

Genetic analysis of yield in drought-prone areas with a scenario-dependent probabilistic approach

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Yield results from month-long feedback processes, whereas mechanisms of drought response operate over minutes following changes in transpiration demand. Evolution has constrained these mechanisms into strategies for stabilizing the water status of leaves and reproductive organs in rapidly varying environmental conditions. These constraints differ from those maximizing yield because of trade-offs between carbon accumulation and the risk of deleterious plant water status. Breeders successfully selected for high and stable yield across environments, including dry environments, but in doing so they selected for constitutive traits. An analysis of the genetic progress showed that the allelic diversity that governs drought acclimation was left largely unexploited because it results in positive or negative effects on yield depending on drought scenarios. We propose a probabilistic approach where the benefits and risks of alleles combinations are estimated for the most likely drought scenarios in each region, under current or future climates. Integrating phenomics, modeling and genomic prediction allowed us to identify the combinations of alleles with positive effects on yield in each drought scenario. For this, we identified traits genetically linked to yield in each scenario with experiments in phenotyping platforms and field networks. One third of the yield variance in a given environmental scenario was accounted for by QTLs of traits measured in phenotyping platforms that co-located with yield QTLs. We converted these traits into model parameters, which were in turn predicted based on allelic values for new genotypes, and allowed yield prediction in 100s fields. This strategy may allow exploiting new alleles for yield in dry regions by explicitly taking into account those alleles that optimize adaptive responses in expected environmental scenarios for each region.

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