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Phenotypes and genes associated with root traits to search for phosphorus acquisition efficiency in maize

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Phosphorus (P) is an essential nutrient to plants and is acquired as inorganic phosphate from the rhizosphere solution. P is one of the least available nutrients particularly in highly weathered, tropical soils, limiting substantially plant growth. An interesting approach to circumvent P deficiency in tropical areas is to explore the genetic diversity available in plants to breed cultivars more efficient in P acquisition. It has been shown that root traits, such as root length and volume, are important to determine if a genotype is P efficient. This study aimed to study root traits that could be involved with P acquisition efficiency and to identify candidate genes with an expression profile consistent with a possible role in root morphology. Field phenotyping results under low and high P conditions enabled us to define two contrasting genotypes for P acquisition efficiency that were used for root traits studies. We standardized the nutrient solution conditions in order to find the best phenotyping parameters for root early screening. Root traits presented overall a high heritability and a low coefficient variation. Also, out of 24 root traits analyzed, 10 presented a correlation above 0.9.These results together with PCA allowed us identify four root traits which adequately represent the variation observed among genotypes. The information described in this study is important for designing early selection strategies for P efficiency in maize, which are needed to support advanced molecular and physiological studies.

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Precision phenotyping gray leaf spot disease using real-time PCR and digital image analysis

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Gray Leaf Spot (GLS) disease of maize is caused by either of two fungal species *Cercospora zeae-maydis* or *Cercospora zeina*. Whole plant phenotyping is currently used to score for resistance to GLS in the field, however methods were lacking for precision phenotyping in glasshouse trials or field screens for quantitative resistance. We developed a specific and sensitive real-time PCR assay for determining the amount of Cercospora DNA relative to maize DNA in a diseased leaf, which is effective for both species of Cercospora. In addition we quantified GLS lesion area by digital image processing of leaf photographs using ASSESS 2.7 software. The methods were validated in glasshouse samples as well as field samples of two maize lines differing in resistance to GLS based on whole plant phenotyping. The amounts of Cercospora DNA within leaves of the susceptible and resistant inbred lines were significantly different (*T*-test, $p<0.001$). The amount of Cercospora DNA detected by the real-time PCR assay correlated well with calculated lesion area (Pearson correlation coefficient = 0.8). These assays will be useful for both basic research into understanding the GLS-maize pathosystem, as well as breeding programmes.

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