

Comparative genomics to improve genotype-phenotype associations in maize and sorghum

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Abstract

Comparing the genomes of two species offers a robust approach to unveil potentially overlooked genes that wield substantial influence on observed agronomic traits. Extensive phenotypic data from maize and sorghum were previously utilized in genome-wide association studies. This project aims to harness the potential of comparative genomics to strengthen confidence in these marker-trait associations and to suggest previously unexplored relationships. To achieve this goal, insights from studies on the genetically diverse Sorghum Association Panel and the maize Wisconsin Diversity Panel were leveraged to classify candidate genes as either shared between the two species or unique to one or the other. Candidate orthologous genes found in both species, associated with shared phenotypes, enhance the reliability of the associations within each species. Additionally, genes unique to each species provide parameters to inform future predictive models. Finally, given the ancient tetraploidy of maize and the biased loss of genes over time, the candidate genes identified in sorghum provide valuable information for understanding the orthologs found in the maize subgenomes.

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