

Resource Summary Report

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PANZEA

RRID:SCR_007846

Type: Tool

Proper Citation

PANZEA (RRID:SCR_007846)

Resource Information

URL: <http://www.panzea.org>

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Description: It contains the genotype, phenotype, and polymorphism data produced by the NSF-funded project; Genetic Architecture of Maize and Teosinte. The PANZEA project will identify genes that control domestication traits and three key agronomic traits: flowering time, plant height, and kernel quality. Genetic linkage, association, and fine mapping analyses will be performed on the largest and most diverse set of mapping families publicly available for any species. A large series of isogenic lines will be used to characterize allelic series and epistatic interactions. The genetic architecture of each of the four trait groups will be compared and contrasted, and the influence of recombination and past domestication bottlenecks on the genomic distribution of functional diversity will be examined. Finally, the ability of genetic architecture-based models to predict phenotype will be evaluated in a broad range of germplasm, including elite US hybrids. This project will take a step toward the ultimate goal of predicting phenotype from genotype.

Synonyms: PANZEA

Resource Type: data or information resource, database

Keywords: FASEB list

Resource Name: PANZEA

Resource ID: SCR_007846

Alternate IDs: nif-0000-03242

Record Creation Time: 20220129T080244+0000

Record Last Update: 20260905T133146+0000

Ratings and Alerts

No rating or validation information has been found for PANZEA.

No alerts have been found for PANZEA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 110 mentions in open access literature.

Listed below are recent publications. The full list is available at [NIF](#) .

Gesteiro N, et al. (2025) Genome-Wide Association Study and Genomic Predictions for Hydroxycinnamate Concentrations in Maize Stover. Journal of agricultural and food chemistry, 73(4), 2289.

Bertolini E, et al. (2025) Regulatory variation controlling architectural pleiotropy in maize. Nature communications, 16(1), 2140.

Wu M, et al. (2025) A multifunctional sesquiterpene synthase integrates with cytochrome P450s to reinforce the terpenoid defense network in maize. The Plant journal : for cell and molecular biology, 124(3), e70575.

Wang Y, et al. (2025) Genome-Wide Association Study and Candidate Gene Mining of Husk Number Trait in Maize. International journal of molecular sciences, 26(7).

Zhang Y, et al. (2025) From function to omics: endophytic Beauveria bassiana promotes maize growth by activating phytohormone signaling pathways under elevated carbon dioxide. BMC plant biology, 25(1), 1759.

Schmidt M, et al. (2024) Fine mapping a QTL for BYDV-PAV resistance in maize. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 137(7), 163.

Guo S, et al. (2024) A genome-wide association study uncovers a ZmRap2.7-ZCN9/ZCN10 module to regulate ABA signalling and seed vigour in maize. Plant biotechnology journal, 22(9), 2472.

Wu C, et al. (2023) A transformer-based genomic prediction method fused with knowledge-guided module. Briefings in bioinformatics, 25(1).

Hartwig T, et al. (2023) Hybrid allele-specific ChIP-seq analysis identifies variation in brassinosteroid-responsive transcription factor binding linked to traits in maize. Genome biology, 24(1), 108.

Chen SP, et al. (2023) A statistical package for evaluation of hybrid performance in plant breeding via genomic selection. Scientific reports, 13(1), 12204.

Hao Y, et al. (2023) Genetic and transcriptomic dissection of host defense to Goss's bacterial wilt and leaf blight of maize. *G3 (Bethesda, Md.)*, 13(11).

F??rster C, et al. (2022) Biosynthesis and antifungal activity of fungus-induced O-methylated flavonoids in maize. *Plant physiology*, 188(1), 167.

Meier MA, et al. (2022) Association analyses of host genetics, root-colonizing microbes, and plant phenotypes under different nitrogen conditions in maize. *eLife*, 11.

Yannam VRR, et al. (2022) Genome-Wide Association Analysis of Senescence-Related Traits in Maize. *International journal of molecular sciences*, 23(24).

Wu X, et al. (2022) Prioritized candidate causal haplotype blocks in plant genome-wide association studies. *PLoS genetics*, 18(10), e1010437.

Xie J, et al. (2021) Optical topometry and machine learning to rapidly phenotype stomatal patterning traits for maize QTL mapping. *Plant physiology*, 187(3), 1462.

Schrauf MF, et al. (2021) Comparing Genomic Prediction Models by Means of Cross Validation. *Frontiers in plant science*, 12, 734512.

Meng X, et al. (2021) Predicting transcriptional responses to cold stress across plant species. *Proceedings of the National Academy of Sciences of the United States of America*, 118(10).

Adak A, et al. (2021) Validation of functional polymorphisms affecting maize plant height by unoccupied aerial systems discovers novel temporal phenotypes. *G3 (Bethesda, Md.)*, 11(6).

Favela A, et al. (2021) Maize germplasm chronosequence shows crop breeding history impacts recruitment of the rhizosphere microbiome. *The ISME journal*, 15(8), 2454.