

GENOME-WIDE PATTERNS OF SPECIATION AND INTROGRESSION IN GIBBONS. B. K. Rosenzweig¹ and M. W. Hahn. B. Author², ¹Indiana University, School of Informatics and Computing, Bloomington, Indiana 47408, USA; bkrosenz@indiana.edu, ²Department of Biology, Indiana University, Bloomington, Indiana 47405, USA; mwh@indiana.edu.

Abstract: The evolutionary history of the gibbon lineage is still poorly resolved [1]. While this state of affairs is generally attributed to the apparently rapid radiation of the four gibbon genera [2], phylogenetic reconstruction can also be complicated by introgressive hybridization post-speciation. In this study we first resolve the branching order of gibbon species, and then apply novel genome-wide analyses to localize signals of introgression across the genome. These methods are relevant to the study of speciation in other systems, and our findings provide insight into the broader role played by introgression in local adaptation and reproductive isolation.

References: [1] Carbone, L. et al (2014) *Nature* 513:195–201. [2] Wall, J. D. et al. (2013) *PLoS ONE* 8, e53682.