Traits measured in a phenotyping platform account differentially for the genetic variability of yield under heat and drought scenarios

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**Context**

Phenomics allows dissection of the genetic variability of adaptation traits to environmental cues. We tested to what extent quantitative traits measured in a phenotyping platform or in genomics installations account for yield measured in diverse environmental scenarios of a multi-site field experiment.

**Experiments**

4 experiments with 2 watering treatments

29 Field experiments

**Traits estimated in the phenotyping platform**

Plant Architecture

Plant Growth

Response of growth to SWP

Stomatal conductance

Aquaporins expression

**Genetic architecture of traits**

Single trait GWAS was performed over all the set of traits under 2 contrasting scenarios, which allowed the unveil of their genetic architecture. From the field network, clustered in environmental scenarios, several scenario-dependent QTLs for grain yield (GY) were discovered.

**Conclusions & Perspectives**

A large proportion of the genetic variance of yield was accounted for by QTLs of traits measured in controlled conditions. Relevant traits differed between environmental scenarios. These results provide insights for understanding the genetic basis of drought tolerance and for designing maize plants adapted to specific drought-prone scenarios.

**QTLs of traits account for yield in scenarios**

A - Grain yield in water deficit - hot colocalizes with response in the platform and PIPs, which reflects in the proportion of genetic variance explained by these QTLs

B - Grain yield in well-watered conditions colocalizes with plant growth and architecture

25 to 40% of the phenotypic variance of grain yield in most represented scenarios were accounted for by allelic effects of traits or transcripts in the platform

**Identification of colocation between platform traits and Grain yield QTLs**

QTLs were defined based on a confidence interval of 0.1 cM for the significant SNP

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