Title Genetic analysis of admixture and patterns of introgression in foundation cottonwood trees (Salicaceae) in southwestern Colorado, USA

Tree Genetics and Genomes

Erika I. Hersch-Green1,5, Gerard J. Allan2,3, Thomas G. Whitham3,4

1 Department of Biological Sciences, Michigan Technological University, Houghton MI, 49931, USA

2 Environmental Genetics & Genomics Laboratory, Northern Arizona University, Box 5640, Flagstaff, AZ 86011, USA

3 Department of Biological Sciences, Northern Arizona University, Box 5640, Flagstaff, AZ 86011, USA

4 Merriam-Powell Center for Environmental Research, Flagstaff, AZ 86011, USA

5 Corresponding Author - Email: eherschg@mtu.edu; Telephone: 906-487-3351; Fax: 906-487-3167
Online Resource 6. Individual admixture proportions ($q_i$) for cottonwood trees using the program STRUCTURE v.2.2 (Pritchard et al. 2000; Falush et al. 2003; Falush et al. 2007), as revealed by 10 nuclear microsatellite markers to determine whether “broadleaf” cottonwood trees collected for this study along the San Miguel River in Colorado, USA are most likely P. deltoides or P. fremontii. We included 26 trees from a known population of P. deltoides (collected and genotyped by H. Bothwell), 163 trees from known populations of P. fremontii (collected by S. Ferrier and genotyped by E. Hersch-Green), and 40 trees from the San Miguel. We limited our analysis to two clusters ($K = 2$). Above individuals we list the category from which the individuals belonged to a priori, where A = P. deltoides, B = P. fremontii, and C = unknown “broadleaf” cottonwood trees collected along the San Miguel River, CO, USA.

LITERATURE CITED

