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Computational methods to identify ionome genes

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The ionome describes the concentration of elements acquired by plants and is heavily influenced by interactions between genes and the environment. Quantitative genetics and high-throughput pipelines have allowed for rapid identification of genomic markers associated with changes in the plant ionome, however, linking those markers to causal genes is more difficult. Many genes may be linked to one marker and annotations are ineffective for unknown causal genes, ultimately impeding candidate gene selection. To identify candidate genes influencing ionic phenotypes, we assembled the known ionome gene (KIG) list: a curated collection of genes experimentally shown to alter elemental uptake in plants and their orthologs in 10 crop species. When compared to ionic GWAS data from Arabidopsis, maize, sorghum, soybean, and rice, more than 90% of significant markers are not linked to a KIG gene, indicating the list is far from complete. We expect a large portion of these unknown causal genes to have orthologs in other species, much like our KIG list genes. To find these orthologous genes, we developed a new comparative approach for GWAS. We start with comparable GWAS markers in multiple species, find genes associated with GWAS markers in each species, then compare each species' marker-associated gene list to identify orthologous genes. Preliminary results from testing on ionic GWAS show this comparative approach finds more trait-linked orthologs in the actual datasets than in 1000 random permutations. Additionally, adding more species to the comparison reduces background noise in the random permutations and retains signal in the actual dataset. Pairing orthologous genes with evidence from analogous GWAS datasets of multiple species produces a prioritized list of conserved candidates in all five species used in this approach- including those with fewer gene annotations. Future research aims to verify ionic candidates and evaluate candidate prioritizing parameters.

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Crop type determines the relation between root system architecture and microbial diversity indices in different phosphate fertilization conditions

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Synthetic phosphate fertilizers are frequently used in agriculture and their overuse can significantly increase production costs and cause negative environmental impacts. Soil phosphorus (P) availability can be increased by the contribution of the rhizosphere microbiota associated with the plant root system. This work aimed to evaluate the effect of different phosphate fertilization conditions on maize and sorghum genotypes. Four commercial genotypes of maize and four of sorghum were cultivated for two seasons under seven treatments, no addition of P fertilizer, and 50 and 100 kg P₂O₅ ha⁻¹ of two rock phosphate (Itafós and OCP) and triple superphosphate. During flowering time, the root system was collected according to the Shovelomics' method and analyzed by a modified version of Digital Imaging of Root Traits (DIRT) system. The modifications made the root system architecture analyses less error-prone and more effective. Moreover, three diversity indices, Shannon-Wiener (H'), Simpson (1-D) and Chao1, were calculated based on the bacteria abundance and richness. The type of crop followed by the genotype and fertilizer were the main factors that affected the root system, grain yield, genetic diversity and abundance of microorganisms. The most productive genotypes had higher root angle and area, increased foraging on the soil surface and P acquisition. Maize presented higher microorganism diversity, root angle and foraging traits while sorghum presented higher abundance of specific taxa, a narrower root angle and smaller foraging. The combined use of less reactive P sources, which could be more soluble over time by the physicochemical processes and soil microbiota activity, together with more efficient genotypes might reduce the amount of soluble phosphate fertilizers applied annually to crops.

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