

Public Abstract

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Title:A comprehensive, systems-biology analysis of the response of soybean root hairs and stripped roots to heat stress

Heat stress is likely to be a key factor in the negative impact of climate change on crop production. Heat stress significantly influences the functions of roots, which provide support, water and nutrients to other plant organs. Likewise, roots play an important role in the establishment of symbiotic associations with different microorganisms. Despite the physiological relevance of roots, few studies have examined their response to heat stress. In this study, we performed a comprehensive systems-biology analysis of the response of soybean root hairs and stripped roots to heat stress. The analysis include a genome-wide transcriptomic, proteomic and metabolomic analyses on isolated root hairs, which are a single, epidermal cell type, and compared their response to whole roots. We identified 2,013 genes differentially regulated in root hairs in response to heat stress. Our gene regulatory module analysis identified ten key modules that controlled the majority of the transcriptional response to heat stress. We also conducted proteomic analysis on membrane fractions isolated from roots and root hairs. These experiments identified a variety of proteins whose expression changed within 3 hours of application of heat stress. Most of these proteins were predicted to play a significant role in thermo-tolerance, as well as in chromatin remodeling and post-transcriptional regulation. The metabolomic analysis identified that heat stress alters the metabolic profile of soybean root hairs. In the current study, we observe the accumulation of amino acids and carbohydrates which is a common defense mechanism that plants employ to cope with heat stress. The data presented represent an in-depth analysis of the heat stress response of a single cell type in soybean.