

T-DNA mutant screen in Arabidopsis to validate candidate genes with predicted ionomic and seed weight phenotypes

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Abstract

Advances in quantitative genetics and high-throughput pipelines have allowed for rapid identification of genomic markers associated with changes in phenotype. However, linking those markers to causal genes is still difficult, as many genes may be linked to one marker. We aimed to improve candidate gene selection by creating a new method that identifies conserved genes underlying GWAS loci in multiple species. So far, we have tested this method in two different experiments: 1) using GWAS from Arabidopsis, soybean, rice, maize, and sorghum measuring 19 elemental uptake (ionomic) traits and 2) GWAS from Arabidopsis, soybean, rice, and maize measuring seed weight traits. We identified 14,336 candidates in the ionomics GWAS comparison. The most likely candidates belonged to ortholog groups linked to GWAS loci in all five species for their given trait according to calculations using random permutations of the data. For the seed weight GWAS comparison, we identified 192 candidates, and again, the most likely candidates belonged to ortholog groups linked to GWAS loci in all species in the comparison. Focusing on these most likely candidate genes from Arabidopsis, we obtained T-DNA lines with mutant alleles for each candidate gene and performed a high-throughput phenotyping screen utilizing ICP-MS for ionomics and the image analysis software PlantCV for seed weight. Preliminary results show 59 ionomic candidates and 9 seed weight candidates have one line with confirmed phenotypes. We plan to further verify these preliminary confirmations by obtaining and screening additional T-DNA lines with different alleles for each candidate gene.

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