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# The genomic landscape of molecular responses to natural drought stress in *Panicum hallii*

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Environmental stress is a major driver of ecological community dynamics and agricultural productivity. This is especially true for soil water availability, because drought is the greatest abiotic inhibitor of worldwide crop yields. Here, we test the genetic basis of drought responses in the genetic model for C<sub>4</sub> perennial grasses, *Panicum hallii*, through population genomics, field-scale gene-expression (eQTL) analysis, and comparison of two complete genomes. While gene expression networks are dominated by local cis-regulatory elements, we observe three genomic hotspots of unlinked trans-regulatory loci. These regulatory hubs are four times more drought responsive than the genome-wide average. Additionally, cis- and trans-regulatory networks are more likely to have opposing effects than expected under neutral evolution, supporting a strong influence of compensatory evolution and stabilizing selection. These results implicate trans-regulatory evolution as a driver of drought responses and demonstrate the potential for crop improvement in drought-prone regions through modification of gene regulatory networks.

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