

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 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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