

Co-localization of QTL for root traits under low phosphorus availability with candidate genes homologues to *PSTOL1* in maize

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Low phosphorus (P) availability is a primary constraint for maize productivity, mainly in tropical soils. This cereal is the most produced in the world and a major staple food in Africa and Latin America, where soils are often degraded. Due to the limited mobility of P in the soil, its acquisition is highly dependent on the proximity to the root system. Thus, the plasticity of root morphology is an important strategy adopted by plants under P starvation, in order to maximize the soil exploitation. Root morphology is a complex trait, and several QTLs have been identified in maize under nutrient solution and field conditions with P contrasting levels. However, few candidate genes related to these traits have been identified. Recently, *PSTOL1* - Phosphorus-starvation tolerance 1 - was identified as the gene underlying a major QTL associated with P uptake in rice, *Pup1* locus. This gene encodes for a protein kinase and was responsible to enhances early root growth, enabling the improvement of P uptake and grain yield in rice. Here we performed a comprehensive QTL study for root traits under low P availability in nutrient solution. Additionally, based on rice *PSTOL1* amino acid sequence we searched for maize putative homologues. Twelve predicted proteins with more than 50% identity with *PSTOL1* were identified. Six predicted proteins sharing more than 55% identity with Os*PSTOL1*, showed the ATP-binding and Serine/Threonine protein kinase domains conserved among maize, rice, and *Arabidopsis*, whereas four of them were clustered together with rice *PSTOL1* in a phylogenetic tree. Using a multi-trait mapping approach, including root morphology traits, total plant dry weight and P content, we identified QTLs on chromosomes 1, 3, 7, 8, 9 and 10. QTLs mapped on chromosomes 1, 3 and 8 co-localized with putative homologues to *PSTOL1* and with other genes controlling root morphology traits. These results will be important to elucidate the genetic factors related to root traits that may contribute to improve P efficiency acquisition in maize. Financial support: Generation Challenge Programme, CAPES, CNPq, FAPEMIG and Embrapa