

## Drought responsive gene expression regulatory divergence between upland and lowland ecotypes of a perennial C4 grass

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### Abstract

© 2016 Lovell et al. Climatic adaptation is an example of a genotype-by-environment interaction (G×E) of fitness. Selection upon gene expression regulatory variation can contribute to adaptive phenotypic diversity; however, surprisingly few studies have examined how genome-wide patterns of gene expression G×E are manifested in response to environmental stress and other selective agents that cause climatic adaptation. Here, we characterize drought-responsive expression divergence between upland (drought-adapted) and lowland (mesic) ecotypes of the perennial C4 grass, *Panicum hallii*, in natural field conditions. Overall, we find that cis-regulatory elements contributed to gene expression divergence across 47% of genes, 7.2% of which exhibit drought-responsive G×E. While less well-represented, we observe 1294 genes (7.8%) with trans effects. Trans-by-environment interactions are weaker and much less common than cis G×E, occurring in only 0.7% of trans-regulated genes. Finally, gene expression heterosis is highly enriched in expression phenotypes with significant G×E. As such, modes of inheritance that drive heterosis, such as dominance or overdominance, may be common among G×E genes. Interestingly, motifs specific to drought-responsive transcription factors are highly enriched in the promoters of genes exhibiting G×E and trans regulation, indicating that expression G×E and heterosis may result from the evolution of transcription factors or their binding sites. *P. hallii* serves as the genomic model for its close relative and emerging biofuel crop, switchgrass (*Panicum virgatum*). Accordingly, the results here not only aid in the discovery of the genetic mechanisms that underlie local adaptation but also provide a foundation to improve switchgrass yield under water-limited conditions.

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