

Arthropod Communities on Hybrid Cottonwood Hosts Show Unique and Persistent Phylogenetic Patterns

IGERT student team: Karl Jarvis*¹, Anjel Craig¹, and Rebecca Beresic-Perrins¹ Collaborators: Gery Allan*¹, Gina Wimp², Thomas Whitham¹, Catherine Gehring¹, Matthew Zinkgraf¹

¹ Northern Arizona University, ² Georgetown University, * lead authors

INTRODUCTION

We examined the hypothesis that insect and other arthropod communities would differ in their phylogenetic (branching evolutionary) patterns on hybrid cottonwood hosts relative to parental species. Hybrids between narrowleaf (*Populus angustifolia*) and Fremont (*Populus fremontii*) cottonwoods have been shown to have differing arthropod communities than either narrowleaf or Fremont cottonwoods, so we postulated that the arthropod communities on hybrids would also exhibit phylogenetic patterns that differ from those found on narrowleaf and Fremont cottonwoods.

Figure 1. Hybrids between Fremont and narrowleaf cottonwoods

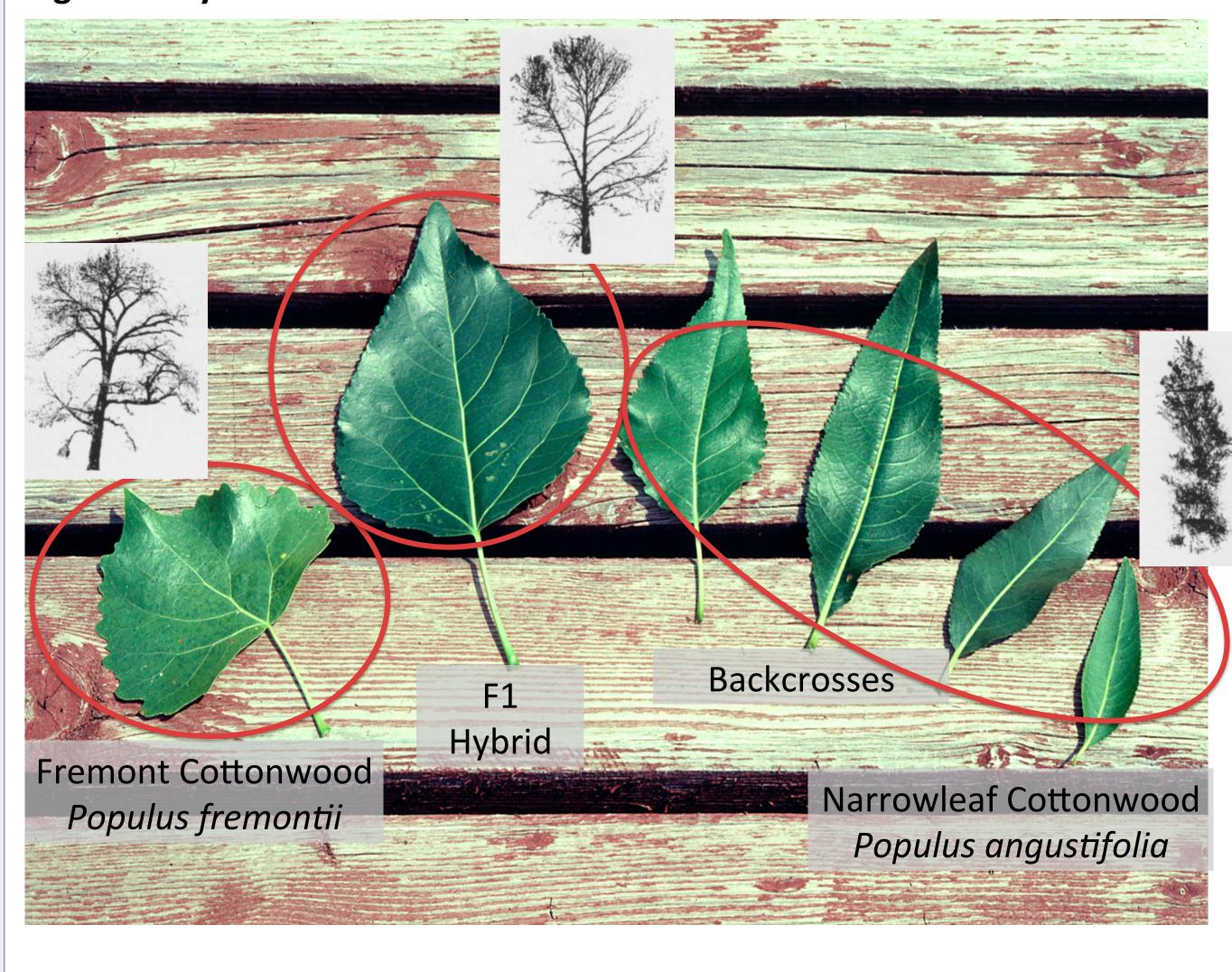


Figure 2a. Communities that are composed of closely related species are considered to be phylogenetically clustered.

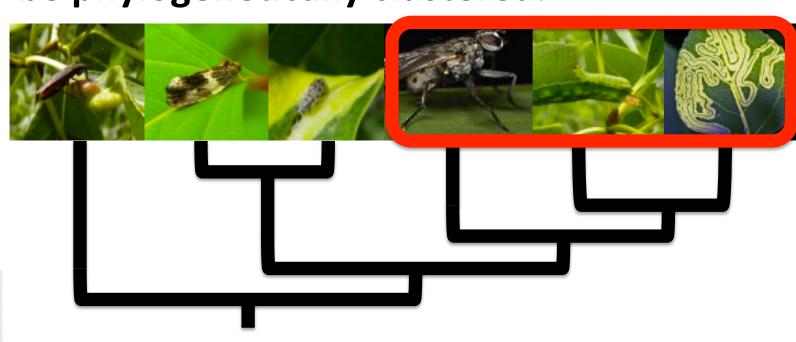


Figure 2b. Communities that are composed of distantly related species are called phylogenetically overdispersed.

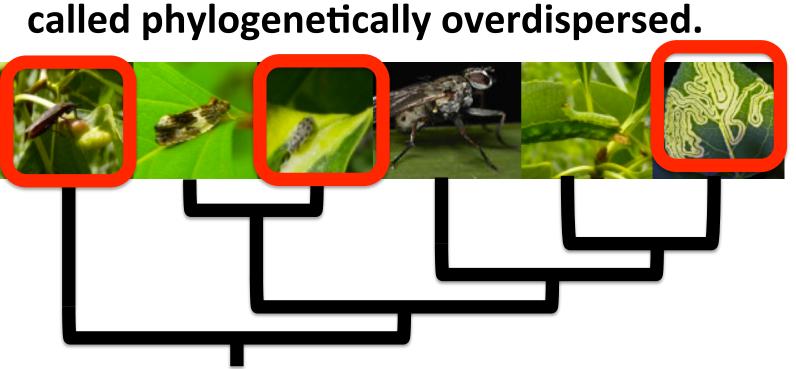


Figure 3. Genetic diversity of cottonwood hosts explains nearly 60% of the variance in arthropod community diversity (Wimp et al. 2004)

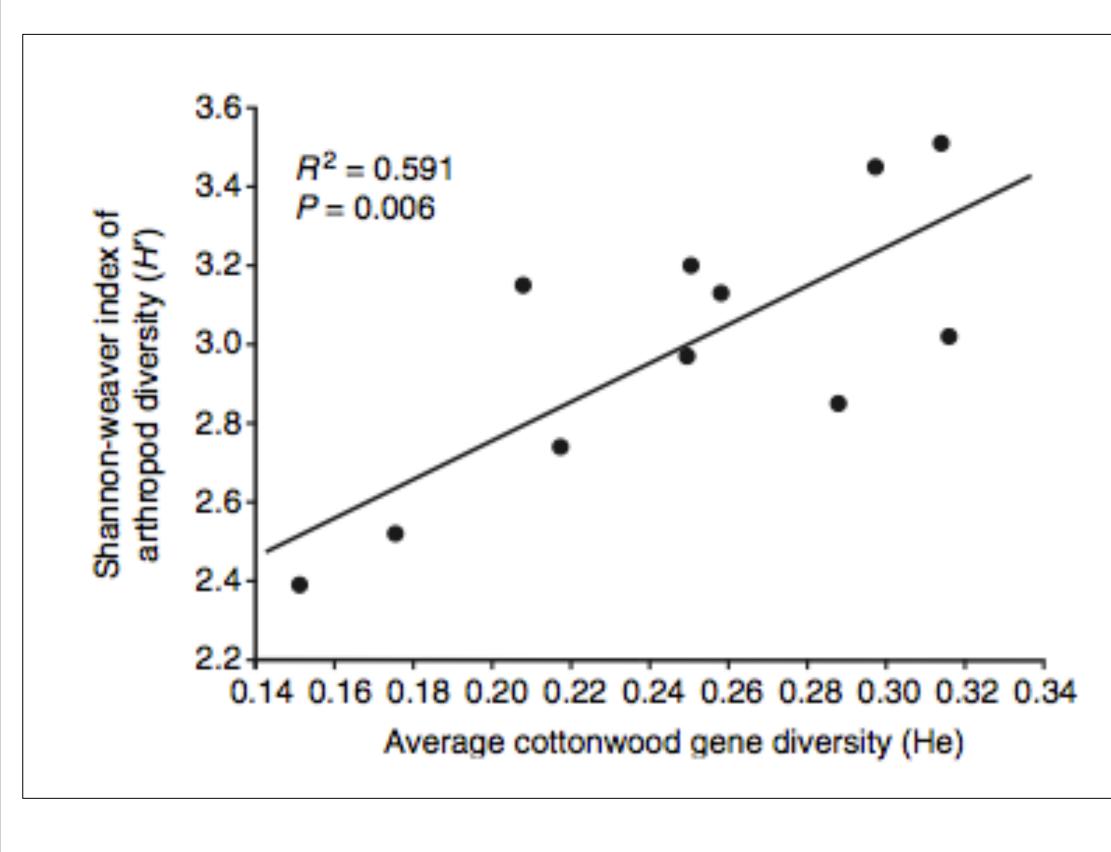
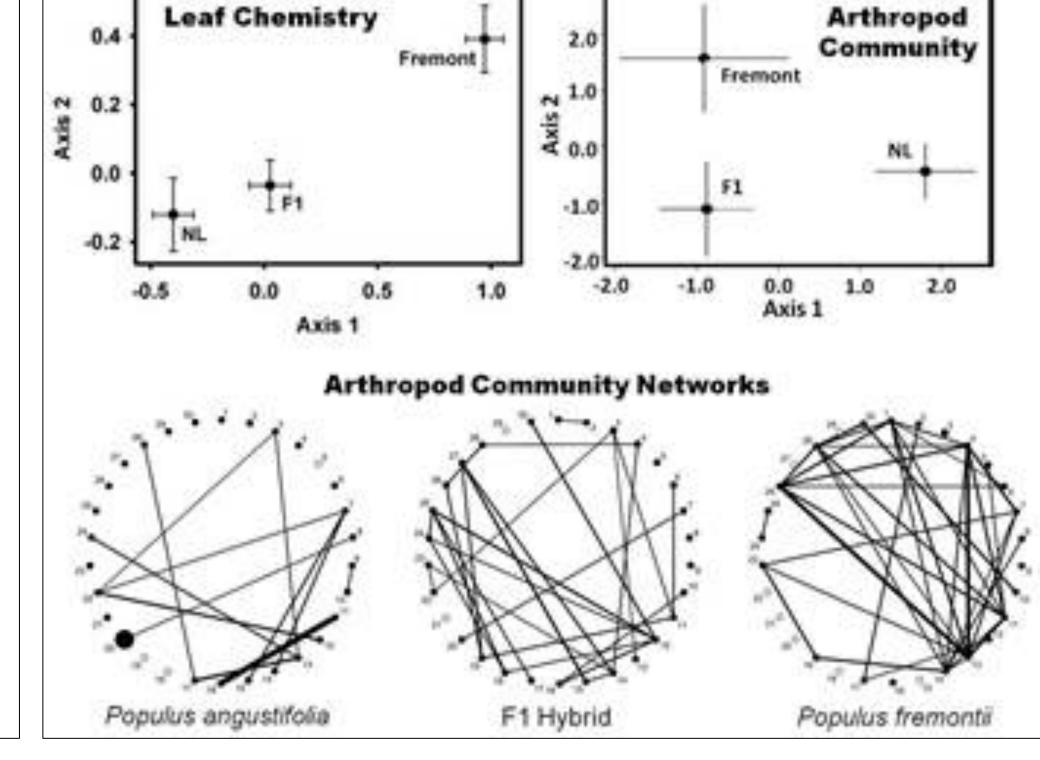


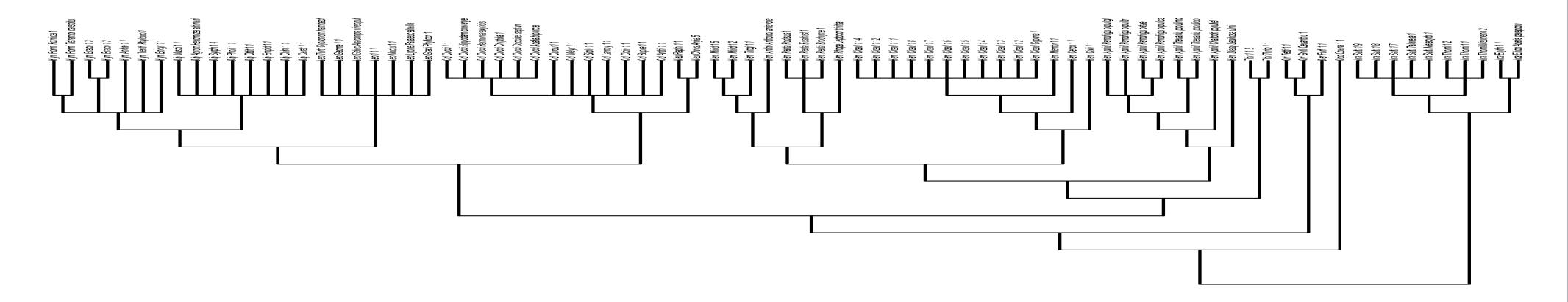
Figure 4. The three host types have unique leaf chemical composition and arthropod communities, and co-occurrence patterns of arthropod communities (Matt Lau unpublished data)



METHODS

We collected community composition and abundance data of arthropods on narrowleaf, Fremont, and hybrid cottonwood hosts growing in a common garden over four years (Wimp et al., 2004). We then assembled a phylogeny of the arthropods we found, based on previous phylogenetic studies (Wheeler et al., 2001). We performed analyses of phylogenetic patterns of the arthropod communities on each individual host tree, as well as on communities pooled by year, host type, and host type within years. These analyses include Phylogenetic Diversity (PD, Faith 1992) and Net Relatedness Index, which measures phylogenetic clustering (NRI, Webb 2002).

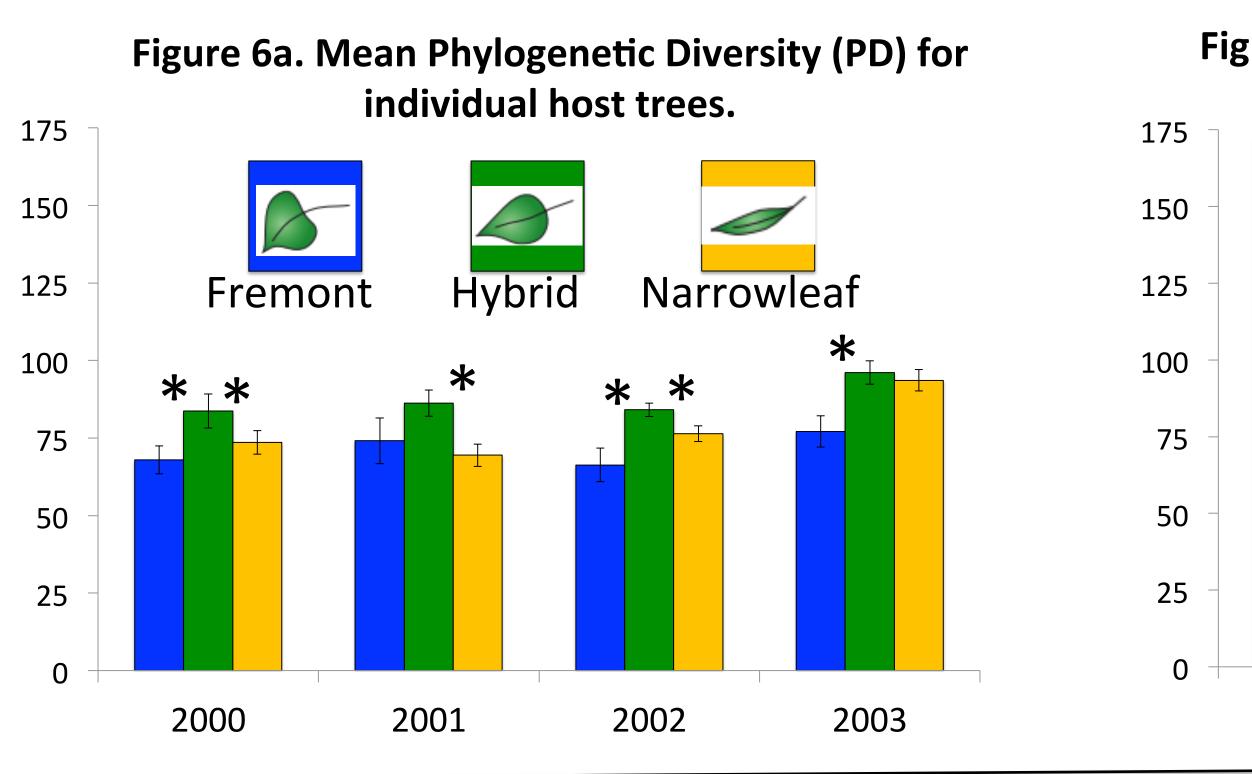
Figure 5. Phylogeny compiled from previous phylogenetic analyses of morphological and molecular data.

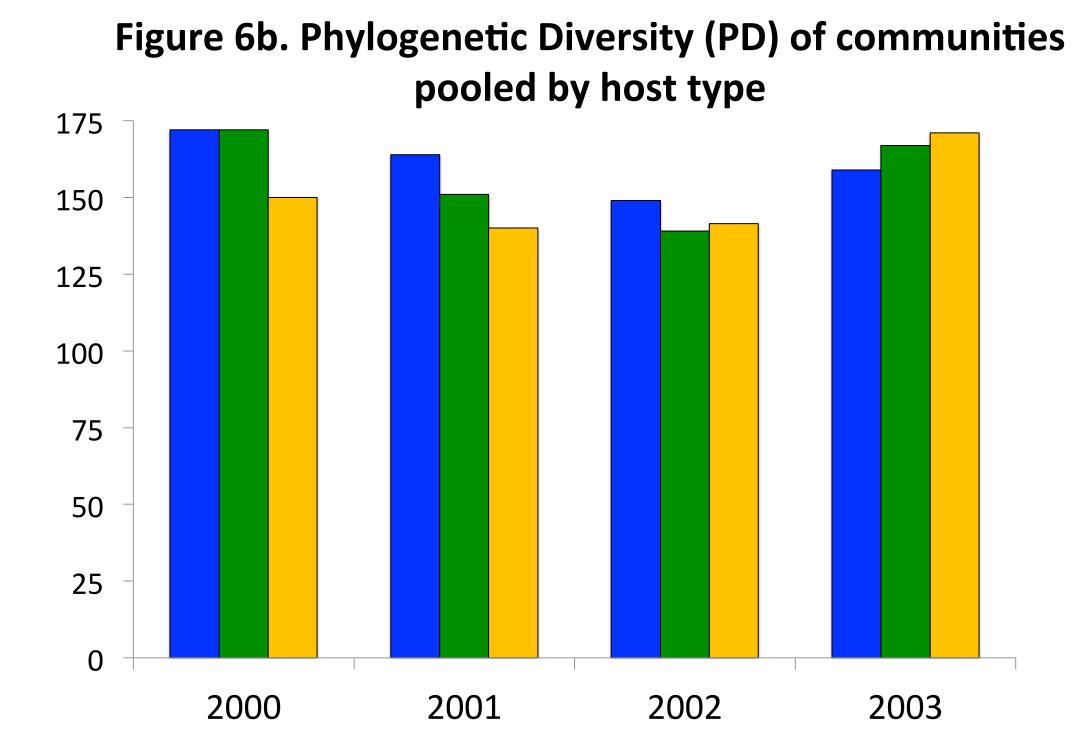


RESULTS

Phylogenetic Diversity (PD) analyses:

- 1) PD of arthropod communities is higher in individual hybrid hosts than in individual hosts of parental species (Fig. 1a), suggesting that hybrid host a greater diversity of arthropods.
- 2) Arthropod communities pooled by host type indicated no such increase in PD in arthropod communities on hybrids (Fig. 1b). This suggests that the high PD in individual hybrid trees is not due to higher PD in the hybrid hosts as a group.

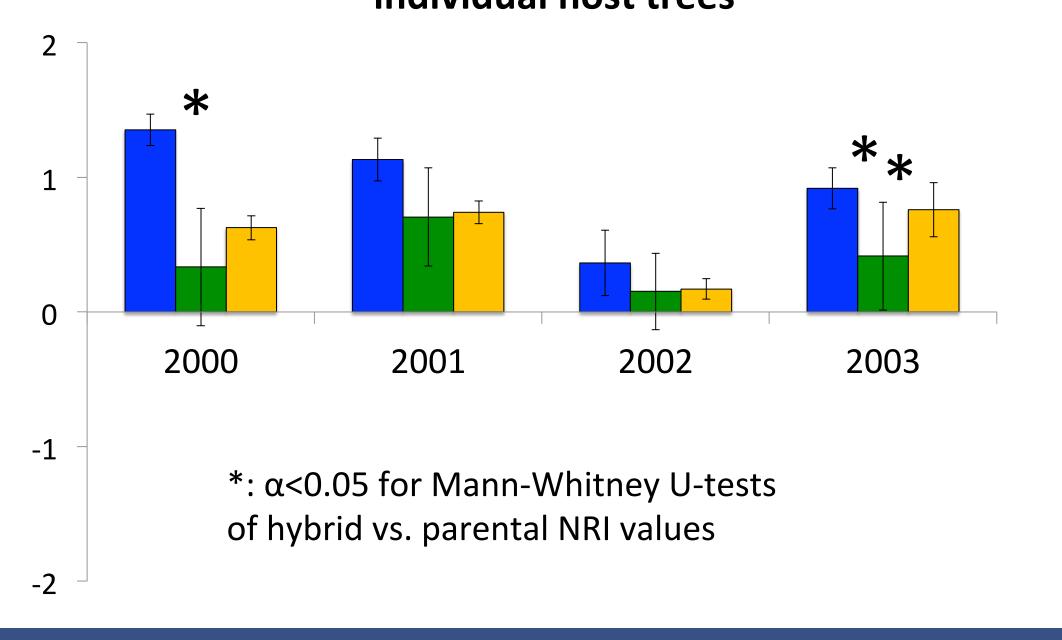


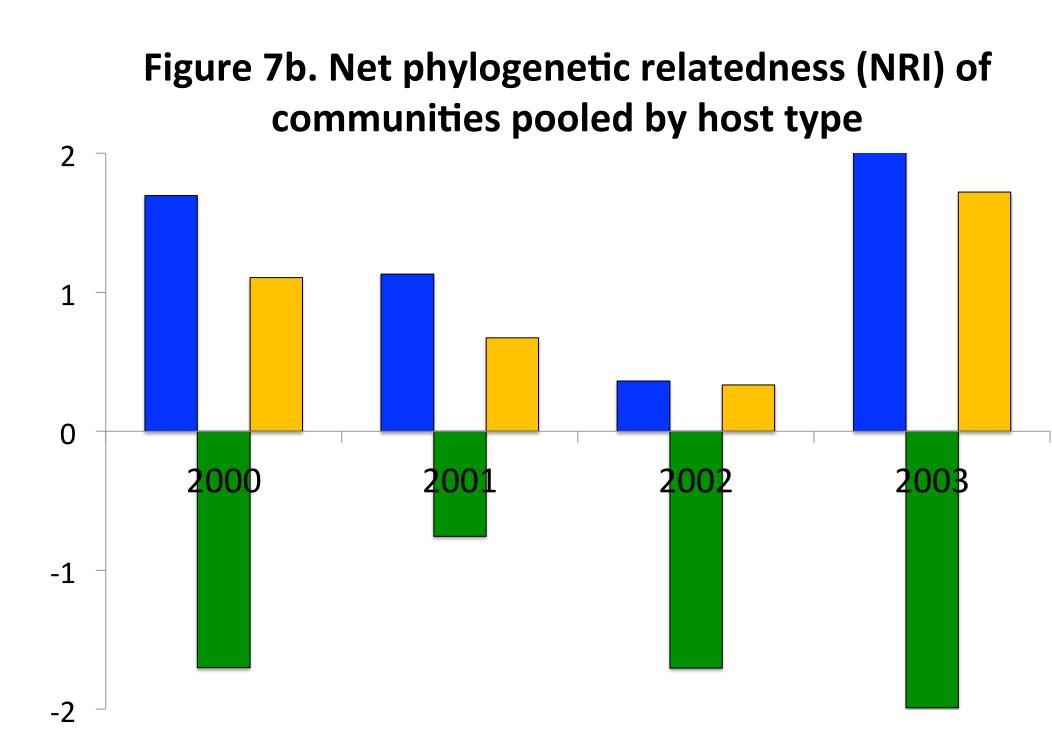


Phylogenetic relatedness (NRI) analyses:

- 1) Arthropod communities on Fremont and narrowleaf hosts are phylogenetically clustered, but arthropod communities on hybrids tend to be less clustered (Fig. 2a), suggesting that parentals host more closely related arthropods.
- Pooled communities of parental hosts are clustered across all four years, but hybrids are phylogenetically overdispersed (Fig. 2b), suggesting that the hybrid trees as a group host a much more diverse community of arthropods than parental hosts.

Figure 7a. Mean net phylogenetic relatedness (NRI) for individual host trees





CONCLUSIONS

Our results indicate that hybrids between Fremont and narrowleaf cottonwoods host a more diverse array of arthropod species, and that hybrids may act as a fundamentally different force in structuring arthropod communities. This suggests that hybrids may play a unique role in the formation of ecological communities, a role that likely extends to entire ecosystems. Ultimately, this supports the consideration of hybrids as evolutionarily significant units of conservation management. Interactions between plants and arthropods are fundamental to all types of ecosystems throughout the world, and hybridization may have a critical but previously ignored role in determining the kinds, amounts, and functions of biodiversity.

REFERENCES

Faith, D. P. 1992. Conservation evaluation and phylogenetic diversity. Biological Conservation 61:1-10.

Kembel, S. W., P. D. Cowan, M. R. Helmus, W. K. Cornwell, H. Morlon, D. D. Ackerly, S. P. Blomberg, and C. O. Webb. 2010. Picante: R tools for integrating phylogenies and ecology. Bioinformatics 26:1463-1464.

Maddison, W. P., and D. R. Maddison. 2010. Mesquite: a modular system for evolutionary analysis 2.74. Retrieved from http://mesquiteproject.org.

Webb, C. O., D. D. Ackerly, M. A. McPeek, and M. J. Donoghue. 2002. Phylogenies and Community Ecology. Annual Review of Ecology and Systematics 33:475-505.

Wheeler, W. C., M. Whiting, Q. D. Wheeler, and J. M. Carpenter. 2001. The Phylogeny of the Extant Hexapod Orders. Cladistics 169:113-169. Whitham, T. G., C. a Gehring, L. J. Lamit, T. Wojtowicz, L. M. Evans, A. R. Keith, and D. S. Smith. 2012. Community specificity: life and afterlife effects of genes. Trends in plant science. In press.

Wimp, G. M., W. P. Young, S. A. Woolbright, G. D. Martinsen, P. Keim, and T. G. Whitham. 2004. Conserving plant genetic diversity for dependent animal communities. Ecology Letters 7:776-780.

ACKNOWLEDGEMENTS

Cottonwood Ecology research group, Merriam Powell Research Center, Art Keith for arthropod images, Steven Shuster, Northern Arizona University NSF IGERT program, Northern Arizona University Biology Department, Northern Arizona University School of Forestry