QTL mapping and identification of putative *PSTOL* homologs associated with phosphorus acquisition traits in maize seedlings

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Modifications in root morphology are important strategies to maximize soil exploitation under phosphorus starvation in plants. Here, we performed a comprehensive QTL mapping to evaluate root traits, biomass accumulation and P content in nutrient solution in a maize RIL population. In addition, we searched for putative maize homologs to *PSTOL1*, a gene responsible for enhanced early root growth, P uptake and grain yield in rice and sorghum. A path analysis revealed that the root surface area presented the highest influence in biomass production and P acquisition. Based in two models for QTL mapping, 13 regions were identified at the chromosomes 1, 2,3,4,6,7,8,9 and 10, ranging from 6.84% to 15.17% and 23.41% to 35.54% for single and multiple traits analysis, respectively. Among the six predicted maize genes sharing more than 55% of amino acid sequence identity with *OsPSTOL1*, four were co-localized with QTLs for root morphology, biomass accumulation and/or P content on chromosomes 3 (*ZmPSTOL3.06*) and 8 (*ZmPSTOL8.05_1*). Expression analysis revealed that these genes were more expressed in roots of the parental lines that contributed with alleles enhancing the respective phenotypes. The QTL mapping strategies adopted in this study revealed complementary results that reflected the correlation between the traits. The combination of QTL and expression data indicated the most promising genes, which may have a functional relationship with root morphology leading to enhance P acquisition in maize, similar to the function of their homologs in rice and sorghum.