

Phenotypic and transcriptomic response of diverse rice accessions to transient heat stress during early grain development

Anil Kumar Nalini Chandran¹, Puneet Paul¹, Balpreet K. Dhatt¹, Jaspreet Sandhu¹, Larissa Irvin¹, Shohei Oguro¹, Yu Shi², Chi Zhang^{2,3} Harkamal Walia^{1,3*}

¹Department of Agronomy and Horticulture, University of Nebraska, Lincoln, NE, 68583, USA

²Department of Biological Science, University of Nebraska, Lincoln, NE, 68588, USA

³Center for Plant Science Innovation, University of Nebraska, Lincoln, NE, 68588, USA

Correspondence: hwalia2@unl.edu

Abstract

Heat stress (HS) occurring during the grain-filling period has a detrimental effect on grain yield and quality in rice (*Oryza sativa*). The development of heat-resilient cultivars could partly solve this issue if tolerant alleles can be identified and incorporated into the germplasm. In this study, we posit that some of the phenotypic variation for heat resilience during grain development could be due to variations in gene expression among accessions. To test this, we characterized the HS response of 10 diverse rice accessions from three major sub-populations using physiological and transcriptomic analyses. At a single grain level, grain width and grain thickness emerged as the most heat-sensitive traits. During a transient HS, IND-3 was categorized as highly sensitive, while five accessions exhibited moderate heat sensitivity, and four accessions were tolerant. Only a core set of 29.4% of the differentially expressed genes was common to the three rice sub-populations. Heat-tolerant accession, TEJ-5 uniquely triggered an unfolded protein response (UPR) under HS, as evident from the induction of *OsbZIP50* and downstream UPR genes. *OsbZIP58*, a gene that positively regulates grain-filling was more highly induced by HS in IND-2 despite it being moderately heat-sensitive. Collectively, our analysis suggests that both unique gene expression responses and variation in the level of responses for a given pathway distinguish diverse accessions. Only some of these responses associate with single grain phenotypes in a manner consistent with the known roles of these genes and pathways.

Keywords: *Oryza sativa*, heat stress, transcriptome, grain development, unfolded protein response