Enhancing Resistance To Combined Stresses by Exploiting Shared Intergenic Regulatory Elements In Rice

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Abstract

Tolerance in crop plants to stresses (*e.g.* heat and disease) involves changes in expression patterns of numerous genes. These changes are controlled by short sequences in promoter areas, specifically *cis*-regulatory elements (CRE) or combinations of CRE organized as modules (*cis*-regulatory modules or CRM). Evidence shows that conserved CRE and CRM are found in promoters of many genes that are co-activated by a single stress, or that they are common to genes co-activated by multiple stresses. We conducted meta-analyzes using publicly available data testing rice responses to diverse pathogens and high temperatures with the goal of identifying genes involved in responses to both conditions. From these, co-expression clusters were identified showing enrichment for genes involved in single or combined stress responses. Analysis of promoter sequences for all these genes from multiple rice genetic backgrounds identified multiple CREs associated with defense responses (DR) and/or thermotolerance, and assembly of CRMs is currently underway. Simultaneously, a rice diversity panel was tested for tolerance to high-night temperatures and immune responses against the multiple pathogens under controlled conditions. We identified ten lines ranging from high-, medium, to low-tolerance to the tested conditions and are currently conducting intermated crosses with elite breeding lines to generate enhanced varieties. Moreover, molecular markers based on the genetic diversity associated to the identified CRE/CRMs were generated and are being validated in the selected rice germplasm. Our goal is to enable genome-wide selection of complex traits governed by multiple genes with a reduced number of markers based on shared stress related CRE/CRMs.