

A FORWARD GENETICS APPROACH INTEGRATING GWAS AND EQTL MAPPING TO DISSECT LEAF DEVELOPMENT IN MAIZE (ZEA MAYS)

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In the post-genomic era, the combination of extensive genomic information with precise phenotyping generated on advanced segregant populations drives the capacity to pinpoint gene functions, hence supporting precision breeding towards global food security.

Maize is established as a model species for monocots since the early characterization of its genome sequence, and is a primary resource for food, feed and energy production. The characterization of the genetic basis of leaf development in maize may contribute to develop plants with higher vigor and productivity. In this study, we employed a three-pronged forward genetics approach integrating transcriptomics, phenotyping, and genome wide associations studies (GWAS) to conduct expression QTL (eQTL) mapping and prioritize candidate genes involved in maize leaf traits determination.

We measured multiple leaf traits and performed RNA sequencing at the seedling stage in a mapping panel of 197 biparental and MAGIC maize recombinant inbred lines (RILs). We derived 373,769 single nucleotide polymorphisms (SNPs) from RNA sequencing data and estimated the transcription levels of 29,573 gene models. First, leaf traits were correlated with gene expression levels to identify transcript-trait correlations; second, marker-trait associations were derived from a GWAS; third, eQTL were derived associating SNPs with gene expression levels.

Finally, we combined all approaches to prioritized candidate genes for leaf development. A weighted gene expression network analysis was used to capture the broader picture of gene interactions controlling the expression of leaf traits.

The integration of our forward genetics approaches led to the identification of 25 candidate genes highly enriched for suggestive functional categories, supporting evidence for the role of vacuole proton pumps, cell wall effectors, and vesicular traffic controllers in early leaf growth. The gene expression grouped the transcripts in 38 co-expression modules some of which correlating with leaf traits. Our results show the value of developing transcriptomic data in segregant populations to derive information about gene networks and their interactions in the determination of traits of interest. When put in relation to trait values, the rapidly expanding body of knowledge on eQTL control and determination will accelerate our understanding of complex trait determination in crops, contributing to break new ground to precision breeding.