

Morphological characterization of two sorghum diversity panels grown in nutrient solution with low phosphorus

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Phosphorus (P) is an essential macronutrient for plants and its acquisition relies on plant root system. In arable land, P is one of the most unavailable macronutrients and frequently limits plant growth, limiting the productivity of crop plants. Therefore, a better understanding of how plants respond to P starvation is necessary to breed crop varieties with enhanced P use efficiency. This study aimed to analyze root traits related to P acquisition efficiency in two sorghum panels, Sorghum Association Panel Subset (SAP), composed of both tropical convert and breeding accessions and the CIRAD Panel, totaling 479 genotypes. Sorghum seeds were germinated for four days on germination rolls and then placed in a paper pouch system with modified Magnavaca nutrient solution (P - 2.5 mM) in controlled conditions. After 13 days, root images were captured using a digital photography setup and analyzed using both RootReader2D program and WinRHIZO software. Root and shoot were dried separately at 65 °C in a forced-air oven until constant weight was obtained. Total root length was highly correlated with all traits, except with root diameter and root:shoot. These suggests that greater root area combined with smaller root diameter contributed to enhanced biomass accumulation. Low coefficient of variation (6.0 - 25.2%) and medium to high heritability (31.6 - 82.1%) was found for all root traits analyzed (total root length, average root diameter, total root volume and volume of fine roots) in both panels. Principal Component Analysis (PCA) was able to differentiate contrasting sorghum lines based in the selected root traits (total root length, average root diameter, total root volume and volume of fine roots) and dry weight (root, shoot, total and root:shoot). The first principal component (PC1) explained 61% while the second principal component (PC2) explained 32% of the phenotypic variation. These data will give support to association analysis in order to identify candidate genes related to root morphology and P acquisition efficiency in sorghum.

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