

# Transcriptomic temperature stress responses show differentiation between biomes for diverse plants

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## Abstract

Plants are foundational to terrestrial ecosystems and because they are sessile, are particularly reliant on physiological plasticity to respond to weather extremes. However, diversity in molecular or transcriptomic responses to temperature extremes is not well described across plants from contrasting environments. Beyond molecular responses, photosystem II (PSII) thermal tolerance traits are widely used to assay plant thermal tolerance. To explore options for improving the prediction of thermal tolerance capacity we investigated variation in the transcriptomic stress responses of 20 native Australian plants species from varied environments, using de novo transcriptome assemblies and 188 RNA-seq libraries. We documented gene expression responses for biological processes, to both hot and cold temperature treatments, that were consistent with transcriptomic stress responses seen in model species. The magnitude of some responses showed differentiation between the species from contrasting arid, alpine and temperate biomes. This variation among biomes indicated that post heat exposure, alpine and temperate species had greater shifts in expression than arid species. Changes in the median expression of biological processes were also compared to plasticity in PSII heat and cold tolerance traits. Gene expression responses showed some expected relationships with PSII thermal tolerance plasticity, but these two response types appeared to be mostly independent. Our findings demonstrate the potential for using conserved gene expression plasticity to characterize the sensitivity or capacity of plants from diverse taxa to respond to temperature extremes. The varied combinations of molecular and physiological responses of plants to temperature stimuli could help define successful strategies under future climates.

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