Phenotyping is essential to enhance phosphorus efficiency in maize and sorghum

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Phosphorus (P) is an essential nutrient to plants and is acquired as inorganic phosphate from the rhizosphere solution. P is one of the least available nutrients particularly in highly weathered, tropical soils, limiting substantially plant growth. An interesting approach to circumvent P deficiency in tropical areas is to explore the genetic diversity available in plants to breed cultivars more efficient in P acquisition. Root traits, such as root length and surface area are key to determine P-efficiency. Our work aimed to study root traits involved with P acquisition efficiency and to identify putative maize and sorghum homologs to Phosphorus Starvation Tolerance 1 (PSTOL1), a gene responsible for enhanced early root growth, P uptake and grain yield in rice. A combined approach of a paper pouch system in nutrient solution with field phenotyping under low-P was used to generate phenotypic data in order to investigate the role of OsPSTOL1 homologs. Association mapping was undertaken in two sorghum association panels phenotyped for P uptake, root system morphology and architecture in hydroponics and grain yield and biomass accumulation under low-P conditions. Root length and root surface area were positively correlated with grain yield under low P in the soil, emphasizing the importance of P acquisition efficiency in sorghum adaptation to low-P availability. SbPSTOL1 alleles reducing root diameter were associated with enhanced P uptake under low P in hydroponics, whereas Sb03g006765 and Sb03g0031680 alleles increasing root surface area also increase grain yield in low-P soil. SbPSTOL1 genes colocalized with QTLs for traits underlying root morphology and dry weight accumulation under low P-soil. For maize, two multiple interval models were used to map QTLs related to root traits, biomass accumulation and P content in a maize RIL population cultivated in nutrient solution. Multiple interval mapping models for single and multiple traits were combined and revealed 13 genomic regions significantly associated with the target traits in a complementary way. Some of these quantitative trait loci (QTLs) were coincident with QTLs for root morphology traits and grain yield previously mapped, whereas others harbored ZmPSTOL1 candidate genes. Maize PSTOL1 candidate genes co-localized with QTLs for root morphology, biomass accumulation and/or P content and were preferentially expressed in roots of the parental lines that contributed the alleles enhancing the respective phenotypes. Our work indicate multiple maize and sorghum PSTOL1 genes that have a role in the modulation of root morphology, which leads to higher P acquisition and yield.

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