

Co-localization of QTLs for root traits, P efficiency indexes and grain yield in maize under low-P soil

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Background

Tropical regions have suboptimal phosphorus (P) availability in the soil for crops, which is a primary constraint for plant growth. In maize, P acquisition efficiency (PAE) has been implicated as crucial for increasing P use efficiency (PUE). Thus, changes in root morphology are strategies that can increase the P uptake by plants. Possibly the genes affecting root development may also affect PAE in maize, and indirectly grain yield in low P conditions. However, information about genetic relationship of root traits, P efficiency and grain yield in maize is limited, and it was addressed by our current study using QTL mapping and QTL meta-analysis in a tropical population in low-P soil.

Methods

Three populations derived from crosses between L3 (P-efficient) x L22 (P-inefficient) were evaluated: Recombinant Inbred Lines (RILs); Testcross population (RILs x L53); and Design III population [1]. The following root morphology traits from RILs were evaluated by Shovelomics method [2]: stalk diameter up first brace (SD), number of brace root whorls (BW), total brace root number (BNT), angle of 2nd arm of brace roots (BA2), number of branching of crown roots (CB) and first 2 cm root diameter (BD). Testcross population was evaluated in field trials with low P (18 kg.ha⁻¹ of P) and high P (106 kg.ha⁻¹ of P) in the soil, and Design III was evaluated in a field trial with low P (10 kg.ha⁻¹ of P). Grain yield (GY), PAE, P internal utilization efficient (PUTIL) and PUE were obtained [1]. QTL for all traits were mapped using a composite interval mapping (CIM) and/or multiple interval mapping (MIM) approaches according to population. QTL meta-analyses were performed to identify overlapping genomic regions.

Results and conclusions

High variability was detected for root traits with heritability ranged 33% for BD to 72% for BW, BA2 and BNT. GY and PUE indexes presented heritability greater than 40%. A total of 53 QTL were identified, 14 for roots traits and 39 for grain yield, PAE, PUTIL and PUE. Meta-analysis identified one cluster on linkage group 1 between 9.69 at

12.13 Mbp, weighing 43%. Individual QTL was identified in this region for BA2, CB, BW, BD and GY. This same region is flanked by root related gene *Rtcs*, which were previously associated with *rootless concerning crown and seminal roots* [3]. On chromosome 3, a consensus QTL (cQTL) was identified between 101.98 at 157.64 Mbp, weighing 52%, and flanked by SNP PZA02044-1. QTLs for SD, BNT, PUE, PAE and GY were mapped in this region. On chromosome 7, a cQTL was identified, weighing 31%, flanked by markers PZA01946/dupssr09 at 123.60/149.71 Mbp. QTLs for BA2, PUE and PAE were identified in this region. These commons regions can be explored in future works to identify genes related with P use efficiency in maize.

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References

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CERTIFICADO

Certifico que o trabalho “**Co-localization of QTLs for root traits, P efficiency indexes and grain yield in maize under low-P soil.**”, tendo como autores, *Flavia Ferreira Mendes, Isabel Regina Prazeres de Souza, Paulo César Magalhães, Lauro José Moreira Guimarães, Sylvia Moraes de Sousa, Sidney Netto Parentoni, Claudia Teixeira Guimarães*, foi apresentado no 6º Congresso Brasileiro de Biotecnologia, realizado de 09 a 13 de novembro de 2015, em Brasília/DF.



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