

PROJECT TITLE

Dissecting components of early plant development in maize

CONSORTIUM

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SUMMARY OF THE REPORT

Selection for accelerated early plant development in maize can increase final biomass yield, improve resource efficiency, preserve soil fertility and reduce the requirement for herbicide treatment. Today's elite germplasm shows only limited genetic variation for early development. For broadening the genetic basis of elite germplasm, introgression of favourable alleles from landraces has been proposed (Sood et al. 2014). We generated doubled-haploid (DH) lines from three pre-selected European Flint maize landraces and evaluated them for early growth and biomass yield in up to 11 field environments as lines per se and/or testcrosses (Hölker et al. 2019; Mayer et al. 2020). The field evaluations indicated that different early development measures, such as early vigour scores and early plant height, target different trait components and correlations with final plant height and biomass yield varied in magnitude.

The present project aimed to dissect early development traits into their genetic components using the phenotyping platform PhenoArch (<https://www6.montpellier.inra.fr/lepse/M3P>; Cabrera-Bosquet et al. 2016). Based on daily RGB imaging, the PhenoArch platform provides high precision phenotypes at high temporal resolution, which cannot be obtained in field trials. A total of 414 DH lines derived from two landraces (plus six checks) and 94 testcrosses (plus six commercial hybrids), with 3 replicates per entry, were evaluated for traits related to plant growth, plant architecture, and radiation use efficiency during plant development up to 11-13 visible leaves. Preliminary analyses revealed high data quality with heritabilities for leaf area, plant height and biomass ranging between 0.60 and 0.85 depending on the measuring time point. The DH lines showed high genetic variability for the traits assessed, as exemplarily shown for leaf area in Figure 1. Part of the testcrosses outperformed commercial hybrids with for example only one hybrid check ranking among the best 20% of leaf area towards the end of the experiment (Figure 2). Traits measured in the platform showed significant positive genetic correlations with early development measures in the field, ranging between 0.25 and 0.7.

The project was successful in generating high quality phenotypic data, providing an ideal basis for i) characterizing genomic regions associated with components of vegetative development and identifying novel favorable haplotypes not present in elite germplasm, ii) advancing genome-based prediction models for vegetative development traits in landrace derived material iii) determining the relevance of individual trait components for increasing final biomass yield and iv) choosing crossing partners for pre-breeding to generate transgressive segregation.



