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W1 : Abiotic Stress

Deciphering Drought Genomics: Integrating Rice And Maize Phenotype Data On The Rice Genome Backbone

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We have used a comparative genomic approach to identify breeding targets for drought resilience in rice and maize. We aligned to a rice genome assembly 503 QTLs for fifty-six traits including measures of most aspects of plant growth and economic yield and its components, root characteristics, and several measures of plant water status. Similarly, 452 consensus positions of multiple QTLs for six measures of maize growth and productivity under water stress were aligned to the maize IBM2N genetic map, which in turn was aligned to the rice genome assembly. One finding to be presented is that quantitative trait loci (QTLs) for drought response seldom correspond in rice and maize. These data suggest that genes underlying drought resilience may not be translatable between grass taxa.