

ARTICLE

<https://doi.org/10.1038/s41467-018-07669-x>

OPEN

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

John T. Lovell^{1,2}, Jerry Jenkins¹, David B. Lowry³, Sujan Mamidi¹, Avinash Sreedasyam¹, Xiaoyu Weng², Kerrie Barry⁴, Jason Bonnette², Brandon Campitelli², Chris Daum⁴, Sean P. Gordon^{4,8}, Billie A. Gould³, Albina Khasanova², Anna Lipzen⁴, Alice MacQueen², Juan Diego Palacio-Mejía², Christopher Plott¹, Eugene V. Shakirov^{2,5}, Shengqiang Shu⁴, Yuko Yoshinaga⁴, Matt Zane⁴, Dave Kudrna⁶, Jason D. Talag⁶, Daniel Rokhsar⁷, Jane Grimwood¹, Jeremy Schmutz^{1,4} & Thomas E. Juenger²

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 C₄ 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.

¹Genome Sequencing Center, HudsonAlpha Institute for Biotechnology, Huntsville 35806 AL, USA. ²Department of Integrative Biology, The University of Texas at Austin, Austin 78712 TX, USA. ³Department of Plant Biology, Michigan State University, East Lansing 48824 MI, USA. ⁴Department of Energy, Joint Genome Institute, Walnut Creek 94598 CA, USA. ⁵Institute of Fundamental Medicine and Biology, Kazan Federal University, Kazan 420008, Russia. ⁶Department of Ecology and Evolutionary Biology, University of Arizona, Tucson 85719 AZ, USA. ⁷Department of Molecular and Cell Biology, University of California, Berkeley 94720 CA, USA. ⁸Present address: Zymergen Inc, Emeryville 94608 CA, USA. Correspondence and requests for materials should be addressed to J.T.L. (email: jlovell@hudsonalpha.org) or to J.S. (email: jschmutz@hudsonalpha.org) or to T.E.J. (email: tjuenger@austin.utexas.edu)