the double haploid R1-nj (Navajo) introduced from International Maize and Wheat Improvement Center (CIMMYT), and emerging deep learning pipelines like to accelerate genetic variant prioritization. To achieve the national target of ending maize imports by 2026, future research is directed toward strategic technologies including using Machine Learning (ML) for selection and genetic prediction and Genome Editing (GE). Enhanced public-private licensing partnerships to scale the distribution of resilient, high-quality seeds to smallholder farmers is also needed to accelerate technology adoption.

Key words: Maize breeding, Climate adaptation, Precision breeding, Doubled haploids

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Evaluation of Glyphosate Tolerance and Pollen Biological Characteristics in Transgenic Maize Co-expressing Cry1C and EPSPS

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Abstract: [Objective] Our study aims to evaluate glyphosate tolerance and pollen biological characteristics of the stacked-trait transgenic maize line C492 co-expressing Cry1C and EPSPS, thereby providing experimental evidence for its biosafety assessment. [Methods] Glyphosate was applied at four times the recommended field dose at the 5–6 leaf stage, and phytotoxicity was assessed using a five-grade injury scale. EPSPS protein levels in different tissues were quantified by ELISA. Pollen viability and fertility were evaluated using TTC and I₂-KI staining. In vitro pollen germination assays were conducted at 25°C, 30°C and 35°C across different storage durations. Pollen grain diameter was determined by microscopic image analysis. Non-transgenic parental lines Zong31 and N-76 served as controls. [Result] C492 exhibited 100% survival under four-fold glyphosate application with a phytotoxicity score of 0, whereas all control plants showed severe injury. EPSPS protein accumulated in a leaf > root > stem pattern (25.81, 15.23, and 11.49 µg/g fresh weight, respectively). Pollen from C492 exhibited normal staining patterns comparable to controls in both TTC and I₂-KI assays. In vitro pollen germination decreased with storage time under all temperature regimes; however, no significant differences were detected between transgenic and non-transgenic lines at any time point. Mean pollen diameter of C492 (101.29 µm) was comparable to that of Zong31 (98.05 µm) and N-76 (100.29 µm). [Conclusion] The Cry1C and EPSPS co-expressing maize line C492 confers strong glyphosate tolerance without detectable adverse effects on pollen viability, fertility, germination capacity, or pollen morphological characteristics. These results indicate that stacked expression of Cry1C and EPSPS does not compromise reproductive biological characteristics, supporting its biosafety evaluation and potential field application.

Key words: Transgenic Maize, Cry1C, Epsps, Glyphosate Tolerance, Pollen Viability, Biosafety Assessment

Funding acknowledgment: This work was funded by the Yuelushan Laboratory Breeding Program (YLS-2025-ZY02037) and the Agricultural Science and Technology Innovation Program in Hunan province (2025CX85).

All-In-One: A Powerful Toolbox for Maize Gene Function Validation In a Single Genetic Transformation, With Feasibility for Gene Knockout, Overexpression, and Complementary Mutation

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Abstract: [Objective] CRISPR/Cas9 genome editing is facilitating crop functional genomic research. However, conventional co-transformation of Cas9 and sgRNA induces lethal albinism and developmental defects when targeting maize essential genes. Furthermore, traditional PCR-based mutation identification is labor-intensive, time-consuming and costly. Here, we have developed an optimized genome editing system integrating split Cas9-sgRNA strategy, tissue-specific visual screening, and an all-in-one vector toolbox to address the lethal editing bottleneck of essential genes and simplify high-throughput genotyping in maize. [Methods] Separate Cas9 and sgRNA overexpression vectors were transformed into the maize inbred line KN5585 via *Agrobacterium tumefaciens*-mediated transformation. In this study, we constructed a dual-fluorescence screening system harboring aleurone- and embryo-specific AmCyan and DsRed2 markers, and a single T-DNA all-in-one vector integrating overexpression cassettes, sgRNA modules and fluorescent reporters. [Results] The split Cas9-sgRNA system eliminated early lethal defects caused by co-editing. Conventional co-transformation only reached 0.51% positive transformation efficiency, while split transformation achieved 12.94%, with F₁ editing efficiency ranging from 38.12% to 100%. Dual-tissue fluorescent labeling enabled 100% accurate visual screening and reduced reliance on PCR. The all-in-one vector system successfully generated overexpression and knockout materials within two generations, with a maximum editing efficiency of 93.75%. High-throughput application of this system produced *Col6* and *Col15* transgenic lines, which exhibited delayed flowering and reduced plant height. [Conclusion] This split Cas9-sgRNA system overcame lethal obstacles in maize essential gene editing. Tissue-specific fluorescence improved mutant screening efficiency and accuracy. The all-in-one vector achieved one-step transformation to generate knockout, overexpression and complementary lines. This efficient, low-cost toolbox supported large-scale gene functional verification in maize.

Key words: Crispr/Cas9, Maize, Split Cas9-Sgrna System, Fluorescent Screening

Funding acknowledgment: This research was supported by National Natural Science Foundation of China (U23A20186).

Mechanism Analysis of RBSDV P5-2 Mediated by the Hypersensitive Response-Related Gene *ZmHIR3* on Maize Rough Dwarf Disease

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Abstract: [Objective] Maize rough dwarf disease (MRDD), caused by rice black-streaked dwarf virus (RBSDV), is a major viral disease that threatens maize production in China. Previous studies showed that the hypersensitive response-related gene *ZmHIR3* participates in the recognition of the RBSDV P5-2 protein and contributes to disease resistance; however, the molecular mechanism underlying this interaction remains unclear. [Method] In this study, an RBSDV P5-2 overexpression vector and an RBSDV P5-2/*ZmHIR3* co-expression vector were constructed, and RBSDV was artificially inoculated to investigate disease phenotypes, chloroplast damage, reactive oxygen species dynamics, Ca²⁺ flux, hormone responses, transcriptomic changes, and metabolic regulation. [Result] RBSDV P5-2 reduced ROS-associated H₂O₂ accumulation, induced H₂O₂ influx and Ca²⁺ efflux, and damaged chloroplast cells, thereby promoting the rough dwarf phenotype. In contrast, *ZmHIR3* complemented the P5-2-induced disease phenotype, alleviated chloroplast injury, and enhanced maize resistance to MRDD. Transcriptome sequencing indicated that maize responses to RBSDV P5-2 were mainly associated with hormone signaling, including abscisic acid and jasmonic acid pathways, as well as photosynthesis-related processes. Hormone-content analysis showed that JA-related isoleucine (Ile) was significantly decreased compared with the receptor control. Integrated metabolomic and transcriptomic analyses further revealed that *ZmHIR3* regulates multiple pathways related to tyrosine, aspartic acid, and glutamic acid metabolism. [Conclusion] These findings indicate that after recognition of RBSDV P5-2 by *ZmHIR3*, the alpha-linolenic acid pathway, a synthetic precursor pathway of JA, is rapidly activated to regulate H₂O₂ and Ca²⁺ signaling, increase JA-Ile-related defense responses, maintain chloroplast integrity, enhance photosynthesis, and improve maize resistance to rough dwarf disease.

Key words: Maize, Rough dwarf disease, RBSDV P5-2, *ZmHIR3*

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Functional and Mechanistic Analysis of the miR164h-ZmNAC21

Module in Regulating Maize Resistance to Head Smut

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Abstract: [Objective] Maize head smut, caused by *S. reilianum*, is a major disease in spring maize-growing regions of northern China and severely compromises grain yield and quality. Elucidating resistance-associated regulatory genes and their mechanisms is therefore important for improving maize resistance to head smut. [Method] This study focused on the *miR164h-ZmNAC21* module associated with maize head smut resistance. Subcellular localization, functional validation, RNA-seq, metabolomic profiling, yeast one-hybrid (Y1H) assays, cellular morphology observations, and measurements of physiological indices were performed. [Result] 5' RACE and Y1H assays confirmed that *zma-miR164h-5p* cleaves *ZmNAC21* transcripts. The *ZmNAC21* promoter drove target-gene expression in roots and seeds, and the ZmNAC21 protein localized to the nucleus. Following SIR and NIM inoculation with *S. reilianum*, hyphal density in vascular bundles increased with incubation time, with hyphae mainly concentrated in the phloem. *ZmNAC21* positively regulated maize resistance to head smut, and overexpression of *ZmNAC21* increased disease resistance by 20% to 29%. In ZmNAC21OE lines, infected cells exhibited apoptosis-like features, and hyphae were confined within dead cells by cell-wall barriers. In contrast, in ZmNAC21CRI lines, cellular autophagy was insufficient to prevent hyphal dissemination. At early maize developmental stages, elevated *ZmNAC21* expression mainly altered peroxidase (POD) and phenylalanine ammonia-lyase (PAL) activities and salicylic acid (SA) content in mesocotyls. Integrated transcriptomic and metabolomic analyses indicated that starch and sucrose metabolism and phenylpropanoid metabolism were involved, thereby contributing to changes in PAL, SA, and other physiological responses. [Conclusion] The *miR164h-ZmNAC21* module regulates starch and sucrose metabolism and phenylpropanoid biosynthesis, modulates PAL activity and SA accumulation, and restricts *S. reilianum* hyphal spread, thereby enhancing maize resistance to head smut.

Key words: Maize, Head smut, miR164h-ZmNAC21, *S. reilianum*, Resistance

Funding acknowledgement: National Natural Science Foundation of China (U24A20397 and 31971956)

Genome-Wide Association Study Identified ZmMYB42 as a Negative Regulator of Resistance to Maize Head Smut

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Abstract: [Objective] Maize head smut, caused by *Sporisorium reilianum*, is a destructive disease that threatens maize production in northern and eastern China. This study aimed to identify resistance-associated loci and clarify the regulatory role of *ZmMYB42* in maize response to head smut. [Method] Head smut resistance was evaluated in 292 maize inbred lines by field inoculation over two years. Genome-wide association analysis, candidate-gene expression profiling, qRT-PCR validation, subcellular localization, and artificial inoculation of *S. reilianum* were performed to screen and verify resistance-related genes. [Result] Three significant SNPs associated with head smut resistance were detected, and 12 candidate genes were identified. Among them, *ZmMYB42* (*Zm00001d053220*) showed contrasting expression patterns between resistant and susceptible lines after inoculation. qRT-PCR supported its involvement in resistance regulation, whereas subcellular localization showed that the ZmMYB42 protein was localized in the nucleus. Overexpression of *ZmMYB42* increased susceptibility and mesocotyl damage after *S. reilianum* infection, indicating that it functions as a negative regulator of resistance. In addition, SNP837 explained 18.11% of the phenotypic variation and was converted into the dCAPS marker DNdCAPS837, which showed 77.78% genotype-phenotype concordance. [Conclusion] These results demonstrate that *ZmMYB42* negatively regulates maize resistance to head smut and provides useful genetic resources and molecular markers for breeding head smut-resistant maize.

Key words: Maize, Head smut, GWAS, ZmMYB42, *S. reilianum*, Resistance

Funding acknowledgement: Natural Science Foundation Project of Heilongjiang Province (U24A20397 and 31971956)

Synergistic Regulation of Ethephon and Ice-6 Improves Photosynthetic Efficiency, Yield and Lodging Resistance

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Abstract: [Objective] High planting density boosts maize yield potential but increases lodging risk. Ethephon improves lodging resistance yet often reduces yield via impaired photosynthesis and fewer kernels. This study developed a novel synergist co-applied of iron chlorin e6, hereafter ICE-6, and DA-6 with ethephon to enhance photosynthetic performance, delay senescence, optimize biomass partitioning and eliminate the yield penalty of conventional chemical regulation. [Method] A two-year (2023–2024) field experiment was conducted at Gongzhuling Experimental Station (124°48'43"E, 43°29'55"N) with Zhengdan 958 at 82,500 plants ha⁻¹. Under the integrated control-and-promotion approach, foliar applications were performed at the 8-leaf (V8) and 11-leaf (V11) stages, respectively. Treatments were: CK (clean water), ETH (ethephon 450 mL ha⁻¹ at V8), CAD (synergist: 22.5 g ha⁻¹ DA-6 + 90 g ha⁻¹ ICE-6 at V11) and PHS (ETH at V8+ CAD at V11). For each treatment, the chemicals were applied after dissolution in 450 L ha⁻¹ of water. Leaf Area Duration, SPAD, net photosynthetic rate (*P_n*), dry-matter accumulation/partitioning, lodging traits and yield components were determined. [Result] The results showed that the spraying of ethephon decreased the photosynthetic potential, *P_n*, and biomass at maturity of maize by 25.70%, 13.93%, and 8.54%, respectively, and the number of kernels decreased by 7.00% without changing the weight of the kernels, which ultimately led to a decrease of 11.00% in yield. The synergist increased the leaf area and chlorophyll content of maize by 17.97% in *P_n*, increasing the biomass at maturity. The proportion of biomass partitioned into stem, leaves, and ear by 3.13%, 1.43%, and 3.55%, respectively, ultimately resulting in a 7.81% increase in yield. The application of synergists based on ethephon effectively mitigated the negative effects of ethephon on leaf area and photosynthetic potential, increasing SPAD by 26.55% at maturity, slowing down the process of plant senescence, and increasing *P_n* by 23.53%, which led to an increase in biomass and harvest index, and an increase of 7.76% in final yield. [Conclusion] Combining the ICE-6+DA-6 synergist with ethephon at V8–V11 improves leaf area and chlorophyll retention, thereby enhancing photosynthetic capacity, biomass and harvest index, resulting in a two-year average yield increase of 7.76% over the water control and approximately 18.8% over ethephon alone. Thereby providing a practical and effective chemical regulation pathway for achieving high yield, stable production, and lodging resistance under high-density planting.

Key words: Ethephon, Plant Growth Regulator, Net Photosynthetic Rate, Biomass, Maize

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Breeding Potential Of Maize Dh Lines From Commercial Hybrids Evaluated by Testcross Performance in Early Zone

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Abstract: [Objective] The genetic diversity of early-maturing germplasm remained narrow over the past decades. While Dent×Flint served as an classic heterotic pattern, and expanding germplasm resources is critical to breeding elite varieties and exploiting heterosis in response to evolving climatic conditions and maize market demands. [Method] A panel consisted of 385 doubled haploid (DH) lines was generated from 14 commercial hybrids adapted in Northern East China. DH lines were testcrossed with four different types of testers (QF4507, QF252, K523, CAVB110), resulted 1505 hybrids and evaluated across five locations. An augmented experimental design was adopted at each testing site; three commercial check varieties (DMY3, Lihe328 and P5697) were selected as controls in every incomplete block to correct environmental variation. In each plot, the grain yield (Yield) and grain dry matter content at harvest (GDMC) were phenotyped. [Result] Among the tested DH lines, those from YNY11, C1563, XY1409, C2188 and DK556 showed higher GCA of grain yield, with a total of 10 DH lines achieving over 95% of average grain yield of check varieties when crossed with four testers. The lines derived from C1563 showed the highest average yield across the four testers, and the top 20% of lines from C1563 exhibited the highest average general combining ability (GCA) at 0.81 for yield, followed by YNY11 with a GCA mean of 0.60. Hence, C1563 and YNY11 are promising germplasm resources for further breeding practices. Of the four testers, QF4507 showed the highest grain yield, while CAVB110 yielded the minimum averagely with four testers. For GDMC, K523 showed the highest average GDMC in tested population, and QF252 the lowest. Testcrosses developed from DH lines derived from A6565 showed highest GDMC and C1210 showed the lowest GDMC. [Conclusion] In summary, this study demonstrates that DH lines derived from early-maturing commercial hybrids harbor substantial genetic variation, with elite germplasm such as C1563 and YNY11 offering valuable resources to broaden the early-maturing genetic base, while appropriate tester selection is critical for fully exploiting heterosis and achieving coordinated improvement in grain yield and quality traits.

Key words: Maize, Doubled Haploid, Germplasm Innovation, Testcross, GCA

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Sustaining Productivity Through Genetic Innovation: Historical Perspectives and Modern Biotechnology in Philippine Corn Breeding

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Abstract: The Philippine corn industry has undergone a significant transformation over the past century, evolving from the selection of native landraces to a modern sector driven by advanced biotechnology. This progression was marked by three distinct technological phases: the early adoption of hybrids, the introduction of genetically modified (GM) varieties, and the current widespread use of high-yielding seeds. These innovations have resulted in a steady upward trajectory in productivity, with average yields for yellow corn hybrids increasing from roughly 5 t ha⁻¹ in the 1990s to current highs of 10 t ha⁻¹. At present, the industry is reliant on biotechnology, with GM corn accounting for approximately 75% of the yellow corn area, providing the needed resistance to pests like corn borer and fall army worm. Despite these genetic gains, the sector continues to face challenges related to high production costs, significant post-harvest losses, and climate vulnerability. The Philippine Yellow Corn Industry Roadmap (2021–2040) outlines strategic priorities for the sector, such as scientific innovation, climate-smart production practices, and strengthened public–private partnerships, which are intended to support productivity, resilience and competitiveness of the Philippine corn industry.

Key words: Philippine corn, Hybrids, Genetically modified varieties

Technical Session 4

Genetic Gain of Multiple-stresses Tolerance with Climate-resilient



Resilience by design: New Generation Maize that Thrives Despite Climate Change

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Abstract: Accelerating climate volatility demands a paradigm shift from incremental improvement to integrated, data-driven breeding systems that deliberately stack resilience traits while maintaining high yield potential. We outline a framework for delivering transformative genetic gains in next-generation climate-adaptive maize for diverse production environments in lowland tropics, where abiotic and biotic stresses increasingly co-occur and interact. We present evidence from recent breeding pipelines at CIMMYT Asia demonstrating sustained genetic gain in yield under managed-stress environments, alongside improved stability across variable seasons. Case examples highlight successful stacking of drought + heat tolerance and drought + waterlogging tolerance, with resistance to major diseases and pests, without yield penalties under favorable conditions. We also discuss product profiling and segmentation, ensuring varieties meet the heterogeneous needs of farmers, rainfed smallholders, intensified systems, and nutritionally enhanced maize, while aligning with seed systems. Transformative gains in climate-adaptive maize are within reach, provided we orchestrate technologies into cohesive pipelines that rapidly stack resilient traits, deliver locally adapted products, and close yield gaps under real-world combinations of stresses across the lowland tropics in Asia and elsewhere.

Key words: Resilience, Genetic gain, Climate change, High-stable yields

58 Years of Maize Breeding Experiences in US, Asia, Africa and Far East Asia including North Korea.

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Abstract: [Objective] to highlight current biomedical black normal and supersweet maize breeding, the development of high-bioethanol *bm3* + leafy maize for climate resilience, and hybrid maize breeding in Northeast China. The breeding principle is based on quantitative gene-controlled stress tolerance. [Method] (1) the introduction of U.S. single-cross (SX) hybrid maize technology into Asia, beginning in South Korea in 1974, followed by technology transfer (from 1978 onward) to other Asian countries including China, India, Thailand, and Indonesia; (2) stress-tolerant maize breeding at IITA for Africa (1979–1995) targeting maize streak virus (MSV), the parasitic weed *Striga* spp., drought, and the development of stress-tolerant hybrids for the first time in West Africa; (3) collaborative maize breeding and seed production in North Korea to combat starvation (1998–2002); and (4) current breeding efforts involving biomedical black maize and high-bioethanol, climate-resilient maize. [Results] both successful and challenging. Major achievements include a threefold increase in the national average maize yield in South Korea through the adoption of U.S. SX hybrid maize technology (1979); control of MSV across the African continent through IITA/CIMMYT collaboration (1986); pioneering *Striga*-tolerant, co-survival maize breeding (1995) and contributing to the saving of more than four million lives in North Korea through increased maize production (1998–2022). Additional challenges and achievements include downy mildew-tolerance breeding in South Asia, particularly in Cambodia, East Timor, Aceh (Indonesia), Nepal, and Myanmar (2023–2025). [Conclusion] the experiences show the importance of co-survival tolerance maize breeding and genetics through QTL genes that guarantee stability and durability with high grain yield under climate resilience. Tips for research fund and time saving maize breeding are suggested. In addition, QUAN RUNDA Co. and Gangwon Maize Research Institute are introduced.

Key words: US single cross maize, Co-survival stress tolerance, Bio-medical black corn, Super bio ethanol *bm3*+ leafy maize

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***NDR1* Coordinates Utilization of Carbon, Nitrogen and Water to Boosts Grain Yields**

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Abstract: [Objective] Amidst global climate change, crop breeding urgently needs to break the trade-off between high yield and resource efficiency to achieve synergistic optimization of carbon assimilation, nitrogen utilization, and water consumption. However, master regulatory hubs capable of integrating all three processes remain largely unreported. [Method] By using chromosome fragment substitution to conduct field and seedling stage drought and low-nitrogen tolerance tests, and combining with GWAS to identify candidate genes; The interactions with downstream target genes were verified through EMSA and ChIP-qPCR experiments; The determination and analysis of physiological indicators such as isotope N¹⁵, photosynthetic rate, and water use efficiency verified that coordinates utilization of carbon, nitrogen and water to boosts grain yields. [Result] We identify a major QTL, nitrogen and drought responsive 1 (*NDR1*), which encodes a G2-like transcription factor that acts as a vascular-enriched central metabolic checkpoint coordinating the utilization of carbon, nitrogen, and water in maize. *NDR1* employs a parallel modular output mechanism: it directly activates a carbon-metabolism module (*ZmSGR1/ZmBGLU1*) to enhance photosynthetic carbon fixation and stay-green traits, a nitrogen module (*ZmNIR1/ZmNPF6.6*) to drive uptake and translocation, and a cytokinin-mediated stress module (*ZmLOG5/ZmCRR2*) to improve water-use efficiency. Importantly, *NDR1* mediates a novel bidirectional physiological compensation: drought signals upregulate nitrogen-utilization genes, while low-nitrogen signals enhance drought tolerance, thus creating a buffering mechanism under dual nitrogen and water deficits. Large-scale field trials and cross-species transformation validate that the superior *NDR1* robustly increases grain yield in maize, rice, wheat, sorghum, and foxtail millet under nitrogen and drought limitation, establishing its broad translational applicability across major staple crops. [Conclusion] *NDR1* coordinates utilization of carbon, nitrogen and water to boosts grain yields in cereal crops. This study reveals a system-level regulatory hub that couple's resource metabolic balance with stress adaptation, providing valuable genetic resources and design targets for breeding climate-resilient, broadly adapted smart crops.

Key words: Maize, Map-based cloning, Nitrogen use efficiency, Drought tolerance, Carbon fixation

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Identification and Validation of MiRNAs and Target Genes

Associated with Low-Temperature Stress during Maize Germination

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Abstract: [Objective] Low temperature during germination is a major abiotic stress that limits seedling emergence of spring maize in cold regions of northern China. Previous studies on maize responses to low-temperature stress have mainly focused on physiological changes and gene discovery, whereas miRNA-mediated regulatory mechanisms remain poorly understood. [Method] The low-temperature-tolerant maize inbred line Zao8-3 and the highly low-temperature-sensitive inbred line Ji853 were used as experimental materials. Small RNA sequencing and degradome sequencing were performed to identify miRNAs and target genes associated with low-temperature stress during maize germination. Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) enrichment analyses were conducted, and key miRNAs and their target genes were validated by qRT-PCR. [Result] Twenty-two key differentially expressed miRNAs and 24 inversely regulated target genes were identified. These target genes were mainly associated with ATP binding, seed germination, RNA splicing, RNA transport, and related biological functions. During germination under low-temperature stress, *zma-miR156h* and *PC-3p-15424* and their target genes showed inverse expression patterns at 2 and 4 h, whereas *zma-miR169o* and its target genes showed inverse expression patterns at 2 and 6 h. At the bud and seedling stages, *zma-miR156h* and its target gene were involved in the response to low-temperature stress, with significant differences in root tissues between the two inbred lines. *zma-miR169o* did not respond to low-temperature stress at the bud or seedling stage; however, its target gene *ZmRLP39* differed significantly in root tissues at both stages, and four other target genes showed significant differences in shoots at the bud stage. *PC-3p-15424* and its target gene showed highly significant differences in root tissues at the bud stage and in stems at the seedling stage between the two inbred lines. [Conclusion] Together with previous findings, these results indicate that maize responses to low-temperature stress during germination are mainly regulated by *zma-miR156h* and *zma-miR169o*. *zma-miR156h* may improve low-temperature tolerance during maize germination by regulating *SPL* target genes, whereas *zma-miR169o* targets *NF-YA* genes to enhance maize tolerance to low temperature during germination, although it did not respond to low-temperature stress at the bud and seedling stages.

Key words: Maize, Low-temperature stress, MiRNA, Degradome sequencing, Expression pattern

Funding acknowledgment: Natural Science Foundation Project of Heilongjiang Province (RC2025QN022 and YQ2022C009)

***ZmBARK1* is Required for Low-temperature Tolerance during Seed Germination in Maize**

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Abstract: [Objective] Low temperature during germination is a major environmental constraint that limits seedling establishment and regional adaptation of maize (*Zea mays* L.). Identifying stable genetic loci and functional genes controlling low-temperature tolerance at this stage is therefore essential for improving maize performance in cold regions. [Method] A panel of 304 maize inbred lines was evaluated under low-temperature and control conditions. Seeds were incubated at 10°C for 31 days followed by recovery at 15°C for 7 days, while control seeds were germinated at 25°C for 6 days. Germination-related phenotypes were integrated with genome-wide genotypic data for association analysis. SNPs with $-\log_{10}P > 6$ and $P < 0.01$ were considered significant, and candidate genes were further examined using RNA-seq data, qRT-PCR, and mutant validation. [Result] Genome-wide association analysis identified 12 stable SNPs associated with low-temperature tolerance during maize germination. Among the candidate genes, *ZmBARK1*, located in bin 4.09 on chromosome 4, was selected as a key regulator. Expression analysis showed that *ZmBARK1* responded to low-temperature treatment, and mutant validation confirmed that disruption of *ZmBARK1* reduced low-temperature tolerance during seed germination. These results indicate that *ZmBARK1* is required for maintaining germination capacity and early seedling establishment under cold stress. [Conclusion] This study identifies *ZmBARK1* as a functional gene underlying low-temperature tolerance during maize seed germination. The stable SNPs and validated candidate gene provide useful targets for marker-assisted breeding and establish a genetic basis for further dissecting cold-stress adaptation during early maize development.

Key words: Low-temperature, Maize, GWAS, RNA-seq, *ZmBARK1*

Funding acknowledgment: Natural Science Foundation Project of Heilongjiang Province (RC2025QN022 and YQ2022C009)

***ZmbHLH30* Enhances Cold Tolerance During Maize Germination**

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Abstract: [Objective] Low temperature is a major abiotic stress affecting maize throughout its life cycle, and the germination stage is particularly sensitive to cold injury. This study aimed to identify the genetic basis of early-stage cold tolerance and clarify the function of *ZmbHLH30* in maize germination under low-temperature stress. [Method] Quantitative trait locus mapping was used to screen candidate genes associated with cold tolerance during maize germination. Subcellular localization, promoter activity analysis, stress-responsive cis-element prediction, overexpression analysis, CRISPR/Cas9-mediated knockout, and integrated transcriptomic and metabolomic analyses were performed to verify the biological function of *ZmbHLH30*. [Result] QTL mapping identified *ZmbHLH30* as a candidate gene regulating maize responses to low temperature. The *ZmbHLH30* protein was localized in the cytoplasm of maize protoplasts, and the *ZmbHLH30* promoter drove beta-glucuronidase (GUS) expression in *Arabidopsis thaliana* leaves. The promoter region of *ZmbHLH30* contained multiple environmental stress-responsive elements, including motifs related to cold and auxin responses. Overexpression of *ZmbHLH30* significantly enhanced cold tolerance at the germination, bud, and seedling stages, with the strongest effect observed during germination, where the cold-tolerance *D*-value increased by 0.366 compared with the control. In contrast, CRISPR/Cas9 knockout lines showed a 0.399 decrease in *D*-value. Under cold stress, *ZmbHLH30* expression was strongly induced in overexpression lines but suppressed in knockout lines. [Conclusion] These results demonstrate that *ZmbHLH30* positively regulates cold tolerance during maize germination and provides a useful genetic target for improving early-stage cold tolerance in maize breeding.

Key words: Maize, Germination stage, Cold tolerance, *ZmbHLH30*, Functional verification

Funding acknowledgment: Natural Science Foundation Project of Heilongjiang Province (RC2025QN022 and YQ2022C009)

The E3 Ubiquitin-Protein Ligase *ZmBOIR3* is a Key Regulator of Low-Temperature Tolerance in Maize Seedlings

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Abstract: [Objective] Low-temperature stress severely restricts maize seedling growth and threatens crop establishment, yield formation, and production stability. This study aimed to identify key genetic factors controlling low-temperature tolerance in maize seedlings and to clarify the regulatory role of *ZmBOIR3*. [Method] Low-temperature tolerance at the seedling stage was evaluated in 299 maize inbred lines using the membership function method. Genome-wide association analysis was integrated with RNA-seq and metabolomic datasets to identify candidate genes, and RT-qPCR analysis was used to verify their stress-responsive expression. Functional evidence was further obtained using an ethyl methanesulfonate (EMS)-induced *zmboir3* mutant. [Result] Twelve SNPs significantly associated with low-temperature tolerance were detected. Integrated multi-omics analysis identified *ZmBOIR3*, which encodes an E3 ubiquitin-protein ligase, as a strong candidate gene. RT-qPCR confirmed that *ZmBOIR3* responded to low-temperature stress during seedling development. Multi-omics evidence suggested that *ZmBOIR3* may regulate secondary-metabolite accumulation and participate in plant hormone- and membrane-associated signaling. The *zmboir3* mutant showed markedly reduced tolerance under low-temperature stress, supporting the positive role of *ZmBOIR3* in cold adaptation. In addition, *ZmBOIR3* may act synergistically with *ZmMYB147* to regulate low-temperature tolerance in maize seedlings. [Conclusion] These findings indicate that *ZmBOIR3* is an important regulator of maize seedling tolerance to low-temperature stress and provide genetic information for improving cold tolerance in maize breeding.

Key words: Maize, Seedlings, Low-temperature tolerance, GWA, *ZmBOIR3*

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Single-Cell RNA Sequencing Resolves Cellular Responses during Waterlogging-Induced Adventitious Root Primordium Formation in Maize

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Abstract: [Objective] Previous phenotypic analyses showed that the waterlogging-tolerant maize inbred line T1162W initiated adventitious root primordia earlier and produced more adventitious roots than the sensitive line B73. This study aimed to characterize the cell-type composition and cellular responses associated with this phenotypic contrast during waterlogging-induced adventitious root primordium formation. [Method] Stem-base tissues of T1162W and B73 were collected before treatment (0 h) and at 6, 12, 18, and 24 h after the onset of waterlogging and profiled by single-cell RNA sequencing. Analyses included marker gene-based cell annotation, cell-frequency comparisons, functional enrichment, and integrated assessment of temporal changes and differences between genotypes. [Result] Marker gene expression profiles supported the annotation of 12 cell populations. Cell-frequency patterns highlighted founder-cell-like (FC), primordium-associated (ARC), and meristematic (MMC) states for detailed analysis. Functional enrichment in FC and ARC was dominated by metabolic regulation and RNA processing during early waterlogging, but shifted toward ribosomal processes and protein translation at 18–24 h, indicating a temporal transition in their functional signatures. Integrating time-series changes with differences between T1162W and B73 yielded nine candidate genes. [Conclusion] Multiple primordium-related cell states displayed distinct responses across treatment stages. These responses may be associated with genotypic differences in adventitious-root formation and waterlogging adaptation.

Key words: Maize, Waterlogging stress, Single-cell RNA sequencing, Adventitious root primordium, Cellular response

Mechanistic Dissection and Breeding Application of *ZmSNAC13* in Regulating Drought Stress Responses in Maize

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Abstract: [Objective] Maize is the most important staple crop in China, and its stable production and yield are increasingly threatened by the frequent occurrence of extreme drought and high-temperature events. NAC transcription factors constitute a plant-specific family that has been widely reported to participate in responses to drought and heat stress. *ZmSNAC13*, a member of the SNAC subfamily of NAC transcription factors, was previously demonstrated to enhance drought tolerance at the seedling stage in transgenic *Arabidopsis*. Therefore, this study aims to elucidate the complete molecular regulatory pathway underlying *ZmSNAC13*-mediated drought responses and to incorporate its superior allele into elite breeding lines through backcross breeding. [Method] Subcellular localization, transcriptional activation assays, seedling-stage and field drought tolerance evaluations, phylogenetic analysis, promoter variation analysis, backcross breeding, PEG-simulated drought treatment, and ABA-induced expression analyses were performed to investigate the biological function and regulatory mechanism of *ZmSNAC13*. [Result] *ZmSNAC13* was localized to the nucleus and exhibited transcriptional activation activity. Phenotypic evaluation of *ZmSNAC13* knockout mutants and overexpression lines at both the seedling and field stages revealed that knockout of *ZmSNAC13* reduced water retention capacity and antioxidant defense at the seedling stage, accompanied by decreased grain yield and chlorophyll content under field drought conditions, demonstrating that *ZmSNAC13* positively contributes to drought tolerance in maize. Expression pattern analysis further showed that *ZmSNAC13* was significantly induced by both drought and ABA treatments, suggesting that it may positively regulate drought tolerance through an ABA-dependent signaling pathway. Analysis of natural variation within the promoter region identified a large insertion/deletion (InDel) polymorphism in the drought-tolerant inbred line Qi319. This favorable promoter allele was associated with a higher drought tolerance index across multiple environments. Furthermore, the polymorphic region was predicted to contain binding sites for 21 stress-responsive transcription factors, including members of the ARF and bZIP families, suggesting that it may regulate stress responses through transcriptional regulation. [Conclusion] This study provides new evidence for understanding the stress-responsive regulatory mechanism of the maize SNAC subfamily. Further elucidation of the complete *ZmSNAC13*-mediated regulatory pathway and the introgression of its favorable allele into elite maize inbred lines will provide a solid theoretical basis and valuable germplasm resources for the genetic improvement of drought tolerance in maize.

Key words: Maize, *ZmSNAC13*, Drought tolerance, Breeding application

Climate-Resilient Maize Breeding for Modern Agriculture in Hilly Areas

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Abstract: [Objective] This presentation highlights maize breeding as a strategic approach to advancing modern agriculture in Thailand's hilly regions, where maize is a major feed crop but production is constrained by rugged terrain, limited mechanization, high labor requirements, and increasing climate variability. Most maize-growing areas in the highlands are rainfed and located outside irrigation systems, making them particularly vulnerable to drought stress. Rising temperatures, erratic rainfall patterns, and prolonged dry spells have become major challenges that negatively affect crop growth, yield, and production stability. Therefore, developing maize varieties with enhanced adaptation to highland environments, particularly drought tolerance, has become a key priority for sustaining maize production. [Method] Recent breeding programs have focused on the development of drought-tolerant maize through the evaluation of diverse germplasm resources, targeted selection, and multi-environment field testing under rainfed highland conditions. [Results] Drought-tolerant maize varieties have demonstrated the potential to maintain yield stability under water-limited conditions, improve production efficiency, and reduce risks associated with climate variability. Their adoption can contribute to increased farm productivity and enhanced economic returns for maize growers in hilly areas. [Conclusion] The development of climate-resilient maize varieties represents a sustainable and cost-effective strategy for strengthening maize production systems in Thailand's highlands. Furthermore, it offers opportunities for regional collaboration in maize breeding and climate adaptation research for hilly agroecosystems.

Key words: Maize breeding, Climate-resilient maize, Drought tolerance, Highland agriculture

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Growth and Recovery of Maize Seedlings under Single and Combined Drought and Saline-Alkali Stresses

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Abstract: [Objective] Drought, salinity, and alkalinity are major abiotic stresses limiting germination and seedling establishment in maize. This study evaluated the effects of single stresses (drought, neutral salinity, and alkaline salinity) and combined stresses (drought–salinity and drought–alkalinity) on germination, seedling growth, and recovery in hybrid maize varieties. [Method] Two single-cross hybrid maize cultivars were subjected to drought, neutral salinity, alkaline salinity, and their combinations, with germination indices, seedling morphology, photosynthesis, and oxidative stress markers assessed during stress and recovery. [Result] Drought reduced radicle emergence percentage (REP) from 99.6% to 61.6% and increased mean radicle emergence time (MRT) from 47.5 to 93.5 hours. Alkaline salinity severely affected seedling quality undetectable by REP alone. Combined stresses reduced REP by over 65% and increased MRT by over 125%. Drought–salinity showed antagonistic interactions on germination, while drought–alkalinity showed synergistic effects on REP. Drought–alkalinity caused the greatest reductions in shoot length (56.5% and 52.3%), root length (55%), and leaf electron transport rate (50%). During recovery, seedlings exposed to alkaline salinity and combined stresses failed to restore normal growth. Although photosynthesis recovered across all treatments, oxidative stress remained elevated in certain variety–treatment combinations, revealing a decoupling between photosynthetic and oxidative stress recovery. [Conclusion] Combined stress responses in maize are complex and governed more by stress mechanisms than stress intensity alone, and single indicators such as radicle emergence percentage are insufficient for fully assessing seedling establishment under alkaline salinity conditions.

Key words: Maize seed establishment, Multifactorial stress combination, Acclimation

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CIMMYT Tropical Maize Breeding in Latin America: Enhancing Productivity and Climate Resilience

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Abstract: [Objective] Maize is a crucial food crop for millions in Central America and Latin America, yet it increasingly faces threats from biotic and abiotic stresses exacerbated by climate change, jeopardizing the livelihoods of smallholder farmers. To adapt maize-based farming systems to these challenges, genetic improvement is essential. CIMMYT's breeding pipelines in Mexico focus on enhancing maize productivity in smallholder systems across Mexico, Central America, and the Andean regions, targeting average genetic gains exceeding 100 kg/ha annually. We implemented a data-driven inbred selection and recycling strategy, introduced temperate germplasm, and utilized predictive breeding techniques, which collectively enhanced grain yield by 2-5% over the mean of hybrids commercialized by local seed companies. This strategic incorporation of temperate germplasm increased genetic divergence (measured as F_{ST}) between tropical heterotic pools, thereby enhancing the yield potential of the hybrids. Our approach successfully identified competitive, stress-tolerant maize hybrids that showed significant performance improvements under stress in trials across various Central American environments. Moreover, the application of predictive breeding methods resulted in a 43% reduction in breeding cycle time, enabling us to better meet the growing demand for resilient maize varieties. These efforts have led to the successful commercialization of stress-tolerant maize hybrids by local seed companies in Latin America, with the elite inbred lines providing essential foundational germplasm for public and private breeding programs. Continued investment and innovation in maize breeding are vital for ensuring food security and enhancing the livelihoods of smallholder farmers, particularly as the impacts of climate change become more pronounced.

Key words: Maize, Genetic improvement, Predictive breeding, Stress tolerance, Temperate germplasm

Functional Characterization of ZmCHN3, a Chitinase Gene, in Maize Salt Tolerance

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Abstract: [Objective] Chitinase participates in plant defense and abiotic stress responses, yet its mechanism under salt stress remains unclear. Elucidating this mechanism is vital for understanding maize salt tolerance and molecular breeding. Here we functionally characterized ZmCHN3, a chitinase-encoding salt-tolerance candidate gene identified from transcriptome data. [Method] Gene family analysis, heterologous expression in pREP1 fission yeast and Arabidopsis, salt-stress phenotyping of maize ZmCHN3 mutants, yeast one-hybrid, transcriptional activation assay, RT-qPCR, yeast two-hybrid, and bimolecular fluorescence complementation (BiFC) were performed. [Result] ZmCHN3 belongs to the ZmCTL gene family, whose members respond to cold, heat, drought, and salt stress. Heterologous expression of ZmCHN3 significantly enhanced salt tolerance of pREP1 fission yeast and Arabidopsis. Maize mutants lacking ZmCHN3 function showed reduced salt tolerance, confirming that ZmCHN3 is a positive regulator. Transcription factors ZmEREB14 and ZmBBR4 interacted with the ZmCHN3 promoter; both were transcriptionally active and salt-responsive, indicating potential positive regulation of ZmCHN3. Four ZmCHN3-interacting proteins were identified: ZmCHN34 (chitinase), ZmEXO4 and Zm00001d013751 (cell wall synthesis/modification), and ZmPDK1 (a key C4 photosynthetic enzyme). Their encoding genes all responded to salt stress. These results suggest that ZmCHN3 may enhance salt tolerance by modulating cell wall architecture and energy metabolism. [Conclusion] This study preliminarily reveals the molecular mechanism by which ZmCHN3 positively regulates maize salt tolerance, and provides a promising elite gene for salt-tolerant breeding.

Key words: Introgression line, Salt tolerance, Chitinase

ZmQKI1 Modulates Circular RNA Biogenesis and Stability to Mediate Drought Response in Maize

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Abstract: [Objective] To investigate the function and molecular mechanism of the RNA-binding protein Quaking 1 (ZmQKI1) in the biogenesis of circular RNAs (circRNAs) in maize (*Zea mays*), particularly in the significant upregulation of circRNA expression under drought stress, and to provide novel insights and approaches for the research and application of molecular mechanisms underlying plant drought responses. [Method] Using nucleocytoplasmic fractionation sequencing of mutants, RIP-Seq, association analysis, EMSA, and FRAP to perform in vivo studies, and elucidate the molecular mechanism by which ZmQKI1 phase separation dynamically regulates circRNA metabolism. [Result] The number of back-splicing events in the coleoptile of the *ZmQKI1* mutant (*qki1-KH*) was significantly lower than that in wild-type plants, whereas no significant difference was observed in canonical splicing events (Student's t-test, $p < 0.01$). Under drought stress, *ZmQKI1* expression was significantly upregulated in maize roots. Combined analysis of circRNA enrichment sequencing and RIP-Seq confirmed that the majority of circRNAs directly regulated by ZmQKI1 were drought-induced, indicating that ZmQKI1 is a key regulator of the massive circRNA expression under drought stress. Phenotypic evaluation of drought tolerance revealed that *ZmQKI1* knockout lines exhibited reduced drought resistance, whereas overexpression lines showed enhanced drought tolerance, accompanied by increased numbers of lateral root primordia and root tips, suggesting that ZmQKI1 promotes lateral root development and positively regulates drought tolerance in maize. Further studies demonstrated that ZmQKI1 facilitates circRNA circularization by binding to flanking introns, as exemplified by *CircZmPOP10*. A 7-bp insertion in its upstream region contains the ZmQKI1 binding site, which is significantly associated with circRNA expression level, root tip number, and drought tolerance in the association panel. Moreover, overexpression of *CircZmPOP10* resulted in increased root tip number and enhanced drought resistance. Additionally, ZmQKI1 undergoes liquid-liquid phase separation (LLPS) and aggregates into stress granules under dehydration stress, whereas deletion of the intrinsically disordered region (IDR) abolishes its phase separation capacity. [Conclusion] This study constructs a ZmQKI1-circRNA-drought tolerance regulatory model from two perspectives: ZmQKI1-mediated intron binding to promote circularization, and phase separation to influence RNA stability. This work reveals a novel mechanism by which plants regulate circRNAs through RNA-binding proteins in response to abiotic stress, and provides theoretical support and genetic resources for molecular breeding of drought tolerance in maize.

Key words: *Zea mays*, Abiotic stress, RNA binding protein, Circular RNA, Liquid-liquid phase separation

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Molecular Mechanism of Maize MiR528 Enhancing Drought Tolerance via Balancing ROS Homeostasis by Targeting *ZmLAC5* and *ZmAo*

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Abstract: [Objective] Drought is a major abiotic stress limiting maize yield. miR528 is a conserved microRNA specific to monocots, playing important roles in development and stress responses. This study aims to elucidate the molecular mechanism by which maize miR528 balances reactive oxygen species (ROS) levels through regulating target genes *ZmLAC5* and *ZmAo*, thereby modulating stomatal movement and enhancing drought tolerance, and to explore its impact on the trade-off between drought resistance and yield. [Methods] We generated Zma-miR528 overexpression and knockout lines as well as *ZmLAC5* overexpression lines. Combined with drought treatments at seedling and adult stages, we performed drought tolerance phenotyping, stomatal aperture and water loss rate measurements, ROS detection via DAB/NBT staining and H₂O₂ fluorescence quantification. RT-qPCR, dual-luciferase reporter assays, and in vivo RNA pull-down were used to verify the interactions between miR528 and its targets, together with photosynthetic parameter and yield trait analyses. [Results] Overexpression of miR528 significantly reduced stomatal aperture and water loss rate and decreased the number of drought-induced dead leaves, while knockout lines showed opposite trends. ROS levels in leaves and guard cells were significantly elevated in overexpression lines and reduced in knockout lines. miR528 targeted both *ZmLAC5* and *ZmAo*, with target preference depending on ROS levels: preferential binding to *ZmLAC5* under high ROS and to *ZmAo* under low ROS. Overexpression of *ZmLAC5* suppressed ROS accumulation, increased stomatal aperture and water loss, and reduced drought tolerance. Yield analysis revealed that miR528 overexpression significantly decreased ear weight and grain weight per ear under both normal and drought conditions, whereas knockout lines showed significantly increased ear weight after drought; *ZmLAC5* overexpression also led to reduced seed setting and yield. [Conclusion] miR528 enhances maize drought tolerance by regulating *ZmLAC5* and *ZmAo* in an ROS-dependent manner to promote stomatal closure, albeit at the cost of yield. This study provides a theoretical basis for balancing drought tolerance and yield through miRNA engineering in maize.

Key words: Maize, MiR528, Drought stress, Reactive oxygen species, Stomatal movement, Yield trade-off

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Molecular Functional Analysis of a Maize Transcription Mediator Complex ZmMED16-Derived Circular RNA in Response to Drought Stress

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Abstract: [Objective] Drought is one of the most severe abiotic stresses limiting maize productivity worldwide. Identifying drought-responsive genes and elucidating their regulatory mechanisms are essential for developing drought-tolerant maize cultivars. Although circular RNAs (circRNAs) have emerged as important regulators of plant stress responses, their molecular functions remain largely unknown. We previously identified a drought-induced circular RNA, CircZmMED16, derived from the exons of the maize transcription mediator complex gene ZmMED16, through circRNA sequencing of maize inbred lines with drought tolerance. This study aimed to elucidate the molecular function and regulatory mechanism of CircZmMED16 in maize drought tolerance. [Methods] The spatiotemporal expression pattern and subcellular localization of CircZmMED16 were determined by qRT-PCR and fluorescence localization assays. Transgenic maize lines overexpressing (OE) or knocking down (KD) CircZmMED16 were generated to evaluate drought tolerance at both seedling and adult stages. RNA pull-down, RNA immunoprecipitation (RIP), electrophoretic mobility shift assay (EMSA), yeast two-hybrid (Y2H), and bimolecular fluorescence complementation (BiFC) assays were performed to characterize the interaction between CircZmMED16 and polyamine oxidase (PAO). Physiological and biochemical analyses were conducted to investigate the downstream regulatory pathway. [Results] CircZmMED16 exhibited distinct spatiotemporal expression patterns, with the highest abundance in the root apical meristem at the seedling stage, broad expression during silking, and preferential accumulation in tassels and roots during grain filling. It was predominantly localized in the cytoplasm and lacked protein-coding potential. Overexpression of CircZmMED16 significantly enhanced drought tolerance, post-rewatering survival, and grain yield under drought, whereas KD plants displayed increased drought sensitivity, impaired root development, and reduced ear yield. Multiple independent assays demonstrated that CircZmMED16 specifically binds PAO, which is localized to the plasma membrane and peroxisomes and functions as a monomer. Under drought stress, OE plants exhibited reduced PAO activity, increased spermidine, proline, and superoxide dismutase (SOD) levels, together with moderate H₂O₂ accumulation, whereas KD plants showed the opposite physiological responses. Mechanistically, CircZmMED16 is proposed to compete with flavin adenine dinucleotide (FAD) for PAO binding, thereby suppressing PAO catalytic activity. [Conclusions] CircZmMED16 positively regulates maize drought tolerance by directly interacting with PAO to inhibit its enzymatic activity, thereby reducing polyamine catabolism.

Key words: Zea mays, Drought stress, CircZmMED16, Polyamine oxidase, Reactive oxygen species homeostasis

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MaizeMind: A Deep Learning Architecture for Genomic Selection in Maize Drought Tolerance Breeding

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Abstract: [Objective] Genomic selection (GS) accelerates genetic gain in crop breeding, yet conventional linear models capture only a limited share of the nonlinear gene–environment interactions ($G \times E$) that dominate performance under abiotic stress. In this study, we develop and evaluate a deep learning (DL) architecture, MaizeMind, for multi-trait genomic prediction in maize under well-watered (WW) and water-stressed (WS) conditions, and applies it to data-driven hybrid design. [Methods] A diversity panel of 185 maize inbred lines was genotyped with 26,939 SNP markers and phenotyped for three core traits — anthesis-silking interval (ASI), plant height, and ear weight — across WW and WS trials. MaizeMind was trained as a multi-trait, multi-environment model and benchmarked against two classes of baselines: machine-learning regressors (Random Forest, SVM, XGBoost) and linear-genetic models (GBLUP, rrBLUP). The trained model was then deployed to predict 9,634 single-cross hybrid combinations, with K-means and agglomerative hierarchical clustering used to partition parental lines and prioritise complementary heterotic groups. [Results] MaizeMind outperformed all five baselines on every trait–environment combination. Under WW conditions, prediction accuracy reached $r = 0.735$ ($R^2 = 0.468$) for plant height and $r = 0.829$ ($R^2 = 0.599$) for ear weight; under WS, the model retained predictive power for ear weight ($r = 0.79$), confirming that nonlinear $G \times E$ signals learned in WW transferred to stress conditions. From the 9,634 in silico hybrids, 254 high-yield combinations with predicted yields in the top 10% were selected for field validation. These combinations exhibited moderate drought tolerance overall, with an average drought tolerance index (DTI) of 0.97. Notably, Tropical $\times$ Tropical crosses showed relatively higher predicted DTI values. [Conclusion] MaizeMind delivers consistent gains over conventional GS models for multi-trait prediction under both optimal and drought-stress conditions, and the WW/WS prediction pair provides a tractable digital pipeline for stacking stress tolerance with yield in maize hybrid breeding.

Key words: Genomic Selection, Deep Learning, Maize Breeding, Drought Stress, Multi-trait prediction

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Responses of Pre-Fertilization Pollen and Silk Biological Characteristics to Salt-Alkali Stress in Maize Varieties with Different Levels of Tolerance

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Abstract: [Objective] Salt-alkali stress is a major environmental factor limiting maize growth and yield formation. It reduces yield primarily by decreasing ear grain number, which is largely determined by the seed-setting success rate. Pollen and silks are essential reproductive organs in the pollination and fertilization process; their physiological activity and functional integrity directly determine pollination success and grain yield. [Method] This study utilized maize varieties with varying levels of salt-alkali tolerance as experimental material. Salt-alkali-tolerant varieties were XY335 and DD1331, and salt-alkali-sensitive varieties were JK968 and JSH2468. Two field conditions were established: saline-alkali land (SA) and non-saline-alkali land (CK). The effects of salt-alkali stress on the biological characteristics of pollen and silks prior to fertilization were investigated; the mechanisms by which salt-alkali stress influences seed-setting rate were elucidated. [Result] Under salt-alkali stress, tassel morphological traits of salt-alkali-sensitive varieties declined significantly ($p < 0.05$): tassel branches decreased by 22.73%, tassel length by 12.35%, tassel diameter by 12.33%, and the number of spikelets by 12.84%. The anthesis-silking interval increased by 1.45 days ($p < 0.05$). Pollen viability and germination rate decreased by 8.83% and 56.25%, respectively. Additionally, silk viability decreased, and silk number declined by 20.56% ($p < 0.05$). In salt-alkali-tolerant varieties, tassel length decreased by 5.30%, and pollen germination rate substantially declined (56.70%); other indicators showed no significant differences relative to CK. Ultimately, the seed-setting rate significantly declined across all varieties under salt-alkali stress, with reductions of 17.17% in salt-alkali-tolerant varieties and 21.95% in salt-alkali-sensitive varieties. [Conclusion] Overall, reduced pollen viability was the primary constraint on seed-setting rate in low-tolerance varieties, whereas reduced pollen germination was the main limiting factor in high-tolerance varieties. These findings provide a theoretical framework for breeding salt-alkali-tolerant maize. Future selection should prioritize screening for high pollen germination rates in tolerant varieties, while enhancing basal pollen viability in sensitive varieties.

Key words: Maize, Salt-alkali stress, Pollen, Silks, Seed-setting rate

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Methyl Jasmonate Alleviates Heat Stress-Induced Impairment of Female Ear Differentiation in Summer Maize

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Abstract: [Objective] Heat stress during ear differentiation severely disrupts floret development, fertilization, and kernel establishment in summer maize, often causing major yield losses. This study investigated how exogenous methyl jasmonate (MeJA) improves heat tolerance during reproductive growth and explored the underlying physiological mechanisms. [Method] Field trials were conducted from 2023 to 2024 using the summer maize hybrid Xianyu 335. Plants were subjected to five days of heat stress at two critical ear differentiation stages, V9 (small trumpet) and V12 (large trumpet). Based on a preliminary concentration test, 1 mmol L⁻¹ MeJA was applied after the heat stress period. We then assessed ear morphology, fertilization and seed-setting traits, endogenous hormone profiles, antioxidant enzyme activities, and oxidative damage indicators. [Result] MeJA application reshaped hormonal balance within developing ears: it elevated levels of trans-zeatin plus trans-zeatin riboside (tZ + tZR), jasmonic acid (JA), and salicylic acid (SA), while suppressing abscisic acid (ABA) accumulation. This shift created a more favorable physiological environment for floret development under heat stress. Concurrently, MeJA boosted antioxidant capacity, as shown by higher activities of superoxide dismutase (SOD), peroxidase (POD), and catalase (CAT), along with lower malondialdehyde (MDA) content. These coordinated responses mitigated heat-induced oxidative damage, promoted ear morphogenesis and floret differentiation, improved silk emergence and fertilization success, and reduced kernel abortion. As a result, kernels per ear and grain yield per plant increased by 48–57% and 49–67%, respectively, compared with the heat-stressed control. Correlation analyses further supported these observations: higher JA and cytokinin levels, stronger antioxidant enzyme activities, and lower oxidative damage were closely linked to better ear development, fertilization efficiency, and yield formation. Notably, MeJA's protective effects were generally more pronounced when heat stress occurred at the V9 stage than at the V12 stage. [Conclusion] Our results show that MeJA alleviates heat-induced reproductive damage through a multi-layered regulatory mechanism involving hormonal reprogramming, activation of antioxidant defenses, and coordinated improvements in ear development and reproductive success. These findings offer new insights into the physiological basis of maize reproductive thermotolerance and highlight MeJA as a promising agronomic tool to stabilize summer maize yields under projected climate warming.

Key words: Heat stress, Fertilization and seed setting characteristics, Hormones, Antioxidant enzyme, Yield

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Pangenome-Wide Identification, Evolutionary Analysis of Maize ZmPLD Gene Family, and Functional Validation of *ZmPLD15* in Cold Stress Tolerance

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Abstract: [Objective] Phospholipase D (PLD) genes play key roles in plant abiotic stress responses, but the systematic identification of maize (*Zea mays* L.) PLD family and its cold tolerance mechanism remain unclear. [Method] Twenty-six maize pangenomes were used to identify 21 *ZmPLD* family genes via HMM search of the PF00614 domain, including five unique genes to avoid gene omission from single reference genomes. Phylogenetic analysis compared PLD conservation among maize, Arabidopsis and rice, and Ka/Ks analysis evaluated gene selection pressure. Five shared structural variations (SVs) with ERF/bHLH binding sites were detected in the *ZmPLD15* promoter; SVs in Region 1 and Region 5 significantly regulate its expression. Protein structure prediction and molecular docking confirmed conserved *ZmPLD15* conformation and stable binding energy with its substrate across germplasms. *ZmPLD15*-overexpressing transgenic maize with B73 background was generated. Three-leaf seedlings of transgenic and wild-type (WT) plants underwent 6 h cold stress at 8–10 °C and 24 h recovery. Leaf cell integrity was observed, and photosynthetic indicators (Pn, Gs, Tr, Ci) were measured to assess cold tolerance. [Result] Most *ZmPLD* genes underwent purifying selection, while *ZmPLD15* and two other genes showed positive selection signals related to maize domestication adaptation. *ZmPLD15* protein features were highly conserved in different germplasms. After cold treatment, transgenic maize had better leaf cell integrity than WT. Transgenic lines retained 45.8% Pn, 47.9% Gs and 55.8% Tr, versus only 7.6%, 21.3% and 13.8% in WT, with balanced Ci levels. In conclusion, *ZmPLD15* enhances maize cold tolerance by protecting photosynthetic systems. This study provides a systematic research framework for the *ZmPLD* family and a key functional gene for cold-tolerant maize breeding. [Conclusion] *ZmPLD15* enhances maize cold tolerance by protecting photosynthetic systems, providing a framework for *ZmPLD* research and a key gene for cold-tolerant maize breeding.

Key words: *Zea mays* L., *ZmPLD15*, Pangenome, Cold tolerance, Photosynthetic system protection

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Alginate Oligosaccharides Enhance Acid Tolerance in Maize Through Phenylpropanoid-mediated Root Lignification

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Abstract: [Objective] Soil acidification is a major worldwide constraint on crop production, and roots are the primary site of proton and aluminum rhizotoxicity, yet how exogenous biostimulants remodel root metabolism to improve acid stress tolerance remains poorly understood. This study aimed to determine whether and how alginate oligosaccharides (AO) enhance acid stress tolerance in maize (*Zea mays* L.) roots, testing the hypothesis that AO redirect carbon away from non-specific polysaccharide deposition toward phenylpropanoid-mediated cell wall lignification in a spatially organized manner across root cell types. [Method] Maize seedlings were grown in soil adjusted to pH 5.8 (control) or pH 3.8 (acid stress), with or without AO supplied at a 1:1000 dilution, and a complementary hydroponic experiment was used to assess root cellular integrity. Growth and root morphological phenotyping, plant nitrogen and endogenous phytohormone determination, relative electrolyte leakage and transmission electron microscopy, and quantification of lignin, callose and uronic acid were combined with untargeted metabolomics, bulk transcriptomics (RNA-seq) and single-cell RNA sequencing (scRNA-seq) of root tips to resolve cell-type-specific responses. [Result] Relative to the pH 5.8 control, acid stress at pH 3.8 reduced plant height, shoot dry weight, total root length and root dry weight by 14.3%, 30.4%, 31.1% and 31.8%, respectively, whereas AO largely restored these traits, lowered relative electrolyte leakage by 24.19%, preserved root ultrastructure, enhanced nitrogen acquisition, and elevated cis-zeatin, indole-3-acetic acid and indole-3-butyric acid. Metabolomic and transcriptomic profiling converged on starch–sucrose metabolism and phenylpropanoid biosynthesis: AO attenuated the acid-induced accumulation of trehalose, UDP-D-glucose and sucrose together with their biosynthetic transcripts (*ZmTPS1*, *ZmUGPA*, *ZmSUS7*), while activating *ZmPAL1*, *ZmCYP73A14*, *CCR1* and *ZmPER1/12/54*, so that callose and uronic acid declined whereas lignin accumulated. scRNA-seq of 14622 root cells resolved 11 cell types and localized the AO-induced *ZmCYP73A14* response to the epidermis, whereas the acid- and aluminum-tolerance genes *ZmMATE1*, *ZmNRAMP4* and *ZmSTOP1-A* were activated in the cortex and endodermis. [Conclusion] Phenylpropanoid-mediated cell wall lignification is a spatially organized mechanism of AO-enhanced acid stress tolerance in maize roots, in which AO reroutes root carbon from non-specific polysaccharide deposition toward targeted wall lignification, deploying the phenylpropanoid programme in the epidermis while partitioning ion-detoxification machinery across the cortex and endodermis. These findings support AO as a residue-free biostimulant for sustainable maize production on acidic soils and provide cell-type-resolved targets for breeding acid-tolerant maize.

Key words: Maize, Acid stress, Alginate oligosaccharides, Phenylpropanoid biosynthesis, Single-cell RNA sequencing, Root lignification

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Identification of Heat Stress-responsive Co-expression Modules and Hub Genes in Maize Leaves Using WGCNA

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Abstract: [Objective] To identify core genes closely associated with heat stress regulatory pathways and stress-resistance traits, and to provide new insights into the molecular mechanisms underlying heat tolerance in maize. [Method] A heat-tolerant inbred line, PHBA6, and a heat-sensitive inbred line, Ji63, were used as experimental materials. Plants were grown under both field and greenhouse conditions, and heat stress was imposed at the early flowering stage. Based on transcriptome sequencing, the molecular response characteristics of leaf from the two genotypes under heat stress were systematically compared. [Result] A total of 3,318 differentially expressed genes (DEGs) were identified in PHBA6, whereas 2038 DEGs were detected in Ji63 under heat stress. Weighted gene co-expression network analysis (WGCNA) was further performed to construct gene co-expression networks associated with stress-resistance phenotypic traits, resulting in the identification of 16 gene modules significantly correlated with tassel heat tolerance. Among them, four modules showing the strongest correlations with target traits were selected, and a set of potential key genes was screened. These genes were mainly involved in transcriptional regulation, protein homeostasis maintenance, reactive oxygen species metabolism, and stress signal transduction. [Conclusion] This study systematically revealed the key regulatory network characteristics of maize leaf under heat stress and identified a group of core genes closely associated with heat tolerance and their potential regulatory pathways. The findings provide new theoretical support for elucidating the molecular mechanisms of heat tolerance during the reproductive stage in maize and offer valuable genetic resources for heat-tolerant germplasm improvement and molecular breeding.

Key words: Maize, Heat stress, Weight gene co-expression network, Transcriptome

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***ZmEREB182* Negatively Regulates *ZmCAND2* to Mediate Melatonin-Dependent Flooding Tolerance in Maize**

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Abstract: [Objective] Flooding is a major abiotic stress that severely restricts maize growth and productivity by disrupting photosynthesis, impairing stomatal function and inducing excessive oxidative damage. Although the melatonin receptor *ZmCAND2* has been implicated in plant stress adaptation, its upstream transcriptional regulation remains largely unknown. This study aimed to identify the upstream regulator of *ZmCAND2* and elucidate its role in melatonin-mediated stomatal regulation and flooding tolerance in maize. [Method] Yeast one-hybrid (Y1H) library screening identified *ZmEREB182* as a direct upstream regulator of *ZmCAND2*, which was validated by dual-luciferase (LUC) and electrophoretic mobility shift assays (EMSA). To assess its physiological function, WT, *cand2*, *ereb182*, *CAND2-OE*, and *EREB182-OE* plants were flooded with or without melatonin, and subsequently examined for stomatal morphology, gas exchange, and oxidative stress parameters. [Result] Subsequent Y1H, LUC and EMSA consistently demonstrated that *ZmEREB182* directly binds to the *ZmCAND2* promoter and represses its transcriptional activity. Flooding markedly impaired photosynthetic performance, resulting in decreases of 61.93%, 77.98% and 4.82% in net photosynthetic rate, stomatal conductance and the maximum quantum efficiency of PSII, respectively, while non-photochemical quenching increased by 42.23%. Meanwhile, flooding triggered excessive accumulation of H₂O₂ and O₂⁻, markedly suppressed CAT and SOD activities, and induced pronounced stomatal closure, collectively indicating severe oxidative damage and photosynthetic inhibition. Melatonin significantly alleviated oxidative damage, restored photosynthetic performance, and promoted stomatal functional recovery in WT, *CAND2-OE*, and *ereb182* plants. In contrast, *cand2* and *EREB182-OE* plants exhibited greater flooding sensitivity and little or no physiological response to melatonin, indicating that disruption of *ZmCAND2* signaling largely abolishes melatonin-mediated protection. [Conclusion] *ZmEREB182* functions as an upstream transcriptional repressor of *ZmCAND2* and negatively regulates melatonin signaling during flooding stress. *ZmCAND2*-dependent melatonin perception alleviates flooding-induced oxidative damage, preserves photosynthetic capacity and subsequently promotes stomatal functional recovery, thereby enhancing flooding tolerance in maize. These findings establish the *ZmEREB182-ZmCAND2* regulatory module as a previously unrecognized mechanism linking melatonin perception with stomatal adaptation under flooding stress and provide promising molecular targets for the genetic improvement of flooding tolerance in maize.

Key words: Flooding tolerance, Melatonin perception, *ZmCAND2*, *ZmEREB182*, Stomatal function, Reactive oxygen species

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Grain Proline: Relation with Maize (*Zea mays* L.) Yield under Managed Drought Conditions

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Abstract: Proline accumulation act as osmoprotectant during water stress, is another critical trait linked to drought resilience. Positive correlation between proline levels and drought tolerance underscoring the importance of genetic diversity. Maize vats genetic diversity is a cornerstone for addressing its vulnerability to drought stress. The present investigation ensure stable productivity and strengthen global food security in the face of climate change. The twenty five genotypes including two checks were arranged in randomized block design with two replications during rabi season at AICRP on Maize Kasba Bawda, Kolhapur farm in Maharshtra state. The experiment was conducted to evaluate the impact of drought stress on various maize genotypes. The key observations included days to tasseling and silking, plant height, cob traits, kernel rows and grain yield. Protein and proline content were assessed by standard biochemical methods. The 27 Maize genotypes were grouped into ten clusters, with Clusters I being the largest (16 genotypes). Based on cluster means, VH1846, VH2052, VH18614, VH19182, and P3302 are ideal for future hybridization. A cross between VH1846 and VH2025 is recommended for maximum yield. Genotypes VH171336, VH201078, and VH201228, with low proline, are drought-susceptible, while VH18614, VH19182, and CAH1511, with high proline, are drought-tolerant, highlighting proline as a key drought resilience indicator. Intra-cluster distances in maize ranged from 7.92 to 8.68, with mono-genotypic clusters (II, III, IV, VI, VII, VII, IX, X) showing no variation. Inter-cluster distances ranged from 7.86 (Clusters II and IX) to 22.97 (Clusters V and VI), indicating distinct differences between clusters. Clusters means revealed significant variation in 13 traits. Cluster III was earliest in tasseling (69 days) and silking (71.50 days), while Cluster IX was the latest (76.50 and 78.50 days respectively). Cluster IX had the tallest plants (137.40 cm), while Cluster III had the shortest (163.18 cm). Cob length and width peaked in Clusters VI (23.40 cm) and VII (16.05 cm), respectively. Clusters VI and VII showed the highest and lowest kernel rows per cob (18 and 12.60), while Cluster V had the highest kernels per row (38). Yield per plant was highest in Cluster VI (190.97 g) and lowest in Cluster IX (118.79 g). Proline content, yield, and 100-kernel weight were the largest contributors to genetic divergence, followed by cob width and protein content. Moderate contributions came from kernel rows, kernels per row, and days to 50% tasseling, while cob traits and plant height had smaller impacts.

Key words: Maize, Drought, Proline, Correlation, Cluster, Genetic diversity

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Heat Use Efficiency as a Physiological Indicator for Identifying Climate-Resilient Maize (*Zea mays* L.) Genotypes under Variable Thermal and Weather Conditions

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Abstract: Climate variability poses a significant challenge to sustainable maize production, necessitating the identification of genotypes capable of maintaining productivity under contrasting thermal environments. A field experiment involving 84 diverse maize genotypes was conducted during the *rabi* season of 2025–26 at the Zonal Agricultural Research Station, Shenda Park, Kolhapur, India, using Randomized Block Design with two replications. The study aimed to evaluate the relationships among thermal indices, genotype-specific weather parameters and grain yield to identify physiological traits associated with climate resilience. Analysis of variance confirmed highly significant ($P < 0.01$) genotypic differences for days to 50% tasseling, days to 50% silking and grain moisture, indicating substantial genetic variability in crop phenology and maturity. Growing Degree Days (GDD), Heliothermal Units (HTU), Photothermal Units (PTU), Sunshine Degree Days (SDD) and Heat Use Efficiency (HUE) were computed, while genotype-specific weather variables were derived for the actual phenological periods from sowing to physiological maturity. Grain yield exhibited weak positive correlations with GDD at tasseling ($r = 0.214$), silking ($r = 0.195$) and physiological maturity ($r = 0.194$), HTU ($r = 0.189$), PTU ($r = 0.194$) and SDD ($r = 0.187$), whereas genotype-specific weather variables, including mean maximum temperature ($r = 0.182$), mean minimum temperature ($r = 0.198$), total rainfall ($r = 0.166$), morning relative humidity ($r = 0.137$), bright sunshine hours ($r = 0.137$) and mean evaporation ($r = 0.199$), also showed weak, non-significant associations with grain yield ($P > 0.05$). Afternoon relative humidity ($r = -0.052$) and wind speed ($r = -0.161$) were weakly negatively correlated with yield. In contrast, Heat Use Efficiency exhibited an exceptionally strong positive correlation with grain yield ($r = 0.994$, $P < 0.0001$), demonstrating that the efficiency with which genotypes convert accumulated thermal resources into economic yield is a more reliable determinant of productivity than thermal accumulation or seasonal weather alone. Multiple regression using thermal indices explained only 5.5% of the variation in grain yield ($R^2 = 0.055$; $P = 0.342$), further indicating the limited predictive ability of thermal indices in isolation. The study demonstrates that Heat Use Efficiency is a robust physiological trait for identifying climate-resilient maize genotypes, whereas accumulated thermal indices and seasonal weather variables alone provide limited discrimination among genotypes grown under similar environmental conditions. These findings provide a practical framework for selecting thermally efficient and climate-adaptive maize germplasm to support resilient production systems under future climate variability.

Key words: Maize (*Zea mays* L.), Heat use efficiency, Thermal indices, Growing degree days, Weather parameters, Phenology, Grain yield, Climate-resilient genotypes

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Waterlogging Duration Determines Root Adaptation and Whole-plant Resource Allocation in Waxy Maize: Differential Regulation by Exogenous Melatonin

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Abstract: [Objective] With the continued progression of global warming, extreme weather events have become more frequent. Rising temperatures accelerate glacier melting and sea level rise, further intensifying the global water cycle and increasing the frequency and severity of heavy rainfall and flooding events. The increase in heavy rainfall often saturates soil water-holding capacity, resulting in waterlogging, which severely impairs the growth and yield of food crops and threatens the sustainable development of agriculture. Globally, approximately 27% of arable land is affected by flooding each year, negatively impacting over 20% of irrigated areas, with this trend continuing to rise. Although waterlogging-induced growth inhibition in maize and the stress-alleviating effects of melatonin have been widely reported, most studies are limited to common maize under single-duration stress. The responses of waxy maize to different waterlogging durations and the mitigating effects of melatonin remain largely unclear. [Method] In this study, waxy maize plants at the jointing stage were subjected to waterlogging for 2, 4, 6, 8, and 10 d, with a non-waterlogged treatment as the control, and were foliar-sprayed with 0 or 100 μM exogenous melatonin. The growth escape and compensatory mechanisms of waxy maize under different waterlogging durations, as well as the regulatory role of melatonin, were systematically analyzed. [Result] The results showed that short-term waterlogging (2–6 d) markedly promoted the development of fine roots (≤ 1 mm), increasing root length, surface area, and volume, and enhancing root bleeding rate, with root growth and nutrient accumulation peaking at 6 d. In contrast, prolonged waterlogging significantly inhibited root growth. Short-term waterlogging induced compensatory increases in plant height, ear height, and stem diameter, whereas aboveground growth was progressively suppressed with increasing waterlogging duration. Waterlogging altered stem structure by increasing epidermal thickness and vascular bundle number and enlarging bundle sheath area, partially enhancing stem mechanical strength; however, waterlogging ≥ 6 d caused xylem deformation and impaired transport function. Waterlogging significantly shifted source–sink relationships, driving preferential allocation of dry matter and nitrogen to roots at the expense of aboveground organs. Exogenous melatonin further enhanced root growth and nutrient accumulation under short-term waterlogging but did not alleviate aboveground growth inhibition and intensified assimilate allocation to roots. [Conclusion] Overall, waxy maize exhibits physiological compensation under short-term waterlogging, whereas prolonged stress leads to structural damage and functional disorder, and the regulatory benefits of melatonin on whole-plant growth coordination are limited.

Key words: Waterlogging, Waxy maize, Root growth traits, Dry matter accumulation, Exogenous melatonin

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Response of Ear Development and Yield Components of Different Heat-Resistant Maize Cultivars to High Temperatures During the Ear Growth Cone Elongation Stage

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Abstract: [Objective] High temperature stress has become a key limiting factor for the yield stability of summer maize in the Huang-Huai-Hai region during the elongation of the ear growth cone. However, the mechanisms that lead to differences in heat tolerance among different genotypes are not yet clear. [Method] This study aims to investigate the effects of high temperature stress during the panicle elongation stage on photosynthetic characteristics, panicle development, antioxidant enzyme activity, endogenous gibberellin content, yield components, and their intrinsic correlations using the heat-resistant variety "Zhengdan 958" (ZD958) and the heat-sensitive variety "Jiyu 3421" (JY3421). [Result] Compared with the long-term baseline of extreme high-temperature days (daily maximum temperature $\geq 38^{\circ}\text{C}$) during 2004–2015 (0.5 d), the annual frequency of such extreme thermal events exhibited a pronounced increasing trend across 2016–2025 (Table 1). The results showed that high temperature significantly reduced the SPAD value of the ear leaves, shortened the peak grain filling period, and exacerbated ear deformities (Figure 1). JY3421 showed an average decrease of 24.3% in seed setting rate and an increase of 74.2% in ear malformation rate; while ZD958 maintained a stable seed setting rate and a slight degree of malformation (Figure 2). Heat stress significantly reduced the number of kernel rows per ear and the number of kernels per ear in JY3421, yet it had no significant effect on the 100-grain weight in either variety (Figure 3). At the same time, high temperature significantly increased the activity of SOD and POD in the panicle organs and decreased the content of GA_4+GA_7 ; among them, the physiological fluctuation of JY3421 was more drastic (Figure 4). Correlation analysis showed that the ear deformity rate and GA_4+GA_7 content were significantly negatively correlated with yield; while SPAD value, antioxidant enzyme activity, number of rows per ear, and number of grains per ear were significantly positively correlated with yield. [Conclusion] In summary, high temperature stress during the spike elongation stage inhibits leaf photosynthesis, disrupts the antioxidant system and hormone balance, damages spike differentiation, and reduces the number of grains per spike, ultimately leading to yield loss. ZD958 maintains its heat resistance and yield stability by maintaining stable photosynthetic capacity, ear development, and physiological homeostasis. This study provides a theoretical basis and excellent germplasm resources for heat-resistant breeding and high-yield cultivation of maize under future climate warming scenarios.

Key words: Cultivar, Ear development, Growth cone elongation stage, High temperature, Yield

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***ZmCOL14* Coordinates the Regulation of Flowering Time and Plant Height in Maize**

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Abstract: [Objective] Flowering time and plant height are two critical agronomic traits in maize that jointly determine yield potential and production stability. This study investigates the genetic basis underlying their coordinated regulation and identifies key loci for breeding improvement. [Method] Genome-wide association studies (GWAS) pinpointed *ZmCOL14* as a major regulator of flowering time. We generated overexpression and knockout lines to evaluate its pleiotropic effects, and applied ChIP-seq and RNA-seq to uncover downstream regulatory pathways. [Result] Multi-year, multi-location surveys of 237 maize accessions confirmed *ZmCOL14* as a key flowering-time regulator. Overexpression delayed flowering and reduced plant height, while knockout accelerated flowering and increased height via altered cell elongation. Integrative analyses identified *ZmCCA1b* and *ZmHY5* as downstream targets, validated by qRT-PCR. [Conclusion] *ZmCOL14* coordinates the regulation of flowering time and plant height by modulating multiple downstream genes, offering new insights into the molecular control of agronomic traits and providing valuable targets for maize breeding.

Key words: Maize (*Zea mays* L.), Flowering, Plant height

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Ear Type Determines Yield Component Responses and Density Adaptation Strategies in Summer Maize

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Abstract: [Objective] The increase in maize (*Zea mays* L.) yield largely depends on the improvement of planting density, but the response mechanisms of different ear-type varieties to density and the optimal density thresholds remain insufficiently quantified. [Method] Based on the multi-site experiments in the Huang-Huai-Hai Plain from 2024 to 2025, a total of 21 maize varieties with small ear, medium ear and large ear were selected. The response differences of yield components to density were systematically analyzed under the density gradient of $1.5\text{--}15 \times 10^4$ plants·ha⁻¹, and the optimal density threshold of each ear type was determined by nonlinear model fitting. [Result] Yield was significantly and positively correlated with kernel number (KN) across all ear types ($r = 0.863\text{--}0.926$). Standardized regression analysis further showed that the contribution of KN ($\beta = 1.247\text{--}1.367$) was substantially greater than that of thousand-kernel weight (TKW, $\beta = 0.482\text{--}0.702$), indicating that grain yield under high-density conditions was primarily driven by KN. Increasing planting density significantly reduced kernels number per ear (KNE) and TKW in all ear types; however, the magnitude of these reductions differed markedly among ear types. Small-ear varieties maintained higher ear-formed rates and greater kernel number stability under high-density conditions, thereby sustaining increases in KN and achieving greater yield potential. In contrast, large-ear varieties were more sensitive to increasing density, exhibiting pronounced declines in ear-formed rate and KNE, which resulted in earlier yield plateaus and lower optimum planting densities. Medium-ear varieties displayed intermediate responses. Bootstrap analysis further demonstrated that the 95% confidence intervals of the optimum planting density were clearly separated among the three ear types, confirming distinct density adaptation strategies. [Conclusion] Ear type determines maize density adaptation by regulating the trade-off between population ear establishment and KN stability, thereby controlling KN and optimum planting density. These findings reveal the physiological basis of ear type-specific density adaptation and provide theoretical support for precision density management to improve maize productivity and resource-use efficiency.

Key words: Maize, Ear type, Planting density, Yield components, Density adaptation

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Physiological Responses and Yield Formation of Summer Maize under Combined High Temperature and Water Stresses at Tasseling Stage

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Abstract: [Objective] Extreme high temperature, drought, and waterlogging stresses exacerbated by global warming severely restrict maize productivity. The tasseling stage is a critical, stress-sensitive period that determines yield formation in summer maize, during which co-occurring high temperature and water stresses exert synergistic inhibitory effects on plant growth and development. [Method] Field soil column pot experiments were carried out from 2022 to 2024 with the summer maize cultivar Denghai 605 as the test material. Six stress treatments were imposed at the tasseling stage : ambient temperature with adequate soil moisture as the control (CK), single drought (D), single waterlogging (W), single high temperature (T), combined high temperature and drought (TD), and combined high temperature and waterlogging (TW). A suite of key physiological and yield related indicators were systematically measured, covering leaf gas exchange parameters, chlorophyll fluorescence kinetics, photosynthetic pigment concentrations, antioxidant enzyme activities, dry matter partitioning, sucrose and starch metabolic enzyme activities, and yield components, to reveal the regulatory mechanisms of the diverse stresses on maize growth and grain yield formation. [Result] T, D, and W disrupted the photosynthetic apparatus of summer maize, significantly reducing the net photosynthetic rate, PSII photochemical efficiency, and photosynthetic pigment accumulation. These stresses suppressed SOD, POD, and CAT activities, triggering excessive reactive oxygen species accumulation and irreversible photooxidative damage to leaves. Combined TD and TW stresses produced prominent additive inhibitory effects, with TW causing the most severe growth impairment. Water related stresses reduced total dry matter accumulation and reshaped biomass allocation, increasing partitioning to vegetative organs while reducing allocation to grains. Combined stresses further inhibited core sucrose metabolizing enzyme activities, delayed sucrose accumulation peaks, hindered photosynthate translocation to grains, and decreased grain starch deposition. Drought reduced yield mainly by decreasing kernel number per ear , whereas waterlogging impaired yield by lowering the 1000 kernel weight, and high temperature emerged as the dominant factor causing severe yield loss. Compared with CK, the grain yields of T, TD, and TW treatments decreased by 72.0%, 75.1%, and 77.9%, respectively. [Conclusion] Co-occurring high temperature and water stresses at the tasseling stage constrain dry matter production and partitioning in summer maize by impairing photosynthetic carbon assimilation, blocking photosynthate translocation, and restraining grain starch deposition, thereby causing substantial yield loss. This study clarifies the core physiological pathways underlying stress induced suppression of photosynthetic assimilation and photosynthate translocation, providing robust theoretical support for stabilizing summer maize yield in warming agroecological regions.

Key words: Summer maize, Tasseling stage, High temperature stress, Water stress, Photosynthetic physiology, Yield formation

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Stage-Dependent Response of Maize Grain Formation to Shading, Waterlogging, and Their Combination: Insights From

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Abstract: [Objective] Climate change has been demonstrated to increase the frequency of complex abiotic stresses in the future, of which the combination of shading and waterlogging caused by persistent rainfall is an important limiting factor affecting maize grain formation and yield. [Method] We investigate grain loss in summer maize induced by shading, waterlogging, and their combined stresses at different stages, and how these stresses affect floret differentiation and floret setting. Maize hybrid Denghai 605 (DH605) was chosen as the test material, with three stress treatments: shading (S), waterlogging (W), and their combined stress (SW) for 6 days at the sixth leaf stage (V6) and tasseling stage (VT). Net photosynthetic rate, plant growth rate, floret differentiation, fertilization characteristics, and ovary development were investigated. [Result] Results showed that shading, waterlogging, and their combined stress during the V6 stage significantly reduced photosynthetic capacity and leaf growth, delayed the ear elongation and led to a decrease in total floret number. Additionally, the decreased floret setting rate during the reproductive growth stage further exacerbated grain loss. Pollen viability and silking rate were more sensitive to shading, waterlogging and the combined stresses imposed at VT than at V6, reducing floret fertilization rate. Additionally, the reduction in starch content in the ovary increased the risk of post-fertilization abortion by an average of 40.6%-67.1%, representing the highest proportion among the other two causes of kernel loss (loss from silking and fertilization) analyzed. Waterlogging at V6 stage was the dominant factor affecting summer maize yield (whereas at VT was shading), and combined stresses showed greater losses compared to single stresses. The yield of V6-SW and VT-SW was decreased by 11.3% and 2.9%, respectively, compared to the S treatment in the same period; and by 2.0% and 12.6%, respectively, compared to the W treatment in the same period. [Conclusion] These findings provide new insights into the responses of maize grain formation to shading, waterlogging, and their combination at different growth stages, and highlight that reducing post-fertilization ovary abortion is an important research objective for mitigating yield losses in maize under persistent rainy conditions.

Key words: Maize, Abiotic stress combination, Photosynthetic characteristics, Ear development, Grain number.

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Evaluation of Thermal Indices and Heat Use Efficiency of Maize (*Zea mays* L.) Genotypes under Winter Season of Western Maharashtra in India

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Abstract: A field experiment was conducted during the *rabi* season of 2025–26 at the Zonal Agricultural Research Station, Shenda Park, Kolhapur, Maharashtra, India. Eighty-four maize genotypes were sown on 27 November 2025 and evaluated for phenological development and grain yield. Agro-meteorological indices, namely Growing Degree Days (GDD), Helio Thermal Units (HTU), Photo Thermal Units (PTU), and Stress Degree days (SDD), were computed from sowing to 50% tasseling, 50% silking, and 50% physiological maturity using daily weather data. Heat Use Efficiency (HUE) was estimated by relating grain yield to accumulated GDD at physiological maturity. Among the different climatic factors temperature influenced on end product i.e. yield. Quantification of thermal indices provides valuable insights into crop development and genotype adaptation under specific agro-climatic conditions. Correlation analysis revealed weak positive associations of grain yield with GDD, HTU, Photo PTU and SDD, with correlation coefficients ranging from 0.187 to 0.214. These relationships were not statistically significant ($P > 0.05$), indicating that variation in accumulated thermal indices alone was insufficient to explain the observed differences in grain yield among the 84 maize genotypes. In contrast, Heat Use Efficiency (HUE) exhibited a highly significant and strong positive correlation with grain yield ($r = 0.994$, $P < 0.0001$), suggesting that genotypes with superior efficiency in converting accumulated thermal resources into grain achieved higher productivity under the prevailing agro-climatic conditions. The results revealed substantial genetic variability in thermal accumulation and thermal use efficiency among the evaluated genotypes. Grain yield varied from 3.70 to 10.22 t ha⁻¹, with an average of 6.75 t ha⁻¹. Heat Use Efficiency ranged from 2.12 to 5.74 kg ha⁻¹ °C day⁻¹, with a mean value of 3.93 kg ha⁻¹ °C day⁻¹. Genotypes exhibiting higher HUE produced greater grain yield under comparable thermal environments, demonstrating superior efficiency in converting accumulated heat units into biomass and grain production. The study indicates that thermal indices can effectively characterize genotype performance and can serve as reliable criteria for identifying climate-resilient and high-yielding maize genotypes. These findings will be useful for maize improvement programmes and for developing weather-based crop management strategies under changing climatic conditions.

Key words: Maize, Drought, GDD, Heliothermal units, Photothermal units, Heat use efficiency.

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Evaluation of Maize (*Zea mays* L.) Genotypes Using Agrometeorological Indices and Heat Use Efficiency under Field Conditions

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Abstract: Temperature is one of the most important environmental factors influencing crop growth, phenological development, and productivity. A field experiment comprising 1200 experimental maize genotypes was conducted during the *rabi* season (26 November 2025 to 15 April 2026) at the Zonal Agricultural Research Station (ZARS), Shenda Park, Kolhapur, Maharashtra, India. The study aimed to quantify seasonal thermal indices and evaluate grain yield performance under prevailing weather conditions. Agrometeorological indices such as Growing Degree Days (GDD), Heliothermal Units (HTU), Photothermal Units (PTU), Sunshine Degree Days (SDD), and Heat Use Efficiency (HUE) are widely used to evaluate crop response to thermal environments and identify superior genotypes. The present investigation was conducted to assess the thermal requirements and productivity of sixty maize (*Zea mays* L.) genotypes under managed drought at field conditions. Thermal indices were computed from sowing to 50% tasseling, 50% silking, and physiological maturity using daily weather data, while grain yield, plant height, grain weight, and Heat Use Efficiency were recorded at harvest. Considerable variability was observed among the evaluated genotypes for thermal accumulation and yield performance. The GDD requirement for physiological maturity ranged from 1592.95 to 1738.10 °C days, indicating significant variation in maturity duration among the genotypes. Among the entries, genotype MGE000016080803 required the highest thermal accumulation to attain 50% tasseling (1008.00 °C days, 5601.46 HTU, 11358.77 PTU, and 46.10 SDD), 50% silking (1051.60 °C days, 5876.93 HTU, 11865.34 PTU, and 54.30 SDD), and physiological maturity (1738.10 °C days, 10601.31 HTU, 20071.02 PTU, and 266.70 SDD), suggesting a comparatively longer crop duration. In contrast, early-maturing genotypes attained these phenological stages with lower thermal accumulation. Grain yield varied from 6025.61 to 12412.61 kg ha⁻¹, whereas Heat Use Efficiency ranged from 2.94 to 6.07 kg ha⁻¹ °C day⁻¹. Genotype MGE000015875616 recorded the highest grain yield (12412.61 kg ha⁻¹) and Heat Use Efficiency (6.07 kg ha⁻¹ °C day⁻¹), followed by MGE000016317860 (11834.82 kg ha⁻¹; 5.78 kg ha⁻¹ °C day⁻¹), VH22501 (11789.36 kg ha⁻¹; 5.76 kg ha⁻¹ °C day⁻¹), and VH22615 (11597.90 kg ha⁻¹; 5.67 kg ha⁻¹ °C day⁻¹). The observed variation in thermal indices and Heat Use Efficiency demonstrates the differential ability of maize genotypes to utilize accumulated thermal resources for grain production.

The results indicate that agrometeorological indices are effective tools for characterizing phenological behaviour and identifying high-performing maize genotypes under specific thermal environments. Genotypes exhibiting higher grain yield and superior Heat Use Efficiency can serve as promising candidates for varietal improvement and breeding programmes aimed at enhancing productivity and climate resilience under changing climatic conditions.

Key words: Maize, GDD, Heliothermal units, Photothermal units, Heat use efficiency, Thermal time, Climate resilience, Crop weather.

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Integrated Multi-Environment and Multi-trait Analyses Reveal Key Determinants of Heat Tolerance and Yield Stability in Tropical Maize

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Abstract: [Objective] Climate change-induced heat stress has emerged as a major constraint limiting maize productivity worldwide, particularly during the reproductive stage. This study aimed to: (1) quantify the magnitude of genotype $\times$ environment interaction (GEI) for grain yield, flowering behavior (days to anthesis, days to silking, and anthesis–silking interval [ASI]), chlorophyll content, and associated yield components using Restricted Maximum Likelihood (REML) linear mixed-model (LMM) ANOVA; (2) determine the morpho-physiological traits that consistently explain and predict heat tolerance and yield stability across highly variable environments; and (3) deploy multi-trait selection tools to identify elite, heat-resilient maize genotypes in a diverse panel of maize evaluated across three distinct heat-vulnerable environments. [Method] Forty-seven tropical maize genotypes were evaluated under natural heat stress across three contrasting agro-climatic locations in India (Varanasi, Kolhapur, and Godhra). Ten agronomic and morpho-physiological traits, including flowering phenology, canopy injury (leaf firing and tassel blast), pollen viability, field weight, and grain yield, were recorded. Variance components were estimated using REML-based linear mixed models, while AMMI and GGE biplot analyses were employed to characterize GEI patterns, genotype adaptation, and test-environment efficiency. Genotype selection was optimized using the Weighted Average of Absolute Scores and Yield (WAASBY) and the Multi-Trait Genotype–Ideotype Distance Index (MGIDI). [Result] Environmental effects accounted for 51.04% of the total grain-yield variation, whereas highly significant crossover GEI (17.97%; $P < 0.001$) confirmed pronounced differential genotypic responses across heat-stress environments. GEI explained 41.88% and 42.35% of the total variation in days to anthesis and days to silking, respectively, demonstrating that heat stress primarily disrupted flowering synchrony, while substantial interaction effects for leaf firing (29.80%) and tassel blast (21.38%) highlighted strong environmental influences on canopy injury. AMMI partitioned the interaction into two significant principal components (IPCA1 = 71.60%, IPCA2 = 28.40%), whereas the GGE biplot captured 90.30% of the total G + GE variation, identifying Kolhapur as the most discriminating and Godhra as the most representative testing environment. Genotype G31 recorded the highest grain yield, while G37 exhibited the greatest environmental stability (WAASB = 0.027). Integrating productivity with stability through WAASBY identified G31, G46, G37, G28, and G29 as the most desirable broadly adapted genotypes. Complementarily, MGIDI selected seven elite ideotypes (G21, G15, G20, G27, G44, G34, and G22) that simultaneously combined higher pollen viability, synchronized flowering, reduced leaf firing and tassel blast, and stable grain yield. This selection resulted in predicted genetic gains of 13.89% for grain yield, 12.42% for field weight, and 9.04% for pollen viability, together with reductions of

15.13% in leaf firing and 13.88% in tassel blast. [Conclusion] The study demonstrates that maintenance of reproductive synchrony, pollen viability, and canopy integrity constitutes the primary biological basis of heat tolerance in tropical maize. Integrating REML-based mixed models with AMMI, GGE biplot, WAASBY, and MGIDI effectively distinguished superior genotypes by simultaneously optimizing productivity, environmental stability, and adaptive physiological traits. The identified elite genotypes represent valuable climate-resilient breeding materials and provide an efficient analytical framework for accelerating the development of heat-tolerant tropical maize hybrids.

Key words: *Zea mays* L., Heat stress, Genotype $\times$ Environment interaction, AMMI, GGE, Biplot, WAASBY, MGIDI

Effects and Optimization of Deliduo and Ethephon on Dehydration and Yield of Maize in Cold Regions

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Abstract: [Objective] In cold regions, the grain moisture content of maize at harvest is generally high, making it difficult to meet the requirements for mechanical grain harvesting. To address this prominent issue and resolve the core contradiction between high yield dependent on a long growth period and machine harvesting dependent on low moisture content, this study investigated the regulatory effects of foliar application of the plant growth regulators Deliduo and ethephon at different stages on maize dehydration and yield. The aim was to identify the optimal application strategy and provide a theoretical basis and technical support for fully mechanized high-yield cultivation of maize in cold regions. [Method] Using the maize variety Jinboshi 825 as the test material, a two-factor split-plot design was employed with three spraying timings at 10d (T1), 20d (T2), and 30d (T3) after silking, and five concentration gradients for Deliduo (D1~D5) and ethephon (E1~E5), respectively. Systematic measurements were taken for green leaf number, leaf area, dry matter accumulation and partitioning, contribution rate of dry matter to grain, grain moisture content, grain-filling characteristics, and yield components. The grain-filling process was fitted using the Logistic equation, and the significance of treatment effects was determined by analysis of variance. [Result] Spraying medium-to-high concentrations of Deliduo (D3~D5) at 20 d after silking significantly delayed leaf senescence, increased dry matter accumulation and its contribution to grains, enhanced grain-filling rate, and increased kernel number per ear and 100-kernel weight. The maximum yield reached 13767.70 kg/ha, which was 9.46% higher than that of the control, while reducing grain moisture content at harvest by 1.7 percentage points. Spraying at 10 d after silking significantly increased yield but showed no significant dehydration effect compared with CK. Spraying low-to-medium concentrations of ethephon (E1~E3) at 30 d after silking effectively induced leaf senescence, accelerated grain dehydration, and reduced grain moisture content by 2.64~3.54 percentage points relative to the control, while increasing grain-filling rate by 7.8%~22.1% and improving yield by 4.37% without significant yield loss. Although spraying ethephon at 10 d after silking had a notable dehydration effect, it caused a significant yield reduction, with a maximum decrease of 5.59%. [Conclusion] Spraying Deliduo at D3~D5 concentrations at 20d after silking effectively promotes yield while reducing late-stage grain moisture content, whereas spraying ethephon at E1~E3 concentrations at 30d after silking effectively accelerates ripening and dehydration while increasing yield. Both combinations achieve a synergistic integration of yield improvement, grain moisture reduction, and maximized economic benefits. These represent the optimal application strategies for auxiliary pre-harvest dehydration of maize in cold regions. Under the premise of maintaining or even increasing maize yield stability, these treatments significantly lower grain moisture content at harvest, reduce drying costs and mechanical harvesting losses, and enhance planting profitability, thereby providing an effective approach to resolving the contradiction between high yield and mechanical harvesting in cold-region maize production.

Key words: Maize, Deliduo, Ethephon, Grain moisture content, Yield

Genetic Variability, Thermal Requirements and Heat-Use Efficiency of Maize Genotypes Under Winter-Season Conditions

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Abstract: A field experiment was conducted during the winter season of 2025–26 at Kolhapur (M.S.), India, to study the yield performance, genetic variability, thermal requirement and heat use efficiency of 60 maize genotypes. The experiment was designed in randomized block with 60 Maize genotypes replicated twice at 60 × 20 cm spacing.

The significant genotypic differences were observed for male flowering, female flowering, anthesis–silking interval and thermal indices accumulated up to flowering. Among the evaluated genotypes, MGE000016080803 recorded the highest thermal accumulation at physiological maturity, requiring 1,738.10°C days GDD, 10,601.31°C day-hours HTU, 20,071.02°C day-hours PTU and 266.70°C days SDD. Grain yield ranged from 60.26 to 124.13 q ha⁻¹, with an overall mean of 89.54 q ha⁻¹. Genotype MGE000015875616 recorded the highest grain yield (124.13 q ha⁻¹) and the highest corrected HUE (7.55 kg ha⁻¹ °C⁻¹ day⁻¹). The first four principal components accounted for 76.05% of the total multivariate variation. The cluster analysis were classified into three genotypes groups. Among the all genotypes, MGE000015875616, MGE000016317860, VH22501 and MGE000016317848 were identified as a promising genotypes in relation to grain yield, HUE, anthesis–silking interval, shelling percentage and ear-placement ratio. These genotypes may be useful in breeding programmes targeting high yield, favourable phenology and efficient utilization of thermal resources under winter-season environments.

Key words: Maize, Genotypes, Thermal requirements, GDD, Heliothermal units, Photothermal units, Heat-use efficiency, Grain yield

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Genetic Control of Maize Flowering Synchrony under Drought Stress

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Abstract: [Objective] Drought severely threatens maize yield stability, especially during flowering. As a monoecious species, its pollination and seed set depend on the synchronous development of male and female inflorescences. Drought, however, often disrupts this synchrony, resulting in a prolonged anthesis–silking interval (ASI) and substantial yield loss. This report presents our recent research progress on genetic dissection of maize drought resilience. [Method] Through QTL mapping, we cloned a quantitative trait locus qDR9 and identified ZmSAUR72, additionally, the pan-genome analysis of 25 newly assembled and 31 existing maize genomes. [Result] ZmSAUR72 promotes silk growth by activating H⁺-ATPase activity. This shortens ASI and stabilizes yield under drought. Revealed the natural variations in ZmASI3 are associated with ASI prolongation under drought stress. The functional transcript of ZmASI3 acts as a chromatin remodeler and confers drought resilience at the flowering stage by alleviating ASI extension. [Conclusion] Thus, the finding offers new insights into the genetic control of maize drought resilience and provides strong candidate genes to breed maize cultivars with enhanced yield stability under water-deficit conditions.

Key words: Maize, Drought resilience, Flowering synchrony, Yield, Gene Cloning

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Identification of heat-tolerance maize inbred lines

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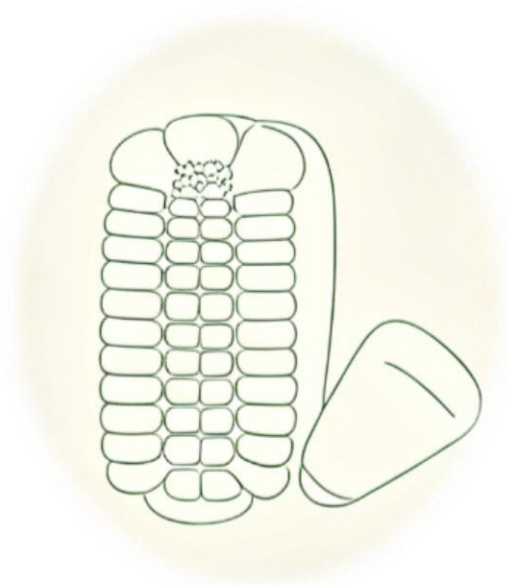
Abstract: [Objective] Heat stress is a major constraint to current and future maize production worldwide. Many traits associated with male and female reproductive organs play important roles in increasing kernel number (KN) under heat stress at flowering, but their contributions to KN under heat stress remains unclear. Besides, heat-tolerant resources are limited, and efficient identification is urgently needed. [Method] In this study, a two-year field experiment including two sowing dates per year and 325 inbred lines was conducted. Traits related to male and female reproductive organs and KN were measured under both heat stress and control condition. [Result] Pollen viability, silk emergence ratio, and anthesis–silking interval (ASI) were the key determinants of KN under heat stress, and their correlation coefficients were 0.87^{***}, 0.63^{***}, and −0.69^{***}, respectively. Based on the kernel number reduction (KNR) between heat stress and control conditions across two years, 325 inbred lines were classified into three groups: heat-tolerant group with 20 inbred lines (KNR below 10%), moderately heat-tolerant group with 74 inbred lines (KNR below 30% and beyond 10%), and heat-sensitive group with 231 inbred lines (KNR beyond 30%). The pollen viability and silk emergence ratio of heat-tolerant group was significantly higher than those in the other two groups, whereas ASI was significantly lower. [Conclusion] We have identified some heat-tolerant maize inbred lines characterized by higher pollen viability and silk emergence ratio, and shorter ASI under heat stress. These lines could serve as valuable resources for breeding heat-tolerant maize varieties.

Key words: Maize, heat stress, kernel number, heat-tolerant, anthesis–silking interval

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Technical Session 5

Nutritional Security through Biofortification and Quality Enhancement



Postharvest Hydro-Cooling for Quality Retention of Sweet Corn Ears

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Abstract: [Objective] The objective of this study was to determine the effectiveness of hydro-cooling in retaining quality of sweet corn ears. [Method] Freshly harvested sweet corn ears were immersed in hydro-cooler to achieve its ½ half and 7/8 cooling time (CT). Pre-cooled and non-pre-cooled ears were then stored at 12±2 and 25±2 °C for 8 days and quality index, weight loss, pH, soluble solids concentration, titratable acidity and ascorbic acid of ears were evaluated at 2 days interval. The experiment was arranged in randomized complete block design with factorial arrangement (three cooling times × two storage temperatures × five storage days) and then repeated thrice. [Result] Differences between cooling time × storage temperature, cooling time × storage day, storage temperature × storage day, and cooling time × storage temperature × storage day significantly affected the quality index of sweet corn ears. Storage temperature × storage day interaction also significantly influenced ear weight loss, soluble solids concentration, and pH. The deterioration of sweet corn ear quality over extended storage was clearly observed. Kernels from all treatments remained turgid with fresh green husks during the first two days of storage at both 12±2 and 25±2 °C. However, by day 4, kernel denting became apparent in most treatments except for ears treated with 7/8 CT and stored at 12±2 °C. Non-hydro-cooled ears maintained acceptable quality for only about four days at 12±2 °C and two days at 25±2 °C. Overall, 7/8 CT combined with storage at 12±2 °C provided the best ear quality, retained higher soluble solids concentration and pH, and resulted in significantly lower weight loss compared to other treatments. [Conclusion] This study demonstrated that hydro-cooling treatment at 7/8 CT followed by storage at 12 ± 2 °C preserves the quality of sweet corn ears more effectively than 1/2 CT. However, hydro-cooling to 1/2 CT is sufficient to preserve ear quality for short-distance markets and short-term storage. Further studies are needed to determine the optimum storage temperature for Malaysian sweet corn varieties.

Key words: Cooling time, Pre-cooling, Quality index, Storage day, Storage temperature

Agronomic Zinc Biofortification of Maize: Integrating Rhizosphere Processes, Plant Traits, and Grain Partitioning for Improved Nutritional Quality

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Abstract: [Objective] This study aimed to develop an integrated framework for zinc (Zn) biofortification of maize by combining agronomic management, rhizosphere processes, and plant physiological traits. It focused on improving grain Zn concentration and bioavailability while maintaining yield. The study also examined how fertilizer strategies, beneficial microbes, root traits, and internal Zn partitioning contribute to better nutritional quality in maize-based systems. [Method] The study synthesized evidence from multi-location field experiments and systems-based analysis. Multi-environment field trials were conducted under contrasting soil conditions. The study evaluated soil and foliar Zn application combined with Zn-solubilizing and plant growth-promoting microorganisms. It assessed root system traits such as root depth, branching, and root hair development, along with rhizosphere processes including organic acid exudation. Physiological analyses were used to study Zn uptake, translocation, and partitioning into grain tissues. Grain quality was further assessed in terms of Zn concentration, protein content, and phytic acid levels. [Result] Targeted Zn fertilization significantly increased grain Zn concentration. Microbial inoculation improved Zn solubilization, uptake efficiency, and transport to grains. Genotypes with deeper and more branched root systems showed better Zn acquisition under low Zn availability. Organic acid exudation, especially citrate and malate, enhanced Zn mobilization in the rhizosphere. Efficient remobilization from vegetative tissues and stronger partitioning into embryo and endosperm improved final grain Zn density. Reduced phytic acid levels increased predicted Zn bioavailability. Integrated management increased grain Zn concentration by 20–55% without yield loss, and some treatments also improved grain protein and kernel quality. [Conclusion] The study shows that effective Zn biofortification in maize requires a systems approach that links soil management, microbial activity, and plant physiological traits. Combining agronomic inputs with improved root and rhizosphere functioning enhances Zn uptake, transport, and grain enrichment. This integrated strategy offers a practical solution to reduce micronutrient deficiency and improve nutritional security in maize-based food systems.

Key words: Zinc solubilizing microorganisms, Rhizosphere organic acids, Root architecture traits, Phytic acid reduction, Grain zinc bioavailability

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Green Extraction of Bioactive Compounds from Organic Corn Silk Waste using Deep Eutectic Solvent and Ultrasound-Assisted Extraction

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Abstract: [Objective] This study aimed to optimize the extraction of phenolic compounds, flavonoids, and antioxidant substances from organic corn silk, an agricultural waste by-product, using ultrasound-assisted extraction combined with deep eutectic solvents (DES), and to evaluate its potential for health-related applications. [Method] Organic corn silk was collected from an organic maize field, dried at 45°C for 48 h, and ground into powder. The extraction process was optimized using a single-factor experiment based on a completely randomized design (CRD) with three replications. Four DES formulations were evaluated, including choline chloride: citric acid (2:1 M), choline chloride: lactic acid (1:2 M), lactic acid: glucose (2:1 M), and choline chloride: citric acid: glycerol (0.5:0.5:2 M). The effects of DES molar ratio, DES concentration (25, 45, 65, 85, and 100% v/v), extraction time (5–30 min), and sample-to-solvent ratio (1:10–1:120 g/mL) on extraction efficiency were investigated. Total phenolic content, total flavonoid content, and antioxidant activities were determined as response variables. [Result] The extraction efficiency varied significantly ($p < 0.05$) among DES formulations and extraction conditions. The DES composed of choline chloride and citric acid was identified as the most effective extraction solvent for recovering bioactive compounds from organic corn silk. The optimal extraction conditions were obtained using choline chloride and citric acid at a molar ratio of 1:1, diluted with 45% water, an extraction time of 20 min, and a sample-to-solvent ratio of 1:110 (g/mL). Under these conditions, the highest total phenolic content, total flavonoid content, and antioxidant activities as determined by DPPH and ABTS assays were achieved, indicating the significant influence of solvent composition and extraction parameters on bioactive compound recovery. [Conclusion] Ultrasound-assisted extraction combined with deep eutectic solvents represents an efficient and environmentally friendly technology for valorizing organic corn silk, a maize processing by-product, into high-value bioactive ingredients. The optimized process supports post-harvest value addition, promotes sustainable utilization of maize-derived waste, and provides opportunities for developing innovative nutraceutical, functional food, and cosmeceutical products, thereby contributing to the diversification and economic development of the maize value chain.

Key words: Bioactive compounds, Antioxidant activities, Choline chloride–citric acid, Green extraction

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Toxicity of Vip Proteins to Maize Stem Borer, *Chilo Partellus* (Swinhoe) and Its larval Parasitoid, *Bracon Hebetor* Say

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Abstract: [Objective] The baseline susceptibility, sub-lethal effects and non-target toxicity of Vip3Aa70, Vip3Aa71 proteins and the Bt formulation Dipel 8L against *Chilo partellus* and its larval parasitoid *Bracon hebetor* under controlled laboratory conditions at PAU, Ludhiana, India (2024-25) were studied. [Method] Bioassays using field populations from Ludhiana and Hoshiarpur, India showed that Dipel 8L was the most toxic ($LC_{50} \approx 1.38-1.40$ ppm), while Vip3Aa70 and Vip3Aa71 exhibited moderate toxicity ($LC_{50} \approx 4.17-5.18$ ppm). LC_{90} values were also lower for Dipel 8L (42.68-53.62 ppm) compared to Vip proteins (62.39-83.28 ppm) at both the locations. The comparatively higher toxicity of Dipel 8L may be attributed to the complementary and combined action of multiple Bt toxins present in the formulation, which enhances its effectiveness against *C. partellus*. Sub-lethal exposure to Bt proteins influenced the biological parameters of *C. partellus*. At LC_{50} , the larval duration was significantly prolonged from 19.47 or 20.43 days in control to 26.45, 26.73 and 25.20 days in Dipel, Vip3Aa70 and Vip3Aa71 protein. [Result] Larval weight were also declined after the exposure of Dipel, Vip3Aa70 and Vip3Aa71 treated larvae, weighing 22.01, 25.53 and 28.86 mg lower than their controls (68.64-79.25 mg). Pupal duration increased from 7.26 days in the control to 9.23-10.87 days across Dipel 8L and both the proteins. Male pupal size were reduced from 10.34-13.68 mm in controls to 7.20-7.62 mm across Bt treated proteins, while female size reduced from 12.68 mm to 10.48 mm. Adult emergence of Bt proteins declined at LC_{50} (48.25-63.33%) compared with 85.50-91.36 per cent in the controls. Fecundity dropped from over 219.27-258.75 eggs in controls to 134-164 eggs in Dipel and both the proteins. Bt protein exposure had mild non-target toxicity on larval parasitoid *B. hebetor* with cocoon size and weight remaining unaffected. [Conclusion] Cocoon formation and adult emergence showed slight reductions of about 7.65 and 10.56 per cent, respectively. These findings support the integration of Vip3Aa-based bio insecticides into sustainable maize IPM strategies.

Key words: Baseline susceptibility, *Bracon hebetor*, *Chilo partellus*, Dipel 8L, LC_{50} , Non-target toxicity, Sub-lethal, Vip proteins

Developing Climate-Resilient Maize Hybrids with Elevated Provitamin A

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Abstract: [Objective] This study aimed at development of a biofortified version of climate-resilient maize hybrid, RCRMH-2. [Method] Marker-assisted backcross breeding was employed using donor lines received from CIMMYT; the favorable *crtRB1* allele was used for foreground selection and 97 KASP SNP markers and 3305 DArT-Tag SNP markers were used for background selection to improve CAL-1514 and CML-451, the parental lines of the climate-resilient maize hybrid, RCRMH-2. [Result] The biochemical estimation of BC₃F₂ progenies of CAL-1514 and CML-451 showed increased β -carotene levels ranging from 4.97–6.44 $\mu\text{g/g}$ and 4.77–5.86 $\mu\text{g/g}$, respectively. Whereas, the β -carotene in original parental lines (CAL-1514 and CML-451) was 0.19 $\mu\text{g/g}$ and 0.13 $\mu\text{g/g}$, respectively. Further, evaluation of 60 new hybrid combinations involving improved provitamin A, across three different environments led to the identification of five hybrids better than or equal to RCRMH-2. [Conclusion] The top five hybrids namely RCRMH-2 β +8, RCRMH-2 β +13, RCRMH-2 β +18, RCRMH-2 β +46, and RCRMH-2 β +58 are undergoing further evaluation for heat tolerance and provitamin A content for their potential deployment as climate-resilient biofortified maize hybrids.

Key words: Biofortification, Climate resilience, *CrtRB1* allele, Marker-assisted backcrossing, Provitamin A

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Effect of Zinc Fertilization on Maize Productivity and Soil Microbial Diversity across Paddy Soils with Different pH Levels

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Abstract: [Objective] Zinc (Zn) deficiency limits maize production in paddy soils. This study evaluated Zn fertilizer strategies across different soil pH to improve nutrient management and soil microbial responses. [Method] Two field experiments were conducted in Chon Daen (pH 5.8) and Lom Sak (pH 7.8), Thailand, using a factorial randomized complete block design with four ZnSO₄·H₂O rates (0, 5, 10, and 20 kgZn/ha) applied at the V6 stage, and two maize hybrids (Suwan 5731 and Suwan 5819). [Result] Moderate Zn application (10 kg Zn/ha) consistently improved maize grain yield and soil Zn availability across contrasting soil pH levels. SW 5819 with 10 kg Zn/ha yielded 7% more than SW 5731 without Zn, whereas no significant yield response occurred at Lom Sak. Soil microbial community composition was primarily determined by soil pH rather than Zn fertilization. *Singulisphaera*, *Abditibacterium*, *Setophoma*, and *Sarocladium* showed a significant positive correlation with soil Zn availability. [Conclusion] These findings demonstrate that Zn fertilization can improve maize productivity without altering soil microbial community composition, supporting site-specific Zn management for sustainable maize production in paddy soils.

Key words: Maize, Zn fertilizer, Zn availability, Soil pH, Soil microbial community

Funding acknowledgment: This research was supported by the Graduate School, Kasetsart University, and the Graduate School of Bioagricultural Sciences, Nagoya University, and the Agricultural Research and Development Agency grant 2021 (grant no. PRP6405032480) and Tyson Foods, Inc.

Soil pH, Zinc Management, and Soil Biological Communities as Pillars of Regenerative Maize Production in Thailand

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Abstract: [Objectives] Thailand's maize sector supplies the animal feed industry that underpins the country's chicken meat exports, yet long-term productivity is constrained by soil degradation in rice-based cropping systems. [Method] Through a decade of collaborative research, our group has pursued a progressive understanding of these constraints from field agronomy to soil ecology to plant physiology converging into a regenerative agriculture (RA) framework for sustainable maize production. We first established that variety choice and soil pH govern both agronomic performance and root-zone microbial structure, with Suwan 5819 emerging as the platform variety best suited to paddy soil conditions. [Result] This guided our investigation into zinc management across contrasting soil pH environments, where calibrated Zn application enhanced grain yield and nutritional quality while soil microbial communities shaped primarily by pH rather than fertilization remained ecologically resilient. Deepening our inquiry to the plant-microorganism interface, we found that arbuscular mycorrhizal symbiosis behaves in context-dependent, sometimes counterintuitive ways under phosphorus and zinc limitation, cautioning against blanket biological inoculation without nutrient diagnosis. Each body of knowledge built upon the last, revealing that productivity, soil health, and feed grain quality are inseparable outcomes of the same decisions. [Conclusion] The RA framework we propose centered on precision Zn nutrition, soil pH management, and ecology-informed biological stewardship simultaneously advances productivity, feed quality, and greenhouse gas emission reduction, positioning Thai maize-fed poultry production to meet the environmental and quality benchmarks of global export markets.

Key words: Regenerative agriculture, Zinc fertilization, Paddy soil pH, Soil microbial community, Maize

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Sensory Acceptability of Corn Grits as a Rice Substitute Among Consumers in San Andres, Quezon, Philippines

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Abstract: The promotion of corn grits as a viable staple substitute requires understanding consumer preferences in regions with established consumption habits. [Objective] This study was to evaluate the sensory profiles and overall consumer preference of three distinct maize accessions against a traditional rice control to identify key drivers of sensory acceptability. [Method] A sensory evaluation was conducted on June 2, 2026, with a panel of 33 habitual corn grits consumers in San Andres, Quezon. The four treatments included an Asian Corn Borer Resistant (ACBR) composite, IPB Var6, APN 426, which was a yellow corn accession, and a sinandomeng rice that served as a control. Panelists assessed the samples using ordinal ranking and preference profiling across seven attributes: aroma, color, flavor, gloss, hardness, stickiness, and overall acceptability. The data were analyzed using the Friedman test, pairwise Wilcoxon signed-rank post-hoc testing, and Principal Component Analysis (PCA). [Results] Analysis of the ranking data revealed a statistically significant preference for the corn grit substitutes over the traditional rice control ($p < 0.001$). Post-hoc testing identified a co-dominance at the top tier between the ACBR flint-type and IPB Var6. PCA of the preference profiles indicated that while general acceptability drove overarching trends, texture—specifically hardness—was the primary differentiator between the top-performing lines. The ACBR flint-type demonstrated broad mass appeal with consistently high, balanced scores, likely delivering a familiar hard-endosperm bite. In contrast, IPB Var6 secured its top-tier rank by appealing to a specific demographic preferring a softer grit texture. [Conclusion] Both the ACBR and IPB Var6 maize accessions proved to be highly acceptable, superior substitutes to Sinandomeng rice for this demographic. The distinct textural divergence between the two top performers highlights the importance of targeted breeding. These findings strongly warrant the commercial advancement and localized deployment of both lines in corn-consuming regions.

Key words: Sensory evaluation, Preference profiling, Corn grits, Rice substitute, Consumer preference, Texture.

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Enhancing the Freeze-Thaw Stability of Maize Starch via Targeted Mutation of Both *Waxy1* and *Sugary2*

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Abstract: [Objective] This study aimed to enhance the freeze-thaw stability of maize starch through targeted mutagenesis of starch biosynthesis genes. [Method] We constructed a CRISPR/Cas9 vector co-expressing Cas9 and two sgRNAs targeting *Waxy1* and *Sugary2*, respectively, and transformed it into the maize inbred line KN5585. Eight types of transgene-free frameshift mutations were obtained, including single mutants of *Sugary2* (S1, S2, S3), single mutants of *Waxy1* (W1, W2), and double-gene mutants (SW1, SW2, SW3). [Result] All frameshift mutations were predicted to produce proteins lacking key catalytic domains. In the T3 generation, double-gene mutants showed no significant differences from WT in plant height or hundred-kernel weight. Freeze-thaw stability assessments revealed that WT and *Sugary2* single mutants exhibited opaque white starch gels with rapid water separation, reaching approximately 60% and 66% syneresis rates by the sixth cycle, respectively. *Waxy1* single mutants showed lower water separation than WT in the first two cycles but surpassed WT by the third cycle. Strikingly, double-gene mutants displayed translucent, highly viscous colloidal solutions with no water loss during the first three freeze-thaw cycles, and even after six cycles, the water separation rate remained below 10%. Scanning electron microscopy showed that SW1 starch granules were irregular with rough surfaces and had a significantly increased proportion of large granules compared to WT. Amylose content analysis confirmed the expected reductions in *Waxy1* mutants and alterations in *Sugary2* mutants. Starch expansibility of SW1 was significantly decreased compared to both S1 and W1 and the WT ($P<0.05$). Viscosity measurements showed that SW1 starches exhibited significant increases ($P<0.05$) in peak viscosity, minimum viscosity, breakdown value, and final viscosity compared to WT, while S1 starches showed significant decreases in all viscosity parameters. [Conclusion] This work provides a foundation for rapidly improving the freeze-thaw stability of elite maize lines through targeted mutagenesis strategies, with potential applications in frozen food quality preservation.

Key words: M maize, CRISPR/Cas9, Freeze-thaw stability, *Waxy1*, *Sugary2*

Engineering High Amylose and Resistant Starch in Maize by CRISPR/Cas9-Mediated Editing of Starch Branching Enzymes

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Abstract: [Objective] To improve the amylose content (AC) and resistant starch content (RSC) of maize kernel starch. [Method] We employed the CRISPR/Cas9 system to create mutants of starch branching enzyme I (SBEI) and starch branching enzyme IIb (SBEIIb). [Result] A frameshift mutation in SBEI (E1, a nucleotide insertion in exon 6) led to plants with higher RSC (1.07%), lower hundred-kernel weight (HKW, 24.71 ± 0.14 g), and lower plant height (PH, 218.50 ± 9.42 cm) compared to the wild type (WT). Like the WT, E1 kernel starch had irregular, polygonal shapes with sharp edges. A frameshift mutation in SBEIIb (E2, a four-nucleotide deletion in exon 8) led to higher AC (53.48%) and higher RSC (26.93%) than that for the WT. E2 kernel starch was significantly different from the WT regarding granule morphology, chain length distribution pattern, X-ray diffraction pattern, and thermal characteristics; the starch granules were more irregular in shape and comprised typical B-type crystals. Mutating SBEI and SBEIIb (E12) had a synergistic effect on RSC, HKW, PH, starch properties, and starch biosynthesis-associated gene expression. SBEIIa, SS1, SSIIa, SSIIIa, and SSIIIb were upregulated in E12 endosperm compared to WT endosperm. [Conclusion] This study lays the foundation for rapidly improving the starch properties of elite maize lines.

Key words: Maize, Amylose content, Resistant starch content, CRISPR/Cas9

Functional Characterization of a PPR Protein Gene Regulating Plant Height via Organellar RNA Metabolism in Maize (*Zea mays* L.)

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Abstract: [Objective] This study aimed to identify the causal gene underlying a novel maize dwarf phenotype and to elucidate the molecular mechanism by which the encoded protein regulates plant height, providing a foundation for developing lodging-resistant maize varieties. [Method] An EMS-induced dwarf mutant (118A), exhibiting approximately 60% reduced plant height and altered ear architecture relative to wild-type B73, was characterized using MutMap-based bulk segregant analysis and whole-genome resequencing to identify the causal gene. Functional validation is planned through CRISPR/Cas9-mediated knockout and genetic complementation, with the underlying molecular mechanisms to be elucidated via RNA editing profiling, RIP-seq, and protein–protein interaction analysis. A de novo redesigned variant of the causal protein will also be engineered to reduce plant height without compromising grain yield, and its breeding potential will be evaluated through multi-environment field trials. [Result] The causal gene, Zm00001eb276220 (*ppr342*), located on chromosome 6, encodes a DYW-class pentatricopeptide repeat (PPR) protein; a causative C→T nonsense mutation results in premature protein termination. This is the first identification of a DYW-class PPR protein directly linked to plant height regulation in maize, revealing a novel pathway of organellar–nuclear communication in plant development. [Conclusion] Although the severe phenotype of *ppr342* currently limits its direct use in breeding, this study establishes the first mechanistic link between PPR proteins and plant height regulation in maize. The planned functional and mechanistic analyses, together with de novo protein redesign, offer a route toward lodging-resistant maize varieties and support seed industry innovation in Hainan Province and China.

Key words: Maize (*Zea mays* L.), Plant height, PPR protein, MutMap, RNA editing, Protein-protein interaction Organellar retrograde signaling, Molecular mechanism, Breeding potential

Funding acknowledgment: Chinese Academy of Agricultural Sciences, Sanya 572000, China

Genome-Wide Prediction of Protein–Metabolite Interactions Provides New Insights into Growth-Defense Trade-Offs in Maize

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Abstract: [Objective] Protein-metabolite interactions play important roles in regulating plant metabolism, development, nutrient utilization, stress adaptation, and defense signaling. In maize, the genome-wide landscape of protein-metabolite interactions remains largely unexplored. This study aimed to establish an integrated computational framework for predicting maize protein-metabolite interactions and prioritizing candidate regulatory links associated with growth-defense tradeoffs. [Method] Maize B73 reference protein sequences were used to construct a genome-wide protein structure resource by integrating homology modelling and AlphaFold-based structural information. Representative protein structures were selected after evaluating structural completeness, confidence, and model reliability. Ligand-binding pockets were predicted using structure-based pocket prediction and maize metabolites were integrated from in-house LC-MS/MS metabolomics data, public databases, and literature sources. The metabolite records were standardized, deduplicated, quality assessed, chemically annotated, and converted into 3D conformers. Protein-metabolite interactions were first screened using a DrugCLIP machine-learning-based virtual screening and then refined by Uni-Dock-based molecular docking. Downstream prioritization was designed to classify candidate proteins into functional groups, including enzymes, transporters, transcription factors or regulators, hormone-related proteins, and nutrient-binding proteins. Schrödinger re-docking, MM/GBSA binding free-energy estimation, molecular dynamics simulation, DFT-based ligand electronic analysis, and experimental validation. [Result] The workflow generated a genome-wide maize protein structure and ligand-binding pocket resource, together with a curated maize metabolite library for large-scale interaction screening. The combined machine-learning and docking strategy reduced the broad protein-metabolite search space into a focused set of strong candidate interactions. These candidates provide a genome-wide structural basis for downstream network analysis, functional classification, and prioritization of maize PMIs related to enzymes, transporters, transcriptional regulators, hormone-related proteins, and nutrient-binding proteins. The downstream validation strategy will help distinguish biologically meaningful interactions from computational false positives by examining binding pose quality, interaction stability, free-energy behavior, ligand electronic properties, and pathway-level relevance. [Conclusion] This study establishes a systematic computational framework for genome-wide prediction and prioritization of maize protein-metabolite interactions. By integrating protein structural modelling, metabolite curation, virtual screening, docking, functional classification, and

multi-level validation strategies, this work provides a foundation for understanding how metabolites may regulate maize growth-defense balance. The predicted interaction candidates can support future experimental validation, functional genomics, metabolomics interpretation, and molecular breeding efforts for improving maize resilience and productivity.

Key words: Maize, Protein-metabolite interaction, DrugCLIP, Uni-Dock, Molecular docking

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Effects of Protein Concentration and Oil Phase Volume Fraction on Physicochemical Properties and Stability of Soy Protein Isolate Complex-Stabilized Corn Oil-Based HIPEs

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Abstract: [Objective] To investigate the regulatory effects of protein concentration and oil phase volume fraction on the physicochemical properties and stability of corn oil-based high internal phase emulsions (HIPEs). [Method] Emulsions were fabricated using soy protein isolate complexes as the aqueous phase and corn oil as the oil phase. Six protein concentrations (10, 15, 20, 25, 30, and 35 mg/mL) and five oil phase volume fractions (76%, 77.5%, 79%, 80.5%, and 82%) were set. The microstructural characteristics and multiple stability mechanisms of the emulsions were systematically analyzed through particle size and zeta potential measurements, confocal laser scanning microscopy (CLSM) observation, and assessments of thermal stability, freeze-thaw stability, centrifugal stability, and water distribution (characterized by low-field nuclear magnetic resonance, LF-NMR). [Result] The results showed that with increasing protein concentration, the particle size of the emulsions showed a decreasing trend, the absolute value of zeta potential rose gradually, and the compactness of the protein film at the oil droplet interface was continuously improved. With increasing oil phase volume fraction, the average particle size and apparent viscosity of the emulsions increased gradually. As protein concentration increased, the tolerance of the emulsion system to extreme environments was enhanced, and protein molecules could better adsorb at the oil-water interface to form a continuous network structure. [Conclusion] Protein concentration and oil phase volume fraction can significantly regulate the microstructure and stability of corn oil-based high internal phase emulsions. This study provides an experimental foundation for the application of plant-based proteins in food-grade high internal phase emulsions, and also offers a theoretical basis for the development and application of corn oil-based functional lipid delivery systems in the food industry.

Key words: Corn oil, High internal phase emulsion, Protein concentration, Oil phase volume, Emulsion stability

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Study on the Effect of Machine Learning to Predict the Characteristics of Different Varieties of Corn Flour on the Texture Characteristics of Biscuits

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Abstract: [Objective] Based on a variety of machine learning algorithm modeling, the effects of basic physicochemical and functional properties of different varieties of corn flour on the quality and structure indexes of biscuits and the internal correlation mechanism were systematically explored. [Method] Four machine learning algorithms, XGBoost, Random Forest (RF), CatBoost, and Support Vector Classification (SVC), were selected to construct prediction models. The pasting rheological properties, pasting texture properties, thermal stability, dough texture properties, total protein content, and zein content of corn flour were used as model input characteristics, and the texture indexes of biscuits were used as model output variables. Based on the machine learning models, the feature correlation analysis was carried out to quantify and summarize the correlation between the characteristics of various raw materials and the texture indexes of biscuits. [Result] The results showed that the three tree models of XGBoost, RF, and CatBoost had similar rules : the thermal stability parameters of corn flour (T_C , T_P , T_0) and the basic texture indexes of dough (gumminess, elasticity, resilience) were the core variables with high contribution ; RF and CatBoost take the thermal characteristic temperature T_C as the primary main control factor, and the dough adhesion Gumminess in XGBoost has the strongest influence. The contribution of elastic storage modulus to rheological parameters is much higher than that of viscous loss modulus. The contribution of zein content in the tree model is low, and the regulation of biscuit texture is weak. The SVC classification model was significantly different from the tree model. The pasting peak temperature, loss modulus, and zein were the top three key features. The influence of T_C was greatly reduced, and the distinction between protein and viscous rheological parameters was significantly improved. [Conclusion] The hot-paste properties of corn flour and the basic texture of the dough are the common core factors that determine the texture of biscuits. Zein and viscous rheological parameters only play a prominent role in the classification model. There are obvious differences in the preference of linear and nonlinear correlation between different algorithms to capture features and biscuit texture.

Key words: Corn flour, Biscuits, Machine learning, RF, XGBoost, CatBoost, SVC

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Construction, Characterization, and Applications of Corn Starch-Based Beagles

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Abstract: [Objective] In this study, corn oil-based oil gels were prepared using a soy protein isolate (SPI)-gum arabic (GA) complex via the emulsion-template method. By combining the oil gels with corn starch (CS) hydrogels, a novel self-assembled Bigels was developed. The effects of the oil-gel-to-hydrogel ratio and the concentration of the cornstarch hydrogel on the macroscopic and microscopic structures, mechanical properties, and stability of the Bigels were investigated. [Result] The results showed that as the hydrogel content (60%–90%) and CS concentration (8%, 10%, 12%) increased, all Bigels samples maintained a consistent semisolid structure without phase separation, and their oil-binding capacities all reached 93.61% or higher, with the highest value reaching 98.39%. Freeze-thaw stability was highest when the hydrogel content was 80%. X-ray diffraction revealed a polycrystalline structure, indicating that the beagles possessed an organized structure. Maximum hardness was achieved when the hydrogel content was 60% and the corn starch concentration was 12%, ranging from 74.464 ± 5.668 to 109.941 ± 5.226 . [Conclusion] This study proposes a novel CS Beagle construct, which may provide a theoretical basis for the customized design of low-fat, healthy foods made from plant-based analogues using 3D printing technology.

Key words: Cornstarch, Bigels, Oil-in-water hydrogel ratio, Cornstarch hydrogel concentration, Oil hydrogel

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pH-Driven Preparation of Zein-Sodium Alginate Composite Emulsions for Lutein Delivery

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Abstract: [Objective] To promote the value-added utilization of protein resources derived from corn processing by-products and overcome the poor aqueous dispersibility, susceptibility to oxidative degradation, and low gastrointestinal bioaccessibility of lutein, this study employed zein obtained from corn processing by-products as the primary raw material and sodium alginate as the polysaccharide component to construct zein–sodium alginate composite emulsions. The protective encapsulation, environmental stability, and gastrointestinal release behavior of lutein in the composite emulsions were systematically investigated. This study aimed to provide a theoretical basis for the high-value processing of corn by-products and the development of delivery systems for lipophilic bioactive compounds. [Method] Zein was solubilized under alkaline conditions using a pH-driven method and was subsequently induced to reassemble by adjusting the pH of the system. The reassembled zein was then complexed with negatively charged sodium alginate to form a zein–sodium alginate composite dispersion. Lutein was dissolved in the oil phase, which was homogenized with the composite dispersion to prepare lutein-loaded oil-in-water emulsions. The formation and structural characteristics of the composite emulsions were evaluated by determining their mean droplet size, particle-size distribution, surface potential, encapsulation efficiency, and microstructure. The effects of pH, ionic strength, temperature, and storage conditions on the dispersion stability of the emulsions and the retention of lutein were further investigated. In addition, an in vitro simulated gastrointestinal digestion model was employed to examine the structural evolution of the emulsions, the release behavior of lutein, and its bioaccessibility during the gastric and intestinal phases, thereby evaluating the protective and delivery functions of the zein–sodium alginate composite interface. [Result] The pH-driven method enabled the formation of stable zein dispersions, and subsequent complexation with sodium alginate produced a dense protein–polysaccharide interfacial layer around the emulsion droplets. This composite layer enhanced electrostatic repulsion and steric hindrance, improving emulsion stability against environmental stresses and protecting lutein from oxidative degradation. In vitro digestion studies revealed that the composite interface maintained partial integrity under gastric conditions, delaying premature lutein release, while intestinal digestion promoted gradual release and micellization. Compared with free lutein and zein-only emulsions, the composite system exhibited superior protection and a more favorable release profile, suggesting potentially enhanced bioaccessibility. [Conclusion] The pH-driven method facilitated the formation of an aqueous zein dispersion while avoiding or reducing the use of organic solvents. The protein–polysaccharide interface formed through the complexation of zein with sodium alginate simultaneously contributed to emulsion stabilization, lutein

encapsulation, and regulation of gastrointestinal release. The composite interface protected lutein during the gastric phase and promoted its gradual release and micellarization during the intestinal phase. Therefore, the zein–sodium alginate delivery system showed considerable potential for improving the stability, modulating the release behavior, and enhancing the gastrointestinal bioaccessibility of lutein. These findings provide a useful reference for the value-added utilization of protein resources from corn processing by-products and the application of lipophilic bioactive compounds in functional foods.

Key words: Zein, Sodium alginate, pH-Driven method, Lutein, Composite emulsion

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Corn Processing as a Driver for Industrial Upgrading and Full-Chain Value Creation

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Abstract: [Objective] Corn processing is a strategic foundation for food, feed, starch, fermentation, bio-based manufacturing and rural industrial development. With the expansion of corn production and consumption, the key challenge is no longer only increasing processing volume, but upgrading the whole industry through specialized raw materials, advanced processing technologies, quality and safety control, and high-value conversion of all processing streams. This study aimed to summarize how corn processing can lead the development of the corn industry and to identify technical pathways for full-chain value creation. [Method] A 2026 industry presentation on corn processing-led industrial development was used as the main framework, and related research materials on corn quality evaluation, full utilization and quality safety were integrated as technical support. The analysis focused on eight aspects: global and Chinese corn production and consumption, development of processing-specific corn varieties, mycotoxin reduction technologies and equipment, food-grade corn flour and grits processing, growth of starch and starch-derived products, industrial scale and equipment upgrading, synthetic biology-based biomanufacturing, and comprehensive utilization of corn processing by-products. [Result] The review indicates that corn processing has become a major engine for industrial upgrading. Corn starch production in China increased from 21.59 million tons in 2015 to 43.61 million tons in 2024, while starch sugars, sugar alcohols, amino acids and organic acids showed marked growth. At the raw-material level, fresh corn, waxy corn, high-amylose corn, high-oil corn and other specialized varieties provide differentiated resources for food products, starch modification, nutritional ingredients and functional applications. At the processing level, mycotoxin reduction by dry abrasion, optical sorting, adsorption, ozone treatment and biological degradation improves raw-material safety, while refined corn flour and grits processing, including conditioning, multi-stage milling, grading, extrusion and enzymatic or fermentation-assisted modification, expands the use of corn in staple foods, noodles, steamed products, bakery foods and restructured rice. At the value-chain level, starch-based fermentation, enzymatic conversion and synthetic biology are generating functional sugars, amino acids, organic acids and green modified starches, and artificial intelligence can support raw-material databases, process control, storage management and product development. Meanwhile, germ, protein, fiber, bran, DDGS and other by-products are increasingly important for oil, feed, edible protein, active peptides, dietary fiber and circular utilization. [Conclusion] Corn processing should be regarded as the central pathway for transforming corn from a bulk crop into a high-value industrial and food resource. Future development should integrate safe raw materials, specialized varieties, refined processing equipment, starch deep processing, food-oriented whole-kernel utilization, by-product valorization, synthetic biology and AI-enabled quality control. Such a processing-led strategy will improve industrial efficiency, food-use value, safety, sustainability and the global competitiveness of the corn industry.

Key words: Corn processing, Industrial upgrading, Starch deep processing, Full-chain utilization, Food-grade corn flour, Biomanufacturing

Compound Enzyme Technology for Corn Starch Processing

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Abstract: [Objective] Corn starch is one of the most important products of deep processing of corn. In the wet milling process of corn starch production, achieving efficient separation of starch and corn husk fibers during the washing step is crucial for improving the starch yield. However, traditional mechanical separation methods are difficult to release the starch particles bound to corn fibers, resulting in low separation efficiency. [Method] The complex structure of hemicellulose glycan chains in corn fiber was analyzed, and a degrading enzyme system was developed accordingly. [Result] The developed enzyme system comprises main-chain-degrading enzymes such as cellulases and xylanases, as well as branch-chain enzymes such as arabinofuranosidases. It can precisely cleave the branched chains of corn fiber polysaccharides, remove steric hindrance, and then efficiently hydrolyze the main chains, fully opening up the fiber structure. During the corn fiber washing process, the dense and complex network structure of corn fiber is disrupted, completely releasing the starch granules and corn protein that are tightly encapsulated within the fiber. This compensates for the low efficiency of conventional mechanical separation in wet milling and improves the yield. At the same time, it reduces material viscosity and the bound water content of corn fiber, thereby lowering the energy consumption required for subsequent fiber drying. This technology has been commercialized by Baiyin Sainuo Biotechnology Co., Ltd., and applied in over 80% of corn starch enterprises in China. [Conclusion] We have developed a corn fiber polysaccharide-specific degrading enzyme system with optimized component ratios. When applied to the washing of corn fibers, it can effectively increase the starch extraction rate and reduce the energy consumption of wet fiber drying.

Key words: Corn starch, Corn fiber, Enzyme, Wet milling.

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Effects of Different Cooking Methods on Nutritional Components of Cassava Variety Huanan No.9

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Abstract: [Objective] To investigate the variations in contents of nutritional components including protein, fat, reducing sugar, polysaccharides, polyphenols and flavonoids in four sample groups: fresh cassava, steamed cassava, boiled cassava and oven-dried cassava. To add the indicator of residual hydrocyanic acid based on the inherent properties of cassava, so as to evaluate the detoxification efficiency of different treatments. To screen out the optimal processing method that can retain cassava nutrients to the maximum extent while achieving effective detoxification. To provide scientific parametric references for household cooking and industrial food processing of cassava. [Method] Experimental Instruments; Electronic balance, electrothermal constant-temperature blast drying oven, ultraviolet spectrophotometer, numerical control ultrasonic cleaner, digital constant-temperature water bath, high-speed refrigerated centrifuge, food steamer, stainless steel cooking pot, constant-temperature frying pan, pulverizer, standard test sieve, sealed sample bags. Experimental Design and Sample Preparation, Experimental Groups; Four treatment groups were set up with three parallel replicates for each group: Control group: Fresh cassava (without heating or drying treatment). Raw cassava slice direct drying group, Steamed cassava slice followed by drying group, Boiled cassava slice followed by drying group. Unified Pre-treatment of Cassava Raw Materials: Rinse cassava thoroughly with room-temperature clean water; Take out and drain surface moisture, then mix evenly and randomly divide into four groups for standby use; Cut uniformly into cuboid slices of $2\text{ cm} \times 2\text{ cm} \times 3\text{ mm}$ to ensure consistent heat-receiving area. Process Parameters for Each Treatment Group Direct drying of raw cassava; Spread cassava slices in a single layer $\rightarrow$ dry at $60\text{ }^{\circ}\text{C}$ for 8 h $\rightarrow$ take out and cool down. Steaming followed by drying; Heat the steamer until steam emerges fully $\rightarrow$ place cassava cubes inside $\rightarrow$ steam for 20 min $\rightarrow$ take out and cool down $\rightarrow$ dry at $60\text{ }^{\circ}\text{C}$ for 8 h $\rightarrow$ take out and cool down. Boiling followed by drying; Fixed material-to-water ratio: cassava: water = 1 : 10. Boil clean water completely $\rightarrow$ add cassava cubes $\rightarrow$ boil for 15 min $\rightarrow$ fish out, drain and cool down $\rightarrow$ dry at $60\text{ }^{\circ}\text{C}$ for 8 h $\rightarrow$ take out and cool down. Control group (fresh cassava); Cut into slices without heating or drying, and prepare samples for immediate testing. [Result] Significant differences were observed across various cooking methods of cassava which greatly influence the nutritional composition of the product. It was observed that the steam cooking had better and strong influence in retaining the nutritional properties of the food for consumption, while the boiling cooking method shows some undesirability due to loss of the loss of nutrients to the water or any solvent used to

achieve boiling of the cassava. [Conclusio] Cooking methods of cassava can greatly influence the nutritional composition of the food as it has direct effects on the physicochemical properties of the food which impacts its nutritional composition for consumption.

Key words: Cassava, Cooking methods, Nutritional composition

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Bioprofiling of Landraces of Maize (*Zea mays* L.) with Diverse Colours and Their Role in Biofortification

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Abstract: [Objective] The present study aimed at bio-profiling of five coloured maize kernels namely white, yellow, orange, red and purple towards the assessment of phytochemicals, biomolecules and minerals. The present study integrates, from fluorescence microscopy to track phenolics in the kernel layers and advanced HPLC analyses to comprehensively profile diverse phytochemicals besides quantifying mineral composition using ICP-MS and analyze starch content and composition which are critical for understanding the functional and therapeutic potential of these maize landraces. [Method] The study employed fluorescence microscopy, SEM-EDAX, Inductively Coupled Plasma Mass Spectrometry (ICP-MS), Gas Chromatogram Mass Spectroscopy(GC-MS), High-Performance Liquid Chromatography (HPLC), amino acid profiling and biochemical assays for starch fractions and bioactive compounds such as flavonoids and anthocyanin.[Result] Fluorescence microscopy revealed that pigmented kernels, particularly red and purple kernel maize, exhibited dense anthocyanin-associated autofluorescence and irregular starch architecture, whereas white and yellow kernels showed prominent ferulic acid-associated blue fluorescence and ordered starch granules. EDAX profiling revealed embryo and aleurone layer exhibited differential elemental distribution while endosperm found with comparatively uniform distribution. Elemental profiling revealed significant variation among kernel colours. Red and purple maize showed higher concentrations of phosphorus, potassium, iron, zinc, manganese, and copper, yellow maize exhibited moderate levels of most elements, while white and orange maize contained relatively higher calcium but lower overall macro- and micronutrient contents. Amino acid profiling showed variation, with glutamic acid as the predominant amino acid across all types. Yellow maize exhibited higher glutamic acid and phenylalanine, orange maize was enriched in lysine, red maize in arginine, and white maize in proline, while purple maize generally showed comparatively lower concentrations of several amino acids. GC-MS detected the abundance of sugars, fatty acids, amino acids and polyols. HPLC analysis for phenolic acids revealed that syringic acid and p-coumaric acid are the major compounds across samples. Yellow maize exhibited the highest overall phenolic acid content, purple maize showed elevated caffeic acid levels, while gallic acid was detected only in white and red maize, indicating distinct phenolic profiles among kernel colours. Biochemical assays indicated that pigmented kernels had enhanced levels of total flavonoids and anthocyanins with purple maize exhibiting the maximum anthocyanin, While white

maize possessed the highest total phenol content, starch and amylose content. [Conclusion] The study unequivocally demonstrated that kernel pigmentation is a strongly and positively correlated with phytochemicals, minerals, and biochemical constituents closely associated with mineral and functional phytochemical composition. By linking composition and functional properties, this work provides the first integrated assessment of coloured maize kernels as complex functional matrices. These findings mark the potential of coloured maize landraces as promising candidates for biofortification and development of nutritionally enhanced maize genotypes. All biochemical data of the above analysis will be presented in detail.

Key words: Bioprofiling, Minerals, Amino acid profiling, HPLC, Biofortification

Active Gluconeogenic Carbon Recycling Counteracts Glycolytic Depletion to Preserve Sugar Homeostasis in Cold-stored Sweet Corn

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Abstract: [Objective] This study aimed to clarify the regulatory mechanism underlying temperature-dependent sugar retention in sweet corn kernels. [Method] Sweet corn hybrid ‘Hetianyü 818’ was stored at 5 °C and 25 °C for 10 days. Kernel quality traits and soluble sugars were measured, and transcriptome profiling, WGCNA, enzyme activity assays, and targeted central-carbon metabolite analysis were integrated to identify sugar-associated pathways and candidate regulatory genes. [Result] Cold storage delayed kernel yellowing and firmness loss and maintained significantly higher glucose, fructose, and sucrose contents than ambient storage. KEGG enrichment and WGCNA identified glycolysis/gluconeogenesis as a central sugar-associated pathway. *ZmPFK6* expression and PFK activity were induced at 25 °C, whereas *ZmPEPCK2* expression, PEPCK activity, and gluconeogenic intermediate accumulation were enhanced at 5 °C. [Conclusion] Low temperature preserves sugar homeostasis in postharvest sweet corn by suppressing *ZmPFK6*-associated glycolytic consumption and promoting *ZmPEPCK2*-mediated gluconeogenic carbon recycling, providing candidate targets for improving postharvest storability.

Key words: Sweet corn, Cold storage, Sugar homeostasis, Glycolysis, Gluconeogenesis

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Efficacy Evaluation of Multi-Effect Foliar Application in Maize

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Abstract: [Objective] Lepidopteran pests including the *Ostrinia furnacalis*, *Helicoverpa armigera*, and *Dichocrocis punctiferalis* not only reduce grain yield but also facilitate fungal colonization and fumonisin contamination, posing serious food safety risks. The use of multi-effect foliar applications incorporating various agrochemicals is a viable pest management approach, though the effects of timing, cultivar choice, and formulation on pest control and mycotoxin levels are not thoroughly understood. This study sought to rigorously assess the effectiveness of these foliar applications in controlling pest populations, minimizing ear damage, and reducing fumonisin levels in maize, while determining the best combination of timing, formulation, and cultivar for integrated management. [Method] A three-factor split-split plot design was utilized, with maize variety as the primary factor, pesticide combinations as the secondary factor, and application timing as the tertiary factor. Forty-eight plots were systematically organized in three replications. The larval populations of the targeted pests were monitored at eight intervals from 47 to 106 days post-emergence. Ear damage was evaluated regularly until harvest, with grain yield and 1000-kernel weight measured at physiological maturity. Total fumonisin (FB1 + FB2), FB1, and FB2 concentrations in harvested grain were determined by liquid chromatography-tandem mass spectrometry (LC-MS/MS) following standard LS/T 6133-2018 protocol. Data were analyzed using three-way split-split plot ANOVA and Tukey's HSD post-hoc tests. [Result] Application timing strongly influenced *Ostrinia furnacalis* suppression ($F = 21.25$, $p < 0.0001$), with the V14+R1 treatment reducing larval counts by 61% versus the control. A similar timing effect was observed for *Helicoverpa armigera* ($F = 4.31$, $p = 0.012$), though at lower densities. The *Dichocrocis punctiferalis* showed a more complex response, with significant variability explained by variety ($F = 69.44$, $p < 0.0001$), reagent ($F = 5.44$, $p = 0.026$), timing ($F = 5.60$, $p = 0.003$), and their three-way interaction ($F = 5.19$, $p = 0.005$), indicating cultivar-specific susceptibility. Overall larval populations were significantly impacted by timing ($F = 17.34$, $p < 0.0001$) and reagent choice ($F = 4.45$, $p = 0.043$), with V14+R1 yielding the greatest cumulative reduction. Ear damage was driven primarily by variety ($F = 60.96$, $p < 0.0001$) and timing ($F = 15.80$, $p < 0.0001$), while the total number of damaged ears was significantly affected by both timing ($F = 10.60$, $p < 0.0001$) and reagent ($F = 7.55$, $p = 0.010$). Grain yield and 1000-kernel weight were determined solely by variety ($F = 77.38$ and 248.06 , respectively; both $p < 0.0001$), with no treatment effects. Variety V1 produced heavier kernels (343.84 g vs. 288.63 g per 1000 kernels), while V2 yielded higher grain output (14,393.69 kg/ha vs. 12,685.30 kg/ha). Mycotoxin analysis showed that total fumonisin concentrations were significantly reduced by timing ($F = 22.27$, $p <$

0.0001) and reagent ($F = 6.87$, $p = 0.013$), with V14+R1 achieving a 71% reduction (from ~7 mg/kg to ~2 mg/kg). For fumonisin B1, the V14+R1 treatment met full EU regulatory compliance, with 0% of samples exceeding the 2 mg/kg limit, while all untreated control samples failed this benchmark. Fumonisin B2 showed a simpler pattern, with V14 alone matching V14+R1 efficacy. [Conclusion] Multi-effect foliar application at the V14 growth stage is critical for effective pest management and fumonisin reduction. The V14+R1 treatment provides optimal efficacy and full EU compliance for FB1. Although no yield effects were observed, varietal genetics being the primary yield determinant, the quality and food safety gains offer strong economic justification for timely applications. These results support integrating precise application timing with cultivar-specific strategies for more sustainable maize production.

Key words: Multi-effect foliar application, Fumonisin, Application timing, Food safety

Responses of Soil Characteristics and Summer Maize Growth to Organic Manure Application in Reclaimed Soil, Southwest China

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Abstract: [Objective] To investigate the effects of organic manure on maize performance and soil properties in reclaimed soils. [Method] A experiment was conducted use typical reclaimed soils in Southwest China with three organic manure treatments: control treatment without organic manure application (CK, 0 kg hm⁻² yr⁻¹), low manure application rate (L, 7500 kg hm⁻² yr⁻¹), and high manure application rate (H, 15000 kg hm⁻² yr⁻¹). The responses of soil chemical properties and summer maize growth to different treatments were evaluated. [Result] After three consecutive years of treatments, soil pH under H treatment (6.8 ± 0.1) was significantly lower than that under CK (7.4 ± 0.1). Soil organic carbon, available phosphorus, available potassium and alkaline-hydrolyzable nitrogen contents were significantly higher in H than in L, which were further significantly greater than those in CK. At the silking stage, maize plant heights were 268 ± 6 cm, 290 ± 3 cm and 313 ± 7 cm under CK, L and H treatments, respectively. The ear leaf area averaged 505 ± 166 cm², 628 ± 85 cm² and 683 ± 56 cm² for CK, L and H, respectively. Chlorophyll fluorescence analysis revealed that treatments L and H increased Fv/Fm and Y(II) in maize ear leaves, facilitating the allocation of absorbed light energy to photochemical reactions. Maize grain yields were 3837 ± 973 kg hm⁻², 5653 ± 1422 kg hm⁻² and 8789 ± 1248 kg hm⁻² for CK, L and H, respectively. [Conclusion] Organic fertilization of reclaimed soil can rapidly enhance soil nutrient availability and organic matter content, promote maize growth and improve grain yield.

Key words: Organic manure, Soil fertility, Reclaimed Soil, Summer maize

Straw Return Enhances Soil Multifunctionality and Maize Yield Through Shifts in Bacterial Community Structure

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Abstract: [Objective] Straw return is widely recognized as an agricultural practice that can improve soil multifunctionality and increase crop yield. However, the mechanisms by which straw return affects soil multifunctionality remain insufficiently understood. [Method] This study was based on a 6-year field experiment conducted in Northeast China, including five straw management treatments: straw removal (CK), straw mulching (SM), straw burial (SB), straw incorporation (SI), and strategic straw return (SR; 1 year of SM, 1 year of SI, and 1 year of SB). [Result] Compared with CK, the SR treatment significantly reduced soil bulk density and improved soil aggregate structure. These changes increased microbial biomass and N-acquiring enzyme activities, thereby promoting soil organic carbon accumulation and nutrient cycling. Consequently, SR significantly enhanced soil multifunctionality and maize yield in the sixth year. Notably, the improvement in subsoil (20–30 cm) multifunctionality contributed more to the increase in maize yield than that in the other soil layers. In contrast, the SB, SI, and SM treatments did not significantly improve soil physical properties, which may have limited microbial growth and activity and thereby weakened their effects on soil multifunctionality and yield. In addition, we found that fungal communities were less resistant than bacterial communities to straw-return disturbance, and the increase in soil multifunctionality was more closely associated with bacterial community structure than with fungal community structure. Bacterial community structure therefore appears to play a particularly important role in maintaining soil multifunctionality. [Conclusion] Straw return enhanced soil multifunctionality and maize yield by improving soil structure, regulating bacterial community structure, and increasing nutrient availability.

Key words: Straw return, Soil multifunctionality, Bacterial community structure, Maize yield

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Drivers of Soil Properties in Different Soil Layers and Maize Yield under Five Years of Deep Ploughing with Straw Return in Saline-alkali Soil

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Abstract: [Objective] Soil salinization poses a threat to agricultural productivity, and deep ploughing with straw return has emerged as a potential strategy to improve saline-alkali land. In this study, we aimed to determine the long-term effects of deep ploughing with straw return on different soil layers and the underlying mechanisms influencing maize yield in saline-alkali soils. [Method] We conducted a five-year field experiment over two sites in which we determined the effects of two tillage treatments—shallow rotary tillage without straw return (CK) and deep ploughing with straw return (DPR)—on soil physical and chemical properties in different soil layers. We also determined the contributions of soil properties in different layers to the yield of the local maize (*Zea mays* L.) variety Dika159. [Result] Overall, deep ploughing with straw return systematically enhanced maize yield (+16.10%) in saline-alkali soil by improving soil physical structure, promoting the accumulation of soil organic matter (+24.28%), and effectively reducing soil salinity (−18.53%). Partial least squares path modeling further indicated that this practice primarily drives yield increase by optimizing topsoil conditions, with the 0–20 cm soil layer playing the most critical role. Deep ploughing with straw return notably reduced soil bulk density (−6.54%) and total salt content (−29.68%) in this layer, thereby directly alleviating salt stress, improving soil moisture and nutrient availability, and ultimately playing a decisive role in increasing maize yield. [Conclusion] Our findings indicate that deep ploughing with straw return is an effective strategy to improve soil conditions and maize yield over a five-year period. The physical and chemical properties of the 0–20 cm layer had the most pronounced effect on yield. Our findings indicate that deep ploughing with straw return is an effective strategy to improve soil conditions and maize yield over a five-year period. The physical and chemical properties of the 0–20 cm layer had the most pronounced effect on yield.

Key words: Deep ploughing, Straw return, Saline-alkali soil, Maize yield

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Microplastics Promoted Cadmium Accumulation in Maize Plants by Improving Active Cadmium and Amino Acid Synthesis

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Abstract: [Objective] Combined microplastic (MP) and cadmium (Cd) pollution may alter soil Cd availability and crop Cd uptake, but the roles of polymer type, particle size and soil type remain unclear. This study aimed to determine how polystyrene (PS) and polypropylene (PP) particles with different sizes regulate Cd bioavailability, maize Cd accumulation, rhizosphere metabolites and bacterial communities in contrasting soils. [Method] Maize was grown for six weeks in Cd-spiked red soil and cinnamon soil under five treatments: Cd alone (5 mg/kg), PS-1 (50 nm PS + Cd), PS-2 (100 nm PS + Cd), PP-1 (5 µm PP + Cd) and PP-2 (10 µm PP + Cd), with four replicates. Plant growth traits, tissue Cd concentrations, rhizosphere pH, electrical conductivity (EC), dissolved organic carbon (DOC), available Cd and sequential Cd fractions were measured. Rhizosphere metabolites were profiled by ultra-high performance liquid chromatography-mass spectrometry, and bacterial communities were characterized by 16S rRNA sequencing. [Result] MP addition did not uniformly inhibit maize growth; the response depended on soil type and particle size. In red soil, MPs had no significant inhibitory effect on maize growth, whereas in cinnamon soil, large PP particles inhibited root growth and small PP particles inhibited aboveground growth. MPs generally promoted Cd accumulation in maize roots and shoots. In red soil, large particles exerted the strongest effect by decreasing pH, increasing EC, enhancing CaCl₂-extractable Cd and promoting the transformation of relatively stable Cd fractions toward active forms. In cinnamon soil, small particles more strongly promoted root Cd uptake. A total of 490 rhizosphere metabolites were identified, and MPs changed carbohydrates, organic acids, lipids and amino-acid-related metabolites. Small MPs in cinnamon soil were associated with enhanced L-serine and 2-methylhippuric acid synthesis/secretion, which may facilitate Cd absorption by roots. Bacterial community analysis further indicated that MPs reshaped taxa related to carbon metabolism and plant growth promotion, including Roseiflexaceae, Arthrobacter, Flavihumibacter and Bacillus, thereby affecting Cd bioavailability. [Conclusion] The ecological effect of combined MP-Cd pollution is strongly soil-type- and particle-size-dependent. Large MPs promoted Cd mobilization mainly by altering soil chemical properties and Cd fractions in red soil, whereas small MPs promoted Cd uptake in

cinnamon soil mainly through rhizosphere metabolite responses. Integrated analysis of soil chemistry, Cd speciation, metabolomics and microbial communities is necessary for evaluating agricultural risks from coexisting MPs and Cd.

Key words: Microplastics, Cadmium bioavailability, Maize, Rhizosphere metabolomics, Bacterial community, Soil type

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Key Technologies for Mycotoxin Prevention and Control and Graded Utilization during Drying and Storage of Maize and Peanut

Fuguo Xing

Abstract: [Objective] Maize and peanuts are important grain and oilseed commodities, but they are highly susceptible to fungal infection and mycotoxin contamination during postharvest drying, storage and utilization. This study aimed to establish an integrated technical system for mycotoxin prevention and control and graded utilization during maize and peanut drying and storage, thereby reducing postharvest losses, improving the safe use of contaminated materials and by-products, and supporting food security and high-quality industrial development. [Method] A full-chain technical route was developed by integrating low-damage drying equipment, mobile drying systems, green and precision storage technologies, rapid visual detection of fungal contamination, nondestructive quality evaluation, intelligent sorting, aflatoxin laser sorting, and chemical and biological detoxification technologies. These technologies were designed to control key risk points from harvest to storage and utilization, with emphasis on reducing mechanical damage, preventing fungal growth, detecting contamination rapidly, and enabling graded utilization of raw materials and processing by-products. [Result] A low-damage air-suction circulating dryer was developed, reducing the kernel damage rate from 2%–5% to below 0.1% and increasing drying efficiency by 50%. An intelligent mobile towed dryer was also created to enable cross-regional operation and dual use under routine and emergency conditions. In addition, green precision technologies for mycotoxin prevention and control during maize and peanut storage, rapid visual detection methods for fungal contamination, nondestructive testing technologies, intelligent color sorting equipment, aflatoxin laser sorting equipment, and detoxification technologies for contaminated raw materials and by-products were established. These achievements have been transferred and applied in 12 enterprises, achieving a 3% reduction in postharvest losses and generating significant economic and social benefits. The technological achievements received the Outstanding Science and Technology Innovation Award from the Chinese Academy of Agricultural Sciences in 2022 and were selected as a main promoted technology by the Ministry of Agriculture and Rural Affairs in 2024. [Conclusion] The established system provides an integrated solution for mycotoxin prevention, contamination detection, precision sorting, detoxification and graded utilization of maize and peanut after harvest. It offers technical support for reducing postharvest losses, improving the safe use of contaminated agricultural products and by-products, and promoting sustainable development of the maize and peanut industries.

Key words: Maize, Peanut, Mycotoxin prevention and control, Drying and storage, Graded utilization, Nondestructive detection

Effects of Waterlogging Duration on Fresh-ear Yield and Grain Quality Traits of Waxy Maize under Exogenous Melatonin Application

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Abstract: [Objective] Waxy maize, a distinct subtype of fresh-eating maize, possesses an endosperm dominated by amylopectin, which imparts its characteristic sticky and glossy texture. Moreover, waxy maize is abundant in phytochemicals and bioactive compounds—including carotenoids and phenolics—that exhibit strong antioxidant potential and contribute meaningfully to its nutritional and health value. However, global warming has increased the frequency and intensity of extreme precipitation and floods, exacerbating waterlogging risks. Waterlogging stress limits nutrient accumulation, reduces maize yield, and deteriorates grain nutritional quality. Previous studies identified the jointing stage as a particularly sensitive period for waxy maize). In the Huang-Huai-Hai Plain, where rainfall is concentrated during jointing, waterlogging is especially likely, yet the effects of varying stress durations on ear development, grain quality, and antioxidant capacity remain unclear. [Method] A three-year field experiment was conducted to examine the effects of waterlogging duration at the jointing stage (2–10 days) on fresh-ear yield and grain quality of waxy maize, with non-waterlogged plants as the control (CK), and exogenous melatonin applied at the V6 stage to assess its regulatory role. [Result] Results showed that waterlogging of ≥ 4 days significantly reduced fresh-ear yield and accelerated grain maturation in waxy maize. In SKN602, 4–6 days decreased ear growth, soluble sugars, and total protein, while increasing starch, especially amylopectin; 8–10 days further reduced ear size and grain traits. For cultivar JKN2000, 4–6 days of waterlogging reduced rows per ear and grains per row, while 8–10 days shortened ear length and width, decreased 100-grain weight, and reduced grains per ear, with 10-day stress causing a 29.3% yield loss ($P < 0.05$). Grain maturation was accelerated under 4–6 days of waterlogging, whereas grain filling was delayed under 8–10 days. Total phenols, flavonoids, total ascorbic acid, carotenoids, zeaxanthin, and lutein, as well as antioxidant capacities (ABTS, DPPH, FRAP), were suppressed under moderate waterlogging but partially recovered under prolonged stress; antioxidant potential was mainly influenced by phenolic compounds, carotenoids, and grain water content. Exogenous melatonin significantly increased fresh-ear yield under 4-day waterlogging and partially alleviated yield loss under prolonged waterlogging. It enhanced total phenols under 2–4 days of waterlogging, increased zeaxanthin content under 6-day stress, and improved ABTS and FRAP antioxidant capacities. Melatonin also reduced starch accumulation and increased soluble sugar and protein contents under 4–6 days of waterlogging. [Conclusion] Overall, melatonin improved yield and ear

traits under 2–8 days, but overall antioxidant improvement was limited.

Key words: Waxy maize, Exogenous melatonin, Waterlogging stress, Fresh ear yield, Nutritional quality, Antioxidant quality

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Maize Methionine Biofortification Through the Regulation of the Cystathionine Beta-ILyase Gene *ZmCBL*

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Abstract: [Objective] Maize nutritional quality is restricted by deficient methionine. This study aims to elucidate the regulatory network of methionine biosynthesis to identify high-efficiency molecular targets for biofortification without yield penalty. [Method] Integrating multi-environment phenotyping with 20 DAP endosperm transcriptomics, we reconstructed the methionine metabolic network. Protein interactions were verified by LCI, BiFC, and Pull-down assays. Gene functions were validated using CRISPR-Cas9, RNAi, and overexpression lines. [Result] We identified *ZmCBL* as a pivotal hub interacting with *ZmCBS*. A hierarchical phosphorylation–ubiquitination–SUMOylation cascade governs *ZmCBL* stability. Targeted mutation of a key phosphorylation site (Ser-223) stabilizes *ZmCBL*, wherein reduced phosphorylation elevates kernel methionine content by approximately 20% without compromising yield. [Conclusion] This work uncovers a critical regulatory mechanism of methionine metabolism. The *ZmCBL*^{S223A} serves as a precision molecular switch, providing an efficient target for rapid biofortification of elite maize lines (SS/NSS) via haploid inducer–mediated genome editing (IMGE).

Key words: Methionine, *ZmCBL*, Phosphorylation, IMGE, Biofortification

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Analysis of Quality Differences in Sweet Corn Seeds between *sh2* and *bt2* Mutation Types

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Abstract: [Objective] Analyzing the differences in grain quality between Sh2 and Bt2 types of sweet corn inbred lines to provide a theoretical basis for improving sweet corn quality and breeding varieties. [Method] Using 4 samples of Sh2 sweet corn inbred lines and 4 samples of Sh2 sweet corn inbred lines as experimental materials, samples were taken 18, 20, 22, and 24 days after pollination to measure grain starch content, sweetness (Brix), total soluble sugars, sucrose, and other soluble sugars, as well as their dynamic changes. Grain volatile flavor compounds were also measured 22 days after pollination. The study analyzed the differences in starch and sugar components between the two types of mutant sweet corn grains, used principal component analysis (PCA) to identify the key soluble sugar factors affecting the two mutants, and compared differences in the composition and aroma contribution of their volatile flavor compounds. [Result] The total starch content in both types of mutant materials continuously increased as the kernels developed, and the starch content in Sh2 material was higher than that in the Bt2 inbred line. The changes in sweetness were closely linked to soluble sugars, and there were noticeable differences between the two inbred lines: the sweetness peak of Sh2 sweet corn kernels appeared 18 days after pollination, while the peak for Bt2 sweet corn kernels was delayed to 20 days after pollination. The dynamics of soluble sugar accumulation and the results of principal component analysis (PCA) showed significant differences in sugar metabolism characteristics between the two genotypes: Sh2 inbred line kernels accumulated more sucrose, whereas Bt2 inbred line kernels had more prominent accumulation of other soluble sugars. Analysis of volatile flavor compounds showed that Sh2 materials had slightly more types of flavor substances than Bt2 materials; both materials mainly had sweet, grassy, and fruity aromas, but Sh2 had a noticeably higher proportion of sweet and fruity aromas and a lower proportion of grassy aroma compared to Bt2. [Conclusion] There are significant quality differences between two types of mutant sweet corn inbred lines. Sh2 sweet corn has lower starch, higher sugar, and a slow sugar decline, with prominent sweet and fruity aromas, making it suitable as a high-sweet, premium sweet corn breeding parent. Bt2 mutant sweet corn has moderate sweetness with noticeable green notes, making it ideal for breeding sweet corn with a fresh, mild flavor.

Key words: Sweet corn, Sh2 mutation, Bt2 mutation, Seed quality, Soluble sugar, Volatile Flavor compounds

Effects of Intercropping Silage Maize with Different Hyacinth Bean Varieties on Forage Nutritive Quality and Soil Microbial Characteristics

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Abstract: [Objective] Monocropping Silage Maize faces two prominent drawbacks: low crude protein content limiting feed value and long-term soil microecological degradation. To explore sustainable Intercropping strategies for high-quality forage production, a field trial was carried out in 2024. [Method] In this trial, silage maize cultivar Jingang Silage 50 was intercropped with four hyacinth bean varieties (BD1–BD4), with sole silage maize set as the control (QC). A randomized block design with three replications was applied to evaluate crop agronomic performance, forage nutritional indicators, soil physicochemical nutrients, and soil bacterial communities via Illumina NovaSeq 6000 high-throughput sequencing. [Result] The results indicated that Intercropping with Hyacinth Beans had no significant negative effects on silage maize plant height, stem diameter and aboveground biomass. Relative to monocropping, all Intercropping combinations significantly boosted crude protein and ash concentrations, while lowering acid detergent fiber (ADF) and neutral detergent fiber (NDF), which greatly improved feed digestibility for ruminants. Water-soluble carbohydrate (WSC) contents declined in intercropped mixtures owing to the low intrinsic sugar content of hyacinth beans. For soil fertility, Intercropping BD1, BD2 and BD3 markedly raised soil total nitrogen, with BD1 increasing total nitrogen by 14.59%; only BD4 significantly enhanced soil potassium by 3.37%, whereas soil phosphorus exhibited no significant difference across all treatments. Soil bacterial sequencing showed Intercropping reshaped rhizosphere microbial assembly. The relative abundances of beneficial phyla Acidobacteriota and Planctomycetota were substantially elevated, balancing the overall microbial community. Alpha diversity analysis revealed BD4 reduced the Shannon index significantly, while BD2 and BD4 lowered Simpson index, indicating more uniform distribution of microbial taxa. PICRUSt functional prediction demonstrated Intercropping upregulated core metabolic pathways including carbohydrate and amino acid metabolism, and suppressed disease-related microbial functions. Among all treatments, the BD1 Intercropping system delivered the best comprehensive performance in forage nutrition, soil nitrogen accumulation and stable microbial diversity. [Conclusion] In summary, silage maize-hyacinth bean Intercropping is an eco-friendly cultivation mode that simultaneously upgrades forage protein quality and ameliorates soil microecology. This research offers theoretical and technical references for developing high-protein silage maize production and sustainable maize farmland ecosystems, matching the high-quality and green development orientation of maize industry.

Key words: Silage maize, Hyacinth bean, Intercropping, Forage nutrition, Soil nutrient, Soil bacterial community

Effects of Nitrogen and Water Stress on Corn (*Zea Mays*) Applied with L-Alpha Free Amino Acid-Based Biostimulant

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Abstract: [Objective] Corn (*Zea mays*) production in Malaysia relies heavily on nitrogen (N) fertilization and adequate soil moisture to achieve good yields. Although Malaysia receives approximately 2,500 mm of annual rainfall, increasingly erratic rainfall patterns associated with climate variability frequently expose maize to periods of water deficit. Furthermore, the country's predominantly highly weathered Ultisols and Oxisols are inherently low in organic matter and nitrogen, resulting in poor soil fertility and a high dependence on external nutrient inputs. While fertilizer application and irrigation remain the primary strategies for maintaining crop productivity, escalating fertilizer prices and increasing climatic uncertainty present major challenges to the corn production. To address this, enhancing plant physiological performance using plant biostimulants maybe a promising strategy to and improve tolerance against drought and nitrogen deficiency. This study evaluated the effectiveness of an L- α free amino acid-based biostimulant (Delfan Plus®, Rovensa Next) in improving the growth, physiology, nutrient uptake, and yield of maize underwater and nitrogen stress. [Method] Five treatments were evaluated: (1) untreated control, (2) biostimulant under non-stress conditions, (3) biostimulant under water stress, (4) biostimulant under nitrogen stress, and (5) biostimulant under combined water and nitrogen stress. Stress treatments were imposed after tasselling, along with the commencement of biostimulant application corresponding to the experimental design. The experiment was conducted in a shade house using a randomized complete block design (RCBD). Plant physiological responses during the vegetative stage were assessed through SPAD chlorophyll readings, stomatal conductance, transpiration rate, photosystem II (PSII) efficiency, and electron transport rate. At harvest, grain yield, shoot dry matter, leaf area index, foliar nutrient concentrations (N, P, K, Ca, and Mg), and nutrient use efficiency were determined. Data were analysed using repeated-measures RCBD analysis of variance (ANOVA) and planned contrast analyses in JASP (JASP Team, 2024). [Result] Biostimulant application significantly increased grain yield, shoot dry matter, leaf area index, and foliar phosphorus concentration compared with untreated plants. However, among the biostimulant-treated maize, water stress and combined water and nitrogen stress significantly reduced grain yield, shoot dry matter, and phosphorus uptake. Photosystem II (PSII) efficiency and electron transport rate remained largely unaffected by the imposed stress treatments, indicating that the photosynthesis was maintained. In contrast, water stress significantly reduced stomatal conductance and transpiration rate, restricting gas exchange and ultimately limiting grain production. [Conclusion] Overall, these findings demonstrate that L- α free amino acid-based biostimulants can enhance maize performance under suboptimal growing conditions by improving physiological resilience and nutrient acquisition, thereby increasing the plant's tolerance to water and nitrogen stress.

Key words: Corn Productivity, L- α Free Amino Acid-Based Biostimulant, Nitrogen Stress, Water Stress

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Effects of Different Light Intensities after Anthesis on Photosynthetic Characteristics, Yield and Quality of Spring Maize

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Abstract: [Objective] Photosynthesis is the core process of driving plant growth, and it is also the basis of material accumulation and yield formation. It is closely related to canopy light distribution, chlorophyll content, photosynthetic rate and fluorescence parameters. However, it is not clear how the changes of light environment after silking affect the carbon metabolism, yield, and quality of spring maize by regulating the above photosynthetic physiological indexes. [Method] The field experiments were carried out with Zhengdan 958 and Fumin 985 as materials from 2024 to 2025. In this experiment, under the conditions of conventional density (D1, 67,500 plants hm^{-2}) and increased density (D2, 90,000 plants hm^{-2}), shading (S, shading 30%) and supplemental light (L, supplemental light intensity of 960~1200 $\mu\text{mol}\cdot\text{m}^{-2}\cdot\text{s}^{-1}$) treatments after anthesis were set up respectively, with natural light conditions as the control. [Result] The effects of different light intensities after anthesis on leaves photosynthetic fluorescence characteristics, dry matter accumulation and distribution, grain starch synthesis related enzymes, yield and quality of spring maize were analyzed. Compared with the control, shading after anthesis decreased leaf area index, canopy light transmittance, chlorophyll content, the maximum photochemical efficiency of PSII (Fv/Fm), the actual photochemical efficiency of PSII (ΦPSII), and net photosynthetic rate (Pn), while increased non-photochemical quenching coefficient (NPQ). Shading reduced the activities of starch synthesis enzymes and the grain-filling rate, resulting in insufficient starch accumulation, decreased grain weight, and significantly reduced yield (38.86%~58.58%). Compared with the Conventional light, the supplemental light increased photochemical efficiency, increased ΦPSII and Fv/Fm, decreased NPQ, and significantly increased Pn. After light supplementation, the grain filling rate increased, the distribution of dry matter to grains increased, the grain weight increased, and the yield increased (10.10%~23.13%). And simultaneously increased the amylose-to-amylopectin ratio, amylose content and total starch content, while decreasing fat and protein contents. The average increases in amylose and total starch contents were 12.35%~13.67% and 2.48%~3.54%, respectively. [Conclusion] Light management has a significant regulatory effect on the yield and quality of spring maize. The post-anthesis light intensity significantly affects the accumulation of photosynthetic products, starch synthase activity and grain filling process by regulating the canopy light distribution and leaf photochemical efficiency of spring maize. Therefore, it is of great significance to implement precise light supplementation strategy under dense planting conditions and formulate differentiated light environment regulation schemes for different densities to give full play to the potential of light yield increase, balance yield and quality traits, and promote the implementation of high light efficiency cultivation techniques for maize.

Key word: Light Intensity, Photosynthetic Characteristics, Dry Matter Accumulation, Starch Synthesis, Yield

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Strip Deep Rotary Tillage Reduces the Optimal Nitrogen Rate for High Maize Yield in the North China Plain: A System-Specific Optimization of Root-Shoot Growth and Soil Nitrogen Availability

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Abstract: [Objective] Long-term no-tillage causes soil compaction and reduces nitrogen (N) use efficiency in maize production in the North China Plain (NCP). Strip deep rotary tillage (ST), which loosens the intra-row soil to 40 cm while retaining inter-row nutrients, may overcome this limitation, but whether it can lower the optimal N rate for high maize yield remains unclear. This study evaluated whether strip deep rotary tillage (ST) could lower the optimal N rate required for high yield, relative to no-tillage (NT) and rotary tillage (RT). Our objectives were to (1) quantify changes in soil properties and N availability under ST compared with NT and RT across different N rates, (2) evaluate the subsequent effects on root-shoot growth coordination, (3) determine and quantify the tillage-dependent shift in the optimal N rate, and (4) identify the key hubs linking soil improvements to yield gains. [Method] Field experiments were conducted at the Xinxiang Experimental Station of Chinese Academy of Agricultural Sciences, Henan Province, China (35°18'N, 113°54'E). A 5-year field experiment (with data reported for 2022-2023) with four N application rates (0, 180, 240, and 360 kg N ha⁻¹) and three tillage practices (no-tillage, NT; rotary tillage, RT; and strip deep rotary tillage, ST) was conducted to examine soil N availability, root-shoot coordination and yield formation. [Result] Across four N rates (0, 180, 240, and 360 kg N ha⁻¹), RT and ST increased maize yield by 12.3% and 17.9%, respectively, compared with NT. Notably, the optimal N rate for maximum yield shifted from 360 kg N ha⁻¹ under NT/RT to 240 kg N ha⁻¹ under ST. In the ST system with 240 kg N ha⁻¹ (ST-N2), soil bulk density decreased and soil porosity increased in the 20-40 cm intra-row soil layer, accompanied by higher mineral N content in the 0-50 cm soil profile. These changes were associated with improved root growth and greater post-silking N accumulation, which in turn increased leaf area index, dry matter accumulation, and root to shoot ratio at silking (R1) compared with NT and RT at equivalent or higher N rates. Nitrogen recovery efficiency (RE_N) and physiological efficiency (PE_N) were also highest under ST-N2. Partial least squares path modeling (PLS-PM) identified root dry weight as the key hub linking soil improvements to yield gains. [Conclusion] In this NCP system, adopting strip deep rotary tillage allows a reduction in the optimal N rate from 360 to 240 kg N ha⁻¹ without sacrificing yield, providing an evidence-based option for reducing N fertilizer input while maintaining high maize yield in the NCP and similar agricultural regions.

Key words: Maize, Tillage practices, Optimal nitrogen rate, Root-shoot growth, Grain yield

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Comprehensive Evaluation of Sweet Corn Germplasm: Genomic Variation and Stress Resistance Profiling

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Abstract: [Objective] Sweet corn is a major type of fresh-market maize, and its yield, quality, and stress resistance directly determine production efficiency and industrial stability. This study aims to systematically assemble and characterize a panel of 450 sweet corn inbred lines, using high-depth resequencing to uncover genomic variation, and to comprehensively evaluate their performance in quality and biotic/abiotic stress tolerance through precise phenotyping, thus providing a material and data foundation for subsequent genome-wide association studies and molecular design breeding. [Method] We subjected 450 sweet corn inbred lines to 20× depth resequencing for systematic genomic characterization. For phenotyping, we performed precise evaluations of key agronomic traits, including yield, quality, and resistance. Resistance to southern corn leaf blight and sheath blight was assessed via artificial inoculation, while tolerance to high temperature and salt-alkaline stress was evaluated under controlled conditions. All assessments were replicated to ensure data reliability. [Result] Through systematic evaluation, we identified 51 accessions with soluble solids content (Brix) $\geq 15\%$, of which two elite accessions reached $\geq 18\%$. For stress resistance, we screened 88 accessions showing resistance or above to southern corn leaf blight (including 9 highly resistant), 6 accessions resistant to sheath blight, 76 accessions with high-temperature tolerance at resistance level or above (including 13 highly resistant), and 50 accessions with salt-alkaline tolerance at resistance level or above (including 6 highly resistant). These germplasm resources provide directly utilizable materials for parental selection in resistance breeding. [Conclusion] This study establishes a preliminary evaluation system that integrates genomic and phenotypic data for sweet corn germplasm. The high-soluble-solids accessions offer valuable genetic material for quality improvement, while the disease- and stress-resistant lines lay a foundation for breeding under multiple stress conditions. In follow-up work, we will integrate high-density genomic variation data with precise phenotypic results to conduct GWAS, aiming to identify key functional loci and favourable allelic variants controlling important quality and resistance traits, thereby providing high-precision targets for molecular design breeding and accelerating the development of elite varieties.

Key words: Sweet Corn, Inbred Lines, Resequencing, Phenotyping, Stress Resistance

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Breaking the Trade-Off Between Grain Yield and Protein in Maize: a Global Meta-Analysis of Optimized Nitrogen Management and Environmental Drivers

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Abstract: [Objective] Protein deficiency is a critical global challenge for public health and Food security. The trade-off between maize grain yield (GY) and grain protein content (GPC) remains a major barrier to enhancing both food quantity and nutritional quality. While nitrogen (N) management is crucial for crop productivity, its potential to synergistically improve both GY and GPC across diverse global environments is not fully quantified. This study aims to identify optimal N practices and the environmental drivers that govern the synergy between maize yield and quality. [Method] A global meta-analysis was conducted with 699 paired observations, and mixed-effects models were used to evaluate effects of N management, soil and climatic factors on GY, GPC and grain protein yield (GPY). [Result] Controlled-release fertilizer boosted GY by 11.53% and GPC by 11.93%. Notably, increasing N application rate predominantly enhanced GPC rather than GY, while a modest reduction in N application rate ($\leq 20\%$) did not significantly affect GY, GPC and GPY. Agronomic adjustments further strengthened these effects, with N topdressing increasing GY, GPC and GPY by 7.90%, 11.65% and 20.47%, respectively. Furthermore, these effects were more pronounced under conditions of lower soil bulk density ($< 1.4 \text{ g/cm}^3$) and warmer climates ($\geq 20^\circ \text{C}$). [Conclusion] This global meta-analysis found that N application rate was the predominant factor of maize GY and GPC, yet increasing N inputs alone reinforced the intrinsic trade-off between them. Crucially, our study demonstrated that optimizing N fertilizer type was a superior strategy for achieving synergistic improvements in GY, GPC and GPY, particularly via controlled-release and bio-based carrier N fertilizers. Furthermore, a strategic reduction in N application rate of no more than 20% was found to maintain both yield and quality without significant losses. The effectiveness of such N fertilizer management was modulated by soil and climate factors, with greater benefits observed under lower bulk density and warmer temperatures. N fertilizer management in practice should follow the principle of defining the appropriate N application rate first, then matching the optimized N fertilizer type, and fine-tuning based on local soil-climate conditions and production objectives. Our findings demonstrate that shifting from conventional N application to synchronized management can achieve a win-win for maize productivity and nutritional security. These results provide a strategic framework for site-specific N management to optimize the soil-plant N balance under a changing climate.

Key words: Food security, Nitrogen fertilizer management, Maize, Grain yield, Protein content

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Multi-Omics Analysis Unraveling the Potential Mechanism of Flavor in Waxy Corn and Sweet Corn

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Abstract: [Objective] Different varieties of corn exhibit diverse and rich flavors, largely determined by the types and ratios of starches and sugars and their volatile substances. However, the processes of flavor compound formation and the mechanisms underlying flavor differences in various corn subspecies during kernel development remain unclear. [Method] We investigated sweet corn (Shenketian 811), waxy corn (Shenkenuo 602), and field corn (Zhengdan 958) using RNA-Seq and GC/LC-MS/MS to identify potential mechanisms of flavor-related compound formation at different developmental stages (14, 22, and 30 days after pollination, DAP). [Result] Sweet corn (Shenketian 811) had higher sweetness, with fructose, glucose, and sucrose levels higher than those in waxy (Shenkenuo 602) and field corn (Zhengdan 958), but lower glutinosity, with significantly lower total starch content and smaller starch granules. Metabolomics and RNA-seq analyses indicated that 22 DAP is a critical period for starch and sugar synthesis and metabolism in corn kernels. Analyses revealed significant differences in structural genes and metabolites related to starch and sucrose metabolism, glycolysis/gluconeogenesis, carbon fixation in photosynthetic organisms, and arginine biosynthesis in sweet and glutinous corn kernels 22 days after pollination. Essential structural genes, including *GPI*, *PGM*, and *SUS* for glucose formation, and *GBE1* for starch synthesis, were upregulated in glutinous corn compared to sweet corn. While the *INV*, *scrK* genes for fructose synthesis, and *WAXY* for amylose synthesis were downregulated in glutinous corn compared to sweet corn. Trend analyses showed significant differences in metabolic product patterns related to fatty acid metabolism, starch and sucrose metabolism, fructose and mannose metabolism, and various amino acid metabolism pathways between sweet and glutinous corn. [Conclusion] The transcription factors such as *AGL5*, *MADS2*, *MADS4*, *MADS6*, *MYB46*, and *MYB26* were highly expressed in sweet corn at all three stages compared to that in waxy corn and field corn. This is the first study to investigate the process of flavor formation in different corn varieties at the transcriptomic and metabolomic levels, identifying potential target genes and transcription factors for the research and regulation of these traits.

Key words: Fresh maize, Flavor variation, Sweet maize, Amino acids, Volatile compounds, Transcription factors

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Technical Session 6

New Challenges of Cross-Border Pests and Diseases



Effects of Maize (*Zea Mays* L.) Seed Treatment with *Beauveria* *Bassiana* on Growth, Endophytic Colonization, and Mortality of the Fall Armyworm (*Spodoptera Frugiperda*)

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Abstract: The objective of this study was to evaluate the effect of seed treatment with the fungus *Beauveria bassiana* Bb02 on maize growth, endophytic colonization, and fall armyworm mortality. The strain was activated on a medium composed of maize flour and wheat bran for 15 days, prepared at 1×10^8 conidia/ml with 0.05% Tween 80. A group of grains was added to the conidial solution, while another was soaked in sterile distilled water with 0.05% Tween 80 for 24 hours, then sown into pots filled with sterile substrate. Vegetative parameters, endophytic colonization, and larval mortality were assessed. The results showed that seed treatment significantly influenced germination rate, root length, and leaf surface area. The leaves were significantly colonized by the fungus compared to the control, and larval mortality was highly significant in larvae fed with leaves colonized by the fungus. These results highlight the effectiveness of strain Bb02 in endophytically colonizing maize plants, thereby reducing the pest population. The high colonization rates 14 days after emergence, coupled with significant larval mortality, suggest that maize can be spared from attacks by this pest at an early stage, as it remains most vulnerable.

Key words: Effects, Endophytic colonization, Mortality, *Spodoptera frugiperda*, *Beauveria bassiana*

Funding acknowledgments: We would like to acknowledge the Gates Foundation, AfricaRice, and National Nanfan Research Institute of CAAS for their support for NARS Capacity Building through the China-Africa Research Partnership (INV-075488) Program fellowship.

National Management and Surveillance Programme for *Spodoptera* *Frugiperda* (FAW) on Maize Crops in Malaysia

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Abstract: [Objective] The fall armyworm (FAW), *Spodoptera frugiperda* (Lepidoptera: Noctuidae), is a highly invasive, migratory, and polyphagous pest capable of causing substantial economic losses in maize production systems worldwide. Following its first detection in Malaysia in February 2019, a nationwide surveillance and Integrated Pest Management (IPM) programme was implemented to monitor infestation dynamics and mitigate crop damage in sweet corn and grain corn production systems. This study evaluated six years (2019–2024) of national surveillance data to assess FAW infestation trends and the effectiveness of coordinated IPM interventions in tropical maize agroecosystems. [Methods] Monthly monitoring data were collected through a nationwide Surveillance and Monitoring Programme coordinated by Plant Biosecurity Division, Department of Agriculture. Surveillance activities quantified monitored areas, infested areas, and FAW infestation rates. Integrated management interventions included farmer capacity-building programmes, systematic field scouting, pheromone trap deployment, and judicious insecticide application within an IPM framework. [Results] Following the initial invasion, FAW infestation rates reached 15.46% in sweet corn and 34.36% in grain maize production systems. Surveillance coverage expanded substantially during the study period, with monitored sweet corn areas peaking at 1,449.55 ha in 2021. Adoption of IPM practices was associated with a reduction in insecticide application frequency from 6–8 sprays to 2–3 sprays per cropping cycle. Concurrently, infestation rates in sweet corn declined to 2.67% in 2022 and subsequently stabilized at 5.86% in 2024. In contrast, grain maize production systems exhibited greater temporal variability, with infestation rates decreasing to 2.15% in 2022 before increasing to 24.23% in 2024. [Conclusion] The findings indicate that coordinated national surveillance integrated with IPM implementation can effectively suppress FAW outbreaks while reducing reliance on chemical control inputs in maize production systems. Nevertheless, the resurgence observed in grain maize suggests the continued invasion and establishment potential of FAW populations and indicates that agronomic factors, including asynchronous planting schedules and landscape-level host availability, may contribute to recurrent infestations. Long-term FAW management therefore requires adaptive surveillance strategies, continuous field monitoring, and sustained IPM implementation to minimize reinfestation risk and support sustainable maize production.

Key words: *Spodoptera frugiperda*, Pheromone traps, Pest surveillance

Mass Production of *Metarhizium Rileyi* Raroeng1 for Field Applications Against *Spodoptera Frugiperda* in Maize

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Abstract: [Objective] The entomopathogenic fungus *Metarhizium rileyi* Raroeng1, a local isolate obtained from naturally infected fall armyworm larvae (*Spodoptera frugiperda* J. E. Smith), has demonstrated vigorous growth on artificial media and high pathogenicity against the host under laboratory conditions. This study aimed to evaluate various low-cost and readily available solid substrates for mycelial growth and conidial production of *M. rileyi* Raroeng1 and to assess its efficacy against fall armyworm under field conditions. [Methods] Mass production of *M. rileyi* Raroeng1 was investigated using different plant-based solid substrates. Substrate performance was evaluated based on conidial yield and concentration. The biological control potential of the isolate was subsequently assessed in on-farm field trials conducted during 2025 and 2026. [Results] The highest conidial production was obtained on ground maize supplemented with ground rice, coconut residue and ground corn husks. Maize-based substrates produced significantly higher conidial yields at a lower production cost than other tested substrates. The addition of coconut residue and corn husks increased the available surface area for fungal colonization and sporulation, thereby enhancing conidial production. Based on these results, maize was selected as the substrate for large-scale fungal production for field application. Field evaluations demonstrated that foliar application of *M. rileyi* Raroeng1 at a concentration of 1×10^7 conidia mL⁻¹ significantly reduced both larval density and plant damage compared with the untreated control. Furthermore, its efficacy was not significantly different from that of the chemical insecticide treatment. [Conclusion] The findings demonstrate that maize is a suitable and cost-effective substrate for the mass production of *M. rileyi* Raroeng1. Furthermore, in planta evaluations confirmed that *M. rileyi* Raroeng1 possesses strong biocontrol potential against fall armyworm, causing high levels of larval mortality under field conditions. Therefore, this isolate represents a promising biological control agent for the sustainable management of *S. frugiperda* in maize production systems.

Key words: Biocontrol agent, Fall armyworm, *Nomuraea rileyi*, *Spodoptera frugiperda*

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Planting Time Shapes Fall Armyworm Infestation Dynamics and Associated Yield Loss of Maize in Bangladesh

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Abstract: In Bangladesh, maize is usually cultivated from early November to mid-December, however, recent intensification of cropping systems has expanded its cultivation period from October to March to accommodate region-specific patterns. The invasion of fall armyworm (FAW), *Spodoptera frugiperda* (J.E. Smith), in 2018 has since posed a serious threat to maize cultivation. This study assessed the seasonal dynamics of FAW infestation and its effects on maize under IPM and control conditions across six planting months over three consecutive years in the Old Himalayan Piedmont Plain (AEZ 1), Bangladesh. Field experiments followed a split-plot design with sowing month as the main plot and treatment as the subplot. Two treatments were applied: (i) IPM plots received seed treatment with cyantraniliprole followed by foliar applications of biopesticides, and insecticides; and (ii) an untreated control. Leaf infestation was assessed from V4-V12 stages, and cob damage, grain yield, and yield loss were recorded at harvest. Heatmap analysis showed consistently high infestation in control plots, peaking at 99.3% during February-March, whereas IPM plots maintained low infestation (<4%). Infestation in untreated control plots exhibited a U-shaped, non-linear response to planting time, described by a cubic polynomial model ($R^2 = 0.456$), with highest levels in October and March and lowest in December. Cob damage and damage intensity mirrored infestation patterns, with maximum damage in March (20.3%) and significantly higher values in control plots than IPM ones. Grain yield was significantly influenced by planting month and treatment, and their interaction. Yield loss also varied across planting month, with the highest losses in March (31.6%) and February (19.4%) and minimal losses during November-January (<3.3%). These findings demonstrate that combining October planting with the recommended IPM approach maximizes maize production, whereas planting from October to January without intervention helps reduce fall armyworm (FAW) infestation and maintain yield stability in Bangladesh.

Key words: Fall armyworm, Planting time, Yield loss, Maize, Bangladesh

Surveillance and Monitoring of Maize Diseases in Bangladesh with Special Emphasis on Fusarium Stalk Rot - An Emerging Threat for Maize Cultivation

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Abstract: [Objective] Maize, the most important cereal crop of Bangladesh faces growing biotic threats. During 2022–2026, assessed disease status across ten major maize growing districts. [Method] BWMRI pathologists recorded disease severity through smartphone-assisted field surveillance. [Result] Turcicum leaf blight was found most prevalent (30–80% severity) in all districts while Fusarium stalk rot (FSR) emerged as a major threat (40–100% severity) since its 2022 outbreak in Lalmonirhat, spreading to Chuadanga and Kurigram districts. Timely sowing and uses of proper fungicide reduces FSR severity at reproductive stage. Other diseases occurred at low levels. [Conclusion] This surveillance provides critical data for developing management strategies, recommending resilient hybrids, and strengthening biosecurity for Bangladesh's maize sector.

Key words: *Zea mays*, Surveillance, Turcicum leaf blight, Fusarium stalk rot, Biosecurity, Bangladesh

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Maize Lethal Necrosis Resistance Breeding: A Success Story from Discovery to Deployment

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Abstract: [Objective] This study summarizes progress in maize lethal necrosis (MLN) resistance breeding, from the discovery of resistance sources and genomic regions to fine mapping, marker development, and deployment of resistant lines and hybrids. It highlights the integration of doubled haploid (DH) technology, conventional breeding, marker-assisted backcrossing (MABC), and forward breeding to accelerate the development and dissemination of MLN-resistant maize germplasm in sub-Saharan Africa. [Method] Following the emergence of MLN in Eastern Africa in 2011, CIMMYT implemented multidisciplinary research strategies to combat the disease, including establishing the largest dedicated MLN screening facility at Naivasha, Kenya. Evaluation of thousands of maize inbred lines identified only a few effective resistance donors, notably KS23-5 and KS23-6. Linkage and association mapping identified a major recessive QTL, qMLN06_157, on chromosome 6, explaining 55–70% of the phenotypic variation and exhibiting stable effects across environments. Fine mapping of the KS23 genomic region led to the development of two tightly linked flanking markers, which are routinely deployed in marker-assisted forward breeding and backcrossing programs. [Results] Since 2013, the MLN facility has screened over 250,000 maize accessions (>400,000 rows) from several seed companies and research programs across sub-Saharan Africa under quarantine conditions. Deployment of the identified donors through DH technology and marker-assisted forward breeding resulted in the development of several MLN-resistant hybrids, some of which have been released in Eastern Africa. MABC converted more than 110 elite drought-tolerant lines into MLN-resistant versions, which subsequently replaced their susceptible counterparts in numerous hybrid combinations. MLN-resistant hybrids maintained grain yields of 3–5 t/ha under severe disease pressure, preventing the 80–100% yield losses observed in susceptible varieties. [Conclusion] A major MLN resistance QTL was identified, fine-mapped, and translated into breeder-friendly markers that are now routinely used in marker-assisted breeding. The integration of DH technology, marker-assisted forward breeding, and MABC has enabled the development of multiple MLN-resistant lines and hybrids, increasing the frequency of favorable resistance alleles to approximately 29% in early-stage breeding materials and strengthening the resilience of maize production systems in sub-Saharan Africa.

Key words: Maize, MLN, QTL, Resistance breeding

QTL Mapping and Candidate Gene Analysis for *Spodoptera frugiperda* Resistance in MTP Maize Introgression Lines

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Abstract: [Objective] Due to scarce resistant maize germplasm and strong *Spodoptera frugiperda* resistance in wild relatives (*Tripsacum* and *Euchlaena*), we developed an allohexaploid MTP combining maize, *Tripsacum*, and *Euchlaena* genomes, and generated introgression line 018 with superior *Spodoptera frugiperda* resistance via successive backcrossing and selfing. [Method] To identify novel resistance genes and elucidate the underlying mechanisms, two F₂ segregating populations were constructed by crossing resistant introgression line 018 with susceptible inbred lines Mo17 and B73. QTL for *Spodoptera frugiperda* resistance were jointly mapped using genetic linkage mapping and BSA-seq. Transcriptome sequencing was performed on leaves of line 018 and B73 at 0, 6, 9, 12, and 24 h post-infestation, and metabolome sequencing at 0 and 6 h. Candidate genes were screened by integrating QTL intervals with differentially expressed genes and metabolites. [Result] Phenotypic evaluation showed that line 018 exhibited resistance slightly lower than tetraploid *Tripsacum*, comparable to tetraploid *Euchlaena*, and significantly higher than Mo17 and B73. Resistance phenotypes in both F₂ populations followed normal distributions, indicating a quantitative trait. Using 170 SSR and 28 InDel markers, a genetic linkage map of 1,891.80 cM was constructed, and four QTLs were identified via ICIM, explaining 22.9% of total phenotypic variation. BSA-seq identified five candidate regions on Chr2, Chr6, Chr9, and Chr10. The Chr10 region (0–3.0 Mb) overlapped with QTL qSF-10-1 and contained 162 genes, of which four overlapped with differential omics data and were considered potential *Spodoptera frugiperda*-resistance genes. qRT-PCR confirmed that ZmRSF1 was significantly upregulated in 018 upon infestation, and homology analysis revealed an 11-bp *Tripsacum*-derived insertion in its promoter region. [Conclusion] Through integrated QTL mapping (linkage analysis and BSA-seq) combined with transcriptomic and metabolomic profiling, four candidate genes associated with FAW resistance were identified. Among them, ZmRSF1 was significantly upregulated in line 018 upon infestation, and an 11-bp *Tripsacum*-derived insertion was detected in its promoter region, which may contribute to its enhanced transcriptional regulation and resistance. This study provides valuable genetic resources and theoretical basis for insect-resistant germplasm innovation and marker-assisted breeding in maize.

Key words: *Spodoptera frugiperda*, Maize, QTL mapping, BSA-seq, Transcriptomics and metabolomics, Homology analysis

Developing Climate-Resilient Maize Against Emerging

Transboundary Pests: CIMMYT's Experience with Fall Armyworm

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Abstract: [Objective] This study identifies lessons from CIMMYT's response to Fall Armyworm that can inform the development of climate-resilient maize and strengthen preparedness against emerging transboundary pest threats. [Methods]: Since the emergence of the invasion of FAW into Africa in 2016, CIMMYT has implemented multidisciplinary research programs focused on host plant resistance. Specialized FAW artificial infestation and phenotyping platforms were established, enabling large-scale evaluation of maize breeding materials under controlled pest pressure. These efforts were supported through partnerships with national agricultural research systems, seed companies, and other stakeholders, facilitating the identification, validation, and deployment of resistant and tolerant germplasm. [Results] More than 10,000 maize genotypes were evaluated using one of the world's largest FAW artificial infestation and phenotyping platforms in public breeding programs. These efforts led to the identification of multiple donor lines with native genetic tolerance and the development of the first generation of FAW-tolerant maize hybrids which have been released in several African countries. The recent achievement is the successful identification of eight new maize hybrids that are now available for deployment through seed system partners across the region. The integration of entomology, breeding, and seed systems significantly strengthened the capacity to address these complex transboundary threats. [Conclusion] The FAW experiences demonstrate that rapid response to emerging transboundary threats requires integrated surveillance and early warning systems, pre-existing breeding pipelines, dedicated screening infrastructure, regional testing networks, and strong seed system partnerships.

Key words: Climate change, Fall armyworm (*Spodoptera frugiperda*), Resistance breeding, Regional collaboration

Factors Driving Nepalese Maize Farmers' Reliance on Inorganic Pesticides for Fall Armyworm (*Spodoptera frugiperda*) Management

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Abstract: This study examines the socio-technical drivers of synthetic pesticide reliance for fall armyworm (FAW), *Spodoptera frugiperda*, management among maize farmers in Nepal. A questionnaire-based survey was conducted among 20 commercial maize farmers and 10 agrovet dealers in western Nepal to assess farmers' pest-management practices, perceptions, access to alternative control options, and institutional constraints. The collected data were analyzed using descriptive statistics to identify the major factors influencing pesticide dependence. The findings revealed that the perceived need for rapid and reliable FAW control was the primary reason for continued reliance on synthetic pesticides. Limited availability of biological control options was reported by 83.3% of respondents, while 80.0% perceived biological and alternative control measures as slower in efficacy than synthetic pesticides. Poor awareness of integrated pest management (IPM) was identified by 73.3% of respondents, followed by weak agricultural extension services (70.0%) and limited access to technical training (66.7%). These findings indicate that pesticide dependence is driven not only by pest pressure but also by gaps in knowledge, technology access, extension support, and the availability of effective alternatives. Reducing dependence on synthetic pesticides requires a coordinated Integrated Plant Health and Ecological Management (IPHEM) approach that combines strengthened extension and farmer training systems, improved access to resistant maize cultivars, promotion and subsidization of effective biological and reduced-risk control products, and stronger technical and policy support. Such an approach can improve farmers' capacity to adopt diversified pest-management strategies, reduce unnecessary pesticide use, and enhance the resilience and sustainability of maize-based agroecosystems in Nepal.

Key words: FAW, Maize farmers, IPM, Pesticide dependence, Nepal.

Funding acknowledgement: CIMMYT International

Efficacy of Pyramid Bt Maize Expressing Cry1Ab + Vip3Aa Against Multiple Lepidopteran Pests, Fumonisin Reduction and Yield Improvement

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Abstract: [Objective] Field trial was conducted in 2025 year to assess the insecticidal efficacy of Bt maize event (Bt11 × MIR162 × GA21, Cry1Ab + Vip3Aa) against four major lepidopteran pests included *Conogethes punctiferalis*, *Helicoverpa armigera*, *Ostrinia furnacalis* and *Helicoverpa zea*, across all reproductive growth stages. To evaluate the effectiveness of transgenic maize in reducing the fumonisin contamination (FB1 and FB2), kernel injury, ear rot disease and grain yield improvement under the stress of major lepidoptran pest. [Method] The experiment was conducted at Xinxiang Experimental station Chines Academy of Agricultural Sciences using randomized complete block design. Larval population density was recorded by visual observation method on randomly selected plants. Insecticidal Bt protein concentration in different tissues and various stages were quantified using ELISA analysis, while fuminosin level was measured by LC-MS/MS technique. [Result] Field trial results reveled Bt maize showed significant reduction in larval density by 97.5-99% across all reproductive growth stages for four major lepidoptran pests. The total Bt protein level (Cry1Ab +Vip3Aa) followed the order Husk > silk> tassel >stem ≈ kernel with Cry1Ab dominant toxin in most tissues containing 72% (13 µg g⁻¹) in Silk, 70% (12 µg g⁻¹) in tassels, 67.8% (8.3 µg g⁻¹) in kernel and stem, while in contrast Vip3Aa was dominant in husk containing 56.7% (11.4 µg g⁻¹). As compared to non Bt maize, Bt maize grain yield increased 8.2%, fumonisin contamination level was reduced significantly FB1 by 84.3%, FB2 86.4% (total fumonisin 84.9%), with significant kernel injury and ear rot reduction as compared to non Bt maize. [Conclusion] The findings demonstrate pyramid of Bt maize expressing Cry1Ab and Vip3Aa insecticidal Bt protein provide broad pest control and contribute sustainable pest management strategy by reducing reliance on chemical insecticides. Genetically modified (GM) crops ensure food security by reducing fumonisin contamination, contribute to yield improvement by reducing losses and play a significant role in reducing the environmental footprint in global maize food system.

Key words: Bt (Cry1Ab +Vip3Aa), Lepidopteran pests, Bt insecticidal protein, Fumonisin, Grain Yield, Food safety, Field efficacy

Validation of QTLs Associated with Native Resistance to Fall Armyworm in Asia-Adapted Maize Lines

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Abstract: [Objective] Host plant resistance is an economical and environmentally sustainable approach for fall armyworm (FAW), *Spodoptera frugiperda*, management in maize. This study aimed to validate quantitative trait loci (QTLs) associated with native FAW resistance in Asia-adapted maize germplasm for use in forward breeding. [Method] A resistant inbred line, CML338, was crossed with the susceptible CML451 to develop 213 F_{2:3} families. The families and parents were evaluated under screenhouse conditions using artificial infestation with three neonate larvae per plant at 14 days after sowing. Leaf feeding damage was recorded at 7, 14 and 21 days after infestation using the Davis et al. (1992) scale. The experiment was conducted in an alpha-lattice design with two replications. The population was genotyped using 3,305 SNP markers, of which 674 high-quality markers were retained for linkage mapping. QTL analysis was performed using Inclusive Composite Interval Mapping with a LOD threshold of 2.5. [Result] Significant genotypic variation was observed for FAW damage, with LFS1 showing moderate heritability (0.29). Six minor QTLs were identified on chromosomes 2, 3, 5, 6 and 10, explaining 4.20–8.90% of phenotypic variation. The QTL qFAW3-1 (bin 3.04) showed the largest effect, while favorable alleles were contributed by CML338. Four QTLs co-localized with previously reported insect-resistance regions, supporting their potential role in broad-spectrum resistance. [Conclusion] These validated QTLs provide useful genomic resources for marker-assisted selection, QTL pyramiding and genomic selection toward durable FAW-resistant maize.

Key words: Fall armyworm, QTL, Linkage mapping, Marker assisted breeding

Funding acknowledgment: International Maize Improvement Consortium for Asia (IMIC-Asia), and the CGIAR Accelerated Breeding Initiative. Prof. Jayashankar Telangana State Agricultural University (PJTU).

Marker Trait Associations and Genomic Prediction for Fall

Armyworm Resistance in Asia Adapted Tropical Maize Germplasm

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Abstract:

[Objective] Fall armyworm (*Spodoptera frugiperda*) is one of the most destructive insect pests of maize, causing severe yield losses across tropical and subtropicals. Identifying genomic regions and molecular markers associated with FAW resistance is essential for accelerating marker-assisted breeding. [Methods] Present study, a panel of 260 Asia-adapted maize inbred lines was evaluated for FAW resistance during the rainy seasons of 2022 and 2023 using three leaf damage scores (LS1, LS2, and LS3) under artificial infestation in a partially replicated experimental design. The panel was genotyped with 3,305 genome-wide DArTag markers, together with 13 previously reported FAW-associated SNPs and 20 SSR markers. Genome-wide Association Analysis using a generalized linear model (GLM) identified six significant marker-trait associations for LS1 in 2022. [Results] Single marker regression analysis detected fourteen significant markers for LS1 and eight for LS2 across seasons. Stepwise regression models explained moderate proportions of phenotypic variation ($R^2 = 0.10-0.20$), with LS1 models ($R^2 = 0.16-0.20$) accounting for greater variation than LS2 models ($R^2 = 0.10-0.12$), indicating stronger genetic control during the early stages of FAW infestation. Genomic prediction using Bayesian Ridge Regression achieved moderate prediction accuracies of 0.54-0.60 for LS1 and 0.40-0.41 for LS2, demonstrating the potential of genomic selection for improving FAW tolerance. Overall, the study identified informative genomic regions and molecular markers associated with FAW resistance and highlighted the usefulness of genomic prediction for breeding resistant maize germplasm. [Conclusion] These findings provide a valuable foundation for validating candidate genes and integrating molecular and genomic approaches into sustainable FAW resistant maize breeding programs.

Key words: Markers, Associations, Candidate genes, Genomic selection

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Screening of Maize Inbreds for Resistance to Maize Shoot Fly(*Atherigona Naqyii*) and Associated Morpho-physiological and Biochemical Traits

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Abstract: [Objective] Shoot fly (*Atherigona naqyii*) is a major pest of maize causing significant yield losses through deadheart formation and plant stand reduction. This comprehensive two-year study screened 37 maize inbred lines against shoot fly under natural field conditions during summer seasons of 2025 and 2026. The evaluation encompassed multiple resistance mechanisms including ovipositional non-preference (antibiosis), larval feeding tolerance, and morpho-physiological traits associated with resistance. [Method] Key parameters recorded on 37 plants per genotype included plant stand, egg-laying patterns, leaf injury index (LII), and deadheart (DH) percentage. Resistance was categorized based on deadheart percentage: Resistant (R: <10% DH), Moderately Resistant (MR: 10-20% DH), Moderately Susceptible (MS: 20-35% DH), and Susceptible (S: >35% DH). [Result] Results revealed significant variation among genotypes for deadheart incidence. Teosinte, BC2F1 (LM13 × Teosinte), and selected BC3F lines exhibited high resistance with <10% deadheart. In contrast, CML139 and certain LM24 × Teosinte crosses were highly susceptible with >40% deadheart. Moderately resistant genotypes including BC3F4 (PML1245 × Teosinte), CM139, and VL109462 exhibited balanced antibiosis and tolerance mechanisms. Correlation analysis demonstrated that egg-laying preference and leaf injury intensity significantly predicted deadheart percentage ($p < 0.01$). These resistant lines represent valuable genetic resources for maize improvement programs and serve as excellent sources of shoot fly resistance in breeding for sustainable maize production. Integration of these resistance sources with high-yielding elite germplasm through strategic breeding will significantly contribute to mitigating shoot fly-related crop losses in shoot fly-prone regions. [Conclusion] This comprehensive two-year screening identified valuable sources of shoot fly resistance in maize inbred lines. The identified resistant and moderately resistant genotypes provide an excellent germplasm base for developing shoot fly-resistant maize cultivars suitable for regions with significant shoot fly pressure. The integration of these resistance sources with high-yielding elite germplasm through strategic breeding will contribute to sustainable maize production and enhanced food security in affected regions.

Key words: Maize, Shoot fly resistance, Antibiosis, Tolerance, Deadheart, Leaf injury index, Germplasm screening, Resistance mechanisms

Single-nucleus Transcriptomics Reveals Hormone Immune Pathway Regulation in Maize during *Cochliobolus Heterostrophus* Infection

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Abstract: [Objective] Southern corn leaf blight, caused by *Cochliobolus heterostrophus*, is an important foliar fungal disease that severely affects maize yield and quality. This study aimed to characterize cell-type-specific immune responses in maize leaves during *C. heterostrophus* infection using single-nucleus RNA sequencing and to identify key responsive cell types and defense-related pathways. [Method] Maize inbred line B73 was inoculated with a conidial suspension of *C. heterostrophus* by foliar spraying, and leaf samples were collected at 0, 6, 18, and 72 h post-inoculation (hpi). Fungal infection processes were observed by WGA-AF488 fluorescence staining combined with confocal laser scanning microscopy. In parallel, nuclei were isolated from maize leaves, and single-nucleus RNA-seq libraries were constructed and sequenced using the DNBelab C4 platform. Raw sequencing data were processed with dnb4tools to generate gene expression matrices. Seurat was then used for quality control, normalization, dimensionality reduction, clustering, and cell-type annotation. Differential expression analysis, Monocle2-based pseudotime analysis, and GO and KEGG enrichment analyses were further performed to dissect the transcriptional responses of distinct cell populations during pathogen infection. [Result] Single-nucleus transcriptome analysis resolved maize leaf cells into five major cell types and two unassigned clusters. Pseudotime analysis indicated that 6 hpi was a critical early response stage to *C. heterostrophus* infection, characterized by extensive transcriptional reprogramming. KEGG enrichment analysis highlighted MAPK signaling and plant hormone signal transduction as major immune-related pathways. Guard cells and vascular bundle cells showed the strongest transcriptional responses. Guard cells mainly activated genes related to metabolism, stress regulation, and defense, whereas vascular bundle cells exhibited stage-specific hormone signaling, with SA-related responses mainly occurring at 18 and 72 hpi and JA/ET-related responses at 6 and 72 hpi. [Conclusion] This study reveals cell-type-specific immune responses of maize leaves to *C. heterostrophus* infection at single-nucleus resolution. The results indicate that 6 hpi is an important time point for early defense activation and that guard cells and vascular bundle cells may serve as key cell types involved in resistance to southern corn leaf blight. MAPK signaling and SA, JA/ET mediated hormone signaling pathways play important roles in maize defense against *C. heterostrophus*, providing a basis for further elucidation of cell-type-specific resistance mechanisms and identification of key disease-resistance genes in maize.

Key words: Maize, *Cochliobolus heterostrophus*, SA/JA

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Resistance of Corn Leaf Aphid *Rhopalosiphum maidis* to Imidacloprid and Lambda-cyhalothrin and Analysis of CYP Gene Expression in Northern China

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Abstract: [Objective] To clarify the resistance status and molecular mechanisms of the corn leaf aphid *Rhopalosiphum maidis* to neonicotinoid insecticides, such as imidacloprid and pyrethroid insecticides, such as lambda-cyhalothrin. [Method] Resistance monitoring and cytochrome P450 monooxygenase (CYP) gene expression analysis was conducted in ten geographical populations collected from northern China, using the leaf-dip method, and key genes were functionally validated by RNA interference. [Result] The results showed that all ten geographical populations of *R. maidis* had developed varying degrees of resistance to imidacloprid and lambda-cyhalothrin, with resistance ratios ranging from 1.6- to 32.7-fold and from 1.1- to 12.5-fold, respectively, showing clear geographical variation. Among them, the Yuanyang (Henan) and Zhenping (Henan) populations showed the highest resistance levels, with resistance ratios of 32.7- and 26.2-fold to imidacloprid and 12.5- and 9.7-fold to lambda-cyhalothrin, respectively. In highly resistant populations, the baseline expression levels of several CYP genes (RmCYP6ER1, RmCYP6C71, RmCYP6C72) were significantly higher than those in the susceptible population. Under exposure to the LC50 of imidacloprid or lambda-cyhalothrin, the expression levels of these genes were significantly upregulated within 24 h and remained high within 48 h. Moreover, resistance levels in different geographical populations were significantly positively correlated with CYP gene expression levels. Silencing these key CYP genes significantly restored the susceptibility of highly resistant populations to both insecticides. [Conclusion] These results indicate that *R. maidis* populations in northern China have developed resistance to both imidacloprid and lambda-cyhalothrin, and that CYP-mediated enhanced metabolism is a key molecular mechanism underlying this resistance.

Key words: *Rhopalosiphum maidis*, Imidacloprid, Lambda-cyhalothrin, Insecticide resistance, CYP gene expression

Fungal Pathogens Causing Maize Leaf Spot in Heilongjiang: Isolation, Identification and Biological Traits

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Abstract: [Objective] Maize is an important global cereal crop and a key guarantee for China's agricultural economy and food security. Maize leaf spot has become a prevalent and serious foliar disease in cold-temperate regions, causing severe yield losses due to its high field incidence rate. However, the species diversity and composition of fungal pathogens triggering maize leaf spot in Heilongjiang Province remain unclear. This study aimed to clarify the fungal pathogenic composition of maize leaf spot in Northeast China, clarify the biological characteristics of dominant pathogens, and provide basic theoretical data for disease diagnosis, pathogen monitoring and scientific prevention and control of the disease in cold-temperate farming areas. [Method] In this study, diseased maize leaf samples with typical leaf spot symptoms were collected from major maize producing areas in Heilongjiang Province. The fungal pathogens were isolated and purified from the symptomatic samples. Combined with morphological observation, biological characteristic determination and ITS sequence molecular identification technology, the pathogenic fungal species of maize leaf spot were accurately identified, and the adaptability of pathogens to different culture conditions was systematically analyzed. [Result] Three fungal strains were successfully identified as the pathogenic fungi of maize leaf spot, namely *Epicoccum sorghinum*, *Didymella pomorum* and *Phoma herbarum*. Biological characteristic tests showed that the three pathogens had strong environmental adaptability and could utilize a variety of carbon sources for growth. The optimal growth conditions for mycelia of the three fungi were temperature of 20–25°C and pH value of 6–8, showing good adaptability to the ecological environment of cold-temperate regions. [Conclusion] This study definitively clarifies the composition of pathogenic fungi of maize leaf spot in Northeast cold-temperate maize producing areas. It systematically reveals the basic biological growth characteristics of the main pathogenic strains. The research results can provide fundamental data and technical support for field disease diagnosis, dynamic pathogen monitoring, and the formulation and application of integrated pest management strategies for maize leaf spot in cold-temperate agroecosystems.

Key words: Maize leaf spot, Fungal pathogens, Isolation and identification, Biological characteristics, Cold-temperate region

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Detection and Genomic Sequence Analysis of Sugarcane Mosaic Virus and Maize Yellow Mosaic Virus in Mixed-Infected Maize from Pu'er, China

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Abstract: [Objective] Maize (*Zea mays* L.) is a major grain and feed crop in China, and maize viral diseases have caused intermittent, large-scale outbreaks in several regions in recent years, threatening yield and quality. Sugarcane mosaic virus (SCMV) and Maize yellow mosaic virus (MaYMV) are transmitted by aphid vectors and can also be seed-transmitted; both have been increasingly reported in southwestern China, yet the virus spectrum and genetic diversity in Pu'er, Yunnan remain poorly characterized. This study aimed to identify the viruses associated with necrotic leaf symptoms in maize from Pu'er and to elucidate their genetic relationships and potential transmission routes. [Method] Diseased maize leaf samples exhibiting necrotic symptoms were collected from Pu'er, Yunnan Province. Reverse transcription-polymerase chain reaction (RT-PCR) was applied for molecular detection of the suspected samples. Metavirome sequencing and whole-genome genetic evolutionary analysis were performed to characterize viral diversity in the samples and reveal the genetic evolutionary traits of viral isolates. [Result] RT-PCR detection showed specific bands of expected sizes for Sugarcane mosaic virus (SCMV) and Maize yellow mosaic virus (MaYMV), whereas no target band of MCMV was detected. Meanwhile, metavirome sequencing verified mixed infection of SCMV and MaYMV at the genomic level and ruled out MCMV infection, the absence of MCMV also ruled out maize lethal necrosis (MLN). Phylogenetic analysis indicated that SCMV isolates from Yunnan shared the closest genetic relationship with the Nakhon Sawan isolate from Thailand (MW248339), while MaYMV isolates exhibited the highest homology with Chinese isolates (MN814307.1). These findings suggest that SCMV in Yunnan may have been introduced through international germplasm exchange or vector insect transmission, whereas MaYMV may be associated with viral spread across other regions of China. Further research on viral transmission routes and insect vectors is required to clarify the origin and dispersal mechanisms of these viruses. [Conclusion] This study Combined RT-PCR detection and metavirome sequencing confirmed that mixed infection of SCMV and MaYMV triggered local leaf necrosis in the investigated area, and clarified the genetic evolutionary characteristics of viral isolates. The results provide important scientific support for the monitoring and management of maize viral diseases, as well as technical references for viral diversity research and novel virus identification. Further investigations into viral transmission mechanisms, pathogenic pathways and integrated management strategies are needed to mitigate the damages caused by viral diseases to maize production.

Key Words: Maize, Maize yellow mosaic virus, Sugarcane mosaic virus, Metavirome sequencing

A Phosphorylation-Gated Sugar Transporter Confers Broad-spectrum *Cercospora* Resistance in Crops

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Abstract: [Objective] Leaf spot diseases caused by *Cercospora* spp. represent a persistent threat to global crop production security, yet the number of broad-spectrum resistance genes identified to date remains extremely limited. [Method] By using map-based cloning and GWAS to identify *ZmPMT1* as the causal gene underlying the resistance effect of *qGLS1.02*; the phosphorylation-gated glucose transport activity was demonstrated through electrophysiological, biochemical, and phosphoproteomic analyses; field trials across multiple seasons and crops (maize, sorghum, and soybean) validated its broad-spectrum resistance against *Cercospora* spp., confirming that *ZmPMT1* confers effective resistance across diverse cropping systems. [Result] Here, we report that *ZmPMT1*, a previously uncharacterized member of the polyol/monosaccharide transporter (PMT) subfamily, confers broad-spectrum resistance to *Cercospora* spp., a not previously attributed function to this family. Unlike previously characterized sugar transporters with intrinsic transport activity, *ZmPMT1* requires phosphorylation by the pattern-triggered immunity (PTI) core kinase ZmCERK1 to activate its glucose transport function. Mechanistically, *ZmPMT1* confers disease resistance via a dual mechanism: it limits pathogen growth by reducing apoplastic glucose, and simultaneously activates MAPK signaling, plant-pathogen interaction and defense genes including *ZmCCoAOMT2* and *ZmWAKL*. Notably, *ZmPMT1* also confers cross-species resistance: it acts against two major maize pathogens, *C. zea-maydis* and *C. zeina*, as well as *C. sorghi* in sorghum and races 1 and 7 of *C. sojae* in soybean. [Conclusion] Our findings identify phosphorylation-gated sugar transport as a broad-spectrum resistance mechanism, providing a genetic strategy for control of *Cercospora* leaf spot diseases in crops.

Key words: Maize, Map-based cloning, Sugar transporter, Apoplastic glucose, Broad-spectrum resistance

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A Jasmonate Pathway Regulator *ZmJAZ12* Modulates Drought Tolerance, Disease Susceptibility, and Reproductive Development in Maize

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Abstract: [Objective] Jasmonic acid (JA) is a plant hormone widely present in higher plants and is recognized as a key regulator in activating plant defense systems against pathogens, insects, and abiotic stresses such as drought and cold. Recent studies have also revealed that JA signaling is involved in regulating plant growth and development in addition to defense responses. This study aimed to dissect the genetic and molecular basis of JA signaling components in balancing growth and defense in maize (*Zea mays* L.). [Method] We selected multiple gene families involved in the JA signaling pathway as candidates and employed more than 500 representative maize inbred lines as experimental materials. Phenotypic data included multi-year and multi-location measurements of flowering-related traits, drought survival rate, and resistance to major foliar diseases including northern leaf blight, southern leaf blight, southern corn rust, and gray leaf spot. Genome-wide association studies (GWAS) and candidate gene association analyses were conducted. Functional verification of candidate genes was performed using overexpression and genome editing lines, combined with transcriptome profiling, as well as molecular interaction assays including LCI, Y2H, and Co-IP. [Result] Genetic variation in *ZmJAZ12*, a member of the JAZ gene family, showed significant associations with drought survival rate, resistance to southern corn rust, anthesis date, and the anthesis–silking interval. Functional assays demonstrated that *ZmJAZ12* overexpression enhanced drought tolerance at the seedling stage but increased susceptibility to southern corn rust at maturity. It also shortened anthesis date and prolonged the anthesis–silking interval. Moreover, *ZmJAZ12* significantly influenced the expression of JA pathway-related genes and interacted with JA-responsive transcription factors *ZmMYC5* and *ZmMYC6*. [Conclusion] Collectively, this study identifies a novel molecular module of *ZmJAZ12* that functions in maize's JA signaling pathway, coordinating the trade-off between growth and defense. These findings provide new insights into the molecular mechanisms underlying growth-defense balance and offer promising genetic targets for maize breeding programs aiming to simultaneously enhance stress tolerance and yield.

Key words: Maize (*Zea mays* L.), JAZ-MYC signaling, Jasmonate-salicylate pathway

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The Dual-Chromosome Defense Axis: Genomic Hubs of *Striga* Resistance in Tropical Maize

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Abstract: [Objective] *Striga hermonthica* remains a major biological constraint to maize production causing large economic losses in sub-Saharan Africa. Dissecting the genetic basis of host defense is essential for identifying elite sources of resistance and designing effective breeding strategies. Genomics-enabled approaches have the potential to accelerate the discovery of *Striga*-resistant germplasm, facilitate the identification of resistant-associated loci, and enhance the efficiency of *Striga*-resistant hybrid development. This study aimed to elucidate the genetic architecture and genomic basis of *Striga* resistance in tropical maize and to evaluate the potential of genomic selection for improving *Striga* resistance. [Method] A panel of 761 tropical maize inbred lines was phenotyped under artificial *Striga* infestation. Data were collected on plant height (PH), the number of emerged *Striga* plants at 8, 10, and 12 weeks after planting (STR8WAP, STR10WAP, and STR12WAP, respectively), *Striga* damage rating at 10 and 12 weeks after planting (SDR1 and SDR2), and the area under *Striga* number Progress curve (AUSNPC). The inbred lines were genotyped using 995,670 GBS markers from which 151,670 high quality markers were retained for association mapping analysis and genomic prediction. [Results] Marker-trait association analysis revealed a major dual-chromosome regulatory axis involving chromosomes 2 and 7 that appears to govern key components of the maize-*Striga* interaction, from early metabolic sensing to late-stage tissue preservation. Chromosome 2, (PVE = 47.6%) emerged as a major multi-trait locus influencing metabolic, homeostatic, and structural defense responses throughout the infestation period. The loci in this region were associated with energy-sensing networks and growth-defense trade-offs via FLZ-type domain-containing proteins, cellular signaling and translation through calcium-transporting ATPase and ubiquitin-specific protease at early-stage host response (STR8WAP and SDR1). Furthermore, chromosome 2 appeared to contribute to the maintenance of shoot elongation under parasitic pressure through genes modulating gibberellin homeostasis (2-oxoglutarate and Fe(II)-dependent oxygenase) and osmotic stress adaptation through an abscisic stress-ripening protein. In contrast, chromosome 7 (PVE = 10.5%) appeared to function as a specialized defense locus associated with post-attachment resistance and preservation of host tissue integrity. Candidate genes in this region were primarily involved in defense signaling, transcriptional regulation, parasite recognition, and cell wall modification, indicating roles in activating immune responses and reinforcing structural barriers against parasite establishment. Additional loci on chromosomes 7 encoded E3 ubiquitin transferases involved in protein turnover, highlighting the importance of

ubiquitin-mediated regulation in sustaining defense responses and maintaining host structural integrity under prolonged parasite pressure. Prediction accuracies across locations ranged from 0.24 to 0.53 for *Striga* resistance-associated traits and reached 0.59 for grain yield, indicating moderate predictive ability. [Conclusion] Together, these findings suggest that *Striga* resistance in tropical maize is governed by an integrated defense network in which chromosome 2 contributes broad-spectrum metabolic and adaptive responses, whereas chromosome 7 provides specialized immune and structural defense functions. Further investigation of these genomic regions could uncover high-impact candidate genes and targets for developing durable, multi-stage *Striga*-resistant tropical maize germplasm with the integration of genomic selection into breeding programs across sub-Saharan Africa.

Key words: *Zea mays* L., *Striga hermonthica*, Gnomonic architecture, Marker-trait association, Genomic selection

Population Genomics of *Cercospora Zeina* Reveals a Clonal, Highly Structured Lineage Causing Maize Gray Leaf Spot in China

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Abstract: [Objective] Gray leaf spot, caused by *Cercospora zeina* and its sister species *C. zeae-maydis*, has become a serious disease of maize in China, yet the population genetics of Chinese *C. zeina* remains uncharacterized using genomic data. Here we characterize the genetic diversity, demographic history and population structure of Chinese *C. zeina* and identify its candidate secreted effector proteins. [Method] We performed whole-genome resequencing for 19 *C. zeina* isolates using an Illumina platform (paired-end 150-bp reads; mean depth ~135×, range 111–156×). Our strain panel consisted of 17 field isolates collected across nine provinces sampled in 2023 (n = 9) and 2024 (n = 8), plus one reference isolate from South African. The publicly available Yunnan *C. zeina* reference genome (accession GCA_022702355.1) was used for read mapping and variant calling. After quality control (Q30 ≥ 96.5%, 99.5–100% of reads mapped), we called 108,962 high-quality biallelic SNPs against the 42.2-Mb reference, then estimated nucleotide diversity (π), FST, and Tajima's D. Population structure was assessed using PCA, LD decay, and model-based clustering (K = 2). Candidate secreted proteins were identified via genome-wide FST scan combined with orthology-based functional annotation. [Result] All Chinese isolates showed uniformly low nucleotide diversity ($\pi \approx 5.6 \times 10^{-4}$). These Chinese isolates were highly genetically differentiated from the South African isolate (mean FST = 0.84). Moderate genetic differentiation was also observed between the 2023 and 2024 collections (mean FST = 0.66). Tajima's D averaged near zero, which pointed to a clonal, demographically stable population. PCA, a flat LD profile that did not decline with physical distance ($r^2 \approx 0.21$ – 0.30 over 1–99 kb), and a clean K = 2 split all indicated a strongly structured, clonal population with little gene flow. Genome scans highlighted 100 candidate 50-kb windows; orthology-based transfer annotated 1,868 genes and recovered 82 secreted candidates, which were dominated by cell-wall-degrading enzymes, with a minority matching known effector-domain families (e.g., SCP/TAPS, thaumatin-like proteins). [Conclusion] The Chinese *C. zeina* population forms a clonal, geographically and temporally structured lineage with little detectable recombination. The 82 secreted candidates represented prime targets for subsequent virulence functional assays. Given its strictly clonal reproduction, any single fungicide-resistance mutation could rapidly disseminate across major maize-producing provinces. Therefore, systematic resistance surveillance is required throughout core maize-growing regions.

Key words: Gray leaf spot, *Cercospora zeina*, Population genomics, Clonal lineage, Maize

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Genomic Dissection of Major Foliar Disease Resistance in Maize

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Abstract: [Objective] Turcicum leaf blight (TLB) and Maydis leaf blight (MLB) are among the most destructive foliar diseases limiting maize productivity worldwide. Identifying resistant germplasm and genomic regions controlling disease resistance is essential for developing durable resistant cultivars through genomics-assisted breeding. This study employed quantitative trait loci (QTL) mapping and genome-wide association studies (GWAS) to elucidate the genetic basis of resistance to MLB and TLB, respectively. [Method] For MLB, 112 maize inbred lines were screened under artificial epiphytotic conditions across multiple locations, identifying 25 resistant genotypes. Generation mean analysis indicated the predominance of dominance effects with significant additive $\times$ additive gene interactions. A recombinant inbred line (RIL) population comprising 198 F₉ lines derived from CML 269-1 (resistant) $\times$ HKI PC4B (susceptible) was evaluated across seven environments (2020–2025) and genotyped using 6,527 SNP markers spanning 2,124.30 cM. [Result] QTL mapping identified 15 QTLs on chromosomes 1, 2, 3, 5, 6, 8, and 10, with LOD scores ranging from 3.0 to 20.3 and explaining 6.2–13.4% of the phenotypic variance. Seven significant epistatic interactions were also detected. A total of 271 candidate genes, including 82 orthologous genes, were identified within QTL intervals. For TLB, a panel of 384 diverse maize inbred lines was evaluated across four disease hot-spot locations and genotyped with 60,227 high-quality SNPs. GWAS identified 16 significant marker-trait associations distributed across seven chromosomes, each explaining 23–30% of the phenotypic variation. Eighteen candidate genes and five orthologous genes were identified within associated genomic regions, primarily involved in cellular organization, molecular binding, and defense-related biological processes. [Conclusion] These findings provide valuable genomic resources and molecular targets for marker-assisted breeding and genomic selection to accelerate the development of maize cultivars with durable resistance to both MLB and TLB.

Key words: Maize, Turcicum leaf blight, Maydis leaf blight, Quantitative trait loci, Genome wide association studies, Candidate genes

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Pan-genomic Dissection of The Genomic Trade-off Between Yield and Disease Resistance in Wheat

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Abstract: [Objective] Conventional breeding theory posits a genetic trade-off between grain yield and disease resistance in wheat. This study seeks to construct an orthology-based wheat pan-genome that includes wild diploid progenitors and modern cultivars. It aims to analyze the patterns of yield-related and disease-resistance ortho-groups, investigating how polyploidization and domestication affect the genetic relationship between these key agronomic traits, with the goal of providing genomic evidence for the simultaneous enhancement of both wheat yield and stress resistance. [Method] A total of 37 high-quality wheat genome assemblies with BUSCO completeness over 90% were collected, including wild diploids, durum tetraploids and Chinese & international hexaploid wheat varieties. OrthoFinder was adopted to generate genome-wide ortho-groups, and eggNOG-mapper was used for functional annotation to classify 1,244 yield-associated and 1,123 disease-resistance-associated ortho-groups. We partitioned ortho-groups into core, shell and cloud pan-genome compartments, applied PCA to analyze functional gene population differentiation, adopted non-parametric Spearman correlation to quantify trait gene co-variation at ploidy, domestication and sub-genome levels, and further characterized chromosomal distribution and PFAM domain composition of two gene categories. [Result] Yield ortho-groups were mainly enriched in the stable core pan-genome (59.7%), while resistance ortho-groups were predominantly distributed in variable shell and cloud compartments (72.2%), showing distinct evolutionary conservation differences. Wild diploid wheat presented a weak negative correlation between yield and resistance gene counts ($\rho=-0.285$, non-significant), whereas tetraploid and hexaploid wheat exhibited strong significant positive correlations; among three sub-genomes, the B sub-genome possessed the strongest coordinated relationship ($\rho=0.855$). Domestication process did not induce overall loss of yield or resistance ortho-groups. Yield gene families were dominated by MYB, GRF transcription factors, while resistance ortho-groups were mainly composed of NB-ARC immune receptor domains. [Conclusion] Polyploidization fundamentally breaks the traditional yield-resistance trade-off constraint in wheat by generating functional genomic redundancy, and the B sub-genome acts as a key coordinator yield-related and disease resistant-related genes. The pan-genomic resources and evolutionary rules identified in this research can guide targeted mining of resistance germplasm and AI-assisted multi-trait genomic selection, supporting the breeding of high-yield and disease-resistant wheat varieties.

Key words: Pan-genome analysis, Wheat genomics, Yield-resistance trade-off, Polyploidy, Artificial intelligence

QTL Mapping of Adult Plant Resistance to Stripe Rust and Leaf Rust in a Fuyu 3/Zhengzhou 5389 Wheat Population

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Abstract: [Objective] Stripe rust (YR) and leaf rust (LR), caused by *Puccinia striiformis* f. sp. *tritici* and *Puccinia triticina*, respectively, are among the most devastating diseases in wheat production worldwide. This study aimed to identify quantitative trait loci (QTL) conferring adult plant resistance (APR) to both rusts in a Fuyu 3/Zhengzhou 5389 recombinant inbred line (RIL) population. [Method] A total of 147 F₂:6 RILs derived from the cross Fuyu 3 × Zhengzhou 5389 were genotyped using the Wheat55K single nucleotide polymorphism (SNP) array and simple sequence repeat (SSR) markers. All materials were phenotyped for YR severity at Mianyang, Sichuan, and Baoding, Hebei, over the 2015/2016, 2016/2017, and 2017/2018 cropping seasons, and for LR severity at Zhoukou, Henan, and Baoding in 2017/2018. QTL detection was performed using the inclusive composite interval mapping (IciMapping). [Result] Eleven QTL for YR resistance and five for LR resistance were identified. Four QTL located on chromosomes 1BL, 2BS, 3AL, and 5AL conferred resistance to both YR and LR where the QTL on 1BL was confirmed as *Lr46/Yr29*, the QTL on 7BL was likely *Lr68*, and six loci including *QYr.hebau-3AL/QLr.hebau-3AL*, *QYr.hebau-5AL/QLr.hebau-5AL*, *QYr.hebau-7DL*, *QYr.hebau-4BS*, *QYr.hebau-6DL*, and *QYr.hebau-2AS* were identified as potentially new resistance loci. An SSR marker for *QYr.hebau-7DL* was developed and validated across a diverse Chinese wheat panel, confirming its effectiveness in different genetic backgrounds. [Conclusion] This study identified multiple stable APR QTL for wheat stripe rust and leaf rust, including several potentially novel loci, and developed a validated molecular marker for *QYr.hebau-7DL* that can be directly deployed in marker-assisted selection for durable rust resistance breeding.

Key words: Wheat, Stripe rust, Leaf rust, QTL mapping, Adult plant resistance, Marker-assisted selection

Effects of Maize Seed Treatment (*Zea mays* L.) with *Beauveria* *Bassiana* on Growth, Endophytic Colonization, and Mortality of the Fall Armyworm (*Spodoptera Frugiperda*)

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Abstract: [Objective] The objective of this study was to test the ability of the Bb02 strain of *Beauveria bassiana*, isolated in 2025 from the carcass of a planthopper (*Sogatella furcifera*), to promote maize growth, to colonize its leaves through seed treatment, and to control the population of *Spodoptera frugiperda*. [Method] The strain was cultured in Goettel medium for 15 days. After this period, spores were prepared using a Malassez cell at a concentration of 1×10^8 conidia/ml, with 0.05% Tween 80. The disinfected seeds were soaked for 24 hours (treated groups), while another untreated group was soaked in sterile distilled water containing 0.05% Tween 80. These grains were then sown in pots filled with sterilized potting soil, with two treatments (treated and untreated) and ten replicates per treatment. Growth parameters were measured at 7 and 28 days after emergence, and endophytic colonization was assessed on the penultimate leaf of the apical and basal positions at 14 and 21 days after emergence. Second-stage larvae were reared in the laboratory and fed colonized and non-colonized leaves inoculated with the fungus to assess mortality. [Result] The results showed that seed treatment significantly influenced some vegetative parameters (germination rate, root length, leaf surface area), that the leaves were significantly colonized by the fungus compared to the control, and that larval mortality was highly significant in larvae fed with leaves colonized by the fungus. The fungus was detected in the leaves after inoculation on PDA culture medium, with a decrease in colonization between samples taken at 14 and 21 days post-inoculation. Leaves colonized by the fungus showed higher larval mortality than non-colonized leaves. [Conclusion] These results highlight the effectiveness of strain Bb02 in endophytically colonizing maize plants, thereby reducing the pest population. The high colonization rates 14 days after emergence, coupled with significant larval mortality, suggest that maize can be spared from attacks by this pest at an early stage, as it remains most vulnerable. These results are only applicable under laboratory conditions and need to be evaluated in real-world settings to confirm the efficacy observed in controlled environments.

Key words: Effect, Endophytic colonization, Mortality, *Spodoptera frugiperda*, Invasion

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The Molecular Mechanism and Application of MAPK Signaling Pathway in Regulating the Cry1Ab Resistance of *Ostrinia furnacalis*

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Abstract: [Objective] The Asian corn borer (*Ostrinia furnacalis*) is a major pest of maize, and the widespread cultivation of Bt maize has imposed continuous selection pressure, increasing the risk of resistance evolution. Although the MAPK signaling pathway has been shown to regulate Bt resistance in *Plutella xylostella*, its role in *O. furnacalis* remains unclear. Therefore, this study aims to identify and characterize MAPK pathway genes in *O. furnacalis* and to investigate their functional involvement in regulating Cry1Ab resistance. [Method] Candidate MAPK genes were screened based on annotated MAPK pathway genes from the *P. xylostella* genome. Three genes (*OfMAP3K4*, *OfP38*, and *OfMAP3K7*) were cloned and subjected to bioinformatics analysis, including sequence characterization, protein structure prediction, and phylogenetic tree construction. qPCR was used to examine their expression across developmental stages, tissues, and in response to Cry1Ab toxin exposure at different concentrations and time points. RNA interference (RNAi) was then employed to silence these genes in both Bt-susceptible and Bt-resistant strains, and the resulting changes in larval susceptibility to Cry1Ab toxin and transgenic Bt maize (Denghai 605D) were evaluated through bioassays. [Result] The three cloned genes encode proteins of 361-1546 amino acids, are localized in the cytoplasm, and show high homology to their counterparts in *O. nubilalis*. They are ubiquitously expressed throughout all developmental stages, with relatively high expression in adults and notably high expression in the midgut of both susceptible and resistant larvae. Cry1Ab toxin exposure significantly upregulated their expression, with distinct temporal patterns depending on concentration. RNAi effectively silenced all three genes, and silencing of any individual gene reduced the expression of the other two, indicating coordinated regulation. Bioassays showed that larval mortality differed significantly from the control group after RNAi treatment, and the susceptibility of the resistant strain to Cry1Ab toxin and transgenic maize was significantly enhanced. [Conclusion] The MAPK signaling pathway genes *OfMAP3K4*, *OfP38*, and *OfMAP3K7* are involved in the regulation of Cry1Ab resistance in *O. furnacalis*. Silencing these genes increases larval susceptibility to Cry1Ab, providing a theoretical basis for the combined application of RNAi-based pesticides and Bt transgenic crops to delay the evolution of insect resistance.

Key words: *Ostrinia furnacalis*, Cry1Ab, MAPK, Resistance management

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A New Plant SUMO Ligase, MPEL1, Synergizes with MAPK16 to Regulate Resistance Against *Fusarium* Pathogens

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Abstract: [Objective] *Fusarium* pathogens cause destructive maize ear and stalk rot with heavy yield losses and mycotoxin hazards. Plant SUMO ligase resources remain limited, and the regulatory link between D-subgroup MAPKs and JA repressor JAZ proteins is elusive. This study aimed to uncover a novel SUMO ligase and its MAPK16-centered cascade conferring *Fusarium* resistance without yield penalties. [Method] We generated MAPK16 overexpression, *mapk16*, *mpel1* and *jaz20* knockout maize lines for pathogen inoculation and yield evaluation. Y2H, BiFC, CoIP and pull-down verified protein interactions, while in vitro/in vivo SUMOylation, ubiquitination, phosphorylation and degradation assays clarified biochemical functions. Transcript and proteome profiling detected defense signaling outputs. [Result] MAPK16 positively regulated broad-spectrum resistance to *F. verticillioides* and *F. graminearum*; its overexpression boosted immunity without yield reduction. MPEL1, a STUB1-homologous protein, functioned as a new cytoplasmic SUMO ligase that bound MAPK16's N-terminus and SUMOylated MAPK16 at Lys526 to stabilize it. Stabilized MAPK16 interacted with JAZ20 via its C-terminal domain and phosphorylated JAZ20 at Thr12/Ser13, triggering 26S proteasome-dependent JAZ20 degradation to release JA defense signals. *jaz20* knockout enhanced disease resistance with no yield loss, whereas *mpel1* mutation weakened stalk and leaf resistance. [Conclusion] We identified MPEL1 as a novel plant SUMO ligase and established the MPEL1-MAPK16-JAZ20 immune cascade. MAPK16 overexpression and JAZ20 knockout are promising breeding targets to develop high-yield maize with durable *Fusarium* resistance.

Key words: SUMOylation, Phosphorylation, Maize, *Fusarium* pathogens, MAPK

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Graphene Oxide Synergistically Enhances *Beauveria Bassiana* for Controlling *Spodoptera Frugiperda*

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Abstract: [Objective] *Spodoptera frugiperda* is a major migratory pest threatening maize production in China, and its current control relies heavily on chemical insecticides, which has exacerbated resistance and ecological risks. *Beauveria bassiana* (Bb) offers biological control potential but suffers from slow action and poor environmental stability. This study introduces graphene oxide (GO) as a carrier to construct GO-Bb complexes and systematically evaluates their synergistic effects, aiming to develop a sustainable and effective integrated management strategy. [Method] GO-Bb complexes were prepared and characterized by scanning electron microscopy, Fourier transform infrared spectroscopy, and thermogravimetric analysis. Their insecticidal activities were assessed via leaf-dip bioassays against 1st and 3rd instar larvae of *S. frugiperda*. Seed germination tests, greenhouse and field efficacy trials, and rhizosphere microbial community sequencing were conducted to evaluate biocompatibility, residual activity, plant growth promotion, and ecological impacts. [Result] GO (10 µg/mL) did not inhibit Bb spore germination (94.00%) and improved the thermal stability of both complexes. GO significantly enhanced toxicity against both 1st and 3rd instar larvae. In field trials, GO-Bb complexes reduced damage and increased the proportion of highly resistant plants at 14 days after emergence. A combined strategy of “GO-Bb seed treatment + broflanilide (Bro) foliar spray” was also proposed, which at 28 days after emergence achieved a damage level of only 0.7 and 90.00% highly resistant plants, significantly outperforming single treatments. Moreover, GO-Bb seed treatment promoted maize growth, enhanced endophytic colonization of Bb in leaves (96.67% at 14 days, maintaining 76.67% at 28 days), and reshaped the rhizosphere microbial community by enriching beneficial bacteria such as *Streptomyces albidoflavus*, while suppressing soilborne pathogens *Fusarium* and *Neocosmospora*, with *B. bassiana* becoming the dominant fungal genus (39.55% relative abundance). [Conclusion] GO synergistically enhances the insecticidal efficacy of Bb, and the integrated strategy of GO-Bb seed treatment combined with Bro foliar spray provides prolonged, effective control of *S. frugiperda* while also improving plant growth and rhizosphere health, offering a promising and eco-friendly approach for sustainable pest management.

Key words: *Spodoptera frugiperda*, Graphene oxide, *Beauveria bassiana*

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Integrated GWAS and Transcriptome Sequencing Reveal Novel Candidate Genes for Southern Corn Rust Resistance in Diverse Maize Germplasm

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Abstract: [Objective] Maize is a globally important crop that serves as a primary source of food, feed and fuel. However, its productivity and quality are increasingly threatened by pathogenic diseases. Southern corn rust (SCR), a fungal disease caused by *Puccinia polysora*, is highly epidemic and spreads through multiple pathways, having emerged as one of the most serious constraints to maize production in recent years. The pathogen causes substantial yield losses and quality deterioration worldwide. Currently, only a limited number of resistant genes are available, underscoring the urgent need to identify novel SCR resistant loci to enhance overall genetic resistance. In this study, we employed genome-wide association studies (GWAS) and transcriptome sequencing to dissect the genetic architecture of SCR resistance. [Method] We utilized three association mapping panels, comprising a total of 896 diverse tropical, subtropical and temperate maize germplasm. Disease resistance was evaluated by scoring SCR severity at 20 days after flowering, and extreme resistant and susceptible accessions were identified for GWAS and subsequent transcriptome analysis. Phenotypic evaluation revealed that SCR scores followed a normal distribution, with tropical germplasm showing higher resistance levels. Heritability was estimated at 95%, indicating that SCR resistance is predominantly governed by genetic factors. GWAS detected a total of 37 significant loci were detected across different populations. By defining 100-kb window flanking each significant locus as the candidate, we screened *Zm00001eb144240*, which encodes a fructose-bisphosphate aldolase and shows differential expression in the leaf protoderm. [Conclusion] Collectively, our phenotypic and genomics analyses have identified resistant germplasm distinctly from previously reported sources and uncovered novel candidate genes for SCR resistance. These findings will facilitate the development of functional markers for application in maize breeding programs.

Key words: Maize, *Puccinia polysora*, Resistance, GWAS, Candidate genes

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Establishment of Rapid Field Identification Technology for Southern Corn Rust

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Abstract: [Objective] Maize (*Zea mays* L.) ranks among the world's top five cash crops. Southern corn rust (SCR), caused by *Puccinia polysora*, is one of the major diseases threatening maize production in China. Under favorable environmental conditions, *P. polysora* can infect maize plants at all growth stages. Early detection of this pathogen during maize development is critical to enable timely disease intervention. [Method] In this study, specific primers and probes were designed targeting the variable region of the rDNA-ITS sequence in the *P. polysora* genome. A visual qualitative detection system was established by combining multi-enzyme isothermal rapid amplification (MIRA) with immuno-recognition and lateral flow chromatography technology, followed by evaluations of its specificity and sensitivity. [Result] The established MIRA-LFIA detection system can specifically identify *P. polysora*, with no cross-reactions against other maize pathogenic fungi, including *Puccinia sorghi*, *Puccinia striiformis*, *Bipolaris maydis*, *Exserohilum turcicum*, *Cercospora zea*, *Curvularia lunata*, *Fusarium graminearum*, and *Fusarium verticillioides*. Under an isothermal condition of 38 °C with a 15-minute reaction duration, the system achieves a detection limit of 1 pg·μL⁻¹ for Southern corn rust pathogen DNA and DNA extracted from 57.6 urediniospores, and exhibits favorable operational stability. A total of 70 field samples collected from the Huang-Huai-Hai region were tested, yielding a positive detection rate of 78.57%. Compared with the highly sensitive single-tube nested PCR method (detection limit: 0.1 fg·μL⁻¹ positive plasmid DNA and DNA from 0.46 urediniospores), the two detection methods shared a consistency rate of 97.14%. [Conclusion] This technology achieves rapid early detection and visual readout for southern corn rust. It greatly lowers technical operation barriers and is suitable for on-site real-time monitoring at grassroots agricultural stations and in field plots.

Key words: Southern corn rust, Visible detection, Rapidity, Sensitivity, MIRA-LFIA

Funding acknowledgment: China Agriculture Research System (Maize) (CARS-02)

Screening and Marker Genotype Analysis of Maize Germplasm Resources for Resistance to Southern Corn Rust

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Abstract: [Objective] Southern corn rust (SCR) is a globally significant plant disease that mainly affects maize leaves. The objectives of this study were to identify resistant germplasm resources and to elucidate their marker genotypes associated with SCR resistance, thereby providing a reference for the efficient use of germplasm and the identification of novel resistance genes. [Method] A total of 1362 inbred lines and 190 hybrids were artificially inoculated and evaluated for field resistance to SCR. Eight SSR primers or SCR markers linked to the resistance genes *RppP25*, *RppD*, *RppCML496*, and *Rpp9* were selected for marker genotype analysis. Based on the diagnostic marker banding patterns of four resistant reference inbred lines (Qi 319, Jing 2416k, CML496, and CML470), accessions showing moderate resistance or higher in the field were subjected to marker genotype identification. [Result] A total of 397 accessions exhibiting moderate resistance or higher were identified through field screening. Based on marker genotype analysis, these accessions were categorized into 39 marker types. AMD402 and CML496 displayed identical genotypes at all 22 amplified loci, while AMD404 and Jing 2416K shared identity at 21 loci. AMD169 and the improved line 738 showed genotype consistency with Qi 319 at 17 loci. At the five specific loci (P091, M271, umc1291, G047, and the *Rpp9*-linked SCR marker), the numbers of accessions sharing genotypes with their respective reference inbred lines were 246, 103, 317, 139, and 153, respectively. At phi048, 116 accessions matched Jing 2416K, 180 matched CML496, and 88 matched both Qi 319 and CML470. At P2913, 135 accessions were consistent with Qi 319, Jing 2416K, and CML470, whereas 183 matched CML496. At P3187, 79 accessions matched Qi 319 and Jing 2416K, while 100 matched CML470 and CML496. AMD443 exhibited distinct genotypes from all four reference inbred lines at loci P091, G047, P2913, and P3187, and Jinyu 528 also differed from all reference lines at G047, the *Rpp9*-linked SCR locus, P2913, and P3187. [Conclusion] Germplasm resources in maize displaying moderate or higher levels of resistance to southern corn rust are still scarce. The resistant accessions revealed substantial diversity in their combinations of resistance genes. Notably, AMD443 and Jinyu 528 may harbor novel resistance loci, which merit further intensive study.

Key words: Germplasm resources, Southern corn rust, Resistance loci

Funding acknowledgment: China Agriculture Research System (Maize) (CARS-02)

Fv*-milR22 Modulates Pathogenicity by Regulating Chitin Synthase Gene *FvCHS8* in *Fusarium Verticillioides

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Abstract: [Objective] MicroRNAs play essential regulatory roles by modulating the expression of their target genes. However, the functions and regulatory mechanisms of fungal microRNA-like RNAs (milRNAs) remain largely unknown. This study aimed to investigate the roles of *Fusarium verticillioides* milRNAs (*Fv*-milRNAs) in fungal growth, development, and pathogenicity. [Method] Fungal milRNAs and their target genes were identified in *F. verticillioides*, the causal agent of maize ear rot, by integrating degradome sequencing, transcriptome sequencing, and quantitative real-time PCR (qRT-PCR). Eight highly expressed *Fv*-milRNAs were selected for overexpression mutant construction. The growth and development of the mutants were evaluated, and their pathogenicity was assessed by inoculating different maize tissues. [Result] *Fv*-milR22 was found to play a crucial role during the infection process of *F. verticillioides* by regulating the chitin synthase gene *FvCHS8*. 5' RNA ligase-mediated rapid amplification of cDNA ends (5' RLM-RACE) confirmed that *Fv*-milR22 directed the cleavage of the *FvCHS8* transcript at the predicted binding site. Co-expression of *Fv*-milR22 and *FvCHS8* in *Nicotiana benthamiana* leaves significantly suppressed the expression of *FvCHS8*. Overexpression of *Fv*-milR22 markedly reduced fungal growth, development, and virulence, accompanied by a significant decrease in *FvCHS8* expression. Compared with the wild-type strain, the *FvCHS8* knockout mutant exhibited slower growth and development and significantly reduced pathogenicity. In addition, deletion of *FvCHS8* resulted in increased sensitivity to hydrogen peroxide, while enhanced tolerance to 0.05% SDS, 100 µg/mL Congo red, and 20 µg/mL Calcofluor White was observed. These findings suggest that *FvCHS8* may participate in the oxidative stress response and contribute to the maintenance of cell wall integrity. [Conclusion] *Fv*-milR22 promotes the infection process of *F. verticillioides* in maize through endogenous regulation of the pathogenicity-related gene *FvCHS8*. These findings provide important insights into the roles of fungal milRNAs and their target genes in the pathogenic process.

Key words: MicroRNA-like RNAs, *Fusarium verticillioides*, Corn ear rot disease, Pathogenicity

Funding acknowledgment: China Agriculture Research System (CARS-02).

Pelletized Straw Return Enhances Soil Fertility but Weakens Fungal Stability in Soda-Saline Maize Systems

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Abstract: [Objective] Soda-saline soils constrain maize production and climate-resilient cropping systems. Crop residue return improves soil organic matter and nutrient availability, but high rates may alter salt chemistry and microbial stability. We assessed fertility-stability trade-offs across pelletized maize straw rates and drivers of bacterial and fungal responses. [Method] A randomized complete block field experiment with five replicates was conducted in the Songnen Plain, Northeast China. Treatments were no straw return (CK), chopped straw at 10 t ha⁻¹ (FS1), and pelletized straw at 10 (KL1) or 30 t ha⁻¹ (KL3). Soils (0–15 cm) were sampled at early grain filling. Soil properties, soluble ions, bacterial 16S rRNA, and fungal ITS communities were assessed using diversity, persistent taxa, β NTI, NST, constrained ordination, and variation partitioning. [Result] Relative to CK, KL3 increased soil organic matter, electrical conductivity, cation exchange capacity, and chloride by 22.9%, 29.9%, 11.4%, and 254.3%, respectively; pH changed little, while total and available N and available K increased significantly. Bacterial diversity and composition remained stable, persistent taxa exceeded 88% of relative abundance, and assembly was dominated by heterogeneous selection (median β NTI > 2). KL3 reduced fungal Shannon diversity from 4.15 to 3.14 and the relative abundance of persistent fungal taxa from 84.08% to 47.03%. Fungal NST decreased from 0.721 to 0.457, indicating stronger environmental filtering within a stochastic-dominated regime ($|\beta$ NTI| < 2). Chloride, Mg²⁺, and total nitrogen were key correlates of fungal reorganization; nutrient and salt variables jointly explained approximately 75% of fungal variation. [Conclusion] Pelletized straw can support sustainable intensification by improving soil organic matter and nutrient availability. However, high-rate application may accumulate soluble salts, especially chloride, and weaken fungal community stability. Optimizing return rates and monitoring ion accumulation are essential to preserve fertility gains and microbial stability, guiding climate-resilient maize production in soda-saline regions.

Key words: Pelletized straw, Soda-saline soil, Maize cropping system, Microbial community stability, Sustainable intensification, Soil organic matter

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Potential Threats of the Moroccan Locust, *Doclostaurus Maroccanus*, to Maize Production in China: Habitat Suitability, Damage Assessment and Rapid Diagnosis

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Abstract: [Objective] The Moroccan locust, *Doclostaurus maroccanus*, is a destructive agricultural pest distributed across parts of Europe, Africa, and Asia. It is characterized by a broad host range, high fecundity, strong dispersal capacity, and a pronounced tendency to form outbreak populations. Following its first detection in Xinjiang, China, in 2023, the species has successfully established local populations, raising concerns about its further spread and potential impacts on agricultural production in northwestern China. Notably, its nymphal and adult occurrence periods largely overlap with the seedling-to-stem-elongation stages of spring maize in Xinjiang, a critical phase of vegetative growth during which crop injury may result in substantial yield losses. This study aimed to assess the invasion risk of *D. maroccanus*, quantify its damage to maize seedlings, and develop a rapid molecular diagnostic method for field identification. [Method] Potential suitable habitats of *D. maroccanus* in China were predicted using the BIOMOD2 ensemble modeling framework under current climatic conditions. Field cage experiments were conducted to evaluate feeding damage caused by third- and fourth-instar nymphs on maize seedlings at the three- to five-leaf stage under five population densities (5, 20, 35, 50, and 100 individuals per cage). In addition, a multienzyme isothermal rapid amplification coupled with a lateral flow dipstick (MIRA-LFD) assay targeting the mitochondrial cytochrome c oxidase subunit I (COI) gene was developed for rapid species identification. [Result] Habitat suitability modeling indicated that extensive suitable habitats for the establishment and spread of *D. maroccanus* are distributed across northwestern China under current climatic conditions, with highly suitable areas primarily concentrated in the Ili Kazakh Autonomous Prefecture of Xinjiang, a major spring maize-growing region. Feeding damage severity increased markedly with locust density. Complete destruction of maize seedlings occurred within 24 h at densities of 50 individuals per cage or higher, and within 2-3 d at 20 individuals per cage, whereas damage progression extended to approximately 8 d at 5 individuals per cage. Under moderate and high infestation levels, nymphs preferentially fed on or severed maize stems, causing rapid lodging and plant mortality. In addition, species-specific primers and probes targeting the mitochondrial COI gene were successfully designed and screened for the MIRA-LFD assay, enabling rapid visual identification of *D. maroccanus* across different developmental stages within 30 min. [Conclusion] This study integrates habitat suitability prediction, maize damage assessment, and rapid molecular identification to provide a comprehensive evaluation of the invasion risk posed by *D. maroccanus* in China. The findings will support surveillance, early-warning systems, and quarantine inspection for this emerging invasive pest in China, thereby contributing to the protection of maize production

and agricultural biosecurity in potentially affected regions.

Key words: *Dociostaurus maroccanus*, Invasive pest, Maize, Habitat suitability, Feeding damage, Rapid detection

Funding acknowledgement: This work was supported by the earmarked fund for China Agriculture Research System (CARS-02-32) and the 2115 Talent Development Program of China Agricultural University.

Dual RNA-Sequencing Unveils *SfNimB* Antifungal Role in *Spodoptera frugiperda* Against *Metarhizium Rileyi*

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Abstract: [Objective] The fall armyworm (FAW), *Spodoptera frugiperda* (J.E. Smith), is a notorious and invasive pest. Due to its wide host range, high reproduction and absence of diapause, it has emerged as a serious economic threat to global corn production. Entomopathogenic fungi (EPF) are thought to be effective biocontrol agents in the integrated management of the fall armyworm. However, their efficacy largely depends on immune interactions between pathogens and hosts. This study aims to elucidate the intricate molecular mechanisms governing the interaction between *Metarhizium rileyi* and *S. frugiperda*, specifically focusing on the critical role of *SfNimB* in mediating host energy reallocation and antifungal immune defense. [Method] Dual RNA-sequencing (RNA-seq) was performed to profile transcriptomes of both *S. frugiperda* and *M. rileyi* during infection. Yeast two-hybrid screening was conducted to identify protein–protein interactions involving SfNimB. RNA interference (RNAi) was used to knockdown expression of candidate genes (*SfNimB*, *SfArylphorin-α*, and *SfRpLP0*), followed by larval mortality assays under fungal infection. Quantitative reverse-transcription PCR (RT-qPCR) was performed to detect the expression levels of antimicrobial peptides (AMPs). [Result] Dual RNA-seq analysis revealed that upon *M. rileyi* infection, *S. frugiperda* shifts energy allocation from growth and development toward immune activation and detoxification responses, while *M. rileyi* secretes effector proteins and secondary metabolites to suppress host defenses. Notably, *SfNimB* was identified as a previously overlooked antifungal immune factor. Knockdown of *SfNimB* significantly reduced AMPs mRNA levels and accelerated larval mortality following fungal infection. Yeast two-hybrid assays revealed SfNimB interactions with SfArylphorin-α and SfRpLP0. Individual RNAi of *SfArylphorin-α* and *SfRpLP0* phenocopied *SfNimB* knockdown, resulting in enhanced susceptibility to fungal infection. [Conclusion] Dual RNA-seq unveils energy reallocation trade-off between growth and immunity in *S. frugiperda* during infection. Among that, SfNimB plays a pivotal role in the pathogen-host interaction, potentially coordinating host energy utilization and mediating downstream antimicrobial peptides synthesis. This coordinated response, involving its interaction partners SfArylphorin-α and SfRpLP0, enhances host antifungal immunity against *M. rileyi* invasion.

Key words: Dual RNA-sequencing, *Spodoptera frugiperda*, *Metarhizium rileyi*, Antifungal immunity

Funding acknowledgement: This work was supported by the earmarked fund for China Agriculture Research System (CARS-02-32), and the Joint Research Program of State Key Laboratory of Agricultural and Forestry Biosecurity (No. SKLJRP2509).

The Prevention and Control of Maize Alien Insect Pests: Invasion Mechanisms, Risk Assessment and Rapid Diagnosis

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Abstract: [Objective] The quarantine pest and invasive alien species present serious influence for crop production and trade in the world. Climate change facilitates the rapid invasion of alien insect pests and threatening global biosecurity. The prevention and control maize alien pests has been supported by the earmarked fund for China Agriculture Research System from 2021. We studied the invasion mechanisms, risk assessment and rapid diagnosis of maize alien insect pests, e.g., *Trogoderma granarium* Everts and *Spodoptera frugiperda* (J. E. Smith), in order to protect maize industry under climate change. [Method] The ecological measurements, transcriptomics, metabolomics, RNAi, and CRISPR/Cas9 technology were used for the invasion mechanisms with high and cold temperature tolerance. The integrated quantitative assessment technology was established, including establishment risk by self-organizing map and potential geographical distribution by MaxEnt model. The multienzyme isothermal rapid amplification coupled with a lateral flow dipstick (MIRA-LFD) assays targeting the mitochondrial cytochrome c oxidase subunit I (COI) gene were developed for rapid diagnosis. [Result] The first chromosome-level genome assembly for *T. granarium* (327 Mb, contig N50 = 883 kb) was generated and functional genomics revealed key gene families and molecular pathways for extreme cold survival, meanwhile, genes *Sf3685*, *Sf8006*, and *Sf3193* linked to chitin binding, extracellular region, and carbohydrate metabolic process were essential for heat tolerance of *S. frugiperda* larvae. A global presence/absence dataset of stored beetles and distribution dataset of *S. frugiperda* were established, the results showed *T. granarium* was the species of highest establishment risk for China, and the year-round potential geographical distribution of *S. frugiperda* included 15 provinces in China. The specific primers and probes of MIRA-LFD were designed for *T. granarium* and *S. frugiperda*, the visualization systems were effective to quickly and uniquely diagnosis within 30 min at 37 °C. [Conclusion] These findings provide highquality genomic resources and theoretical foundations for understanding the invasion mechanism of maize alien insect pests. It offers an improved solution for invasion risk assessment and early detection of insect pests, thereby contributing to identify actionable targets for the development of quarantine measures and invasion prevention strategies.

Key words: Maize alien pests, Invasion mechanism, Risk assessment, Rapid diagnosis

Funding acknowledgement: This work was supported by the earmarked fund for China Agriculture Research System (CARS-02-32), the Joint Research Program of State Key Laboratory of Agricultural and Forestry Biosecurity (SKLJRP2509), and the 2115 Talent Development Program of CAU.

Identification and Functional Characterization of Avirulence Gene

AvrHtn1 in *Setosphaeria turcica*

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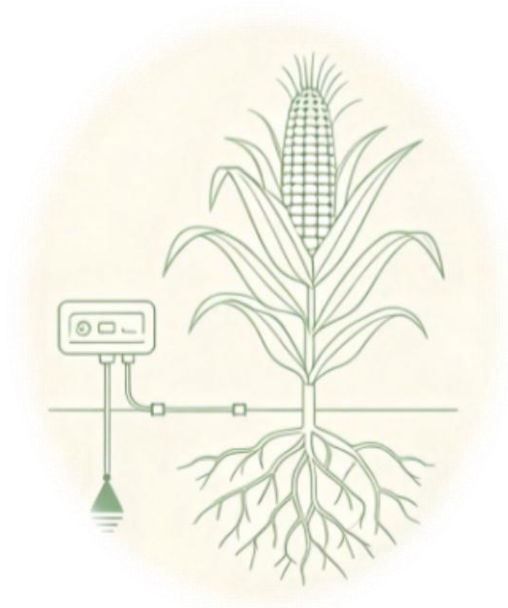
Abstract: [Objective] Northern corn leaf blight (NCLB) is a devastating foliar disease that severely reduces maize yield and quality. The pathogen *Setosphaeria turcica* is heterothallic, genetically variable, and contains diverse physiological races, bringing great challenges to disease management. The avirulence genes *AvrHt2*, *AvrHt3* and *AvrHtn1* matching maize resistance genes *Ht2*, *Ht3* and *Htn1* remain largely unknown. This study intended to identify these unreported avirulence genes, characterize their effector functions, and reveal the molecular basis of race pathogenic differentiation in *S. turcica*. [Method] Genome-wide association study (GWAS) was performed on resequencing data of characterized physiological races of *S. turcica* to screen candidate avirulence loci. SignalP 5.0 and EffectorP 3.0 were used for effector prediction. Combined with quantitative real-time PCR and cell death suppression assays, the protein features of AvrHtn1 were characterized. Physical interaction between AvrHtn1 and ZmWAK-RLK1 was validated via Y2H, LCA and Co-IP assays. RNA interference and overexpression mutants of AvrHtn1 were constructed to dissect its biological functions. [Result] A total of 10, 22, 16 and 25 candidate loci linked to AvrHt1, AvrHt2, AvrHt3 and AvrHtn1 were separately obtained. Subsequent effector prediction with SignalP 5.0 and EffectorP 3.0 prioritized AvrHtn1 for further verification. Quantitative transcription analysis revealed that AvrHtn1 was highly induced during infection. Sequence analysis showed that AvrHtn1 is a cysteine-rich protein carrying a functional secretory signal peptide and could suppress BAX-triggered programmed cell death, confirming it as a secreted effector. Y2H, LCA and Co-IP assays verified the physical interaction between AvrHtn1 and ZmWAK-RLK1 encoded by maize resistance gene *Htn1*, thereby defining *AvrHtn1* as an avirulence gene. Functional characterization via RNAi silencing and overexpression mutants of *AvrHtn1* in *S. turcica* demonstrated that this gene exerted no obvious effects on fungal vegetative growth and stress tolerance, yet negatively regulated asexual reproduction, spore germination and pathogenicity of the pathogen. [Conclusion] The avirulence gene *AvrHtn1*, identified by GWAS and experimental validation, encodes a cysteine-rich secreted effector highly expressed during infection that suppresses BAX-triggered cell death, physically binds maize ZmWAK-RLK1 via its extracellular WAK domain, and negatively regulates conidiation, appressorium formation and pathogenicity of *S. turcica*.

Key words: *Setosphaeria turcica*, Physiological race, Effector

Funding acknowledgement: China Agriculture Research System (CARS-02), Hebei Natural Science Foundation (C2025204211).

Technical Session 7

High Resource Efficient Crop Production and Smart Agriculture



Integrated Agroecological Intensification Strategies for Climate-Resilient Maize Production in Water-Limited Environments

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Abstract: [Objective] This study aimed to develop a climate-resilient maize production framework for arid and semi-arid regions of Asia. It focused on evaluating how different sustainable practices—such as conservation agriculture, biological nitrification inhibition (BNI), intercropping, optimized planting patterns, mulching, biochar, and improved nutrient management—affect crop yield, resource-use efficiency, and system stability under water- and nutrient-limited conditions. [Method] The study synthesized evidence from multi-location field experiments and systems-based analysis. It examined individual and combined effects of several practices, including conservation agriculture with reduced tillage and residue retention, maize-legume intercropping, BNI-based nitrogen management with slow-release fertilizers, optimized planting geometry, organic and biodegradable mulching, biochar application, and allelopathy-based weed control. Key measurements included soil moisture, temperature regulation, root growth, light interception, nutrient use, weed suppression, nitrogen efficiency, and water productivity. A structural pathway analysis was used to understand the mechanisms behind yield stability. [Result] Integrated management practices consistently improved maize performance compared to conventional farming. Conservation agriculture increased soil moisture retention, stabilized soil temperature, and supported better root development, improving water productivity. Intercropping and optimized planting improved light capture and nutrient use, while reducing weed pressure. BNI and slow-release fertilizers reduced nitrogen losses and improved nitrogen recovery. Mulching reduced evaporation and improved soil hydrothermal conditions, while biochar enhanced soil fertility, microbial activity, and carbon storage. Overall, grain yield increased by 18–42%, while water- and nitrogen-use efficiencies improved by 15–38%. Results showed that improved root–shoot balance, better canopy light use, and stronger soil buffering capacity were key drivers of yield stability. [Conclusion] The study shows that combining complementary sustainable practices can significantly improve maize productivity and resilience in dryland systems. These approaches reduce dependence on external inputs while improving soil health, water use, and nutrient efficiency. Overall, this integrated strategy offers a practical and scalable solution for climate-resilient maize production in vulnerable agricultural regions.

Key words: Soil moisture retention, Nitrogen use efficiency, Conservation agriculture, Intercropping systems, Biochar amendment

Funding acknowledgement: Sultan Qaboos University

Genetic Diversity, Biological Variation, and Host Plant Adaptation of Invasive Fall Armyworm (*Spodoptera frugiperda*) Populations in Nepal

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Abstract: [Objective] Since its invasion of Africa in 2016, fall armyworm (FAW), *Spodoptera frugiperda*, has spread rapidly across Asia, causing substantial yield losses, particularly in maize. In Nepal, FAW was first reported in May 2019 and subsequently spread throughout the country. [Method] This study investigated the geographic distribution, genetic diversity, and biological variation of FAW populations collected from different locations in Nepal. [Result] Genetic characterization based on the triose phosphate isomerase (*Tpi*) gene confirmed that all populations belonged to the corn strain, with no evidence of the rice strain. Three *Tpi* subgroups- Ca1, Ca2a, and Ca2b-were identified, with Ca1 being predominant (87%). Comparative biological studies revealed significant differences between Ca1 and Ca2. Pre-adult survival was higher in Ca1 (86%) than Ca2 (72%). Ca1 exhibited a female-biased sex ratio (37.2:62.8), whereas Ca2 was male-biased (61.1:38.9). Oviposition duration was longer in Ca1 (8.68 days) than Ca2 (6.92 days), while Ca2 showed significantly greater food intake and assimilation efficiency during the sixth larval instar. Furthermore, comparative studies of Ca1 reared on rice and maize for three generations showed significantly prolonged development on rice, with F0, F1, and F2 generations requiring 21.7%, 18.3%, and 18.9% longer developmental periods, respectively. Rice-fed colonies also exhibited lower larval and pupal body weight, pre-adult survival, and fecundity. [Conclusion] These findings demonstrate substantial genetic and biological variability within Nepalese FAW populations and highlight the potential of the predominant Ca1 subgroup to adapt to rice, posing a potential risk to rice-based agroecosystems and emphasizing the need for continued surveillance and integrated pest management.

Key words: Fall armyworm, Genetic diversity, *Tpi* gene, Host plant adaptation, C-strai

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Development of Cytosine and Adenine Base Editors for Maize Precision Breeding

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Abstract: [Objective] The limited efficiency of current base editing systems in maize constrains their application in precision breeding. This study aimed to systematically evaluate evolved cytosine (CBEs) and adenine base editors (ABEs), establish the high-efficiency base editors for maize, and develop herbicide-resistant germplasm through targeted genome engineering. [Method] Previous reported seed fluorescence reporter (SFR) system was implemented for rapid identification of base-edited transformants and transgene-free progenies. Four CBEs (evoAPOBEC1, evoFERNY, evoCDA1, RrA3F) and two ABEs (TadA8.20, TadA8e) were engineered and functionally characterized through maize protoplasts transient expression assays and stable transformations. Chimeric *35S-CmYLCV-ZmU6* promoter and tRNA-HDV ribozyme processing elements were used for tandem sgRNA expression. Mutation profiling were analyzed via Hi-TOM deep sequencing. Herbicide resistance phenotypes and agronomic impacts were quantitatively assessed through field trials under herbicide treatment. [Result] The evoCDA1-CBE and TadA8.20-ABE demonstrated superior base-editing performance, achieving multiplex editing efficiencies of 78.6% and 100.0% at the tested loci, respectively, with some homozygous and biallelic mutants exceeding 72.4% and 73.7%. Precise editing of *ZmACCI/2* (acetyl-CoA carboxylase) improved herbicide resistance, with *ZmACC2*-edited lines displayed superior resistance. The *ZmACCI/2* double mutants exhibited no significant growth penalty under 4× herbicide treatment when intercropped with soybean in the field and maintained acceptable fitness even under 8× herbicide application. [Conclusion] This study establishes evoCDA1 and TadA8.20 as the high-efficiency base editors, advances crop genetic engineering by facilitating robust, multi-locus modifications without altered agronomic performance, enhancing herbicide tolerance in maize. The successful utilization of base editors will forward in agricultural biotechnology and precision breeding.

Key words: *Zea mays*, Cytosine BE, Adenine BE, Multiplex editing, *ZmACC*

Soil Moisture and Nutrient Mobility Influence Nitrogen Partitioning and Translocation in Maize (*Zea mays* L.) under Various Water-nitrogen Regimes

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Abstract: [Objective] Optimizing water and nitrogen (N) management is crucial for improving crop yields, yet the soil water dynamics and nutrient mobility on N partitioning and yield information remain insufficiently understood. [Method] To address this gap, field experiments were conducted from 2020 to 2022 in the western Songnen plain (SARs), a cold semi- arid region of northern China. The study examined three soil moisture levels (40%, 60%, and 80% of field capacity) and four N fertilization rates (0, 100, 200, and 300 kg N ha⁻¹) to evaluate their impacts on soil nutrient dynamics (SNs), soil water utilization (SWU), soil enzyme activities (SEAs), N accumulation (NA), N translocation (NT), N utilization (NU), biomass accumulation (BA), and maize yield. [Result] Results showed that maintaining soil moisture at 80% field capacity (W3) significantly enhanced SWU and partitioning, particularly under the N200 treatment. Specifically, W3-N200 increased SWU by 4.15–26.13%, SNs by 5.06–35.49%, and SEAs by 6.57–38.78% compared with W1 (40%) and W2 (60%). Regression analysis indicated that W3 advanced the time to peak BA rate by 11.76–17.85 days and increased maximum biomass, and average BA rate, peak BA rate. Under N200, structural equation modeling (SEM) revealed increases in NA (13.95–34.65%), NT and NU (3.14–27.49%), resulting in a 4.99–28.81% higher BA and 4.44–10.73% greater yield. The W3-N200 treatment achieved the highest grain yield (10437 kg ha⁻¹), with superior water use efficiency and N use efficiency. Optimal water and N management regulated SNs and SEAs, which in turn improved N transformation and BA, ultimately increased maize yield. [Conclusion] These findings provide valuable guidance for sustainable water and nutrient management in SARs agricultural regions. This study quantified the effects of optimized water and N management strategies on maize yield and N losses in semi-arid regions (SARs). These findings confirm that W3-N200 is an effective water-fertilizer management strategy. However, while W3 irrigation achieved optimal agronomic results, it also requires higher water input, which may increase production costs and pressure on limited water resources. Therefore, future management strategies should balance agronomic gains with economic feasibility and water sustainability to ensure that water–N optimization remains both productive and practical for farmers in semi-arid regions.

Key words: Semi-arid regions (SARs), Water availability, Nitrogen partitioning; Soil nutrient, Grain yield

Subsurface Split Manure Application Increased Soil Organic Carbon Stability by Enhancing Aggregation and Recalcitrant Carbon Fractions with Depth-dependent Mechanisms in a Wheat-maize Rotation

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Abstract: [Objective] Subsurface manure application has been identified as an important strategy to improve soil properties and enhance soil organic carbon (SOC) sequestration. However, how do SOC stabilization response to manure application frequency remain unclear. [Method] To solve this knowledge gap, a two-year field experiment in the North China Plain of wheat-maize rotation was conducted, including a control without manure application (T_0); single application of manure every two years (T_1); split applications of manure (once a year) with the same total amount (T_2). [Result] Across 0–40 cm, compared to T_0 , T_1 and T_2 increased SOC by 23–28%, particulate organic carbon (POC) by 57–118%, and mineral-associated organic carbon (MAOC) by 7–16%, with greater increases by T_2 in topsoil (0–20 cm). Compared with T_0 , T_2 increased SOC in macroaggregates and increased the mean weight diameter (MWD). Moreover, T_2 increased the chemical stability of SOC by enriching recalcitrant organic C content (aromatic-C, aliphatic-C, and phenol-C) and reducing labile organic C content (carboxyl/amidogen-C and polysaccharide-C) in soil aggregates of all sizes. Compared with topsoil, subsoil exhibited greater increases in POC, aggregate stability, and chemical recalcitrance, indicating depth-dependent responses to subsurface manure application. Moreover, chemical recalcitrance exhibited the strongest direct positive effect on SOC content in both soil layers. Compared to T_0 , T_1 and T_2 improved wheat yield by 10% in the second year, while there were no significant differences in the maize yield. [Conclusion] Overall, these findings reveal that subsurface manure application has the potential to enhance stable SOC accumulation via synergistic physical and chemical stabilization pathways, with a better performance of split manure application, aiding SOC sequestration and soil fertility improvement.

Key words: Subsurface manure application, Fertilization frequency, Soil organic carbon, Mineral-associated organic carbon, Soil aggregate

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Synergistic Enhancements in Maize Yield and Water Productivity: Dense Planting with Regulated Deficit Irrigation Versus Conventional Practice

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Abstract: [Objective] Enhancing both grain yield and water productivity (WP) under water scarcity is a critical challenge for sustainable maize production. Conventional farmer practices—characterized by low planting density (D_1 : 9.0×10^4 plants·ha⁻¹) and excessive irrigation (I_5)—often limit the potential for both. To advance the high density production system enabled by precision stage specific regulation (HD-PSR), we conducted a multi-region field experiment across arid to sub humid climates in Xinjiang, China. [Method] This study is positioned within the emerging high density production system enabled by precision stage-specific regulation (HD-PSR) framework. Replacing the conventional practice (low density + over irrigation) with an optimized practice (high density + regulated deficit irrigation). Treatments included region-specific full irrigation (I_5) and four deficit levels (I_1 - I_4 , each reduced by 90 mm relative to I_5), elucidate the physiological mechanisms (e.g., dry matter accumulation, canopy cover, soil water, E/T partitioning) underlying any synergistic effect. [Result] Compared with the conventional model (D_1+I_5), the HD-PSR based optimized model (D_2 , 12.0×10^4 plants·ha⁻¹ plus regulated deficit irrigation, I_{opt}) synergistically increased grain yield by 18.8-25.0% and WP by 8.7-20.0% across sites, while saving 11.1-50.0% of irrigation water. This synergy was driven by improved canopy coverage and sustained dry matter accumulation under precision regulated irrigation that maintained soil water storage at ~70% of field capacity, thereby reducing non-productive water losses (soil evaporation in arid/semi arid areas and excessive transpiration in the semi humid area). [Conclusion] The HD-PSR approach integrates increased plant density with growth-stage-specific irrigation regulation to maximize both yield and WP. Our study provides a quantitative irrigation module for the HD-PSR and identifies a translatable soil water threshold (~70% FC) for sustainable intensification of maize in water limited regions.

Key words: Regulated deficit irrigation, Water productivity, Synergistic effect, Soil water threshold, Arid agroecosystems

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AI-Ready Nutrient Decision Spaces for Precision Maize Fertilizer Management in South Asia

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Abstract: [Objective] This study develops AI-ready nutrient decision spaces to improve maize yield potential while reducing fertilizer inefficiency and environmental costs in South Asia. [Method] Harmonised treatment-level evidence from agronomic trials was integrated with genotype groups, ecological zones and yield-response functions to estimate N-rate decision spaces and P05–P95 yield envelopes. [Result] The framework identifies spatial domains of nutrient surplus, deficit and low NUE, and quantifies lower, average and optimum fertilizer decision ranges for precision targeting. The Nepal database includes 3,021 treatment records from 52 sources, with 2,245 NUE-screened records. Applied N is available for 2,544 records, and 4R/precision nutrient management is represented by 230 records. Spatial workflows identify NUE hotspots and fertilizer-saving domains. [Conclusion] The approach links field evidence, spatial intelligence and smart input management to support scalable maize advisories and fertilizer-demand reduction pathways.

Key words: Maize, Nutrient-use efficiency, Precision input management, Yield-response functions, Smart agricultur

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When Low-input is Not Enough: Implications of Nutrient-limited Environments for Maize Genotype Evaluation

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Abstract: [Objective] Maize breeding for low-input and organic production systems must address highly heterogeneous environments, where soil fertility varies widely due to land use history and farmer management. Organic fields can range from recently converted paddy land to intensively managed vegetable systems, resulting in substantial variation in nutrient availability. In mixed crop–livestock systems, maize serves dual purposes, with grain as concentrate feed and stover as high-energy roughage with superior digestibility compared to conventional forage grasses. Consequently, breeding programs must develop hybrids adapted to organic conditions while enhancing nutrient-use efficiency under variable environments. This requires evaluation systems capable of effectively discriminating genotypic differences; however, organic systems are often assumed to inherently provide such conditions, particularly when organic amendments are applied. [Methods] This study assessed the capacity of contrasting nutrient environments within a certified organic system to differentiate maize hybrids based on nutrient-use efficiency. Fifteen genotypes, including ten F₁ crosses and five commercial checks, were evaluated under compost-amended and non-amended conditions using a split-plot randomized complete block design with three replications. Nutrient-use efficiency was quantified based on stover yield response (stover-based NUE) to capture genotype-specific performance under contrasting nutrient availability, while grain-based NUE was examined to provide a complementary perspective on reproductive performance. [Results] Genotype discrimination was strongly environment dependent. Under compost-amended conditions, variation in nutrient-use efficiency was limited across hybrids. In contrast, nutrient-limited conditions revealed clear differentiation in stover-based NUE, while grain-based NUE showed minimal variation. This highlights that genotype discrimination depends not only on environmental stress but also on the trait used. Overall, moderate nutrient availability can mask genetic variation, whereas controlled nutrient limitation is essential for revealing differences relevant to selection. [Conclusion] These results highlight that effective genotype discrimination for nutrient-use efficiency depends critically on the design of evaluation environments. Controlled nutrient limitation is essential to reveal genotypic variation, particularly for stover productivity, while grain-based responses may remain less sensitive. This distinction underscores the importance of tailoring selection environments to target traits. By improving the detectability of NUE-related performance, this approach can enhance breeding efficiency and support the development of maize hybrids better suited to integrated crop–livestock systems under resource-limited conditions.

Key words: Nutrient-use efficiency, Low-input systems, Organic maize, Genotype discrimination, Stover yield

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Effects of Optimized Nitrogen Application under Shallow Buried Drip Irrigation on Soil Nutrients, Microbial Communities and Water-nitrogen Utilization in Semi-arid Maize Fields

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Abstract: [Objective] This study explores the effects of optimized nitrogen application under shallow-buried drip irrigation on soil nutrients, soil microbial communities and water-nitrogen utilization efficiency in semi-arid maize fields. It aims to provide scientific basis for the precise and efficient implementation of maize shallow buried drip irrigation fertilization management in the semi-arid area of Heilongjiang Province. [Method] Three planting densities were tested: M1 (67,500 plants ha⁻¹), M2 (82,500 plants ha⁻¹), and M3 (97,500 plants ha⁻¹). The experimental design included one-time nitrogen fertilization (Y), conventional fertilization treatment: D3 (three nitrogen topdressings), and optimized fertilization treatment: D4 (four nitrogen topdressings), D5 (five nitrogen topdressings), and D6 (six nitrogen topdressings). The changes of soil nutrients, soil microbial community and diversity, water and nitrogen use efficiency in different growth seasons and different soil layers of maize were comprehensively and systematically explored. [Result] Compared with Y treatment, in the 0-10 cm soil layer and 10-20 cm soil layer, D6 treatment significantly increased soil nutrient content. With the deepening of soil depth, nutrient content gradually decreased. The optimized nitrogen application treatment significantly affected the soil bacterial community structure and increased the bacterial microbial diversity in the 0-10 cm and 10-20 cm soil layers. D6 treatment increased the relative abundance of beneficial bacteria such as *Sphingomona*, *Rokubacteriale* and RB41. TN is the main environmental factor affecting the bacterial community structure, and it shows a highly deterministic bacterial assembly process in the 0-10 cm and 10-20 cm soil layers. Optimized nitrogen application treatment significantly increased fungal microbial diversity in 0-10 cm and 10-20 cm soil layers. D6 treatment was characterized by beneficial fungal biomarker species such as *Tausonia* and *Mortierella*, and Y treatment was dominated by pathogenic fungi such as *Fusarium*. SOC are the main environmental factors of fungal community structure. In the 0-10 cm soil layer, the homogeneous selection of D6 was the most prominent, and the random process in the deep soil (such as 20-30,30-40) dominated the fungal community construction. In addition, D6 treatment significantly reduced crop ET, WUE and PUE by 23.83 % and 25.23 %, respectively. [Conclusion] In summary, the optimized nitrogen application treatment can improve the soil nutrients of 0-40 cm soil layer. The optimized nitrogen application treatment also improved the soil microbial community structure. In particular, the D6 treatment effectively increased the abundance of beneficial microorganisms. Finally, maize water and nitrogen use efficiency were significantly improved. Therefore, in the semi-arid area of western Heilongjiang Province, it was determined that M2D6 (82500 plant ha⁻¹, nitrogen topdressing 6 times) was a more suitable water and nitrogen management strategy.

Key words: Maize, Shallow buried drip irrigation, Soil nutrients, Microbial community, Water and nitrogen use efficiency

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Investigation of yield-limiting nutrients for rain-fed lowland rice production in the Fogera floodplain of the Amhara Region in Northwest Ethiopia

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Abstract: The productivity of rice (*Oryza sativa* L.) in Ethiopia is below the potential due to spatial and temporal soil fertility variability and sub-optimal fertilization. This on-farm study was conducted in 2019 and 2020 to determine yield-limiting nutrients, quantify yield gaps, and determine indigenous soil nutrient supply (ISNS) for lowland rice in Fogera floodplain of Northwest Ethiopia. The study comprised the following treatments: NPKSZnB, -N (PKSZnB), -P (NKSZnB), -K (NPSZnB), -S (NPKZnB), -Zn (NPKSB), -B (NPKSZn), and zero fertilizer (F0). The treatments were arranged in a randomized complete block design considering farmers' fields as replications. The results revealed that the growth and yield of rice were significantly affected by the -N and F0 treatments. However, the other nutrient omissions did not significantly influence the mentioned parameters. The highest (2299.5 kg ha⁻¹) yield response was recorded from the -N treatment. However, very low and insignificant yield responses were recorded from the other nutrient omissions. The average agronomic N use efficiency was 16.7 kg kg⁻¹, which indicated a high probability of yield response to the application of N fertilizer. The lowest (42.4%) ISNS was found for N, while the highest ISNS (>90%) was recorded for P, K, S, Zn, and B. The yield gaps due to the omission of N were 57.6%, while the yield gaps due to the omission of P, K, S, Zn, and B were very low. Therefore, N was found to be the most yield-limiting and most deficient nutrient for the lowland rice production in the study area.

Key words: Fertilizer, Fogera, Nitrogen, Nutrient omission, Phosphorus, Potassium, Rice, Yield gaps, Yield response

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Mycoflora of Wheat Seeds (*Triticum aestivum* L.) and Antifungal Activity of Essential Oils of *Cymbopogon Citratus* and *Lippia Multiflora* in Burkina Faso

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Abstract: [Objective] This study aimed to improve phytosanitary management of wheat in Burkina Faso by characterizing the mycoflora associated with wheat seeds and evaluating the antifungal efficacy of essential oils from *Cymbopogon citratus* and *Lippia multiflora* as alternatives to synthetic fungicides. [Method] Six wheat varieties (Borlaug 100, Norman, Diré 15, Achtar, Kanz, and Diré 12) were analyzed using the blotter paper method to identify fungi associated with the seeds. The antifungal activity of the essential oils was then evaluated in vitro by the direct contact method, using a completely randomized block experimental design, against *Fusarium moniliforme*, *Curvularia lunata*, and *Bipolaris maydis*. [Result] The analyses identified 12 fungal genera, with *Curvularia* (30.59%), *Fusarium* (15.01%), *Cladosporium* (14.74%), *Alternaria* (11.9%), *Phoma* (7.37%), and *Bipolaris* (7.08%) dominating. Significant variability in contamination rates was observed among the varieties, with the highest infection rates recorded in Norman and Borlaug 100. Biological efficacy tests showed that the essential oil of *C. citratus* completely inhibited the mycelial growth of *F. moniliforme* at 200 ppm, and of *C. lunata* and *B. maydis* at 400 ppm. Conversely, *L. multiflora* exhibited generally low effectiveness against *F. moniliforme* and *B. maydis* at all tested concentrations (200, 400 and 600 ppm), and only moderate activity against *C. lunata* at 600 ppm. [Conclusion] This study highlights the diversity of the mycoflora in wheat seeds in Burkina Faso and demonstrates the strong antifungal potential of *C. citratus* essential oil. These results provide a scientific basis for developing environmentally friendly biological control strategies, although additional culture-based trials are necessary before their integration into sustainable wheat disease management programs.

Key words: *Triticum aestivum* L., Seeds, Fungi, Essential oils, Burkina Faso

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Identification of Genomic Regions Associated with Nitrogen Use Efficiency in Maize under Low and Optimal Nitrogen Conditions

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Abstract: [Objective] Nitrogen is the most crucial macronutrient for maize, profoundly influencing growth, photosynthesis and grain yield. Efficient uptake and utilization of nitrogen are therefore essential for maximizing productivity with minimal inputs. To facilitate genomics-assisted breeding for enhanced nitrogen use efficiency (NUE), we conducted genome-wide association studies to identify NUE-associated genomic regions under both low (LN) and optimal (ON) nitrogen conditions. [Methods] A panel of 410 genotypes was evaluated for agronomic and yield-related traits under LN and ON environments. Phenotypic correlations among anthesis days (AD), ear height (EH), plant height (PH), and grain yield (GY) were stronger and significantly positive under ON compared to LN. [Results] We identified 26 significant marker trait-associations (MTAs) corresponding to 30 candidate genes under LN and 20 MTAs corresponding to 21 candidate genes under ON. One common MTA for EH was detected under both conditions, associated with *Chitobiosyldiphosphodolichol beta-mannosyltransferase ALG1-like* (GRMZM2G045979), a gene implicated in shortening internodes below the ear and reducing ear height. Under LN, *WUSCHEL-related homeobox 8/9-like* (GRMZM2G133972) was associated with PH and is known to regulate plant height, while *WAT1-related protein* (GRMZM2G125731) was associated with AD and contributes to anthesis timing via auxin flux regulation. *AT-hook motif nuclear-localized protein* (GRMZM2G405559) identified for GY under LN, acts as a transcriptional regulator of maize panicle development. Under ON, *Villin/Gelsolin* (GRMZM2G180988) was associated with DA, EH and PH, playing key role in stalk structure and developmental processes that directly impact ear height and lodging resistance. The *MADS-box/MEF2 Transcription Factor* (GRMZM2G005155) was identified for anthesis-silking interval (ASI), influencing development and emergence of silk. For GY under ON, *Chloroquine-resistance transporter-like* (GRMZM2G162250) was identified, which functions in efficient soil nutrient capture. [Conclusions] Collectively, these genes provide biological insights into the mechanisms underlying NUE in maize and represent valuable targets for validation, functional characterization, and marker development for future breeding efforts.

Key words: Nitrogen use efficiency, GWAS, candidate genes, Marker

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Field Efficacy Evaluation of Clothianidin Seed Coating Against *Monolepta hieroglyphica* on Maize

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Abstract: [Objective] *Monolepta hieroglyphica* has become a destructive primary pest threatening maize production in Northeast China, while resistant transgenic maize varieties available for field control remain scarce. This study aims to clarify the field control performance of clothianidin seed coating against *M. hieroglyphica* and its yield-promoting effect on maize. [Methods] Field cage and open-field experiments were conducted in combination with yellow sticky trap captures and sweep net sampling to systematically evaluate the effects of a 48% clothianidin flowable concentrate for seed treatment (FS) on *M. hieroglyphica* populations and crop yield. [Results] The results showed that seed coating with 48% clothianidin FS at an active ingredient rate of 7.68 g per kg seed provided corrected control efficacies of $56.3\% \pm 2.7\%$, $45.8\% \pm 13.3\%$, and $55.6\% \pm 1.8\%$ in open fields at Qiqihar, Gongzhuling, and Taonan, respectively. In the cage experiment at Gongzhuling, the corrected control efficacy reached $96.9\% \pm 1.5\%$, and the corrected maize yield was relatively increased by $13.6\% \pm 1.3\%$ compared with the untreated control. [Conclusions] Seed coating with 48% clothianidin delivers favorable field suppression against adult *M. hieroglyphica* and significantly cuts down local adult population density. Large-scale application is capable of substantially lowering the regional pest source, thereby providing feasible technical support for the sustainable, green management of this pest in the Northeast maize production region.

Key words: Clothianidin, *Monolepta hieroglyphica*, Seed-coating, Pest suppression, Maize yield improvement

Variable Rate of Nitrogen Application in Maize. The Greek research experience

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Abstract: [Objective] The purpose of this paper is to provide a concise overview of the major research conducted in Greece on the variable-rate application (VRA) of nitrogen (N) to maize. [Method] We reviewed the main research studies in Greece on the VRA of N fertilizers, both solid and liquid, using precision agriculture technologies based on active multispectral canopy sensors. These sensors produce modulated radiation at 40 Hz in the visible (VIS, 400–700 nm) and infrared (NIR, 700–1000 nm) regions of the electromagnetic spectrum. Nitrogen requirements are monitored weekly using the multispectral sensors and the chlorophyll index (CI), based on the model by Holland and Schepers (2010). [Result] The VRA fertilization, using the NDVI vegetation index, reduced the total amount of N required by 38% compared to the conventional method and increased NUE by about 20%. Even in plain maize fields, liquid VRA of N reduced in-season N rates by 23–46% and the total N dose by 12–24% compared to the conventional N application method. The reduction in N fertilization translated into benefits of 44–88 €/ha. [Conclusion] VRA of N in maize results in significant economic and environmental benefits.

Key words: VRA of N, Maize fertilization, Precision farming

Drip Fertigation with UAN Reduces Gaseous Nitrogen Emissions and Increases Maize Yield via Modulating Soil Physicochemical and Microbial Environments

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Abstract: [Objective] Extensive water and fertilizer practices represent a primary source of reactive nitrogen (N) loss in agriculture and a critical barrier to green and sustainable intensification. This study clarified how improved irrigation and N management influence N loss potential, pathways, and mechanisms in summer maize production, supporting the transition to precision agriculture. [Method] The experiment comprised seven treatments, with border-irrigated controlled-release urea serving as the control (BC). The remaining six treatments were: micro-sprinkler with controlled-release urea (SC), drip with controlled-release urea (DC), micro-sprinkler fertigation with urea (SN), drip fertigation with urea (DN), micro-sprinkler fertigation with UAN (SU), and drip fertigation with UAN (DU). [Result] Compared with BC, grain yield in DC and SC increased by 11.82% and 6.62%, respectively, while gaseous N emissions were reduced by 37.51% and 18.74%. DU, DN, SU, and SN exhibited even greater emission reductions, with gaseous N losses decreasing by 65.48%, 60.58%, 59.87%, and 52.04%, their N footprint decreasing by 43.61%, 42.00%, 41.84%, and 39.32%, and grain yield increasing by 18.72%, 11.40%, 12.27%, and 6.14%, respectively. DU also improved agronomic N efficiency by 13.81% over BC. However, no significant yield differences were found between DN and DC or SN and SC. Soil Water-Filled Pore Space (WFPS) directly and positively affected N₂O emissions. Optimized irrigation, particularly drip irrigation, lowered WFPS and associated denitrification intensity. DU, DN, SU, and SN attenuated peak gaseous N emissions and shortened their duration relative to BC, DC, and SC. Furthermore, DU and DN increased soil microbial diversity and reduced the relative abundance of denitrifying functional microorganisms compared to SU and SN. UAN similarly inhibited these microbes relative to urea. These microbial responses, together with lower WFPS and soil NO₃⁻-N and NH₄⁺-N concentrations under drip fertigation, synergistically mitigated gaseous N losses. [Conclusion] Drip fertigation reduced gaseous N emissions by shaping soil physicochemical and microbial environments, while simultaneously improving maize yield and N use efficiency. UAN drip fertigation achieved the greatest emission reduction and yield increase, demonstrating the feasibility of the relevant technology for practical production.

Key words: Summer maize, Reactive nitrogen loss, WFPS, Soil bacterial abundance

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AI-Powered Climate and Agronomic Intelligence for Supporting Maize Production and Decision-Making

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Abstract: Agronomists advising maize production increasingly rely on multiple sources of information, including seasonal climate outlooks, satellite-based crop monitoring, market prices, nitrogen management, and carbon-footprint considerations. However, these inputs are usually delivered separately and rarely translated into field-level recommendations. The main challenge is therefore no longer a lack of data, but the need to integrate diverse information into practical decisions such as when to plant, whether to irrigate, and how much nitrogen to apply. We present early-stage work on KUCCI (Kasetsart University Climate & Crop Intelligence), a prototype designed to support this integration for maize production. Climate reanalysis and seasonal forecast data are linked with a maize growth-stage model so that weather anomalies can be expressed as stage-specific agronomic risks, such as heat stress during flowering, rather than as climate statistics requiring further interpretation. Carbon considerations are incorporated in the same decision framework. Potential emission reductions from improved nitrogen management are estimated against a baseline using an established carbon-accounting approach and linked directly to fertilizer practices. In this way, carbon reduction becomes an additional benefit of good agronomic management rather than a separate burden for farmers. The objective is to provide a single field-level view combining climate risk, agronomic recommendations, carbon implications, and price information. KUCCI is currently a prototype and has been tested only in small pilot areas in Lopburi and Saraburi. We welcome discussion with agronomists and researchers developing similar decision-support approaches elsewhere in Asia.

Key words: Climate intelligence, Decision support system, Maize production, Artificial intelligence (AI), KUCCI

Responses of Three Widely Grown Rice Varieties to Water And Nutrient Management in West African Inland Valleys

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Abstract: Rising rice demand in West Africa calls for higher yields, yet improved varieties often respond inconsistently across farmers' fields and management conditions. [Objective] This study assessed how three widely grown rice varieties in West Africa (Nerica L19, IR841, and Orylux6) respond to combined water and nutrient management in West African inland valleys. The responses measured were phenology, yield, and nitrogen use. [Method] A two-year split-split-plot experiment was run in 2022 and 2023 at two contrasting sites in Benin, Ouinhi and Savalou. It crossed two water approaches, Smart-Valleys and undeveloped valleys, with three fertilization regimes across the three varieties. Fertilization included no input (F0), a blanket lowland recommendation (F1), and location-specific fertilization (F2). We measured days to anthesis, grain yield, grain nitrogen uptake, and agronomic nitrogen efficiency, then analyzed them by ANOVA. [Result] Variety significantly influenced all responses ($p < 0.001$). Days to anthesis increased in the order Orylux6, Nerica L19, then IR841. IR841 required 1.24 times longer than Orylux6 and showed a longer vegetative cycle. This cycle gap widened between sites, exceeding 11 days for IR841. Under Smart-Valleys with F1 or F2 fertilization, IR841 reached the highest yields, near 5.7 t/ha at Ouinhi in 2023. IR841 and Nerica L19 reached about 5.9 to 6.0 t/ha at Savalou, while Orylux6 stayed consistently lower. Smart-Valleys raised grain nitrogen uptake by 36%, from 166 to 226 kg/ha, and Ouinhi exceeded Savalou by 20%. IR841 accumulated the most nitrogen, near 213.6 kg/ha. The Smart-Valleys and F2 combination peaked near 320 kg/ha in 2023, showing a synergistic rather than additive interaction. Agronomic nitrogen efficiency was highest for IR841 under F1 Smart-Valleys at Ouinhi, near 23 kg·kg⁻¹. Nerica L19 reached the experiment maximum under F2 Smart-Valleys at Savalou, near 26 kg·kg⁻¹. [Conclusion] Varietal performance depended strongly on water and nutrient management. IR841 and Nerica L19 clearly outperformed Orylux6 under Smart-Valleys with F1 or F2 fertilization. Their advantage still varied with site and cycle length. Pairing stress-adapted, high-yielding varieties with Smart-Valleys and location-specific fertilization offers the most reliable path to higher productivity and nitrogen efficiency. Varietal recommendations should therefore be tailored to each site rather than applied uniformly.

Key words: African rice varieties, Smart-Valleys, Nitrogen use efficiency, Site-specific fertilization, West Africa

Exploring the Link Between Maize Seed Quality and Water Use Efficiency at Seedling and Grain-Filling Growth Phases

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Abstract: [Objective] Seed quality plays a critical role in early crop establishment, while water use efficiency acts as a bridge between plant physiology and field performance. Yet existing research treats seed quality and water use efficiency (WUE) as independent traits, leaving a gap in understanding their interaction. This study investigated the predictive capacity of seed quality traits like viability and vigour (Emergence %, Germination %, and Accelerated ageing %, Germination rate index, Accelerated ageing rate index, and Conductivity test) on WUE traits (Seedling and Grain-filling water use, Seedling and Grain-filling water use efficiency, Seedling and Grain-filling dry weight, Seedling and Grain-filling growth rate) at the seedling and grain-filling growth phases of maize. [Method] Four extra-early drought-tolerant maize genotypes were planted in a completely randomized design, while their WUE was established in a randomized complete block design, all in three replications. Seed quality traits were evaluated in the laboratory, while water use efficiency data were collected from the field at the maize seedling and grain-filling phases. This study adopted weekly destructive sampling to evaluate water use efficiency traits. [Result] While there were no significant associations between viability and WUE traits ($p > 0.05$), a significant association was observed between vigour and WUE traits at the grain-filling phase ($p < 0.05$). Accelerated ageing rate index had a negative association with grain-filling water use efficiency and grain-filling drying weight (-0.90 ; $p < 0.01$). Among the WUE traits at the seedling phase, seedling WUE significantly correlates positively with seedling water used and seedling dry weight (0.91 ; $p < 0.01$). At the grain-filling phase, grain-filling dry weight significantly correlates positively with grain-filling water used (0.63 ; $p < 0.05$). The grain-filling growth rate significantly correlated positively with germination percentage, accelerated ageing percentage, grain-filling dry weight, and grain-filling water use efficiency ($0.59, 0.64, 0.69, 0.74$; $p < 0.05$ & 0.01). Meanwhile, a significant negative association was observed between grain-filling growth rate and germination rate index (-0.59 ; $p < 0.05$). However, there were no significant individual effects of seed viability and WUE traits nor their interactions on maize grain yield ($p > 0.05$). [Conclusion] This study underscores the importance of seed vigour as a metric to improve maize water use characteristics at critical growth phases, with a prospect for future breeding to enhance climate change resilience.

Key words: Maize growth phases, Accelerated ageing index, Biomass accumulation, Seed quality assessment.

Technical Session 8

Climate-resilient Farming System and Agroecological Intensification



Development of a Field Assessment and Data Management System for "Insee 2" Hybrid Sweet Corn Production Using the AgriSpace Application under Smart Agriculture Framework

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Abstract: [Objective] Integrating smart agricultural technologies and geospatial data management is essential for optimizing economic crop supply chains. This research developed a standardized field assessment and spatial data management system for "Insee 2" hybrid sweet corn production using the AgriSpace digital application, aiming to enhance production efficiency and decision-making under the smart agriculture framework. [Method] The system was implemented and evaluated within the contract farming network of the National Corn and Sorghum Research Center, Faculty of Agriculture, Kasetsart University, spanning Nakhon Ratchasima, Saraburi, and Lopburi provinces. This network operates on a year-round production scheme designed to ensure a continuous daily supply of 8–10 tons of fresh corn ears from an average active cultivation area of 5–7 rai per day. The developed digital workflow integrates the acquisition of geospatial coordinates and continuous crop phenological (growth-stage) data via the AgriSpace application, linking them directly to a centralized cloud database. [Result] This integration enables advanced spatial analysis, yield forecasting, and precise harvest date prediction. The results indicate that the system significantly mitigates data discrepancies, improves data integrity, and establishes high consistency in field monitoring and evaluation. [Conclusion] Consequently, this digital approach optimizes supply chain logistics and enhances the overall climate-resilient production efficiency of Insee 2 sweet corn across diverse environments.

Key words: Smart agriculture, AgriSpace application, Field assessment, Contract farming, Insee 2

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Elite Purple Waxy Corn Hybrid Of DOA; CNW23099

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Abstract: [Objective] This research aims to develop a purple waxy corn hybrid with high yield and desirable eating quality. [Method] CNW23099 was developed from a cross between CNSW08, a white-kernel waxy corn inbred line with good eating quality, and CNSWP46, a purple-kernel inbred line with anthocyanin pigmentation in the aleurone layer, during 2019-2022 at CNFCRC, Thailand. The hybrid was evaluated in preliminary, standard, and regional trials during 2023-2025. [Result] CNW23099 produced fresh ear yields with and without husk of 13.3 and 8.5 t/ha, respectively. CNW23099 had ear yield with husk higher than commercial varieties range from 4-17%. Moreover, it exhibited desirable tenderness and flavor. Furthermore, CNW23099 presented attractive purple kernels and good agronomic traits, including 64 days to harvest, ear size (diameter x length) of 4.1 x 17.2 cm and 14 kernel row per ear. [Conclusion] CNW23099 shows promising potential as a new purple waxy corn hybrid for commercial cultivation in Thailand. Further multi-environment trials will be conducted to evaluate its yield stability and support its potential release to farmers.

Key words: Waxy corn, Hybrid, Anthocyanin

Funding acknowledgement: This study was supported by the Thailand Science Research and Innovation (TSRI).

Breeding of Red Sweet Corn

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Abstract: [Objective] To develop red-purple pigmented sweet corn inbred lines as a source of anthocyanin and to produce experimental hybrids for cultivar development. [Method] Red-purple pigmented inbred lines were developed through successive self-pollination and pedigree selection. A total of 175 elite inbred lines were identified, of which 58 were selected as parental lines and crossed using factorial and line $\times$ tester mating designs to generate 110 experimental hybrids. The hybrids were evaluated in a preliminary yield trial with three commercial check varieties under field conditions at the Chai Nat Field Crops Research Center. Data were collected from the 10 best ears per plot to evaluate agronomic performance and eating quality. [Result] A total of 193 red-purple pigmented inbred lines (S1–S6) were developed. Husked and dehusked ear weights ranged from 1.1–5.0 and 0.8–3.5 kg, respectively. Sweetness ranged from 13.4–17.4 °Brix, and harvest maturity ranged from 72–79 days. Based on agronomic performance, ear characteristics, and sweetness, 21 promising hybrids were selected. [Conclusion] The selected hybrids will be advanced to standard yield trials for further evaluation and future sweet corn cultivar development.

Key words: Sweet corn, Breeding, Hybrid, Inbred line, Anthocyanin

Funding acknowledgement: This study was supported by Thailand Science Research and Innovation (TSRI).

Multi-Environment Yield Trials and Stability Analysis of Promising Hybrid Waxy Corn Varieties in the Upper Northern Region of Thailand

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Abstract: [Objective] The project on development of F₁ hybrid waxy corn varieties suitable for cultivation in the upper northern region of Thailand aims to evaluate and select high-yielding hybrid waxy corn varieties with good eating quality and suitability for the regional environment. [Method] The study was conducted during the rainy season of 2024, assessing the yield and eating quality of 6 promising hybrid combinations with 4 commercial check varieties across 6 environmental conditions: (1) Mueang District, Phayao Province; (2) Mueang District, Lampang Province; (3) Dok Khamtai District, Phayao Province; (4) Ngao District, Lampang Province; (5) Rong Kwang District, Phrae Province; and (6) Thoeng District, Chiang Rai Province. The experiment was arranged in a randomized complete block design (RCBD) with three replications. [Result] The results indicated that two elite hybrid, UP15 × T7, exhibited high yield potential and good eating quality. This hybrid an average with husk yield of 18,863 kg ha⁻¹ and an average without husk yield of 12,588 kg ha⁻¹, performing well across various environmental conditions in the upper northern region. The hybrid has a harvesting age of 65 days, an average ear length of 18.6 cm, an ear width of 4.1 cm, and 14 kernel rows. The second-highest yielding hybrid was KCU59 × T7, which produced an average with husk yield of 15,850 kg ha⁻¹ and an average without husk yield of 12,044 kg ha⁻¹. It reached harvesting age of 65 days, with an average ear length of 17.4 cm, an ear diameter of 4.1 cm, and 14 kernel rows per ear and good eating quality. When compared with the highest-yielding commercial cultivar, Black Pink, which produced an average with husk yield of 20,206 kg ha⁻¹ and an average without husk yield of 13,494 kg ha⁻¹ with a harvesting age of 66 days, an ear length of 17.1 cm, an ear diameter of 4.4 cm, and 14 kernel rows per ear, while also good eating quality. Yield stability was evaluated using the Eberhart and Russell method, the hybrid UP15 × T7 exhibited regression coefficients (b) of 1.20 and 1.32 for with husk yield and without husk yield, respectively. Similarly, KCU59 × T7 exhibited regression coefficients of 1.29 and 0.81 for with husk yield and without husk yield, respectively. In all cases, the regression coefficients were not significantly different from unity, indicating broad adaptation and stable performance across environments. The GGE biplot analysis explained 93.64% of the total variation in with husk yield (PC1 = 86.86% and PC2 = 6.78%) and 95.69% of the total variation in without husk yield (PC1 = 87.32% and PC2 = 8.37%). [Conclusion] Therefore, these hybrids demonstrated high yield potential and stable performance across environments and are recommended for cultivation and dissemination to farmers in the Upper Northern Region of Thailand.

Key words: Waxy corn, Yield trial evaluation, Stability, Elite hybrid

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Community Structure and Diversity of Migratory Maize Aphids in Jilin Province

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Abstract: [Objective] This study clarified species composition, migration dynamics and community structure of migratory maize aphids in Jilin Province to support pest monitoring and early warning. [Methods] Winged aphids were collected via suction traps at Dunhua, Gongzhuling, Meihekou and Taonan from 2019 to 2025; 141,072 maize-associated aphids of four species were identified, and community diversity, dominant species and interannual similarity were analyzed. [Results] The four aphid species had obvious spatiotemporal differences in population dynamics. All four regions had low aphid community diversity with low evenness and high dominance. Gongzhuling and Meihekou had higher diversity than Dunhua and Taonan. July–September Shannon–Wiener index (0.2195–0.6425) and Pielou index (0.1583–0.4635) peaked in Gongzhuling, while Simpson dominance index was the lowest there. Aphid communities had low inter-site similarity, with dominant species shifting across locations and years. Taonan’s community structure was the most stable. [Conclusion] Migratory maize aphid communities in Jilin show obvious spatiotemporal variation, which offers evidence for regional targeted monitoring and control.

Key words: Maize aphid, Suction trap, Population dynamics, Species diversity

Evaluation of Genotype $\times$ Environment Interaction of Reciprocal Pro-Vitamin A Maize Hybrids

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Abstract: The tendency of genotype $\times$ environment interactions to complicate the selection process of superior genotypes and lessen the selection efficiency gives rise to the necessity to evaluate multi-environment trial data. Sixty-three reciprocal pro-vitamin A maize hybrids were evaluated at four locations in South Africa. Data was analysed using Genstat statistical software. The objectives of the study were to determine existence of genotype $\times$ environment interaction on grain yield of 63 pro-vitamin A maize genotypes tested across four locations and to determine if cytoplasmic effects influenced the behaviour of pro-vitamin A maize hybrids across environments. Data was analysed using Genstat software package. The chief observation was the presence of genotype $\times$ environment interaction among the 63 maize hybrids evaluated at four locations. Additionally, three mega-environments were present in the study and Dundee and Ukulinga were in the same mega-environment. Makhathini and Ukulinga had a strong crossover genotype $\times$ environment. Cedara and Dundee were the most discriminating (informative) environments. Hybrids 14PVA-120 and 14PVA-44 were the best yielding experimental hybrids although they had poor static stability. Standard commercial hybrid DKC80-40BRGEN was the best hybrid at Dundee and Ukulinga but among the experimental hybrids, hybrid 14PVA-62 is recommended for both environments. Hybrid 14PVA-120 is recommended for environments that exhibit same characteristics as Cedara. Hybrid 14PVA-80 shined at Makhathini hence it is recommended for similar environments. Hybrids 14PVA-101 and 14PVA-124 showed the highest static stability. Cytoplasmic effects were present for both yield and stability. Yield and static stability were inversely proportional as the high yielding hybrids were lowly stable. Evaluation of the genotype $\times$ environment interaction generally showed that cytoplasmic effects were significant for mean yield and homeostatic stability performance of pro-vitamin A maize hybrids.

Key words: Pro-vitamin A maize, Genotype $\times$ environment interaction, Cytoplasmic effects, Grain yield, Yield stability

Effects of Exogenous Carbon Input on Soil Microbial Functions and Greenhouse Gas Emissions in a Wheat–Maize Cropping System

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Abstract: [Objective] To elucidate the effects of different exogenous carbon inputs on soil microbial functioning and greenhouse gas emissions in a winter wheat–summer maize rotation system, [Method] six treatments were established: no fertilization (CK), conventional fertilization (N), sole application of commercial organic fertilizer (M1), straw return combined with conventional fertilization (NJ), replacement of 20% of mineral nitrogen fertilizer with commercial organic fertilizer (M2), and replacement of 20% of mineral nitrogen fertilizer with manure (M3). Soil CO₂ and N₂O emissions were monitored, and the underlying microbial mechanisms were investigated by determining microbial biomass carbon and nitrogen and extracellular enzyme activities. [Result] The results showed that: (1) all exogenous carbon inputs reduced cumulative N₂O emissions, whereas their effects on CO₂ emissions depended on the type of carbon source. Compared with the N treatment, M2 reduced annual cumulative CO₂ and N₂O emissions by 3.4% and 17.1%, respectively, exhibiting the greatest simultaneous mitigation effect. Although M3 and NJ reduced N₂O emissions by 10.3% and 5.3%, respectively, they increased CO₂ emissions by 7.0% and 17.3%. (2) Organic amendments generally promoted microbial biomass accumulation in the surface soil layer (0–10 cm). During the summer maize season, MBC and MBN under M2 increased by 66.8% and 86.1%, respectively, indicating enhanced microbial retention of carbon and nitrogen resources. (3) Extracellular enzyme responses exhibited pronounced seasonal differentiation. Organic amendments mainly enhanced nitrogen- and phosphorus-acquiring enzyme activities during the winter wheat season, whereas NJ increased β -glucosidase activity by 72.0% during the summer maize season, suggesting that straw decomposition under warm conditions intensified microbial carbon acquisition. (4) Enzyme stoichiometry indicated that microorganisms tended to adopt a “low enzyme investment–high growth efficiency” strategy during the summer maize season, whereas straw and manure inputs increased enzyme production per unit microbial biomass in deeper soil during the winter wheat season. [Conclusion] Overall, M2 coordinated carbon supply with reduced nitrogen fertilizer input and reshaped microbial carbon–nitrogen allocation and nutrient-acquisition strategies. This treatment simultaneously increased microbial biomass and reduced soil CO₂ and N₂O emissions, highlighting its potential as a low-carbon fertilization strategy for winter wheat–summer maize rotation systems in the North China Plain.

Key words: Exogenous carbon input, Winter wheat–summer maize rotation system in the North China Plain, Greenhouse gas emissions, Soil microbial biomass, Extracellular enzyme activity

Enhancing Crop System Sustainability by Optimizing Straw Returning and Nitrogen Management: A Multidimensional Evaluation of Energy, Economy, And Environment

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Abstract: [Objective] Straw return to the field and nitrogen fertilizer application are widely recognized as effective measures for improving resource use efficiency; however, there is currently a lack of comprehensive assessments covering energy, economic, and environmental dimensions. [Method] This study explores methods to improve yield, profitability, and environmental management by evaluating the sustainability performance of different maize straw return schemes combined with varying nitrogen application rates. [Result] Compared to the control group (no straw return + 210 kg N ha⁻¹), the SN group (full straw return + 210 kg N ha⁻¹), the S-15%N treatment (full-rate straw return + 178.5 kg N ha⁻¹), and the 1/2SN treatment (half-rate straw return + 210 kg N ha⁻¹) showed increases in the value of agricultural ecosystem services increased by 17.49%, 12.87%, and 11.40%, respectively. Further comparisons showed that, compared to the SN treatment, the 1/2SN or S-15%N treatments achieved higher sustainability performance indicators and a lower carbon footprint while maintaining comparable crop yields. [Conclusion] In summary, promoting the practice of “straw incorporation with nitrogen fertilizer application” combined with optimized measures such as “nitrogen fertilizer reduction” (S-15%N) or “half-rate incorporation” (1/2SN) represents an effective pathway toward achieving sustainable agricultural development.

Key words: Straw return, Nitrogen fertilizer management, Sustainability performance index, Carbon footprint, Agroecosystem service value, Eco-economic benefits

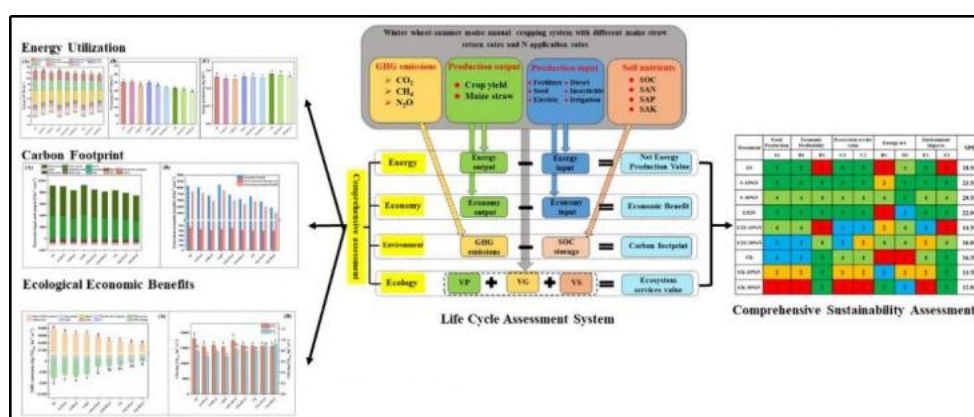


Fig. 1 An assessment of sustainability based on yield, energy, economy and environment.

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Optimizing sowing date and variety maintain stable maize yield under strip tillage in the Northeast China

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Abstract: [Objective] Strip tillage, one of conservation tillage, is beneficial for improving soil quality but may reduce maize yield due to low soil temperatures under straw mulching in high-latitude areas of northeast China. Optimization of sowing date and variety offers a cost-effective solution to maintain or enhance crop productivity. [Method] In the present study, a split-plot field experiment was conducted to evaluate the effects of four sowing dates (2nd May (D1), 9th May (D2), 16th May (D3), 23rd May (D4)) and three maize varieties (early-, medium-, and late-maturing) on maize yield and resource use efficiency under strip tillage during 2022 to 2023. [Result] D1, D2, and D3 increased maize yield by 10.7%, 8.4%, and 9.8%, heat use efficiency (HUE) by 6.5%, 5.2%, and 7.4%, water use efficiency (WUE) by 5.5%, 6.8%, and 9.9% and nitrogen fertilizer partial factor productivity (NPFP) by 10.6%, 8.3%, and 9.9% as compared to D4 on average, respectively. The soil temperature use efficiency (TUE) of D3 was significantly increased by 7.8%, 8.2%, and 9.9% in contrast with D1, D2, and D4. Compared with EV, MV and LV increased yield by 22.5% and 28.9%, HUE by 18.9% and 23.8%, TUE by 19.0% and 23.9%, WUE by 18.9% and 24.0%, and NPFP by 22.4% and 29.0% on average, respectively. [Conclusion] The present study suggests that under strip tillage, moderately delayed sowing date and long-growth varieties application can enhance maize productivity with higher resource use efficiency in high-latitude areas of northeast China.

Key words: Conservation tillage, Sowing date, Variety, Grain yield, Resource use efficiency

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Effects of Maize and Soybean Rotation on Soil Microbial Necromass Carbon in the Mollisols Region of Northeast China

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Abstract: [Objective] Soil organic carbon (SOC) is a major component of the global carbon cycle, and microbial necromass carbon (MNC) is increasingly recognized as the dominant contributor to SOC accrual. Crop rotation diversifies plant litter inputs and increases root biomass, thereby shaping rhizosphere microbial communities that are closely associated with litter decomposition and necromass transformation, which in turn influence SOC stability. Although MNC has been reported to account for approximately 50% of SOC, its response to different rotation systems remains poorly understood. To address this, the present study combined straw returning, conservation tillage, and crop rotation to investigate the accumulation and transformation of microbial necromass in soil, with the aim of providing insights into SOC sequestration and nutrient enhancement. [Method] A field experiment was established in Harbin City, Heilongjiang Province in 2022, comprising three treatments: continuous soybean (CS), continuous maize (CM), and soybean–maize rotation (SM) with straw mulching and strip tillage. Soil samples (0–20 cm) were collected after harvest in 2024 and 2025. [Result] Compared with CS and SM, CM significantly increased fungal necromass carbon (FNC) by 9.51% and 16.23%, respectively, and total MNC by 8.49% and 14.68%, respectively. No significant difference in bacterial necromass carbon (BNC) was observed between CS and CM ($P>0.05$). Both SM and CM significantly increased the FNC/BNC ratio relative to CS, by 11.14% and 9.08%, respectively. Among all treatments, CM exhibited the highest contribution of MNC to SOC (42.72%), and FNC was the predominant fraction of MNC across all treatments. [Conclusion] Short-term soybean–maize rotation significantly enhanced the FNC/BNC ratio compared to CS treatment, whereas CM treatment significantly increased soil necromass carbon fractions. Although short-term soybean–maize rotation clearly altered soil MNC pools, no significant increment was detected compared with CS treatment. Further research is therefore needed to investigate the long-term effects of soybean–maize rotation cropping system.

Key words: Conservation agriculture, Microbial necromass carbon, Soil organic carbon, Northeast China

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Effects of Sowing Date-dependent Hydrothermal Conditions on Maize Yield and Soil Physical Properties under Strip Tillage in Northeast China

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Abstract: [Objective] Northeast China is the most important maize production area and commodity grain base in China, which is of great significance for ensuring national food security. Conservation tillage practice, e.g. straw returning and strip tillage, is beneficial to maintaining soil moisture and reducing soil erosion. However, such tillage system may reduce soil temperature, consequently affecting the growth and development of maize and yield formation. Furthermore, mechanical sowing under excessive soil moisture can aggravate the risk of soil compaction. Optimizing sowing timing is therefore essential to improve maize productivity and sustain soil physical quality. [Method] In the present study, a field experiment was conducted in Harbin, Heilongjiang Province, China, with five sowing-date treatments: April 25th (D1), May 2nd (D2), May 9th (D3), May 16th (D4), and May 23rd (D5). The maize yield and key soil physical indices during critical maize growth stages were measured to clarify the responses of maize yield and soil physical properties to sowing date under strip tillage. [Result] The results revealed that treatments D1, D2, D3 and D4 maintained relatively high grain yields without statistically significant inter-treatment differences, demonstrating that moderately delayed sowing exerted no remarkable negative effect on crop productivity. D4 produced the maximum yield, which was primarily driven by elevated ear number and grain number per ear. Sowing operations were implemented at soil moisture contents of 271%, 23.6%, 21.6%, 22.4% and 23.3% for D1 to D5, respectively, with corresponding soil bulk density increments of 7.4%, 5.3%, 2.7%, 6.0% and 6.7%. Mechanical seeding operations substantially aggravated soil bulk density under excessive soil moisture conditions. [Conclusion] Sowing date significantly regulates maize yield and soil physical properties under strip tillage in Northeast China. Appropriate delay of sowing alleviates low-temperature constraints on maize growth and effectively reduces machinery-induced soil compaction risks. Therefore, sowing within optimal soil moisture range can minimize tillage induced soil compaction and preserve soil quality. Collectively, selecting a rational sowing date based on in-situ soil moisture conditions is a vital agronomic strategy to coordinate high maize yield and sustainable soil quality under conservation tillage.

Key words: Conservation tillage, Maize yield, Soil compaction, Soil moisture, Sowing date

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Effect of Rotational Tillage Pattern on Crop Yield and Carbon Footprint under Soybean-Maize Rotation System in Northeast China

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Abstract: [Objective] Northeast China, a major maize and soybean production area, has suffered from continuous monoculture, straw removal, and inappropriate tillage practices, resulting in crop yields instability, soil degradation, high production costs, and high carbon emissions. Conservation agriculture, characterized by crop rotation, straw mulching, and reduced or no tillage, is effective in improving soil fertility and sustaining crop productivity. However, slow decomposition of surface straw mulch in this cold temperate region lowers soil temperatures in spring, restrict crop growth and compromise the potential for carbon sequestration and emission reduction. Accordingly, optimization of matched tillage regimes is urgently required. [Method] To address this, a two-year field experiment was conducted in Jiamusi, Heilongjiang to evaluate four tillage systems with straw returning: rotary tillage with ridge sowing for both maize and soybean (RR); no tillage for maize and strip tillage for soybean with sowing on original ridges (MR); rotary tillage with flat sowing for both crops (RF); and no tillage for maize and strip tillage for soybean with flat sowing (MF). [Result] Results showed that MR maintained higher soil moisture in the 0-40 cm layer than RR, while no significant differences were observed in 0-20 cm soil temperature. MR also tended to increase total nitrogen and organic carbon stocks, but the increases were not statistically significant. Although crop yields did not differ among treatments, MR produced the highest economic returns (4.9-10.0% above others) and benefit-cost ratio. Furthermore, MR enhanced grain nitrogen accumulation, post-anthesis dry matter and nitrogen contribution to grains, and increased nitrogen use efficiency (NUE) by 7.4% for maize and 10.4% for soybean, as well as nitrogen partial factor productivity (NPFP) by 6.3% and 0.2%, respectively, relative to RR. In contrast, RR significantly reduced N₂O emissions, global warming potential (GWP) by 20.9-28.9%, and greenhouse gas intensity (GHGI) by 18.2-30.8% compared with MR and MF. MR exhibited the highest net energy and energy use efficiency (4.5-8.4% and 2.4-7.6% higher, respectively), whereas RR showed lower area-based and energy-yield carbon footprints, though economic-equivalent footprints were similar across RR, MR, and RF. [Conclusion] Overall, MR offers superior productivity, nutrient/energy efficiency, and profitability, making it suitable for yield-oriented objectives; conversely, RR is more environmentally friendly due to its lower emissions and carbon footprint. Therefore, tillage strategies should be formulated according to specific production and ecological priorities.

Key words: Conservation tillage, Crop rotation, Yield, Nitrogen use efficiency, Carbon footprint

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Yield Advantage in Wide Strip Intercropping: Border-row Effects and Adding a Third Crop in Double Relay Intercropping

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Abstract: [Objective] Intercropping provides a vital way to enhance productivity, resource use efficiency, and other ecosystem functions in agroecosystems. Traditional strip intercropping is based on narrow strips and is hard to mechanize. Wide strip intercropping offers improved compatibility with mechanization, but the yield advantage and the underlying mechanisms require examination. We compared the yield advantages of narrow and wide strip intercropping, explored the potential of including a fodder crop after harvest of the early-sown species and we quantified the border row effects in wide strip intercropping. [Method] We conducted a two-year field experiment in northwest China with wheat/maize, pea/maize, oilseed rape/maize, and wheat/soybean intercropping in both narrow and wide strip intercrops, and corresponding monocultures. In wide strip intercropping, Sudangrass was planted after wheat, while common vetch was planted after harvesting peas and oilseed rape. Productivity, border row effects, and plant functional traits were measured to illuminate mechanisms underlying the advantages of intercropping. [Result] Both narrow and wide strip intercropping showed a productivity advantage. The land equivalent Ratio (LER) of wide strip intercropping ranged from 1.04 to 1.20 based on grain yield, which was lower than the range of the LER of narrow strip intercropping (1.11 to 1.36). This difference was primarily due to a lower maize partial LER in wide strip intercropping. Planting a fodder or green manure crop after the harvest of early-maturing crops increased the biomass-based LER of wide strip intercropping. Maize exhibited higher productivity in border rows compared to inner rows, especially in pea/maize and oilseed rape/maize intercropping, which was related to functional traits. [Conclusion] The results demonstrate that the wide strip intercropping sustains yields through border row recovery (resource reallocation post-harvest) and optimized planting strategy with temporal niche exploitation. Mechanization-adaptable wide strip intercropping offers a scalable solution for sustainable agricultural intensification.

Key words: Wide strip intercropping, Border-row effect, Double relay intercropping, Land equivalent ratio (LER), Mechanization, Forage crop

Biotech Maize, Conservation Tillage Adoption, and Their Joint Effects on Maize Production and Pesticide Use

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Abstract: [Objective] Biotech maize and conservation tillage are important technologies for promoting the green transformation of Chinese agriculture and safeguarding food security. However, evidence remains limited on whether biotech maize facilitates the joint adoption of conservation tillage practices among smallholders and whether the two technologies generate joint effects on agricultural production and pesticide use. This study examines the effects of biotech maize cultivation on farmers' adoption of conservation tillage and evaluates the joint effects of biotech maize and conservation tillage on maize yield and herbicide and insecticide use. [Method] Using farm household survey data collected in 2023 and 2024, covering 2,451 households and 5,052 maize plots across 17 Chinese provinces, we employ discrete-choice models to estimate the effects of biotech maize cultivation on the joint adoption of conservation tillage practices and on the adoption of no-till or reduced tillage and straw incorporation separately. We further distinguish among insect-resistant, glyphosate-tolerant, and stacked-trait maize varieties. Interaction terms between biotech maize cultivation and conservation tillage practices are then included in ordinary least squares regressions for maize yield and pesticide application. We also examine heterogeneity across China's major maize agroecological zones. [Result] Biotech maize cultivation increases the probability of jointly adopting multiple conservation tillage practices by 6.8 percentage points and the probability of adopting straw incorporation by 9.6 percentage points, with both effects significant at the 1% level. The estimated effects vary across transgenic traits. Stacked-trait varieties increase the probabilities of joint conservation tillage adoption and straw incorporation by 9.9 and 10.2 percentage points, respectively. Insect-resistant varieties increase the probabilities of joint conservation tillage adoption, no-till or reduced tillage, and straw incorporation by 7.4, 4.4, and 7.3 percentage points, respectively. Glyphosate-tolerant varieties increase the probabilities of joint conservation tillage adoption and straw incorporation by 8.1 and 8.6 percentage points, respectively. The adoption effects also exhibit substantial regional heterogeneity: biotech maize promotes conservation tillage adoption in northern and southwestern China but reduces the probability of joint adoption in the Huang-Huai-Hai region. The interaction between biotech maize and conservation tillage has no statistically significant effect on maize yield. However, it is positively associated with herbicide application and negatively associated with insecticide application. These joint effects differ considerably across agroecological zones. [Conclusion] Biotech maize cultivation promotes farmers' adoption of conservation tillage, although the magnitude and direction of this effect vary across transgenic traits and agroecological zones. Combining biotech maize with conservation tillage does not produce a detectable yield gain but changes the composition of pesticide use by

increasing herbicide application while reducing insecticide application. The commercialization of biotech maize should therefore be coordinated with conservation tillage programs and region-specific pesticide-management policies. Particular attention should be paid to preventing excessive herbicide use while leveraging the potential of biotech maize and conservation tillage to reduce insecticide use and promote greener agricultural production.

Key words: Biotech maize, Conservation tillage, Pesticide use

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Physiological Regulatory Mechanisms of Exogenous Spermidine and Brassinolide in Alleviating Saline-Alkali Stress in Maize

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Abstract: [Objective] Saline-alkali stress is a major abiotic constraint on global maize (*Zea mays* L.) production. Exogenous application of plant growth regulators is an effective strategy to improve crop stress tolerance. In this study, we investigated the physiological regulatory effects and yield responses of maize to exogenous spermidine (Spd) and brassinolide (BL), applied alone or in combination, under saline-alkali stress, and explored their synergistic mechanisms. [Method] Field experiments were conducted using the maize cultivar Leidan 198 grown in natural saline-alkali soil. Six treatments were designed: control (CK, water spray), T1 (0.3 mmol·L⁻¹ Spd), T2 (0.2 mmol·L⁻¹ Spd + 0.1 mmol·L⁻¹ BL), T3 (0.15 mmol·L⁻¹ Spd + 0.15 mmol·L⁻¹ BL), T4 (0.1 mmol·L⁻¹ Spd + 0.2 mmol·L⁻¹ BL), and T5 (0.3 mmol·L⁻¹ BL). Multiple physiological indices (antioxidant enzyme activities, osmotic adjustment substances, endogenous hormone contents, and key metabolic enzyme activities) were measured at the seedling (V3), jointing (V6), and grain-filling (R3) stages. [Result] All treatments mitigated saline-alkali stress damage, with combined applications showing more pronounced effects than individual ones. Treatment T4 (0.1 mmol·L⁻¹ Spd + 0.2 mmol·L⁻¹ BL) exhibited the optimal effect, significantly increasing grain yield by 15.6% compared with the control, and also enhancing plant height, soil plant analysis development (SPAD) value, and aboveground and belowground dry matter accumulation. Moreover, T4 markedly elevated the activities of superoxide dismutase (SOD), peroxidase (POD), and catalase (CAT), while decreasing malondialdehyde (MDA) content. It effectively maintained homeostasis of endogenous hormones (indole-3-acetic acid (IAA), cytokinin (CTK), abscisic acid (ABA), gibberellin (GA)) and enhanced activities of key metabolic enzymes (sucrose synthase (SuSy), ribulose-1,5-bisphosphate carboxylase/oxygenase (Rubisco), nitrate reductase (NR), and glutamine synthetase (GS)). [Conclusion] These findings demonstrate that the combined application of 0.1 mmol·L⁻¹ Spd and 0.2 mmol·L⁻¹ BL comprehensively enhances saline-alkali tolerance throughout maize growth and ultimately increases grain yield. This study provides a new technical approach and theoretical basis for saline-alkali-tolerant cultivation in saline-alkali regions.

Key words: Spermidine, Brassinolide, Maize, Saline-alkali stress, Yield

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Reduced Phosphorus Input Under Split Drip Fertigation Alters Maize Root Distribution, Phosphorus Uptake, and Grain Yield in Irrigated Inner Mongolia, China

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Abstract: [Objective] In the irrigated spring maize region of Inner Mongolia, China, low phosphorus mobility and basal fertilization create a mismatch between P supply and maize root demand, reducing P-use efficiency. Optimizing P rates and split drip fertigation is crucial for sustaining yield with lower P inputs. [Method] To address this issue, a two-year field experiment was conducted in 2022 and 2023 with five treatments: no P application (CP0), split P application through drip irrigation with a 30% reduction (CP1, 105 kg P₂O₅ ha⁻¹), split P application through drip irrigation with a 15% reduction (CP2, 127.5 kg P₂O₅ ha⁻¹), split P application through drip irrigation at the conventional rate (CP3, 150 kg P₂O₅ ha⁻¹), and conventional one-time basal P application (CK, 150 kg P₂O₅ ha⁻¹). At silking, root morphology, root length density (RLD), and Olsen-P distribution were quantified in the 0–40 cm soil profile. Plant P accumulation, post-silking P accumulation, grain yield, and P-efficiency indices were also determined. [Result] Compared with CK, CP2 and CP3 significantly increased root dry weight (RDW), root surface area (RSA), and root volume (RV). Compared with conventional basal P application, CP2 increased Olsen-P availability in the 30–40 cm soil layer and promoted root proliferation in the middle and lower parts of the sampled profile. Descriptive root-P spatial analysis suggested that CP2 was associated with closer co-localization of RLD and Olsen-P in the 20–40 cm layer than CK, while maintaining grain yield comparable to CP3 and increasing grain yield by 4.07% relative to CK. CP2 also increased apparent P recovery efficiency and P agronomic efficiency by 47.34% and 54.62%, respectively, relative to CK. [Conclusion] These results indicate that a moderate reduction in P input under split drip fertigation can improve the spatial efficiency of P acquisition by aligning P supply with active root distribution within the upper 40 cm soil profile. Under the conditions of this study, applying 127.5 kg P₂O₅ ha⁻¹ through split fertigation was a promising strategy for maintaining spring maize yield while improving P-use efficiency in the irrigated spring maize region of Inner Mongolia, China.

Key words: Phosphorus fertigation, Spring maize, Root length density, Root-phosphorus spatial concordance, Phosphorus use efficiency

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Dynamic Interference of Combined High Temperature and Drought Stress on the Source-Sink-Transport System in Summer Maize

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Abstract: [Objective] High temperature and drought often occur simultaneously in Huang-Huai-Hai Plain and severely restrict summer maize yield, while the systemic physiological mechanism of combined stress disrupting maize source-sink-transport system and reducing grain yield remains unclear. This study aimed to clarify the synergistic damage pathway of combined heat-drought stress on source, transport and sink organs, identify the critical stress-sensitive stage limiting sink capacity, quantify the water regulation effect and its application boundary, and provide theoretical support for stress-resistant high-yield maize cultivation. [Method] A two-year (2024–2025) lysimeter experiment was carried out with heat-sensitive summer maize cultivar Denghai 605. Two temperature levels (normal temperature NT, high temperature HT) and three soil moisture gradients (low L, medium M, high H) were set at tasseling stage to form six treatments. We systematically measured root morphology and bleeding intensity, stem mechanical properties, dry matter and nitrogen accumulation & distribution, dynamic grain filling characteristics, yield components and grain quality. Two-way ANOVA, Logistic grain-filling fitting and PLS-PM path model were adopted to analyze the systemic response of source-sink-transport system to compound stress. [Result] Combined high temperature and drought (HT-L) produced synergistic inhibitory effects on the whole source-sink-transport system. HT-L reduced total root surface area and root bleeding intensity by 54.3%–58.1%, leaf total nitrogen accumulation by 66.7%, and stem mechanical indicators by 19.7%–29.6%. The early grain filling stage (7–14 days after silking) was confirmed as the irreversible critical sensitive window for sink formation; kernel dry matter accumulation rate of HT-L only reached 48.5% of the control (NT-H), leading to annual grain yield decline of 38.7%–41.8%. Sufficient irrigation (HT-H) effectively alleviated heat-induced damage to source and transport functions, yet failed to eliminate direct thermal injury to sink development, resulting in an average yield loss of 13.4%. PLS-PM revealed that compound stress mainly suppressed yield through the chain pathway of Stress → Source System → Transport System → Yield. Meanwhile, combined stress deteriorated grain quality by lowering starch and test weight while raising crude fiber content. [Conclusion] Tasseling-stage combined heat and drought stress triggers systemic dysfunction of summer maize source-sink-transport system via three coordinated approaches: inhibited root absorption and leaf assimilation damage source capacity, stem structural degradation blocks assimilate transport, and irreversible endosperm cell development damage in early grain filling limits sink potential. Maintaining adequate water supply from tasseling to early grain filling can

stabilize source and transport functions, but water regulation has a clear efficacy boundary and cannot offset heat damage to sink organs. Integrating water management, heat-resistant genetic improvement and targeted agronomic regulation during early grain filling is the optimal strategy to stabilize summer maize yield under compound heat-drought stress in Huang-Huai-Hai Plain.

Key words: Combined heat and drought stress, Tasseling stage, Source-sink-transport system, Grain filling, Summer maize

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How Deep Tillage Combined with Organic Inputs Increased Soil Organic Carbon Storage and Crop Productivity in Northeast China

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Abstract: [Objective] Soil organic carbon (SOC) sequestration in agricultural systems is strongly influenced by tillage practices and organic inputs, yet their interactive effects on microbial necromass formation and its contribution to SOC stabilization remain unclear. [Method] To address this, a three-year field experiment was conducted with three treatments: conventional tillage with straw (CT_S), deep tillage with straw (DT_S) and deep tillage with straw plus organic manure (DT_S_M). [Result] Our results showed that compared to CT_S, DT_S and DT_S_M improved crop yield by 7.0%–11.5%. DT_S_M increased SOC content by 11.5%–16.5% relative to CT_S across soil layers. This treatment also increased microbial biomass carbon (+25.5%) and nitrogen (+19.1%) in the subsoil, while boosting extracellular enzymes (+3.8%–19.6%) relative to CT_S. Crucially, DT_S_M promoted microbial necromass accumulation, with total microbial necromass C increasing by 13.3%–14.3%, primarily driven by bacterial-derived contributions (+24.1%–26.7%) rather fungal sources (+9.9%–11.6%). Partial Least Squares Path Modeling indicated that tillage, organic materials and SOC exerts positive influence on crop yield, whereas organic materials and tillage primarily also promoted bacterial necromass C formation by enhancing microbial biomass in the topsoil and alleviating microbial resource limitation in the subsoil, thereby promoting SOC sequestration. [Conclusion] Overall, these results demonstrated that the incorporation of deep tillage and organic materials promote SOC sequestration and crop productivity, and represents a sustainable approach for managing cropping systems in the Northeast China Plain.

Key words: Deep tillage, Straw, Subsoil carbon, Microbial necromass, Yield

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Biochar Combined with DCD and NBPT Alleviates Greenhouse Gas Emissions by Regulating Soil Nitrogen Cycling

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Abstract: [Objective] Excessive nitrogen fertilizer application in summer maize production leads to low nitrogen use efficiency and exacerbates environmental issues such as increased greenhouse gas emissions. This study aims to investigate the combined effects of biochar with nitrification inhibitor (DCD) and urease inhibitor (NBPT) on soil nitrogen transformation, greenhouse gas emissions, and nitrogen-cycling microbial communities, in order to evaluate their potential for achieving synergistic enhancement of crop yield increase and emission reduction. [Method] A two-year field experiment (2024-2026) was conducted with five treatments: no nitrogen fertilizer (N0), conventional nitrogen application (N210), conventional nitrogen with biochar (BN210), conventional nitrogen with DCD+NBPT (N210DN), and conventional nitrogen with biochar+DCD+NBPT (BN210DN). Soil inorganic nitrogen content, nitrogen-cycling enzyme activities, and N₂O and CO₂ emission fluxes were measured at key growth stages, and high-throughput sequencing was employed to analyze changes in the structure and abundance of soil nitrogen-cycling microbial communities. [Result] Compared with conventional nitrogen application, the BN210DN treatment significantly increased soil NH₄⁺-N content, reduced nitrate reductase and urease activities, suppressed the expression of denitrification functional genes (nirK, nirS, nosZ), and decreased the abundance of nitrifying bacteria (Nitrospirota). This treatment significantly reduced cumulative N₂O and CO₂ emissions, lowered global warming potential (GWP) and greenhouse gas intensity (GHGI), and improved nitrogen use efficiency by 44.81% and 44.95% over the two years, respectively. [Conclusion] The combined application of biochar with DCD+NBPT can extend the effective duration of the inhibitors through complementary mechanisms of physical adsorption and retarded degradation, while synergistically regulating the soil nitrogen-cycling microbial community structure. This effectively inhibits nitrification and denitrification processes, reduces gaseous nitrogen losses, and achieves the dual goals of increasing crop yield and mitigating greenhouse gas emissions. This strategy provides theoretical basis and technical support for establishing a low-carbon and high-efficiency nitrogen management model in farmland.

Key words: Biochar, Nitrification Inhibitor, Urease Inhibitor, Nitrogen Cycling, Greenhouse Gas Mitigation

Legume-Based Double-Cropping Rotations Improve Soil Nutrient Status and Subsequent Winter Wheat Yield Through Changes In Soil Bacterial Network Complexity in the North China Plain

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Abstract: [Objective] Although legume inclusion in crop rotations is widely considered an effective strategy to mitigate agroecosystem degradation associated with long-term cereal monoculture, the coordinated responses of soil physicochemical properties, soil microbial communities, and crop productivity to double-cropping cereal–legume rotations remain incompletely understood. [Method] We conducted a field experiment comparing a conventional winter wheat–summer maize (WM) with two legume-based rotations: winter wheat–summer peanut (WP) and winter wheat–summer soybean (WS). [Result] Relative to WM, legume-based rotations reduced soil bulk density by 2.27–6.10% and increased total nitrogen content (4.05–12.30%), soil organic carbon content (5.43–9.57%), and mineral N content by 17.93–37.35%. Activities of enzymes associated with C and N turnover also increased, with urease and sucrase rising by 27.47–83.17% and 12.39–21.92%, respectively, and subsequent winter wheat yield increased by 5.93–15.46%. Bacterial profiling showed that legume inclusion shifted community composition from oligotroph-dominated toward copiotroph-dominated assemblages. Co-occurrence network analysis indicated that WS formed a more topologically cohesive and structurally stable bacterial interaction network. The neutral community model (NCM) results were consistent with a greater role of environmental filtering in community assembly under legume-based rotations. Furthermore, partial least squares path modeling (PLS-PM) showed that rotation effects on winter wheat yield were consistent with an indirect pathway involving changes in bacterial network complexity coupled with soil physicochemical drivers, with soil physicochemical properties showing the strongest direct positive association with yield. [Conclusion] These results elucidate the mechanisms by which legume-based double-cropping rotations enhance subsequent wheat productivity, offering empirical support for optimizing crop rotation practices in the North China Plain.

Key words: Diversified crop rotations, Crop yield, Soil properties, Soil microbial community

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Density-Exacerbated Developmental Heterogeneity Constrains Grain Yield and Quality in Maize

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Abstract: [Objective] Population heterogeneity is an inherent feature of biological populations, yet its role in determining collective productivity remains poorly understood. We aimed to determine whether density-induced population heterogeneity constitutes a fundamental constraint on crop productivity and to quantify its contribution to yield loss and quality formation under high-density planting. [Methods] Maize was used as a model crop in a two-year field experiment involving three hybrids grown under four planting densities. Individual plant performance was continuously monitored from vegetative growth to maturity to characterize the emergence and progression of population heterogeneity. Reproductive performance was quantified at the plant, ear, and kernel levels, and quantitative analyses were conducted to evaluate the relative contributions of planting density and population heterogeneity to grain yield and quality. [Results] Increasing planting density significantly intensified population heterogeneity, which emerged early during vegetative development and progressively propagated across multiple biological scales. This developmental divergence resulted in pronounced reproductive inequality among dominant, intermediate, and suppressed plants. Although dominant individuals exhibited enhanced reproductive performance, their gains were insufficient to compensate for the substantial losses of suppressed individuals, leading to incomplete compensation at the population level. Consequently, both grain yield and quality declined under high-density conditions. Quantitative analyses further demonstrated that population heterogeneity exerted a stronger negative effect on grain yield than planting density itself and accounted for approximately 62.4% of the yield reduction observed under high-density conditions. [Conclusion] Our findings identify population heterogeneity as a major determinant of crop productivity and establish a quantitative framework linking developmental heterogeneity to system-level yield formation. These results demonstrate that improving population uniformity represents a previously overlooked strategy for simultaneously enhancing yield and grain quality in high-density cropping systems.

Key words: Maize, High density planting, Population heterogeneity, Asymmetric competition, Yield formation, Grain quality

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Effects of Different Straw Returning Methods on Soil Greenhouse Gas Emissions and Microbial Communities

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Abstract: [Objective] Straw returning to the field, by returning crop residues to the soil, can effectively improve soil structure, increase soil organic matter content, enhance soil fertility and water retention capacity, and thereby ensure stable and increased crop yields. However, as an exogenous organic material input into the soil, the decomposition process of straw profoundly alters the soil's water, heat, gas, nutrient, and microbial environments. This changing process inevitably exerts complex influences on the production, consumption, and emission of soil greenhouse gases. Therefore, there is an urgent need to explore the optimal method for maize straw returning and utilization under the condition of integrated crop-livestock farming in the agro-pastoral ecotone of northern China. [Method] Based on the straw returning modes in the Hinggan League region of Inner Mongolia, this study took maize straw as the research object and set up five treatment groups: traditional planting control (CK), straw returning after animal digestion and composting, full-amount straw returning, half-amount straw returning, and high-stubble straw returning. The effects of different straw returning methods on soil greenhouse gas emission characteristics and microbial community structure were analyzed. [Result] Different treatments resulted in differences in soil greenhouse gas emissions. Compared with the CK group, the half-amount straw returning group significantly increased CO₂ and N₂O emissions (by 48.6% and 147.8%, respectively; $P<0.05$), but promoted CH₄ absorption (by 249.4%; $P<0.05$). The full-amount and half-amount straw returning groups intensified the global warming potential (GWP) due to high CO₂ release, and their greenhouse gas intensity (GHGI) was significantly higher than that of the other three groups ($P<0.05$). In contrast, the straw returning after animal digestion and composting group and the high-stubble straw returning group achieved emission reduction through synergistic carbon and nitrogen metabolism. Regarding the impact on bacterial communities, compared with the CK group, straw returning increased the relative abundance of Proteobacteria and Actinobacteria. Among them, the full-amount straw returning group significantly increased the relative abundance of Proteobacteria by 30.48%. Regarding the impact on fungal communities, the full-amount straw returning group significantly decreased the relative abundance of *Ascomycota* by 15.25% and significantly increased the relative abundance of the *Tausonia* genus in Basidiomycota by 42.42%. The bacterial community diversity in the straw returning after animal digestion and composting group was significantly higher than that in the CK and half-amount straw returning groups; the fungal community diversity was significantly higher than that in the full-amount straw returning group. The differential microorganisms, Rhizobiales and Xanthomonadaceae, in the straw returning after animal digestion and composting group were positively correlated with CO₂ and N₂O emissions ($P<0.01$). [Conclusion] In conclusion, the straw returning after animal digestion and composting

group has a better ability to inhibit the warming effect, with significant differentiation in soil bacterial and fungal community structures, and has dual advantages in improving bacterial and fungal diversity. There is a certain correlation between soil microbial diversity and the emission or absorption of CO₂, N₂O, and CH₄.

Key words: Straw return to field, Soil greenhouse gas emission, Microbial diversity

Funding acknowledgement: We sincerely thank Shuyuan Xue for her/his valuable suggestions and constructive discussions during this study. This research was supported by the Xing'an League Comprehensive Experimental Station of the National Maize Industry Technology System.

Regulating the Rhizosphere with SynComs for Reshaping Agroecosystem Resilience

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Abstract: [Objective] The agricultural ‘Green Revolution’ has substantially mitigated global food scarcity; however, over-reliance on chemical inputs—including fertilizers and pesticides—has triggered severe soil degradation and widespread environmental pollution, which exacerbates agroecosystem vulnerability against the pressure of climate change. We identify synthetic microbial communities (SynComs) as a core mechanism for regulating rhizosphere and reshaping agroecosystem resilience, which is the pivotal entry point for the transition from conventional intensive farming to low-carbon green agriculture. [Method] We propose quantitative breakthroughs with SynComs for this transition: a 30% reduction in chemical fertilizer and pesticide use, a 20-50% increase in water- and nutrient-use efficiencies, and a 10-30% increase in water-to-carbon biotransformation in rainfed dryland ecosystems. By regulating rhizosphere microbial communities, we construct a framework, encompassing the design of climate-smart SynComs, exploration of biophysical pathways for water-to-carbon biotransformation, development of bio-based nitrogen fixation, and exploitation of water-sensed bio-enhancers, all oriented to the triple-goals of safeguarding food security, maintaining soil health, and cutting greenhouse gas emissions. Leveraging rhizosphere microbial communities, we establish a pipeline for novel SynComs via high-throughput isolation of functional microorganisms, single-cell Raman-based sorting of active microbial strains, and precise assembly of functional microbiomes. [Result] Large-scale field trials under Zhejiang Province’s agricultural science and technology program validate the efficacy of the SynComs. The bio-enhancers increased rice yields by 16.6–17.8%, while biofertilizers effectively enhance soil health. [Conclusion] These findings reveal that microhabitat regulation on soil rhizosphere can be an effective pathway for the transformation of global agriculture to a resilient system.

Key words: Synthetic microbial communities, Rhizosphere regulation, Agroecosystem resilience, soil health, Climate-smart agriculture

Conservation Agriculture as a Sustainable Approach for Maize Production: A Comparison with Conventional Agriculture in a Maize-Based Cropping System

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Abstract: [Objective] conservation agriculture can improve soil health, preserve moisture, lessen soil degradation, and increase cropping systems' long-term resilience; it is becoming more widely acknowledged as a sustainable production method. In a maize-based cropping system, this study aimed to examine the effects of conservation and conventional agriculture on soybean performance and maize productivity. [Method] A field experiment was conducted to compare conservation and conventional agriculture practices. Plant height, stem girth, internode length, and grain yield were among the growth and yield parameters for maize that were measured. Grain yield and soybean growth were also recorded. To identify variations between the two production systems, a statistical analysis was performed on the collected data. [Result] The results indicated that there were no statistically significant variations in maize plant height, stem girth, internode length, or grain yield between conservation and conventional agriculture. However, maize cultivated under conservation agriculture generated a slightly greater numerical grain yield than conventional agriculture. With the exception of plant height, the production system had no noticeable effect on the majority of soybean measurements. [Conclusion] Although conservation and conventional agriculture achieved comparable maize and soybean performance under the experimental conditions, conservation agriculture maintained maize productivity while giving a slight numerical yield advantage. Conservation agriculture is a viable management strategy for resilient maize-based production systems because of its established advantages for enhancing soil quality, conserving water, lowering erosion, and promoting long-term agricultural sustainability. It is advised to conduct additional long-term research to measure its productivity and environmental advantages under various circumstances.

Key words: Conservation agriculture, Conventional agriculture, Maize productivity, Soybean yield, Sustainable intensification, Maize-based cropping system.

Funding acknowledgement: This study was financially supported by the Ethiopian Institute of Agricultural Research (EIAR).

Accelerating climate-resilient maize varietal turnover to foster a functional hybrid maize seed systems in Nepal

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Abstract: Maize is the second most important cereal crop after rice in Nepal, cultivated on approximately 0.91 million ha with an annual production of around 3.0 million tons and an average productivity of 3.60 t ha⁻¹, which remains substantially below the attainable yield of modern hybrids. Maize cultivation area is gradually declining in the mid-hills of Nepal, while hybrid maize cultivation is expanding rapidly in the Terai and Inner Terai, particularly during the winter and spring seasons. Despite gradual improvements in domestic production, the country continues to face a widening demand-supply gap driven by the rapidly growing poultry and livestock farming. The release of heat-resilient maize hybrids such as CAH151 and CAH153 in 2017 with the support of HTMA project of CIMMYT opened new opportunities for hybrid maize seed production and commercialization in Nepal. This was followed by the release of CAH1715 in 2022, while CAH1511 is currently being promoted through private seed companies and NMRP is going to release very soon for general cultivation. The development and commercialization of these climate-resilient hybrids provide a strategic pathway to enhance maize productivity, strengthen climate resilience, and contribute to national food and feed security. However, the adoption and dissemination of these hybrids remain limited compared with hybrids developed by multi-national companies, due to weak marketing strategies, inadequate domestic hybrid seed production, limited public-private partnerships, fragmented seed distribution networks, and insufficient farmer awareness. Enhanced collaboration among the different value chain actors such as research (Nepal Agricultural Research Council), universities (Agriculture and Forestry University, Institute of Agriculture and Animal Science/Tribhuvan University, Madhesh Province University, Sudurpaschim University, Purbanchal University) seed companies (8-R&D licensed, and 11-hybrid seed production), 75- community seed producer groups, and development partners will be critical for scaling improved hybrids adapted to diverse agroecological zones. Coupled with supportive seed policies, climate-informed advisory services, and investment in local seed enterprises, accelerated varietal turnover can substantially increase maize productivity, reduce dependence on imports, improve farmers' income, and build resilient maize production systems capable of sustaining Nepal's food, feed, and climate adaptation goals.

Key words: Nepal maize, Climate-resilient hybrid, Seed value chain, Public-private partnership, Food & feed security

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Policy Frameworks and Economic Drivers for Sustainable Value Chains



On-Farm Research from Researchers to Farmers

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Abstract: Thai Maize National Program has been established among Thai Researchers and the Rockefeller Foundation as the “Co-ordination Project for Corn Improvement Program” since in the year 1962. After that, it was transferred to coordinate with the CIMMYT International Maize and Wheat Improvement in the year 1967. Then, the Thai maize research in the farmers’ fields started successfully when the CIMMYT’s expatriate came to develop the program since in the year 1984. The main objective of the On-Farm Research is to transfer the new appropriated technologies from the On-Station research program to improve the productivities and the profitability for farmers. One of the good examples of the On-Farm testing was the collaborative research among the breeding program, agronomic testing and crop protection as well as the economic evaluation, which led to develop the maize variety namely “SUWAN 2301”, the first Thai maize hybrids which has been recognized as the “Research Award” from the National Research Council of Thailand in the year 1989. The step of conduction the On-Farm Research is to bring the successful on-station maize material both the elite hybrids and the pre-commercial hybrids to test in the various growing conditions. Moreover, the agronomic trials and the crop protection arrangements at the testing location are the support data of the selection. During the operation, the data collections for the national variety registration as well as for the international standard are required. Moreover, the analysis of the stability for the testing varieties specific to the location and the variety wide adaptation are needed. The most important to bring the appropriated technologies to farmers are the “Verification Trials with the Economic Evaluation” and the “Demonstration Plots” which will promote the sustainable agricultural development. Five major stakeholder groups who involve as the key success of the On-Farm Research are the On-Station Researchers, On-Farm Researchers, Product Development section, Market Development section and Farmers. The clearing define roll and sharing among all stakeholders are essential for achieving successful research outcomes and sustainable agricultural development.

Key words: On-farm research, Maize, Technology transfer, Demonstration plots, Sustainable agriculture

Development and Policy of China's Corn Industry

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Abstract: [Objective] This report reviews recent developments in the global and Chinese corn industries, identifies the main constraints facing China's corn sector, and examines the evolution and future direction of related policies. Policy implications are provided for strengthening production capacity, stabilizing market expectations, and safeguarding food security. [Method] Using data from the United States Department of Agriculture, the National Bureau of Statistics of China, the General Administration of Customs of China, and the National Food and Strategic Reserves Administration, the report combines trend analysis, international comparison, and policy review to assess production, consumption, trade, prices, import sources, and policy instruments. [Result] Global corn production and consumption have grown steadily, with feed demand remaining the main driver. International markets are increasingly affected by weather conditions, geopolitical conflict, energy prices, and macroeconomic changes. China produced 3.01 million tons of corn in 2025. Feed and industrial uses accounted for about 67 percent and 25 percent of domestic consumption, respectively. However, China's corn yield was only 58 percent of the United States level, while production costs were substantially higher. Rising feed and processing demand is expected to increase the gap between domestic supply and demand to about 40 million tons by 2035. Imports have also increased, although their sources have become more diversified, particularly through greater imports from Brazil. China's corn policy has shifted from temporary stockpiling toward producer subsidies, crop structure adjustment, corn and soybean strip intercropping, yield improvement, and the commercialization of biological breeding technologies. Tariff rate quotas and import diversification have also been used to balance domestic supply and demand. [Conclusion] Future policies should strengthen market monitoring, coordinate domestic production and trade, accelerate seed innovation, and promote high value corn processing. More diversified import channels and deeper international cooperation are also needed to improve the resilience of China's corn industry.

Key words: Corn industry, Supply and demand, Agricultural policy, Yield Improvement, Food Security

Effects of Biotech Maize Cultivation on Farmers' Pesticide Inputs in China

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Abstract: [Objective] As climate change intensifies, the risks posed by weeds and insect pests may increase, thereby raising uncertainty in agricultural production and farmers' reliance on chemical control. Biotech maize provides a new technological option for managing crop pests and weeds, but herbicide-tolerant and insect-resistant traits may affect pesticide inputs through different pathways. China is at a critical stage in the commercialization of biotech maize, yet evidence from smallholder production systems remains limited. This study evaluates the effects of biotech maize cultivation on farmers' pesticide inputs and examines how these effects vary across maize agroecological regions and different levels of weed and insect pressure. [Method] This study uses farm survey data collected in 2023 and 2024, covering 2,451 households and 5,052 maize plots across 17 provinces. Maize traits are matched with plot-level pesticide input decisions. Ordinary least squares models are used to estimate the effects of herbicide-tolerant maize on herbicide inputs. Given the large proportion of zero values in insecticide inputs, Poisson pseudo-maximum likelihood models are used to estimate the effects of insect-resistant maize. Pesticide inputs are measured in terms of both formulated-product quantities and active-ingredient quantities, with a further distinction between glyphosate and non-glyphosate herbicides. [Result] Cultivating herbicide-tolerant maize increases total herbicide use and herbicide active-ingredient use by 78.5 and 28.8 mL/mu, respectively. These increases are driven mainly by higher glyphosate inputs, while neither non-glyphosate herbicide use nor its active-ingredient use changes significantly. Across regions, glyphosate inputs increase markedly in the northern spring-maize, Huang-Huai-Hai summer-maize, and southwestern maize regions, whereas increases in total herbicide use and active ingredients are concentrated in the Huang-Huai-Hai and southwestern regions. The positive effect of herbicide-tolerant maize on glyphosate inputs becomes stronger as weed pressure increases. Insect-resistant maize has no statistically significant average effect on either formulated insecticide use or insecticide active ingredients, and insect pressure does not significantly alter these effects. Further analysis nevertheless indicates that insect-resistant maize is associated with reductions in the southwestern region and in farmers' decisions to use insecticide active ingredients and the intensity of their application. [Conclusion] The effects of biotech maize on pesticide inputs vary by genetic trait, pesticide category, and production region. Herbicide-tolerant maize mainly increases glyphosate inputs without significantly reducing non-glyphosate herbicides, indicating that it currently changes the composition of herbicide use rather than producing a clear reduction in total herbicide inputs. Although insect-resistant maize has no statistically significant average effect on total insecticide inputs, it has the potential to reduce insecticide active-ingredient use in certain regions and at

specific stages of farmers' application decisions. As China advances the commercialization of biotech maize, pesticide management strategies should be tailored to different genetic traits. Insect-resistant traits should be integrated with sustainable integrated pest management and precision pesticide application to better realize their potential for pesticide reduction and environmental improvement.

Key words: Biotech maize, Pesticide use, Smallholder agriculture

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Seed Quality Assessment and Agronomic Performance of Zagatala 68 Corn Variety

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Abstract: [Objective] Conservation tillage systems increase soil resistance to erosion, prevent water loss from the soil, and improve soil structure. This is particularly conducive to the conservation of soil and water resources in rainfed maize cultivation. This research aimed to evaluate the effect of different field conditions (I–IV) on key seed quality traits of the maize variety Zagatala-68. [Methods] Within the experimental field, biomorphological characteristics—namely, plant height, height of ear attachment to the stem, leaf number at the ripening stage, as well as leaf length and width—were assessed across the treatment variants based on the data obtained from each plot. Were used standard protocols (AZS 134-2005, 137-2005, 138-2005) to determine germination energy, germination capacity, moisture content, test weight, and 1000-seed weight across four replicates (n=100 seeds per replicate). [Results] The results revealed significant field-dependent variation: 1000-seed weight ranged from 343 ± 5.2 g (Field II) to 389 ± 4.1 g (Field III), while test weight varied between 76.5 ± 0.8 kg·hL⁻¹ and 79.3 ± 0.6 kg·hL⁻¹. Field III consistently showed superior seed quality (lowest moisture: 15.7%; highest 1000-seed weight: 389.3 g). [Conclusion] Site-specific agronomic management significantly affects both seed quality parameters and biomorphological traits of Zagatala-68. The variety demonstrates high productivity and superior phenotypic performance under advanced agrotechnical conditions.

Key words: Seed quality, Seed vigor, Germination capacity, 1000-seed weight, Yield indicators

Optimized Prediction of Maize hybrid Performance Using Advanced Predictive Modeling Approaches

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Abstract: [Objective] To optimize predictive models through optimizing training population composition to predict maize hybrids performance. [Method] Using a real partial design two data set and cross-validation, we evaluate a G-BLUP model to predict possible hybrids, and compare selection method and size of the training population to predict all possible hybrids among all lines. Seven different traits were analyzed, including grain yield. [Result] Negative distance based training and a new method using the n closest individuals to individuals for prediction achieved the highest prediction accuracy. Smaller training sets perform worst than larger ones. Conclusion] Using a well selected set of hybrids and predictive models, it is possible to accurately predict the performance of potential hybrids, avoiding the need to generate and evaluate all possible crosses.

Key words: Maize hybrid, Hybrid performance prediction, G-BLUP model, Training population, Cross-validation

Funding acknowledgement: This work is funded by the Gates foundation through the AGG project.

Integrated Transcriptomic and Metabolomic Insights into Fall Armyworm Resistance Mechanisms in Maize: Identification of Candidate Genes, Pathways, and Defence Metabolites

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Abstract: [Objective] Fall armyworm (FAW), *Spodoptera frugiperda*, is a devastating pest of maize worldwide, threatening productivity and food security. Host plant resistance offers a sustainable strategy for FAW management; however, its molecular basis remains poorly understood. This study aimed to elucidate the genetic and biochemical mechanisms of FAW resistance by integrating transcriptomic and metabolomic analyses in contrasting CIMMYT maize inbred lines, CML338 (resistant) and CML451 (susceptible). [Method] Plants were subjected to FAW infestation under controlled conditions, with uninfested controls maintained in parallel. Leaf tissues were collected 48 h after infestation for RNA sequencing (RNA-Seq) and untargeted liquid chromatography–high-resolution mass spectrometry (LC-HRMS). Differential expression, pathway enrichment, weighted gene co-expression network analysis (WGCNA), and transcriptome–metabolome correlation analyses identified resistance-associated genes, pathways, and metabolites. Selected metabolites were further evaluated through molecular docking against the FAW gut enzyme Aminopeptidase N1. [Result] RNA-Seq datasets showed high mapping efficiencies (84-87%) and extensive transcriptional reprogramming in resistant plants. Defense-related genes were enriched in phytohormone and calcium signaling, MAPK cascades, transcriptional regulation, fatty acid metabolism, flavonoid biosynthesis, and secondary metabolite pathways. WRKY, MYB, MYC, NAC, and ERF transcription factors were strongly induced. Metabolomic profiling revealed higher accumulation of defense-associated fatty acids, including linoleic and arachidonic acids, and terpenoids such as α -terpineol and carotenoid derivatives in resistant plants. Integrated network analysis identified coordinated relationships involving TPS, DXS, PLD, LOX, and FAD genes. Molecular docking indicated strong binding of α -terpineol to Aminopeptidase N1, suggesting potential anti-herbivore activity. [Conclusion] Overall, integrated omics analysis revealed coordinated signaling, transcriptional, and metabolic mechanisms underlying FAW resistance. Identified genes and metabolites provide promising targets for marker-assisted and genomic-assisted breeding toward durable FAW-resistant maize.

Key words: FAW, Transcriptomic, Metabolomic, Defence, Signaling pathways

Funding acknowledgement: International Maize Improvement Consortium for Asia (IMIC-Asia), and the CGIAR Accelerated Breeding Initiative.

Marker-Based Quality Control for Improving Seed Quality

Assurance in African Maize. Learning and prospects

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Abstract: [Objective] Maize is the staple food for more than 300 million people in Africa, making access to high-quality seed essential for food and nutrition security. However, maintaining varietal purity from breeding through commercial seed production remains a major challenge due to fragile seed systems, limited quality assurance infrastructure, and the widespread cultivation of three-way hybrids. Reliance on phenotypic quality control alone is insufficient, resulting in genetic contamination, poor seed quality, and increased circulation of counterfeit seed. This study presents the implementation of a DNA marker-based quality control (QC) system in African maize breeding and seed production, highlighting its progress, adoption, and impact over the past five years. [Methods] CIMMYT, in collaboration with partners, developed and deployed a standardized DNA marker-based quality control (QC) panel to verify genetic purity and identity throughout the maize seed value chain. The QC panel was made accessible to breeding programs, seed companies, and national partners through multiple genotyping service providers. To accelerate adoption, CIMMYT conducted hands-on training programs and webinars for breeders, seed companies, and regulatory agencies. Initially implemented within CIMMYT's breeding programs, the marker-based QC system has since been scaled across African NARS, private seed companies, and seed certification agencies, providing a rapid, accurate, and cost-effective alternative to conventional phenotypic QC methods. [Results] The initiative enabled seed companies to establish DNA fingerprint reference profiles for founder and breeder lines, while NARS and regulatory agencies increasingly adopted marker-based QC for germplasm management, variety registration, and seed certification. Through extensive training and technical guidance, the technology has been implemented by approximately 20 partner organizations, collectively submitting over 5,000 samples annually for QC genotyping. The proportion of samples failing genetic purity and identity tests declined from 25% in 2020 to less than 10% in 2025, demonstrating substantial improvements in seed quality assurance and the effectiveness of DNA marker-based QC systems across Africa. [Conclusion] The adoption of DNA marker-based QC is a major and more accurate means to improved seed quality in African maize. It will increase confidence in seed supply systems, enhance farmer access to genuine and high-quality seeds, and ultimately improve profitability for seed enterprises and seed value chain actors. More efforts are therefore required from regulatory authorities, public and private seed producers to embrace DNA fingerprint markers to maintain seed quality assurance across the seed production and delivery chains. Beyond maize, this initiative can be replicated in other crops' seed production and supply chains to secure farmer's seed investments and food security in Africa.

Key words: African maize, Seed quality assurance, DNA fingerprint, Seed value chain, Food security

Determinants of Farmers' Willingness to Try New Yellow Maize

Varieties: A framework for Farmer-Centric Agricultural Policy

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Abstract: Farmers' acceptance for new yellow maize varieties is often constrained by multiple factors, including socio-economic barriers, and differences in technical knowledge. [Objective] This study aimed to identify the key determinants influencing farmers' willingness to try new varieties and to provide insights for the development of a more farmer-centered and location-specific agricultural policies. [Method] Primary data was gathered using a structured questionnaire and focus group discussion to establish a comprehensive sociodemographic profile of 91 maize farmers in Alfonsolista, Ifugao, Philippines. Factors affecting willingness to adopt new maize varieties were determined using inferential and descriptive relational statistics. [Result] A binary regression analysis combining socio-demographic and institutional determinants revealed that factors such as age (OR = 1), years of maize farming experience (OR = 1.01), were entirely neutral, meanwhile completing a college degree (OR = 2.14) increases the willingness of trying a new variety. Interestingly, taking in the institutional determinants, it was revealed that private-led trainings triple the farmers' odds of willingness to try the variety (OR = 3.2), whereas public-led training compresses these odds (OR = 0.29). These findings suggest that high participation in public training activities does not necessarily translate into greater willingness among farmers to try a variety, highlighting the need for more farmer-oriented and needs-based agricultural policies that are aligned with farmers' local practical concerns. Additionally, multiple response analysis revealed that among hesitant farmers (i.e., those unwilling to try new varieties), the most identified condition for acceptance was the establishment of localized field demonstrations, with 72.7% of the farmers expressing this demand, suggesting that farmers in Alfonsolista, Ifugao are hesitant to adopt new varieties due to uncertainty in adaptability and performance of these varieties under the region's microclimatic conditions. An inverted weighted preference analysis further revealed a socio-cognitive divide between willing and unwilling farmers. Hesitant farmers prioritized pest resistance (score = 32, weighted mean = 4.57 out of 5) indicating a strong emphasis on crop security and mitigating risks. Contrastingly, receptive farmers showed stronger preference for high yielding varieties (score = 287, weighted mean = 4.34 out of 5), which reflects interest in productivity and increased economic gains. These results demonstrated the critical need to tailor the institutional support based on the localized risks faced by smallholder farmers in Alfonsolista, Ifugao, towards a more farm-centric and responsive policy intervention.

Key words: Maize variety acceptance, Socio-demographic determinants, Institutional support, Binary regression analysis, Alfonsolista (Ifugao)

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Seed Production Technologies to Simplify Hybrid Maize Production

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Abstract: [Objective] To validate and deploy a seed production technology for three-way maize hybrid production to simplify hybrid seed production for Africa. [Method] To quantify benefits of genetic male sterility technology on maize seed yields and yields in farmers' fields a range of trials were conducted on-station and on-farm. [Result] Manual detasseling process removes up to nine leaves and 2.9 leaves on average. Seed yields are estimated to reduce by 5.2% per leaf removed, equating to an average seed yield reduction of 14%. Hybrids produced using Ms44-SPT segregate 50:50 for non-pollen producing and pollen producing plants and are referred to as 50% non-pollen producing (FNP). FNP hybrids yield 200 kg ha⁻¹ more in farmers' fields and provided a small yield benefit should farmers choose to recycle. [Conclusion] This technology is the first documented example of a single gene conferring a yield advantage of this magnitude in farmers' fields in Africa. Trait integration strategies are underway to facilitate large scale deployment.

Key words: Hybrid maize, Seed production technology, Genetic male sterility, Three-way hybrid, Detasseling

Transforming India's Maize Sector for Connecting Farms to

Industry: Economic, Policy and Market Drivers

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Abstract: In South Asia, India's maize sector is undergoing a structural transformation from a predominantly food and feed crop to a strategic industrial commodity, driven by rising demand from grain-based ethanol industries, starch, food processing etc. This policy triggered transition presents significant opportunities to strengthen farmer incomes, enhance value addition, and contribute to national energy security, industrial growth, and sustainable agriculture. The poultry and fuel sectors have become the major consumers of maize, together accounting for about 65-70% of its total use, a share that is expected to continue increasing in the coming years. During the Year 2024-25, maize contributed 51.5% (12.6 Mt) of the total ethanol feedstock in India to meet the E20 ethanol blending program targets, which is projected to rise by 20-25Mt by 2030 to address the E30. However, realizing this potential requires a resilient and integrated maize value chain that effectively connects producers with expanding industrial markets. Transforming India's maize sector requires coherent policies, efficient markets, and strategic investments across the value chain. Climate-resilient technologies, sustainable production, mechanization, improved logistics, storage, and market intelligence must be supported by stable pricing, Farmer Producer Organizations (FPOs), contract farming, and public-private partnerships. Aligning production with the growing demand from feed, ethanol, and agro-industries will create a globally competitive, farmer-centric maize value chain that strengthens economic growth, rural livelihoods, and national food, feed, fuel, and industrial security.

Key words: Agriculture transformation, Policy, Markets, Drivers

Participatory Breeding Approaches for Breakthrough Product Development and Validation

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Abstract: [Objective] Moving testing and selection into farmers fields can help overcome shifting environment-types within the target population of environments (TPE) and validate new technologies under real-world conditions. [Method] Advances in host-farmer sampling, sparse testing strategies and phenotyping can help facilitate on-farm testing within breeding programs [Result] Delineating farm types ensured testing strategies adequately sample socio-economic diversity within the TPE while sparse-testing facilitated increasing the size of the network. Simple, cost-effective phenotyping tools were deployed to quantify key traits in farmers fields. [Conclusion] Cost effective approaches to scale on-farm testing can help validate new varieties and technologies under real world conditions.

Key words: On-farm testing, Target population of environments, Sparse testing, Phenotyping, Breeding program

Seasonal Dynamics of Stem Borer Composition, Diversity, and Damage on Maize (*Zea mays* L.) in Ghana: Insights from Historical Field Records

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Abstract: This study evaluated seasonal differences in infestation levels, species composition, diversity, and damage indicators of stem borers infesting maize during the major and minor cropping seasons in Ghana. The study utilized historical data derived from field experiments conducted in 2009 at the Teaching and Research Farm of the Department of Crop and Soil Sciences, Kwame Nkrumah University of Science and Technology (KNUST), Kumasi, Ghana. Weekly observations of stem borer infestation were recorded over five weeks during the major season and four weeks during the minor season. Three stem borer species were identified: *Busseola fusca*, *Eldana saccharina*, and *Sesamia calamistis*. Mean larval abundance was comparable between seasons, with values of 2.47 larvae per plant during the major season and 2.49 larvae per plant during the minor season. Independent sample t-tests indicated no statistically significant differences in seasonal infestation levels ($p > 0.05$). Harvest assessments indicated slightly higher plant damage during the minor season. Species diversity, as measured by Shannon indices, was similar between the major and minor seasons (1.00 and 1.02, respectively). These findings provide valuable baseline information on maize stem borer communities in Ghana prior to the invasion of fall armyworm (*Spodoptera frugiperda*). The study highlights the importance of continuous monitoring and integrated pest management strategies for sustainable maize production.

Key words: Stem borers, Seasonal infestation, Species diversity, *Busseola fusca*, *Eldana saccharina*, *Sesamia calamistis*

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Ecosystem Development Approach Required for Bridging the Yield Gaps of Maize in India

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Abstract: Bridging the maize yield gap is imperative for meeting India's rapidly increasing demand for food, feed, fodder, starch, and bioethanol, while enhancing farmers' incomes and resource-use efficiency and promoting climate-resilient agricultural systems. Owing to its high productivity, wide agro-climatic adaptability, and multiple industrial applications, maize has emerged as a strategic industrial crop in India. During 2024-25, maize was cultivated on 12.09 million ha, producing 43.41 million tonnes with an average productivity of 3.60 t/ha in India. The Government of India's Ethanol Blended Petrol (EBP) Programme, targeting E20 by 2025-26 and E30 by 2030, is expected to increase demand for maize as a sustainable ethanol feedstock in addition to the existing demand for poultry and animal feed, starch and food processing. However, productivity remains below potential due to limited adoption of improved technologies, inadequate improved seed and mechanization access, weak linkages and poor institutional framework across value chain. Therefore, an integrated maize ecosystem involving capacity building, input and machinery support, digital advisory services, and market linkages is required. Accordingly, ICAR-Indian Institute of Maize Research (IIMR), Ludhiana undertook a catchment area development project sponsored by the Ministry of Agriculture & Farmers Welfare, Government of India across 15 states involving over 88 districts to enhance productivity, strengthen procurement, improve farmers' market access, and develop a sustainable maize-based ethanol supply chain in catchment areas of utilizing industries. To operationalize this ecosystem development approach, a large number of on-farm farmers' participatory trials (n=3375) of maize were conducted across seasons to evaluate the performance of improved maize production technologies under farmers' field conditions. The trial yields were compared with corresponding state average yields to quantify the extent of productivity enhancement achievable through technology-led interventions. Descriptive statistical measures, including seasonal mean, minimum, maximum, and percentage yield advantage, were used to assess the effectiveness of the ecosystem-based interventions across diverse agro-ecological regions of India. Results revealed highly significant inter-states and seasonal variations in maize productivity under the ecosystem-based intervention. During rainy season, mean on-farm trial yields ranged from 4.06 t/ha (Assam) to 6.09 t/ha (Madhya Pradesh). The maximum yield realized in rainy season was 5.0 to 8.7 t/ha which is much higher than national productivity of 3.0 t/ha which shows great potential to raise the yield of maize in India. During winter season, on-farm trial yields varied from 6.31 to 9.68 t/ha, with the highest mean yield (9.68 t/ha) and maximum recorded yield (12.60 t/ha) observed in Assam. During spring season, on-farm trial yields ranged from 6.35 to 9.88 t/ha, with the highest mean yield recorded in West Bengal (9.88 t/ha), followed by Punjab (9.25 t/ha) and Haryana (9.18 t/ha). Overall, the ecosystem-based approach across seasons demonstrated substantial potential to bridge maize yield gaps through integrated technology dissemination, institutional convergence, and assured market linkages. The approach improved productivity, accelerated adoption of

improved practices, and strengthened collaboration amongst research institutions, extension agencies, FPOs, aggregators, input providers, and ethanol industries, thereby fostering development of a resilient maize value chain in India. Scaling this integrated model through sustained policy support, public-private partnerships, and coordinated stakeholder action can enhance national maize production, improve farm profitability, ensure sustainable feedstock availability for the expanding ethanol sector, and contribute to India's long-term food, feed, industrial, and biofuel security while promoting climate-resilient agriculture. **Key words:** Maize productivity, Yield gap analysis, Ethanol, Maize value chain, Sustainable intensification

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Quantifying Contributions of Efficiency-enhanced Nitrogen Fertilizers to Maize Production and Environment: Evidence for Sustainable Agriculture Policy Framework

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Abstract: [Objective] Maize is crucial for global food security, and China's Golden Maize Belt is a major production region. However, sustainability is threatened by high nitrogen fertilizer rates, low utilization efficiency and severe nitrogen losses. Efficiency-enhanced nitrogen fertilizers (controlled-release urea and nitrification inhibitors) can improve nitrogen use efficiency and deliver ecological benefits, yet high costs often limit their economic attractiveness to farmers. This study aimed to quantify the agronomic, environmental and economic impacts of these fertilizers in maize production and to develop a multi-stakeholder cost-sharing policy framework for sustainable agriculture. [Method] A split-plot field experiment was conducted with nitrogen fertilizer types as the main plots (including no nitrogen application, application of common urea and application of mixture with 50 % common urea and 50 % controlled-release urea), and nitrification inhibitor as the sub-plots (including no application and application of 3,4-dimethylpyrazole phosphate). Maize productivity, agronomic nitrogen use efficiency, nitrogen-saving potential, greenhouse gas emissions, and eco-economic benefits were measured. [Result] Efficiency-enhanced nitrogen fertilizers significantly increased maize productivity by 3.1%–11.4% and agronomic nitrogen use efficiency by 7.3%–26.8% compared with common urea, with controlled-release urea showing a more prominent effect on grain yield. They also reduced global warming potential by 11.0%–24.7% and greenhouse gas intensity by 10.2%–29.1%. The combined application of controlled-release urea and nitrification inhibitor exhibited a subadditive effect on greenhouse gas mitigation. Addition of the nitrification inhibitor incurred similar farmer economic input (34.3 versus 34.5 \$ ha⁻¹) but required a lower ecological premium from government and the public (105.8 versus 151.0 \$ ha⁻¹) and achieved a higher return on investment (4.2 versus 2.5) than controlled-release urea alone. Although the combined use generated ecological benefits of 248.9 \$ ha⁻¹, farmers still needed economic support of 97.9 \$ ha⁻¹ from government and 104.9 \$ ha⁻¹ from the public. [Conclusion] Efficiency-enhanced nitrogen fertilizers improve both productivity and environmental performance of maize systems. Controlled-release urea is particularly effective for yield gain, while the nitrification inhibitor is more cost-effective for greenhouse gas mitigation and delivers higher returns. A well-designed cost-sharing policy framework that internalizes ecological benefits is essential to overcome economic barriers for farmer adoption and to promote sustainable maize production.

Key words: Efficiency-enhanced nitrogen fertilizer, Maize, Greenhouse gas, Nitrogen loss, Trade-offs

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Agronomic Performance and Technological Quality of Maize Varieties: A Farmer-led Participatory Evaluation for Varietal Adoption in Smallholder Farming Systems of Benin (West Africa)

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Abstract: In Benin, maize cultivation faces rainfall scarcity and irregularity, which reduces productivity. The preference of smallholders for specific agronomic and technological traits, coupled with their exclusion from breeding programs, undermines their effectiveness and perpetuates the use of low-yield maize varieties. [Objective] This study aimed to support breeding programs by evaluating smallholder farmers' preferences for agronomic traits in ten maize varieties in drought-prone regions of Benin, including their willingness to trade off specific traits. [Method] Using a mixed-methods approach over three years, this study evaluated 135 smallholders' preferences for maize traits during the vegetative and post-harvest stages in Guinirou, Miniffi, and Awanla-Kpèloundè. [Result] Results revealed that drought tolerance is the most important criterion at the vegetative stage ($r = 0.33$). At harvest, estimated productivity is the key factor in variety ranking ($r = 0.531$). After evaluations, the varieties TZE-W POP DT STR, DT STR Syn-W/TZL COMP1-W, and QPM-Faaba were the most preferred by farmers, while PVA SYN-13 and TZL COMP1-W/DT-SYN-1-W were the least appreciated. Technologically, DT STR Syn-W/TZL COMP1-W and QPM-Faaba had the longest cooking times (6.3 minutes), whereas F2SCA 1413-36 had the shortest (3.0 minutes). [Conclusion] Promoting these varieties could help improve maize yields in areas most affected by climate variability.

Key words: Adoption, Technological aptitude, Zea mays L., Productivity, Drought tolerance, Benin

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Technical Session 10

Market Dynamics and Agribusiness Innovation in the Global Maize Economy



Genetic Dissection of Endosperm Mutants in Commercial Sweet and Waxy Corn Hybrids in Thailand

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Abstract: [Objective] Sweet and waxy corn are high-value specialty crops in Thailand, where distinct market segments demand specific combinations of sweetness, texture, and kernel appearance. These eating-quality traits are largely controlled by recessive endosperm mutations in starch biosynthesis genes, particularly *sugary1* (*su1*), *brittle2* (*bt2*), *shrunk2* (*sh2*), and *waxy* (*wx*). This study aimed to genetically dissect and classify endosperm mutant backgrounds in widely grown commercial sweet and waxy corn hybrids in Thailand. [Method] Forty commercial F₁ hybrids (18 sweet and 22 waxy) obtained from major public and private seed organizations in Thailand were genotyped using five diagnostic single-nucleotide polymorphism (SNP) markers targeting the *su1*, *bt2*, *sh2*, and *wx* loci. [Result] Genotypic profiling of sweet corn hybrids (SWH1–SWH18) indicated that most hybrids carried the single recessive *sh2/sh2* genotype associated with the “shrunk” high-sugar phenotype, whereas five hybrids (SWH3, SWH6, SWH9, SWH11, and SWH18) carried double-recessive *su1/su1* and *sh2/sh2* combinations with variable *bt2* alleles, thereby diversifying eating quality. Among waxy corn hybrids (WXH1–WXH22), three major market-oriented groups were identified: standard waxy, “Tian” (glutinous/chewy), and “sweet waxy”. Standard waxy and Tian hybrids predominantly carried the amylose-free *wx/wx* genotype, while sweet waxy hybrids combined *wx/wx* with sweet alleles to integrate chewiness with enhanced sweetness; notably, WXH13 possessed a triple-recessive *su1/su1*, *sh2/sh2*, *wx/wx* genotype. Overall, these results highlight diverse but targeted genetic strategies used by breeders to tailor endosperm starch architecture to specific consumer and processing preferences. [Conclusion] The genotypic information generated here provides a practical baseline for marker-assisted selection (MAS) and supports the rational design of next-generation specialty corn hybrids for domestic and regional markets.

Key words: Specialty corn, Endosperm mutants, *shrunk2*, *waxy*, Marker-assisted selection, Sweet-waxy corn

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Advances in Maize Breeding in Thailand: The Role of the Department of Agriculture

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Abstract: [Objective] Maize is a key crop for Thailand's feed industry, but production is constrained by climate change, drought, and changing farming systems. The Department of Agriculture has implemented a maize breeding program to develop hybrids with drought tolerance, adaptation to high planting density and dry-season cultivation after rice, high and stable yields, and suitability for silage. Conventional breeding integrated with biotechnology, systematic germplasm management, and multi-stage evaluation accelerates variety development. Released hybrids and parental lines support seed production, strengthen food security, and enhance Thailand's agricultural competitiveness.

Key words: Climate change, Drought, Variety development

Heterotic Grouping of Field Corn Lines Derived from Commercial Hybrids Using Grain Yield, Kernel Size, and Kernel Type for Inbred Line and Hybrid Development

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Abstract: [Objective] This study aimed to (1) classify heterotic groups of field corn lines derived from commercial hybrids, and (2) evaluate the use of testcross grain yield together with kernel size and kernel type of S2 ears for heterotic grouping. [Method] The study comprised two parts: (1) evaluation of testcross hybrids developed from 44 S1 populations and four inbred testers (Tak Fa 1, Tak Fa 3, Ki 48, and Ki 60) using a 14 x 14 Simple Lattice design during the 2020 rainy season, followed by heterotic grouping based on grain yield; and (2) classification of kernel size, type, and shape of the corresponding S2 lines and the four inbred testers. [Result] Based on testcross grain yield, the 44 S1 populations were classified into three heterotic groups: 26 populations in the Suwan group, 10 populations in the Non-Suwan group, and 8 populations in other heterotic groups. All four testers exhibited positive, but non-significant, GCA effects. Kernel size and kernel type of the S2 lines could not be effectively combined with grain yield for heterotic grouping. However, the highly homozygous inbred testers showed distinct kernel characteristics: the Suwan group (Tak Fa 1 and Ki 48) was predominantly medium-sized flint, whereas the Non-Suwan group (Tak Fa 3 and Ki 60) was characterized by medium to large, predominantly semi-flint kernels. [Conclusion] Heterotic grouping based on grain yield was influenced by the choice of inbred tester, whereas the use of kernel size and kernel type requires highly homozygous inbred lines.

Key words: Commercial field corn hybrid, Inbred tester, Heterotic group, Grain yield, Kernel traits

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Development of Field Corn Inbred Lines through Heterotic Grouping of Commercial Hybrid-Derived Lines

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Abstract: [Objective] This study aimed to (1) develop field corn inbred lines with potential for commercial hybrid development and (2) evaluate the performance of testcross hybrids derived from crosses between lines developed from commercial hybrids and elite inbred testers. [Method] Eight sets of 25 S₃ lines derived from eight commercial hybrids assigned to two heterotic groups were crossed with two inbred testers from the opposite heterotic group. Eight testcross experiments were conducted using a Randomized Complete Block Design with two replications, comprising 56 entries (50 testcrosses and six hybrid checks). The trials were carried out at Salaeng Phan Research Station, Charoen Pokphand Produce Company Limited, Saraburi, Thailand during the 2024/25 dry season and the 2025 rainy season. [Result] Grain yield differed significantly among entries in all experiments in both seasons. The five highest-yielding testcrosses in each experiment were not significantly different from the best hybrid check. S₃ lines that produced these superior testcrosses and exhibited good per se performance were selected for further line and hybrid development. DK9979C was the best hybrid check in the dry season (5,375–6,794 kg/ha), whereas SW6481 was the best hybrid check in the rainy season (3,763–5,419 kg/ha). All testers showed significant positive GCA only in the dry season. [Conclusion] Approximately 30% of the S₃ lines were selected for further breeding. Ki 60 and Kei 1723 were the most effective testers in the dry and rainy seasons, respectively, whereas Kei 1601 and Kei 1614 consistently produced superior testcrosses across both seasons, depending on the genetic background of the female parent.

Key words: Field corn, Inbred line development, Heterotic group, Testcross, Commercial hybrids

Funding acknowledgement: The authors gratefully acknowledge Salaeng Phan Research Station, Charoen Pokphand Produce Co., Ltd. for providing the research facilities and field sites for this study.

A Hybrid Approach for Accelerating the Scaling of Stress-tolerant Maize Varieties in Southern Africa

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Abstract: [Objective] Maize production in Southern Africa is increasingly threatened by recurrent droughts and other climate-related stresses, posing significant risks to food and nutrition security in a region where maize is the principal staple crop. Although stress-tolerant maize varieties provide an important adaptation option, achieving their rapid and widespread adoption by smallholder farmers remains a persistent challenge. While agricultural technology scaling has been widely discussed in the literature, practical evidence on effective pathways for accelerating the large-scale deployment of improved crop varieties remains limited. This study addresses this gap by examining the experiences of the Accelerated Innovation Delivery Initiative (AID-I) in Southern Africa. [Methods] A mixed-method approach combining qualitative and quantitative data was used to identify the key drivers of rapid scaling of drought and pest tolerant maize varieties. Under the AID-I project, we endeavor to deploy drought and pest tolerant maize to farmers in Zambia, Malawi, Tanzania and DR Congo. The scaling model integrated four complementary components: (i) multi-stakeholder partnerships, (ii) demand creation, (iii) capacity strengthening, and (iv) seed production and commercialization. [Results] The partnerships established involved 24 key players, including 17 private seed companies and 7 public institutions. Significant achievements were recorded in the four target countries. A total of 69 multi-stress-tolerant maize hybrids were promoted. Certified seed production reached 26,548 metric tons against 13,726 metric tons in year 2. The seed produced is estimated to plant close to 1,000,000 ha benefiting over 800,000 households and reaching about 5.5 million people across target countries. The approach was effective in reaching a substantial number of beneficiaries in a short period of time. [Conclusion] The approach has contributed to strengthening the resilience of farming communities within maize production agroecological zones undergoing recurrent climatic threats. These outcomes serve as a valuable learning model for similar ongoing and future agricultural initiatives. Beyond maize, other crops could be target for further learning.

Key words: Climate smart maize, Strategic partnerships, Rural livelihoods, Smallholder farmers, Last mile, Climate change

Occurrence Dynamics and Population Source of Maize Aphids in Northeast China Under the New Context

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Abstract: [Objective] Northeast China is a major maize-producing region in the country. In recent years, due to climate change and shifts in maize cropping patterns, maize aphids have become increasingly destructive, rising from secondary pests to major pests. However, research on maize aphids in this region remains relatively limited, and their species composition and damage status are poorly understood. This knowledge gap poses challenges for effective pest monitoring and management. [Method] This study employed a combination of field system surveys—including a suction trap network, drone with attached traps, and adjustable-height yellow sticky traps—along with molecular markers and trajectory analysis, to investigate the population dynamics, occurrence and damage, overwintering, and migration of maize aphids in Northeast China. [Result] (1) Based on a summary of maize aphid species in China and other countries, eight species were identified as damaging maize in Northeast China. Combined with field observations, four major species were recognized: *Rhopalosiphum maidis*, *R. padi*, *Aphis gossypii*, and *Sitobion miscanthi*. (2) Compared with other aphids, *R. maidis* colonizes maize fields later in the season, mainly infests the ear, and causes light damage. It is anholocyclic, with an unclear overwintering boundary; it may overwinter in southern Northeast China and migrate northward. Both *R. padi* and *A. gossypii* are holocyclic, overwintering as eggs on hosts, with populations comprising both locally reproducing and migrating individuals. *R. padi* is widely distributed across the plant, increases sharply in autumn, and is the dominant and most threatening species. *A. gossypii* is mostly on lower leaf undersides and is a minor pest. *S. miscanthi* infests maize in small populations, causes light damage, is anholocyclic, does not overwinter locally, and originates from long-distance migration from the winter wheat areas of the Yangtze River middle-lower reaches and the Huang-Huai-Hai region. (3) The eastern Asian insect migration belt lies between 15°N and 45°N, oriented southwest–northeast, covering a vast area from the Indochina Peninsula (Vietnam, Laos, Myanmar) through eastern China to the Northeast China Plain, the Korean Peninsula, and the Japanese archipelago. The populations of *R. maidis* and *S. miscanthi* in Northeast China originate from this migration belt. (4) Due to the short maize growing season, Tajima's D of maize aphid populations indicates a recent historical outbreak, likely associated with large-scale planting. [Conclusion] The findings of this study provide a theoretical basis for accurate prediction and integrated management of maize aphids in this region.

Key words: Maize aphids, Migration, Molecular marker, Overwinter, Population dynamics

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Stability Analysis of Coffee (*Coffea arabica* L.) Bean Yield Using GGE Biplot in South Western Ethiopia

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Abstract: Coffee is the largest export crop, and the backbone of the Ethiopian economy. The experiment was conducted at Metu, Gore and Chora for two consecutive years with the objective of determining the nature and magnitude of genotype x environment interaction, to classify environment based on genotype performance and identifying stable genotypes on coffee yield by using GGE biplot analysis. A total 17 advanced coffee genotypes were laid out using randomized complete block design with three replications. The analysis of variance for coffee bean yield revealed the presence of highly significant difference ($P<0.01$) among genotypes, environments and genotype by environment interaction. Results of GGE biplot showed that the first two principal components (PC1 and PC2) justified 65.66% of the sum of squares with PC1=49.12% and PC2=16.54% of the GGE sum of squares. The six test environments were divided into four different coffee growing mega-environments. Among the test location Metu2 and Gore2 were the most representative and most discriminating environment while Chora2 was less powerful to discriminate genotypes or less desirable as a testing location for coffee bean yield. Genotype G5 (236/71), followed by G8 (872/74) and G12 (227/71) were stable and high yielder across coffee growing environments and it recommended for mega environment production.

Key words: Bean Yield, Discriminating, Genotype x Environment Interaction, Stable

Evolution of Maize Business in Asia: Major Challenges, Drivers, and Future Prospects

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Abstract: Maize (*Zea mays L.*), the “Queen of Cereals,” has transformed from a local staple into a global commodity, surpassing rice and wheat in production. Asia, excluding China, now contributes 31% of global maize output and 34% of harvested area, with India, Thailand, the Philippines, Indonesia, Vietnam, and Bangladesh emerging as key players. The sector’s growth is driven primarily by rising demand for livestock feed, particularly in poultry, reflecting changing diets and higher per capita incomes. Between 2010 and 2016, Asian maize production rose 27.7%, aligning with projections of a 45% global demand increase by 2020, with Asia’s demand nearly doubling compared to 1995. Beyond feed, industrial uses such as ethanol and starch derivatives are reshaping markets. India’s ethanol blending target of 20% by 2026 exemplifies policy-driven acreage shifts from water-intensive crops like paddy to maize, alongside breeding for higher starch content. Historically, hybrid technology spread from the U.S. to Asia between 1921 and 1970, revolutionizing production despite uneven adoption. By 2000, two-thirds of maize acreage was planted with single cross hybrids. Today, breeding has advanced from conventional phenotypic selection to molecular approaches. Rapid Cycle Genomic Selection (RCGS) and Doubled Haploid (DH) technology are shortening breeding cycles and accelerating genetic gains. However, breeding programs in Asia remain younger and less developed than in Europe, leaving scope for improvement. Strengthening breeding efforts, coupled with agronomic innovations, is essential to close yield gaps and adapt to diverse growing conditions. Climate change adds complexity, demanding resilient varieties and sustainable practices. The future of Asia’s maize industry lies in integrating advanced breeding, supportive policies, and technological innovation to meet rising feed and industrial demand while ensuring sustainability. Major Challenges: The Triple Threat Despite growth, the Asian maize business faces a “triple threat” of heat, drought, and waterlogging, compounded by the fact that 80% of maize in the Asian tropics is rainfed. In rainfed systems, productivity is typically less than half of irrigated systems. Climate change manifestations are already evident: in Vietnam, annual average temperatures have risen by 0.5 to 0.7°C over 50 years, while shifting monsoon patterns have reduced the number of rainy days, leading to extreme moisture fluctuations—waterlogging followed by drought—within a single season. Around the year planting, corn after corn planting has created a bigger challenge on biotic stresses, including Leaf disease all over, downy mildew in Indonesia and various stalk rots all over, further threaten yields, particularly in rice-maize rotation systems. Productivity Gaps and Facts A significant challenge remains the productivity gap between Asia and the West. While the U.S. reached mean yields of 10,555 kg/ha in recent years, India’s average stands at 4100 kg/ha. Although India demonstrated a high annual production growth rate of 6.60% in the early 2000s, absolute yields remain sub-optimal due to genetic limitations and

varied agronomical practices. Indonesia and the Philippines show promising trajectories, with projected 2025 productions of 14.10 million metric tons (mmt) and 8.46 mmt, respectively and India has exceeded from the target and achieve the mark of 55 mmt production from 13.4 million ha. **Future Prospects** The future of Asian maize lies in stress-resilient germplasm that offers "upside yield potential with downside risk reduction". Regional targets are ambitious; India aims to double its maize output to 100 million tons by 2047. To meet this, scientists are realizing significant genetic gains through RCGS, with recorded improvements of 110 to 135 kg/ha/year under drought stress and nominal gains under heat stress. Trade dynamics will also shift; by 2025, Asian maize imports are expected to reach 75 million metric tons, accounting for over 60% of the projected global maize trade. In conclusion, the maize industry in Asia has journeyed from subsistence farming to a dynamic, industrial value chain. Over the next quarter-century, its success will hinge on the seamless integration of systematic breeding programs, advanced genomic tools, precision phenotyping, and robust germplasm exchange. Public-private partnerships will be vital to navigating the uncertainties of climate change, while agronomists must champion a systematic approach that unlocks maize's full potential. Only through this coordinated effort can the sector rise to meet the surging demand of feed and fuel industries, transforming challenges into opportunities for sustainable growth.

Key words: Ethanol, Climate change, Advance breeding tools, Stress resilient, Germplasm exchange

Effects of Calcium Peroxide on Root Morphology and Yield

Formation of Summer Maize in Waterlogging Farmland

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Abstract:[Objective] With global climate change, extreme precipitation events are becoming more frequent, aggravating waterlogging stress, one of the main abiotic constraints on stable and high yields of summer maize. This study aimed to clarify how calcium peroxide (CaO₂) regulates soil oxygen conditions, root morphogenesis, and yield formation under waterlogging, providing both theoretical and practical support for mitigating this stress. [Method] Field experiments were carried out over the 2023 and 2024 summer maize growing seasons at the Huang-Huai-Hai Regional Maize Technology Innovation Center of Shandong Agricultural University. The maize cultivar Denghai 605 (DH605) was used in a randomized complete block design. Waterlogging was imposed at the three-leaf (V3) stage, with two treatments: CaO₂ amendment and a non-amended control (CK). Multiple indicators were measured, including soil oxygen status, root morphology, canopy photosynthetic physiology, dry matter accumulation, and grain-filling characteristics. [Result] Averaged across the two seasons, CaO₂ notably improved soil oxygen conditions under waterlogging. From the onset of waterlogging to 10 days after stress relief, mean oxygen concentrations in the 0–20 cm and 20–40 cm soil layers increased by 7.38% and 7.44%, respectively, compared with CK. Root morphology was greatly improved at anthesis: total root length, root surface area, root volume, and root dry weight rose by 39.81%–51.98%. Canopy photosynthetic capacity also benefited. At anthesis, ear leaf net photosynthetic rate (P_n), stomatal conductance (G_s), and transpiration rate (T_r) increased by 23.84%, 30.63%, and 85.99%, respectively. Aboveground dry matter accumulation at physiological maturity was 22.70% higher under CaO₂ treatment. Grain-filling dynamics were positively affected, with the maximum grain-filling rate rising by 7.29%. Kernel number per ear and 1000-kernel weight increased synergistically by 39.98% and 5.00%, leading to a 50.77% increase in grain yield over CK. [Conclusion] Calcium peroxide effectively alleviates waterlogging stress and substantially boosts grain yield in summer maize. By improving soil oxygen availability, CaO₂ reshapes root architecture, strengthening water and nutrient uptake. This triggers a cascade of improvements in canopy photosynthesis, dry matter partitioning, and grain filling, ultimately raising yield through coordinated gains in both kernel number and kernel weight. This study clarifies the functional pathway of CaO₂ in mitigating waterlogging stress at the seedling stage and provides an innovative agronomic strategy for stabilizing and increasing summer maize yields in the Huang-Huai-Hai Plain.

Key words: Waterlogging, Calcium peroxide, Root morphology, Grain filling characteristics, Yield, Maize

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Functional Analysis of Zinc Finger Protein Transcription Factor ZmZFP69 Under Low-Temperature Stress at Maize Seedling Stage

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Abstract: [Objective] Maize (*Zea mays L.*) seedlings are highly susceptible to low-temperature stress, which significantly impacts maize yield and quality. [Method] A zinc finger protein transcription factor (*ZmZFP69*) mutant and a control (B73) maize inbred line were subjected to low-temperature treatment, and changes in the phenotypic characteristics, hormone levels, and other indicators before and after the treatment were systematically identified. Subsequently, a combined RNA-seq and DAP-seq analysis was conducted to explore the influence of *ZmZFP69* on the promoters of downstream genes. Finally, the proteins interacting with *ZmZFP69* were examined using InterProDesign combined with BiFC and subcellular localization. [Result] The *zmzfp69* homozygous mutant maize inbred line exhibited enhanced low-temperature tolerance compared to the control. RNA-seq and DAP-seq analyses revealed that *ZmZFP69* binds to the *ZmAUX* gene promoter, significantly suppressing its expression. The interaction between *ZmZFP69* and the downstream protein ZmBG6 was confirmed by InterProDesign, subcellular localization, and BiFC assays. [Conclusion] *ZmZFP69* negatively regulates maize seedling low-temperature tolerance by inhibiting *ZmAUX* expression and interacting with ZmBG6.

Key words: Zinc finger protein, *ZmZFP69*, Maize, Low-temperature stress

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CRISPR/Cas9-Mediated Mutagenesis of Melatonin Synthesis Genes Enhances Maize Tolerance

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Abstract: [Objective] Water stress, including increasingly frequent sudden shifts between drought and flood, poses a serious threat to corn yields. Melatonin can enhance the resilience of crops, but its regulatory mechanism still requires further exploration. This study elucidated whether and how endogenous melatonin, elevated via CRISPR/Cas9-mediated mutagenesis of biosynthesis rate-limiting enzymes, enhances tolerance to both stresses and dissected the underlying physiological, transcriptomic, and metabolic network mechanisms. [Method] We concurrently edited *ZmCOMT*, *ZmSNAT*, and *ZmASMT1* to generate a stable *comt snat asmt* triple mutant. Sanger sequencing was used to identify indels and deduce amino acid substitutions. The mutant and negative control (NC) plants were subjected to well-watered, progressive drought, and a controlled DFAA treatment (drought followed by rapid re-watering and waterlogging). We measured endogenous melatonin and phytohormone (ABA, IAA, CTK, GA) contents, assayed antioxidant enzyme activities, nonenzymatic antioxidants AsA/GSSG, osmotic regulators and reactive oxygen species (ROS) levels. And we performed RNA-seq transcriptomic profiling to compare global gene expression changes and targeted metabolomics of tryptophan metabolites under stress conditions. [Result] The CRISPR-induced mutations caused key amino acid changes (Gly168→Ala in *ZmSNAT*, Asp175→Glu in *ZmCOMT*, and Asp150→Glu in *ZmASMT1*) within conserved domains, subtly altering protein tertiary conformations. Contrary to gene disruption, these modifications significantly enhanced enzymatic activities of SNAT, ASMT, and COMT, leading to an 86.70% increase in endogenous melatonin content in the mutant under CK. Under drought and DFAA stress, the mutant exhibited markedly elevated antioxidant enzyme activities, resulting in substantially reduced H₂O₂ and O₂⁻ accumulation compared with NC. Concurrently, endogenous ABA, IAA, and CTK levels were significantly upregulated, while GA content decreased. Transcriptomic analysis revealed that the mutant reprogrammed hormone signaling pathways. Crucially, path analysis uncovered a metabolic rewiring: in NC, L-kynurenine exerted a direct negative effect on AsA, indicating intrinsic competition; this suppression was completely eliminated in the mutant (non-significant). Concurrently, the nicotinic acid→NADP⁺ path, blocked in NC, became highly activated in the mutant, reflecting efficient NADPH regeneration to fuel the AsA-GSH cycle. [Conclusion] Endogenous melatonin confers DFAA and drought tolerance through dual actions: enhanced ROS scavenging and, more importantly, global metabolic rewiring that alleviates the kynurenine-AsA antagonism while activating the nicotinic acid-driven NADPH engine. This reprogramming, coupled with upregulated defense transcripts and osmotic adjustment, ensures redox homeostasis under fluctuating water stresses, providing a novel paradigm for breeding climate-resilient maize.

Key words: Maize, CRISPR/Cas9, Melatonin, Abiotic stress, Phytohormone homeostasis

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Interval Control Algorithm for Plot Precision Seeder Based on BeiDou RTK

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Abstract: [Objective] Plot seeding in crop breeding experiments demands extremely high precision, requiring both accurate control of alternating plot and spacing lane sections and alignment of actual seed landing points with theoretical spatial boundaries for precise plot length measurement. This study aimed to address the shortcomings of traditional methods in boundary identification, length control, and system delay compensation. [Method] A collaborative control algorithm integrating centimeter-level BeiDou RTK positioning was proposed, comprising two core components. First, a projection accumulation and dynamic state switching trigger algorithm was developed, which constructed a dual-state machine model (seeding-spacing lane) and employed a distance accumulation method based on along-track projection with a dynamic state judgment mechanism to achieve precise boundary identification and mode switching. Second, a kinematics-based feedforward landing point prediction model was established to create a mapping relationship between seed landing lag distance and real-time velocity, enabling advance triggering of seeding actions to compensate for landing deviations. [Result] Field experiment results demonstrated the following: in tracer marker comparison tests, the projection accumulation algorithm achieved a cumulative error of only 3.5 cm over 100 m, representing an 81.2% improvement over the traditional Euclidean distance accumulation algorithm. In state switching tests within the speed range of 0.5-3.0 km/h, the mean absolute deviation of plot length was 1.8-3.2 cm, with a 100% switching success rate. In landing point prediction tests, the average deviation between the first seed's landing point and the theoretical starting point was 3.3 cm, with a standard deviation of 2.5 cm. [Conclusion] The proposed algorithm provides a comprehensive technical solution for achieving high-precision automated plot seeding operations, significantly enhancing the accuracy and comparability of breeding experiments.

Key words: Plot seeding, BeiDou RTK positioning, Projection accumulation, State switching, Landing point prediction

Funding acknowledgement: Heilongjiang Provincial Scientific Research Institutes Research Operating Expenses Project (CZKYF2025-1-B018)

Deep Learning-Based Detection of Emerged and Missing Maize Seedlings Using UAV Multispectral Imagery for Precision Crop Management

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Abstract: [Objective] Maize seedling establishment is a key factor affecting subsequent crop growth and yield formation, while accurate monitoring of emerged and missing seedlings remains challenging under complex field conditions. This study aimed to develop an automated approach for detecting emerged and missing maize seedlings using UAV multispectral imagery. [Method] An end-to-end transformer-based detection framework, Seedling-DETR, was developed to simultaneously detect emerged and missing maize seedlings. The framework incorporated hybrid-scale feature fusion and multispectral information to enhance feature representation for small seedlings and missing regions. The proposed method was evaluated using field datasets collected under different emergence conditions and further validated through field-scale deployment based on UAV orthomosaic imagery. [Result] The results show that, under a random train–test split (8:2), when using RGB images as input, our Seedling-DETR achieves a mean average precision (mAP) of 83.1% at an IoU threshold of 0.5, outperforming YOLOv11x and RT-DETR by 2.5% and 1.1%, respectively. The proposed method achieves an AP of 69.3% at an IoU threshold of 0.5 for missing seedling detection, which increases to 71.7% when multispectral inputs are incorporated. Similar performance trends are observed on an independent validation set collected on a different date. Although the model introduces moderate computational overhead (282 GFLOPs for RGB input and 418 GFLOPs for multispectral configuration, with 84.0 M and 85.1 M parameters, respectively), it can maintain efficient detection performance suitable for actual agricultural field deployment. [Conclusion] Overall, this study provides an effective and scalable framework for the detection of emerged and missing maize seedlings under complex field conditions. The proposed framework supports accurate reseeding decisions, and contributes to automated maize production.

Key words: Maize seedling, RGB imagery, Multispectral imagery, Deep learning.

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Effects of Different Straw Returning Methods on Maize Yield, Nutrient Accumulation, and Soil Nutrients in a Semi-Arid Region

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Abstract: [Objective] In the semi-arid region of western Heilongjiang Province, black soil degradation due to long-term intensive use, low straw utilization efficiency, and constrained maize productivity are critical issues. This study systematically investigated the effects of different straw returning methods on soil nutrient pools, nutrient accumulation characteristics and organ-distribution patterns in maize plants, and further explored their regulatory effects on yield components. The aim was to provide a theoretical basis and technical support for achieving high and stable maize yields and efficient straw utilization in the chernozem soils of semi-arid areas. [Method] Four treatments were established: straw removal with rotary tillage (CK), straw mulching (SM), deep plow returning (DP), and straw incorporation (SI). From 2024 to 2025, using CK as the control, the effects of different straw returning methods on soil nutrients, maize nutrient accumulation, yield, and yield components were systematically analyzed. [Result] The overall performance of different treatments on maize yield traits followed the order $DP > SM > SI > CK$. Compared with CK, the DP treatment significantly increased nutrient contents in the 10~40 cm soil layer, with average increases of 13.01% for organic matter, 16.79% for alkali-hydrolyzable nitrogen, 31.86% for available phosphorus, and 10.11% for available potassium. The DP treatment also significantly promoted the accumulation of nitrogen, phosphorus, and potassium in maize at maturity, with average increases of 22.63%, 12.72%, and 16.73%, respectively. Regarding yield, the DP treatment performed best, increasing yield by 11.23% and 21.00% over CK in the two years, respectively. [Conclusion] The deep plow returning (DP) treatment effectively improved the nutrient pool in deeper soil layers, enhanced the absorption and accumulation of nitrogen, phosphorus, and potassium in maize plants, and achieved stable and increased yield through increased kernel number per ear and 1000-kernel weight. With its significant advantages in improving soil fertility, promoting nutrient accumulation, and increasing maize yield, deep plow returning is a promising agronomic practice suitable for promotion in semi-arid regions.

Key words: Semi-arid region, Straw returning, Soil nutrients, Maize nutrient accumulation, Maize yield

Interpretable Prediction of Maize Grain Protein Yield Using UAV Multispectral Imagery and Meteorological Data Acquired at an Optimal Physiologically Informed Growth Stage

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Abstract: [Objective] Unmanned aerial vehicle (UAV) phenotyping has emerged as a transformative tool in crop breeding. UAV-based crop models mainly target grain yield or canopy biomass. We developed an interpretable Grain protein yield (GPY) prediction framework using UAV multispectral imagery, cumulative meteorological variables, and machine learning. [Method] The experiment included 55 maize varieties under spring and summer sowing at one site in one year. Growth-stage screening and single-kernel protein accumulation kinetics jointly identified R4 as a physiologically supported monitoring window. [Result] The R4-only random forest (RF) model outperformed the full five-stage model. Their R^2 values were 0.57 and 0.45, respectively. The R4 strategy also reduced UAV acquisitions from five to one. Nested leave-one-variety-out validation assessed prediction for varieties excluded from training. The RF model using UAV and meteorological variables achieved an R^2 of 0.5985 and an RMSE of 181.96 kg hm⁻². Meteorological variables increased the number of varieties meeting the operational $R^2 > 0.6$ threshold from 16 to 27. SHAP analysis showed distinct prediction patterns between sowing cohorts. Canopy structural and textural features were more important under spring sowing. Solar radiation and precipitation evenness gained importance under summer sowing. Error analysis linked low predictability to compressed within-variety GPY variation and incomplete cross-variety transfer of input-GPY relationships. [Conclusion] This study extends UAV-based crop phenotyping from the prediction of grain quantity alone to GPY, an integrated measure of grain yield and crude protein concentration that represents grain-protein output per unit area. Within the present single-site and single-year experiment, the dough stage (R4) was the most informative single monitoring stage, and incorporating meteorological variables improved pooled prediction accuracy and prediction coverage among held-out varieties. SHAP analysis further showed that canopy and environmental variables contributed differently between sowing seasons, helping explain why canopy vigor alone was insufficient for GPY assessment. The LOO design demonstrates leakage-free predictive ability for varieties excluded from training within this dataset; however, it does not establish external generalizability across years, locations, soil conditions, or management regimes. The proposed approach should therefore currently be regarded as a physiologically informed proof of concept for high-throughput GPY screening under comparable experimental conditions.

Key words: Maize, UAV remote sensing, Grain protein yield, Machine learning, SHAP

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Technical Session 11

Terrain-Specific Solutions: Modernizing Maize Production in Hilly and Mountainous Regions



Technical Advances and Yield Benefits of Drought-Resistant and Water-Saving Maize Production on the Loess Plateau from A Climate Resilience Perspective

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Abstract: [Objectives] Maize production across the Loess Plateau accounts for nearly 11% of China's maize area and total output. The region hosts the China's largest contiguous rainfed spring maize zone and serves as a pivotal dryland "reserve grain base" for western China. Nevertheless, ongoing climate warming destabilizes agroecosystem. Developing drought-resistant, water-saving and yield-enhancing technologies centered on efficient precipitation utilization is therefore essential for establishing climate-resilient maize cultivation systems. [Method] Multi-year datasets collected across sub-regions of the Loess Plateau were synthesized. Grain yield and water use efficiency (WUE) of dryland maize were quantified to identify key drivers of yield improvement and corresponding technical solutions. [Results] Over the past six decades, the accumulated temperature above 10 °C on the Loess Plateau has risen by 300–1000 °C, accompanied by a 10–30 day extension of the frost-free period. Every decade, the growing season of spring maize shortens by 5–6 days: sowing is delayed by 1.7 days, while harvesting advances by 5.5 days. Dryland maize exhibits a yield potential of an additional 200 kg per mu, with achievable WUE ranging from 2.0 to 2.5 kg·mm⁻¹·mu⁻¹. Loess highlands, aeolian sandy zones along the Great Wall, and the Yellow River Valley possess the greatest capacity for yield improvement. In a long-term continuous maize cropping system spanning thousands of mu and maintained for over 40 years, grain yield per mu rose sequentially from 230 kg to 550 kg and then to 770 kg, representing an almost 2.4-fold total increase. Technological advances have been realized over the last two decades. First, integrated agronomic-machinery technologies including full film double-ridge furrow rainwater harvesting, water-responsive dense planting for cost-efficient production, and delayed low-moisture grain harvesting were developed. A multi-functional integrated machine that performs ridging, film mulching, fertilization and in-film hill-seeding in one pass was invented, laying the foundation for a ridge-furrow rainwater harvesting cultivation system. This technology captures nearly all rainfall within farmland and enables a "1-ton maize per mu" yield benchmark, lifting WUE and grain yield by over 30%. We established the framework of "targeting yield and planting density based on available water", and proposed a water-adaptive dense planting quantitative guideline of 10 maize plants per millimeter of annual precipitation. High-density, machine-harvestable maize hybrids were screened. A post-physiological maturity harvesting protocol was formulated: stalks are left standing for 50–60 days to allow ear dehydration until grain moisture drops below 20%, which facilitates direct mechanical grain harvesting. Second, an integrated soil-moisture probing precision seeding

system was innovated, paired with a dedicated seeder that removes dry topsoil to place seeds into moist subsoil, a practice termed "seeding in wet soil by stripping dry topsoil". Under mild drought stress, seedling emergence rate increased by 7.1–13.4 percentage points, translating to a 11.8%–20.7% yield boost. Seedling survival remained consistently between 85% and 92% during moderate continuous spring-summer droughts. Under extreme drought conditions, plot yield reached 717.4 kg per mu, marking a 20.8% yield increment. Third, a holistic drought-resilience regulation theory for dryland maize was proposed, covering the coupled soil–surface–canopy continuum. We clarified the synergistic eco-friendly mechanisms of deep subsoiling, straw incorporation, reduced/no-tillage for erosion and moisture conservation during fallow seasons, fully biodegradable mulch films, and water-responsive dense planting with reduced chemical fertilizer inputs. [Conclusions] Future dryland maize production will prioritize coordinated management of rainwater collection, soil water storage, topsoil moisture retention, water conservation and efficient water use. Anticipated breakthroughs will cover drought-tolerant water-saving maize varieties, compact-stalk high-population planting architectures, AI-driven smart farming, in-situ soil reservoir construction, eco-friendly mulching materials, and targeted limited supplementary irrigation at critical growth stages.

Key words: Loess Plateau, maize, Drought resistance and yield improvement, Water use efficiency

Optimizing Sowing Date for Green Cob Yield of Sweet Corn in the Hill Tracts of Bangladesh

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Abstract: [Objective] Sweet corn has the potential to significantly improve agricultural productivity and rural livelihoods in the hill regions of Bangladesh, as it is a sustainable, adaptable, and high-value crop. Optimizing sowing dates for year-round sweet corn cultivation in the hilly areas of Bangladesh is crucial for enhancing productivity, ensuring a continuous market supply, and improving farmers' livelihoods. The present study is undertaken to investigate the performance of sweet corn at different sowing dates and to identify appropriate sowing schedules for sustainable and year-round production under hilly agro-ecological conditions. [Method] In the Khagrachari Hill Tracts of Bangladesh, sweet corn (cv. BARI Sweet Corn 1) was assessed under on-farm conditions from December 2025 to March 2026. From December 10, 2025, to March 12, 2026, the experiment was conducted in a randomized complete block design with two replications across 19 producers' fields. The experiment consisted of ten sowing dates placed at 10-day intervals. The protocol of crop husbandry from seeding to drying was followed as per the recommendation of Bangladesh Wheat and Maize Research Institute. The collected data were analysed at 5% levels of significant using Duncan's Multiple Range Test. [Result] Results revealed that both plant height and cob yield were substantially influenced by the sowing date, according to the results. The plant height increased gradually as the sowing date was postponed, reaching a maximum of 199.5 cm on March 12, and a minimum of 149.6 cm on December 10, the date of the latest sowing. In contrast, the yield of cobs decreased as the sowing date was postponed. The sowing on December 10 yielded the highest cob yield (10.54 t ha⁻¹), with 20 and 30 December yielding 10.35 t ha⁻¹ and 10.30 t ha⁻¹, respectively, as statistically comparable results. An additional delay in sowing led to a significant decrease in yield, with the lowest value of 5.90 t ha⁻¹ recorded during the 12 March sowing. Results also found a strong negative correlation between sowing time and cob yield revealing the $R^2 = 0.959$, which means about 95.9% of the variation in cob yield is explained by time. Generally, the most effective

method for maximizing cob yield was early sowing, notably on 10 December. [Conclusion] Conversely, delayed sowing facilitated vegetative growth at the expense of productivity.

Key words: Hill agriculture, High-value crops, Year-round production, Chittagong Hill Tracts, Crop productivity, Agronomic management.

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Deploying Climate-resilient Maize Germplasm for Food and Fodder Security in Hilly Regions of Pakistan

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Abstract: Traditional maize landraces cultivated in the hilly regions of Pakistan are generally characterized by low yield potential, limited access to improved seed, and increased vulnerability to climatic stresses, constraining both food and fodder security of smallholder farming communities. To address these challenges, a collaborative partnership between the International Maize and Wheat Improvement Center (CIMMYT) and Pakistan's National Agricultural Research System (NARS) has focused on the introduction, evaluation, and deployment of genetically diverse and climate-resilient maize germplasm adapted to the agro-ecologies of northern Pakistan. Elite CIMMYT-derived hybrids and open-pollinated varieties (OPVs) were systematically evaluated through multi-location testing and National Uniform Yield Trials, followed by varietal release, seed multiplication, and dissemination to farming communities. These efforts resulted in the release of Saad in 2020, followed by the stay-green OPVs NARC-3 in 2025 and NARC-2 in 2026. The newly released OPVs combine improved grain productivity with enhanced fodder potential, offering an important dual-purpose option for mixed crop–livestock production systems. Their stay-green characteristics provide additional value through prolonged availability of green biomass and improved fodder utility, particularly in hilly environments where quality feed resources are often limited. The integration of improved CIMMYT germplasm with efficient national testing, varietal release, seed multiplication, and farmer-oriented deployment provides an effective pathway for accelerating varietal turnover and replacing low-yielding traditional materials. Strengthening this germplasm-to-farmer pipeline can contribute to climate resilience, increased maize productivity, improved fodder availability, and enhanced food and livelihood security of resource-poor farming communities in Pakistan's hilly regions.

Key words: Maize, Climate resilience, CIMMYT germplasm, Open-pollinated varieties, Stay-green, Food security, Fodder security, Pakistan

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A Brief Overview of the Maize Industry in Nepal

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Abstract: Maize (*Zea mays* L.) is one of Nepal's major food-security crops, supporting the livelihoods of million rural households. It is cultivated approximately 0.91 million hectares, producing about 3.19 million tons across diverse agro-ecological regions from the Terai plains to the high-hills, making it one of the country's most widely adapted crops. Despite steady growth from 2013 to 2022, the area under maize cultivation has declined in recent years, particularly in the hilly regions. In the mid and high-hills, maize is a staple food, with nearly 86% of production consumed by households, whereas about 80% of maize produced in the Terai is used as feed for the rapidly expanding poultry and livestock sectors. The maize sector has gradually modernized since 2008 with the introduction of hybrid maize for general cultivation through government-led interventions. Hybrid maize now occupies about 80% of the Terai maize-growing area during the winter and spring seasons, driven by higher yield potential and feed industry demand; in the hills, hybrid cover roughly 10% of the area. More than 115 registered feed industries operating in Nepal, yet domestic maize production remains insufficient, requiring imports to meet over 50% of feed industry demand. The Nepal Agricultural Research Council, in collaboration with International Maize and Wheat Improvement Center, has developed 10 national hybrid maize varieties and 31 open-pollinated varieties (OPVs), while over 90 hybrids from multi-national companies have been registered to date. Despite some fluctuations, private seed companies and farmers' cooperatives have produced hybrid maize seed since 2018, with current annual production of about 150 tons- a significant step toward the commercializing the maize seed sector. However, this positive growth in maize production is constrained by low productivity (3.5 t ha⁻¹), limited supply of high-yielding and stress-resilient varieties, pest and disease outbreaks (including fall-army worm), labor shortage, and weak post-harvest and marketing systems. Nevertheless, Nepal's maize industry has strong potential for growth through wider adoption of improved seeds and varieties, advanced agronomic practices, and stronger market linkages, which could better support domestic industries and reduce imports.

Key words: Maize industry, Nepal, Hybrid maize, Open-pollinated varieties, Food security

Hybrid Maize Seed Systems as A Catalyst for Rural Agribusiness Transformation in Nepal

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Abstract: Nepal's dependence on imported hybrid maize seed has prompted growing investments in domestic seed production through public-private partnerships. This study documents the transformation of Satbariya, a village traditionally focused on maize grain production, into an emerging hybrid maize seed production hub through coordinated interventions involving CIMMYT, the Nepal Agricultural Research Council (NARC), government agencies, private seed companies, and farmers' cooperatives. The initiative introduced and strengthened technical capacity in hybrid seed production, field management, quality assurance, mechanization, and post-harvest handling, while improving farmers' access to formal seed markets and commercial services. The engagement of private seed companies and cooperatives created stronger market linkages and provided farmers with more predictable opportunities to produce and market hybrid seed. The model also generated new income and employment opportunities, with women farmers and women-led groups playing an increasingly important role in seed production and agribusiness activities. Beyond increasing local seed availability, the Satbariya experience demonstrates how community-based seed production can evolve into a commercially oriented rural enterprise when supported by appropriate technology, institutional coordination, market incentives, and capacity development. The initiative represents an important example of agribusiness innovation in Nepal's maize sector, linking smallholder farmers to formal seed value chains while strengthening local entrepreneurship. The experience offers lessons for scaling decentralized hybrid seed systems to other production hubs and reducing Nepal's dependence on imported seed while contributing to seed security, farmer livelihoods, and national maize self-reliance.

Key words: Hybrid maize seed, Village-based agribusiness, Mid-hills of Nepal

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Overview of Maize Production, Challenges, and Recent Research

Developments in Lao PDR

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Abstract: [Objective] This study looks at the current state of maize farming in Lao PDR. It identifies the main economic and farming challenges that small farmers face, and reviews recent research on testing new maize varieties and improving the seed system. [Method] The study uses national crop data from 2021 to 2025 and a survey of 235 small farming households in Oudomxay and Xiengkhouang provinces. It also includes results from field and station yield tests done between 2023 and 2025. These tests compared different plant materials, like CIMMYT hybrids and local Lao experimental crosses, against the most common commercial seeds. [Result] Maize is very important for the rural economy in Lao PDR, especially in the northern mountains, making up about 16.6% of the agricultural GDP in 2023. From 2021 to 2025, the area planted with "hard maize" ranged from 92,759 to 110,910 hectares. Even though maize is a key export for animal feed, crop yields have stopped growing (averaging 4.8 to 5.2 tons per hectare). Farmers also rely too heavily on imported commercial seeds, making the crops too genetically similar. For example, in Xiengkhouang province, just two imported varieties make up 92% of the planted area in the survey. Recent research by the Rice and Cash Crop Research Center (RCCRC) has tried to fix these problems through many field and station yield tests from 2023 to 2025. These tests compared different maize types against standard commercial seeds. The research found several good varieties, like VH19392, VH171309, and local crosses like W3 x LW3 and CML563 x 170. These varieties produce high yields, grow well, and are well-liked by farmers. The studies also show that it is important for the plants to be stable and adapt well to different local environments, like in Oudomxay and Xiengkhouang provinces. Even with this progress, maize farming still faces big challenges. Production costs are high (averaging 7.1 to 8.3 million LAK per hectare) because farmers depend on imported seeds and chemicals. There are also pest threats like the Fall Armyworm (FAW). Weather risks, like too much rain flooding the soil, can also lower yields a lot. However, these challenges are a chance to build a Lao Maize Innovation System (LMIS). By supporting local seed businesses and connecting research centers with small farmers, Lao PDR can create a stronger farming system. Using High-Quality Tropical Maize (HQTM) can help improve food security and make the local maize industry more competitive. [Conclusion] Right now, the maize farming system in Laos has high costs and is easily damaged by problems, which threatens food security. To fix this, Lao PDR should move toward a Lao Maize Innovation System (LMIS). This system will support local seed businesses and connect research centers directly with small farmers so they can plant stronger, locally adapted maize varieties.

Key words: Maize production, Food security, Hybrid trials, Lao PDR, Smallholder livelihoods

Transforming Nepal's Maize Future: Science and Innovation for Scalable Value Chains

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Abstract: [Objective] Maize commercialization has the potential to be a major driver of economic transformation in Nepal in line with the country's Agriculture Development Strategy (ADS) 2015–2035. Nepal's formal livestock industry requires approximately 0.8 million tonnes of maize annually, of which more than 50%—valued at around US\$120 million—is met through imports. Since 2021, CIMMYT has designed, implemented, and tested the Maize Commercialization Model (MCM), an inclusive, science-based cropping system and market innovation approach that promotes maize cultivation in spring fallows through partnerships with government, private sector, and farmers. The model aims to sustainably increase domestic maize production to contribute to national food and feed security while reducing maize imports by 50% by 2030. This paper presents the results and lessons from MCM implementation during 2021–2026, highlighting its scaling and mainstreaming into Government of Nepal programs for sustainable maize value chain development. [Method] A mixed method approach was used for the assessment with data collected from 700 randomly selected farmers households in 2022 focusing on farmers' maize production, knowledge and practice, and maize marketing. More than 100 focus group discussions with members from 70 farmers cooperatives, 20 multi stakeholder group meetings, interviews with 200 micro small and medium enterprises, 100 key informant interviews with public and private actors and 6 national and provincial stakeholder workshops were held between 2022 and 2026 to generate data and information on the production, utilization, incomes, and market linkages created by the MCM. Data was analyzed using qualitative statistics and quantitative tools including regression analysis, probit, multinomial probit, and the Inverse Probability Weighted Regression Adjustment (IPWRA) method. [Result] In 2026, the MCM was found to be in a scaling trajectory. Between 2021 and 2026, the number of households in the MCM increased from 830 to 30,000; area under spring maize increased from 278 ha-15,000 ha, maize yield increased from 5.5 MT to 7 MT and average income from maize increased from NRs 48,000 (USD 400) to NRs 138,000 (USD 985). About 58% of the respondents mentioned that their maize yields increased compared to 2020. The reasons accorded to higher yield were use of hybrid seed (43%) and better availability of irrigation (25%). The likelihood of participating in MCM is 25% higher for farmers who received agricultural training and those who received information from agrovets are 15% more likely to participate. The farmers mentioning lack of technical knowledge about maize farming reduced from 37% in 2020 to 14% in 2022 ($P < 0.01$). Results show that female headed households increased maize yield by 0.70 MT/ha ($p < 0.05$) as compared to male headed HHs. Over the years the average farm gate price of maize increased from NPR 21/kg in 2021 to NPR 35/kg in 2026. The number of feed mills and micro, small and medium enterprises (MSMEs) engaged in maize aggregation increased from 5 to 23 in

2026. About 84% of MCM farmers sold on average 76% of their produce, of which 41% was sold for processing feed, 4% for food processing and 18% for producing local animal feed. The Government of Nepal invested USD 5 million since 2021 in MCM focusing on irrigation, agriculture machineries and storage. Farmers invested more than USD 600,000 on improved inputs while the private sector invested about USD 800,000 on market infrastructure. In 2025, the Government of Nepal included the MCM into its regular program and allocated USD 72,000 to support 6 rural municipalities including in Eastern Nepal. In 2026-27, the support was extended to 10 municipalities across 3 provinces. [Conclusion] The MCM could create incentive for the stakeholders to learn and catalyze investment in the maize sector. The scaling of national maize value chains should focus on strengthening the entire system—from breeding (short duration, stress tolerant) and seed production to sustainable crop management, post-harvest handling, processing, and market integration. Simultaneously, investments in aggregation, storage, feed industries, and market infrastructure can create stronger demand pull and better returns for farmers. By embedding research, monitoring, learning, and evidence-based policy support within scaling efforts, Nepal can accelerate the development of a competitive, climate-resilient, and inclusive maize value chain that contributes to agricultural transformation, import substitution, employment generation, and sustainable economic growth.

Key words: Maize, Value chains, Innovations, Public-private partnerships, Financing

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Optimizing Row Spacing to Improve Stalk Lodging Resistance by Regulating Light Distribution Under High Maize Planting Density

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Abstract: [Objective] With frequent extreme weather caused by climate change, stalk lodging seriously restricts high-yield production of summer maize under dense planting. Reasonable row spacing can optimize canopy light distribution, improve stalk morphological quality and enhance lodging resistance. This study aimed to clarify the physiological mechanism of row-spacing regulating stalk lodging resistance for summer maize in hilly areas. [Method] A two-year field experiment was carried out. Treatments with different planting densities and row-spacing patterns were set up. We continuously measured canopy light transmittance, basal internode growth, stalk mechanical characteristics and lodging rate during maize growing seasons. [Result] Stalk mechanical strength had a quadratic correlation with canopy photosynthetically active radiation. Basal light transmittance was positively correlated with internode thickness, unit-stem dry weight, lignin and cellulose accumulation. High planting density reduced light transmission in the lower canopy, restrained basal internode development, decreased stalk mechanical strength and increased lodging risk. Optimized equal row spacing improved light environment of population lower layer, promoted basal internode growth, and effectively lowered lodging risk under dense planting. [Conclusion] Appropriate row spacing improves internal light distribution of maize population, strengthens stalk lodging resistance and stabilizes grain yield under high density. For hilly areas of central Sichuan, the optimal cultivation mode is 67,500 plants ha⁻¹ with 60 cm equal row spacing.

Key words: Planting density, Row spacing, Canopy light transmittance, Internode characteristic, Stalk lodging resistance

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The Development Potential and Strategy of High Protein Maize in Southwest China

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Abstract: [Objective] Against the background of national strategies to reduce and substitute soybean meal in feed and to adopt the all-encompassing approach to food, this study analyzes the current foundation, potential, and development strategies for high-protein maize in Southwest China, aiming to provide a basis for national feed grain security and high-quality development of regional agricultural industry. [Method] Based on statistical data, combined with meta-analysis and field experiments, the potential for developing high-protein maize in Southwest China (Sichuan, Yunnan, Guizhou, and Chongqing) was systematically evaluated from the aspects of current planting status, industrial demand, and regional advantages. Strategies for genetic improvement and cultivation regulation were also explored. [Result] The average planting density ($48000 \text{ plants ha}^{-1}$) and grain yield (7700 kg ha^{-1}) of maize grown by farmer in Southwest China were significantly lower than those in other major production regions of the country, indicating considerable room for improvement in both density and yield. Recently, five high-protein maize varieties (protein content $>12\%$) suitable for cultivation in Southwest China have been approved. Field experiments showed that spring-sown maize achieved both higher average yield and higher average grain protein content than summer-sown maize. The maize and *Ophiopogon japonicus* intercropping system achieved synergistic improvement in maize yield (12228 kg ha^{-1}) and protein content (11.26%). Southwest China possesses potential for developing high-protein maize, yet it needs to break through the bottleneck of insufficient high-yield and high-quality varieties as well as supporting key cultivation techniques. [Conclusion] Future efforts should focus on precision breeding of high-protein maize varieties, establishment of a cultivation technology system centered on precise nitrogen regulation, and development of a collaborative innovation mechanism involving government, industries, universities, research institutes, and end-users to realize the high-quality development of the high-protein maize industry.

Key words: High-protein maize, Southwest China, Potential, Strategy, Food security

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Development of Fall Armyworm-Resistant and High-Yielding Maize

(*Zea mays* L.) Open-Pollinated and Inbred Lines from Kalahari

Early Pearl (KEP) Maize in Namibia

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Abstract: This study aims to develop high-yielding, fall armyworm-resistant maize (*Zea mays* L.) open-pollinated varieties (OPVs) and inbred lines derived from the Kalahari Early Pearl (KEP) maize variety to improve maize productivity and strengthen food security under Namibia's dryland farming conditions. The research will be conducted during 2026–2027 at Omahenene, Mannheim, and Bagani Crop Research Stations. Conventional selection, irradiation-induced mutation breeding, and successive selfing will be used to develop improved OPVs and inbred lines. Genotypes will be evaluated for agronomic performance, grain yield, fall armyworm resistance, phenotypic stability, and generational performance across different environments. Data will be analysed using analysis of variance and selection indices to identify superior breeding materials. The study is expected to produce locally adapted, high-yielding, and fall armyworm-resistant OPVs suitable for farmer seed recycling, together with stable inbred lines and improved germplasm for future hybrid development. The resulting breeding materials are anticipated to enhance maize productivity, reduce dependence on pesticides, lower production costs, and strengthen Namibia's national maize breeding programme. The development of improved KEP-derived maize varieties will contribute to sustainable maize production, increased resilience to fall armyworm infestation, enhanced food security, and greater national capacity for maize improvement in Namibia.

Key words: Maize breeding, Fall armyworm resistance, Open-pollinated varieties, Inbred lines, Kalahari Early Pearl, Namibia

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