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Depth and vertical distribution of roots in tropical maize inbred lines

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ABSTRACT

We need a better understanding about the distribution of roots in soil and the genetic variation available to alter this distribution. There is evidence that root traits are indirectly selected by breeders. For example, indirect selection for a deeper root system may improve drought avoidance (Hund et al., 2009) and even be related to historic yield increase (Hammer et al., 2009) in maize. We investigated a diverse panel of 33 tropical maize inbred lines for basic root characteristics. Leaf area increments did not increase beyond root elongation rates above 200 cm d^{-1}. Genotypes were separated into those with a relatively deep or shallow root system given their leaf area. This knowledge may be utilized to select model genotypes for the mapping of quantitative trait loci (see posters of Hund et al. and Reimer et al.) and for simulation studies (poster of Herter et al.).

METHODS

The target traits assessed using the panel of inbred lines were the temporal development of the leaf area and the vertical distribution of the roots. Roots, grown in 40 to 80-cm growth columns, were destructively sampled at 8 different depths when 2-, 4- and 6-leaves were fully developed. Root lengths in these sections were measured using the methylene-blue staining method (Sattelmacher et al., 1982): roots were stained, the dye was removed in $CaCl_2$ solution and the solution’s color intensity was measured. Obtained intensities were calibrated using subsamples additionally scanned and analyzed digitally (Figure 1). Three basic characteristics were used to describe the root system: i) root length, ii) rooting depth, i.e. the depth above which 95 % of the roots were located (D_{95}) and iii) root system shape, i.e. the proportion of deep roots (DR) below $D_{95}/2$ (Figure 1).

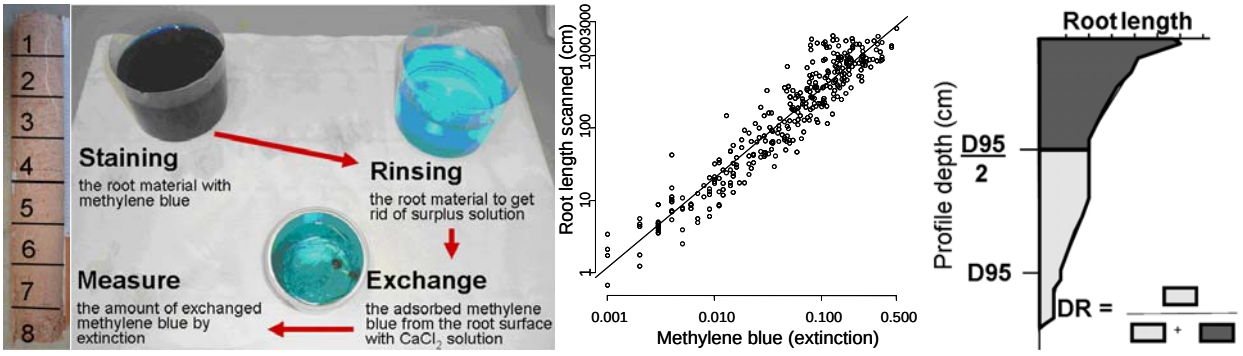

Figure 1. Methylene-blue staining to estimate root length in each column section (left), calibrated using root lengths measured by WinRhizo© (middle) and summarized as overall root length, rooting depths (D_{95}), and the proportion of deep roots (DR)(right).

RESULTS AND DISCUSSION

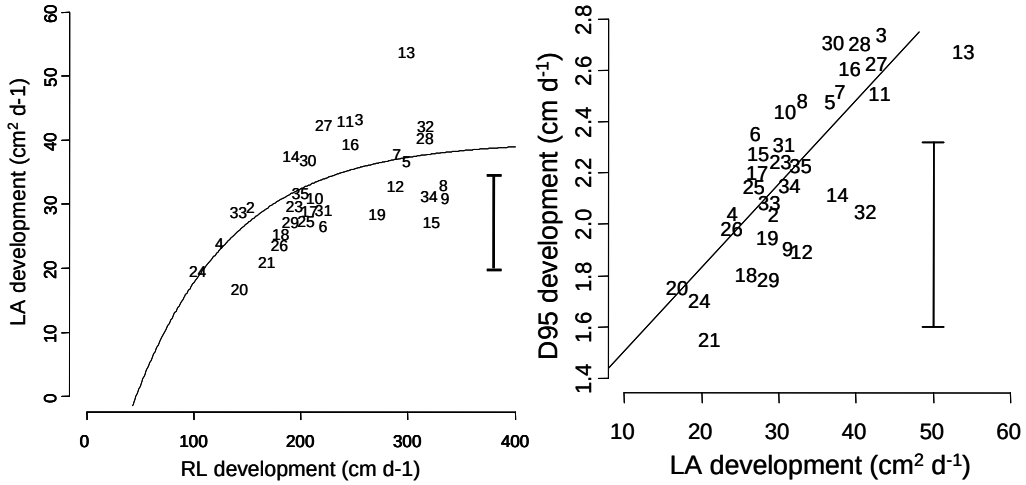

Figure 2. Increment of leaf area (LA) in dependency of the development of root length (RL) between the 2-leaf and the 6-leaf stage (left); rooting depth (D_{95}) in dependence of the increment in leaf area (LA)(right). Numbers indicate different genotypes. Vertical bars indicate the least significant difference.

Staining saved up to 50% of the time needed for the analysis of root length compared to scanning. The leaf-area growth rates increased asymptotically with root elongation rates: above elongation rates of ~200 cm d^{-1}, the leaf area did not increase further (Figure 2, left). Possible causes of this stagnation with increasing root length are elevated respiratory costs and inter-root competition, both reducing the benefits of a better nutrient uptake. By contrast, the leaf-area increment increased linearly with the D_{95} increments (R^2 = 0.6; Figure 2, right). Thus larger plants had deeper roots. However, genotypes positively or negatively deviating from the regression line were respectively classified as deep and shallow rooting, given a certain leaf area. Next, we aim to combine our data with those of our Generation-Challenge Programme partners at CIMMYT (Mexico), INRA (France) and KARI (Kenia) to elucidate if the root characteristics are predictive for the genotypes’ development under drought in the field.

REFERENCES

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