www.sbg.org.br - ISBN 978-85-89109-06-2

Root system variation among maize inbred lines grown under differential phosphorus levels

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Keywords: P efficiency, diversity, root traits, P efficiency, phenotype

Phosphorus (P) is one of the most important nutrients for plant growth and development. Changes in root morphology are particularly important to increase P uptake in plants due to low mobility of this nutrient in the soil. One promising approach to help overcoming P deficiency in tropical soils is to explore the diversity in root morphology. This study aimed to analyze maize root traits that could be involved in P acquisition efficiency. We used a paper pouch system with Magnavaca's nutrient solution (low P - 2.5 µM and high P - 250µM) under a controlled environment to evaluate root traits (total length, total surface area, average diameter and surface area of roots with diameter between 0-1, 1-2, >2 mm) and root and shoot dry weight. The 182 inbred lines from Embrapa Maize and Sorghum collection were analyzed in a completely randomized experimental design with three biological replicates, each one composed of three plants per pouch. High heritability and low coefficient of variation were detected for the majority of the analyzed traits in both conditions, except for root surface area with diameter between 1-2 mm and root dry weight. There was a significant difference among genotypes and treatments considering all traits. Interactions between genotype and P concentration were significant for total root surface area and root dry weight. Overall, genotypes under low P condition presented lower values for all traits compared to those grown under high P condition. Root average diameter showed a significant negative correlation with most of the root traits that were evaluated. All root traits, except for root diameter, presented high phenotypic correlations with each other and with total dry weight, suggesting a proportional advantage of increasing shoot dry mass by the enhancement on root dry mass. We concluded that the maize collection presented morphological diversity concerning all analyzed traits and these phenotypic results will be used in the discovery of root morphology related genomic regions/genes that are involved on P acquisition efficiency in maize.

Financial support: Embrapa, CNPq, Fapemig and Generation Challenge Program (GCP).