

The Genomic Basis of Ecotype Evolution in Switchgrass

Thomas E. Juenger¹, John T. Lovell^{2,3*} (jlovell@hudsonalpha.org), Adam Healey^{2,3}, Shengqiang Shu³, Jason Bonnette¹, Kerrie Barry³, Dan Rohksar³, Jane Grimwood² and Jeremy Schmutz^{2,3}

¹University of Texas, Austin, TX, USA; ²HudsonAlpha Institute for Biotechnology, Huntsville, AL, USA; ³Department of Energy Joint Genome Institute, Berkeley, CA, USA;

Project Goals: Land use change, resource limitation and climate extremes threaten the sustainability of both agricultural and natural ecosystems. In plants, breeding can improve crop resilience to novel stresses, and successful ecological restoration can buffer the effects of ever-shrinking natural habitats; however, these efforts require sufficient knowledge of the traits, genes and environments that underlie productivity and adaptation. Here, we demonstrate how the development of genomic resources in the biofuel crop and widespread tallgrass prairie species, Switchgrass, permits inference of the processes of climate adaptation and definition of genetic loci that underlie climate-dependent growth.

Funding Statement: This research was supported by the US Department of Energy, Office of Science, Office of Biological and Environmental Research Award DESC0014156 to T.E.J. and DE-SC0017883 to D.B.L. Funding was provided by National Science Foundation Plant Genome Research Program Awards IOS0922457 and IOS-1444533 to T.E.J. and NSF/IOS-1402393 to J.T.L. This research was also based upon work supported in part by the Great Lakes Bioenergy Research Center, US Department of Energy, Office of Science, Office of Biological and Environmental Research under Awards DESC0018409 and DE-FC02-07ER64494. The work conducted by the US Department of Energy Joint Genome Institute is supported by the Office of Science of the US Department of Energy under Contract DE-AC02-05CH11231.