

Understanding the natural variation in heat stress response in Pigeonpea and crop wild relatives through time-series transcriptome analysis

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Abstract

As the temperatures are projected to increase across the world due to global warming, heat stress (HS) is a major concern for all crop plants. We report here, a time-series transcriptome analysis of one Pigeonpea cultivar (*Cajanus cajan*) and two Crop Wild Relatives (CWRs), *Cajanus acutifolius* and *Cajanus scarabaeoides* under heat stress (HS) at $42\pm 2^{\circ}\text{C}$. A total of 9521, 12447, 5282 transcripts were identified to be differentially expressed in *C. cajan*, *C. acutifolius* and *C. scarabaeoides* respectively. In this study, we also examined alternative splicing (AS) during HS and revealed that a significant number of DEGs undergo AS in a species-specific pattern. Both transcriptome and qRT-PCR analysis showed that the HS caused the down-regulation of photosynthetically important genes such as Curvature Thylakoid protein, RuBisCO small chain, and NDH complex subunit; fatty acid modulating genes and up-regulation of defense mechanisms such as expression of HSPs and anti-oxidant enzymes in all *Cajanus* species. The results of histochemical assay showed higher lipid peroxidation in *C. acutifolius* inferring the presence of high quantity of PUFA in the plasma membrane which might have led to severe damage of membrane-bound organelles like chloroplast during HS, coupled by high electrolyte leakage during HS.

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