



# Exploring QTLxE in a network of fields: identification of QTLs associated with scenarios of heat and drought for predicting yields in future climates

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## Elaborating a unique regulon for rice yield under drought: component genes underpin or are affected by transcriptional, post-translational, biochemical and epigenetic mechanisms

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A limited number of regulons have been characterized in the eukaryotes. Similarly, limited information exists on characterization of large-effect QTLs (LEQ). We recently suggested that an LEQ for rice yield under drought was composed of multiple genes that were necessary for its full impact, and which functioned in a manner similar to that of a regulon. Here we report characterization of four of the nine essential genes at this locus. Each of the four genes highlights a separate component of the complex panoply of regulatory mechanisms at play in response to drought stress. One of the genes is a transcription factor. It regulates two downstream target genes in *cis*. One, an amidohydrolase, modulates the epigenome, and other, a phosphodiesterase, affects critical biochemical components in the reproductive organs. The fourth gene, a kinase, potentially affects transcrip-

tional splice variants. In parallel, the transcription factor is differentially SUMOylated under drought and this post-translational modification potentially alters the genes regulated by the transcription factor. Transcriptomics, proteomics and metabolomics-mediated analyses of a near isogenic line (NIL) containing the LEQ reveal novel features and present a holistic overview, captured by its unique regulon like gene content, on the plants' response to drought stress. The LEQ is already part of rice varieties released for drought tolerance. Dissection of the molecular mechanisms in breeding lines generated through molecular genetics is useful because markers/genes can be easily tracked. The molecular genetics and molecular biology interface generates field-relevant, and gene and/or mechanism-based data that is robust and dependable for other varieties/crops.

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Genetic analysis of tolerance to climate change is hampered by climatic variability that generates GxE interactions depending on the timing and intensity of water or heat stresses. We have performed a genome-wide analysis of yield in 29 fields over Europe, with irrigated and rainfed treatments in each location. Six scenarios of heat and drought were first identified by clustering observations over 60 European sites x 35 years. A detailed environmental characterisation was carried out in all experiments, which were ascribed to environmental scenarios. A panel of 244 maize hybrids genotyped with 832K polymorphic SNPs was analysed in these experiments, together with a characterization of phenology in a phenotyping platform. We have first identified by GWAS genomic regions (QTLs) associated with grain yield. Nearly all QTLs had scenario-dependent

allelic effects, with positive, negative or null effects depending on heat/drought scenarios. Second, by combining information coming from the field and the platform, we have estimated the responses of yield components to environmental conditions via regression analysis over the whole dataset. We have identified in this way massive effects of temperature and water deficit at flowering time, and of intercepted light during the vegetative stage. The slopes of these responses largely differed between hybrids and were dissected into QTLs. A model combining environmental conditions with QTL of responses accounted for 72% of the variance of yield, including in eight new experiments. This work, therefore, allows prediction of genotypes to cope with climate changes. (Millet et al 2016, *Plant Physiology* 172:1).