

Computation methods to identify elemental accumulation genes

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Abstract

High throughput phenotyping and quantitative genetics have enabled researchers to identify genetic regions, or markers, associated with changes in phenotype. However, going from GWAS markers to candidate genes is still challenging. When selecting candidate genes for ionomic GWAS markers, we curated a collection of well-known ionomic genes (KIG) experimentally shown to alter plant elemental uptake and their orthologs in 10 crop species: 2066 genes total. Yet when compared to ionomic GWAS markers, over 90% of significant markers were not linked to a KIG - indicating the list is incomplete and many causal genes are unknown. Continuing to use only functional annotations as candidate selection criteria will keep efforts biased toward well-known genes and hinder the characterization of unknown genes. We propose an unbiased computational approach that compares analogous GWAS markers from multiple species and searches for conserved genes linked to trait markers. Like the KIG list, we expect many of these unknown candidate genes to have orthologs in other species. By leveraging the evolutionary relationship of these conserved genes, rather than prior knowledge and gene annotations, this method: 1) finds more candidate genes than we expect from random chance, 2) selects and prioritizes candidates in poorly annotated species, and 3) includes unknown genes in the results. With this approach, we now have an unbiased list of gene candidates across 19 ionomic traits in model species and crop species to verify in future experiments.

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