

The Evolutionary History of Forest Tree Communities: A New Tool for Assessing Forest Health

Kevin M. Potter and Frank H. Koch

Department of Forestry and Environmental Resources, North Carolina State University,
Research Triangle Park, NC 27709; kpotter@ncsu.edu



Pine-fir forest, Plumas National Forest, California



Hardwood forest, Canaan Valley State Park, West Virginia

Introduction

Recent advances in gene sequencing and molecular systematics have vastly improved how well we understand evolutionary relationships among plant species. Phylogenetic “family trees” of species, which are generated using this knowledge, represent a new and promising tool for assessing forest health from an evolutionary perspective, in terms of both biodiversity and community resilience to stress.

Key Concepts

1) **Phylogenetic diversity** represents the total phylogenetic tree branch lengths (measured in millions of years) of the species in a community. It is a more meaningful measure of biodiversity than species richness (the number of species present) because it calculates the cumulative evolutionary ages of the species, rather than weighting them equally regardless of relatedness.

2) **Phylogenetic community structure** quantifies whether species in a community are more clustered or dispersed on the phylogenetic tree than expected by chance. Overdispersed communities have higher-than-chance evolutionary diversity, and should therefore encompass a higher proportion of species unaffected by a given stressor, or able to adapt to it.

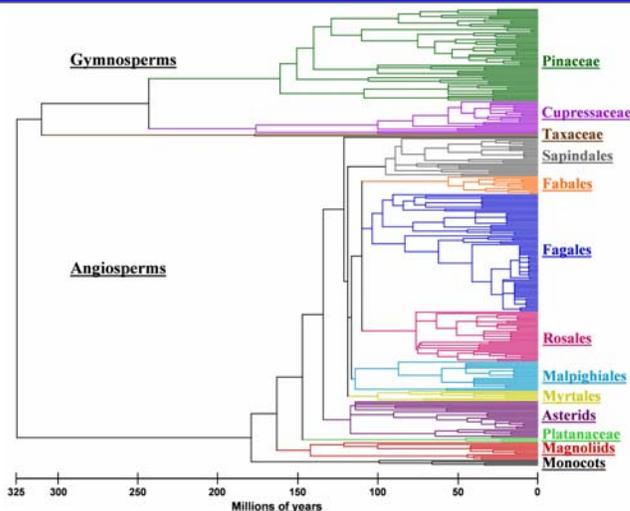


Figure 1: The phylogenetic tree of the 311 North American forest tree species inventoried by FIA was constructed in part using the BLADJ module of Phylocom (Webb et al. 2007). Evolutionary relationships and branch lengths were based on a survey of recent molecular systematic studies, except for basal angiosperm relationships, which were from Wikström et al. (2001).

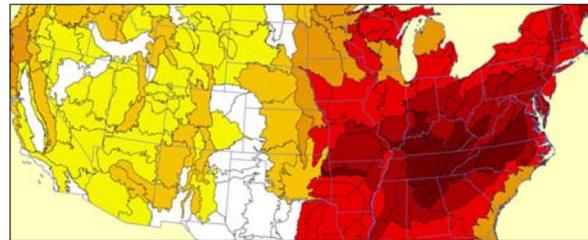
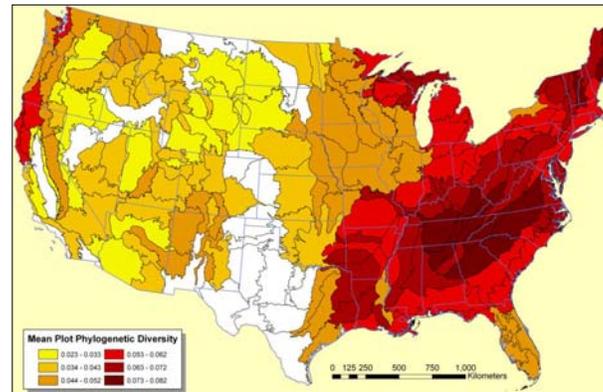


Figure 2 (above): The highest mean plot-level species richness (α diversity) occurs in sections of the Appalachians, Piedmont and Cumberland Plateau.

Figure 3 (below): Phylogenetic diversity is high in sections of the Northeast as well as the Southeast. Sections on the West Coast are also moderately high.



Methods

- ❖ Construction of phylogenetic tree of all 311 tree species inventoried by Forest Inventory and Analysis (FIA) (Figure 1).
- ❖ Compilation of most recent FIA tree inventory data, of trees ≥ 1 inches dbh, from 102,304 one-sixth-acre plots across 48 states.
- ❖ Generation of phylogenetic diversity and community structure statistics using Phylocom (Webb et al. 2007), with means calculated by ecoregion section. Sections with < 25 plots excluded.
- ❖ Structure quantified with Nearest Taxon Index (NTI), with a t test for section means significantly $\neq 0$. NRI scores > 0 are more phylogenetically clustered than by chance, < 0 are less clustered.

Results

- ❖ Although there is a generally similar pattern between species richness (Figure 2) and phylogenetic diversity (Figure 3) at the section scale, important geographical differences exist between these measures of biodiversity. These include higher relative phylogenetic diversity in the Northeast and along the West Coast.
- ❖ The analysis of phylogenetic structure (Figure 4) found strong regional differences in overdispersion (in the Interior West and Southeastern Coastal Plain) and clustering (in the Upper Midwest, the Great Plains, the Appalachian Mountains, and the Northwest).

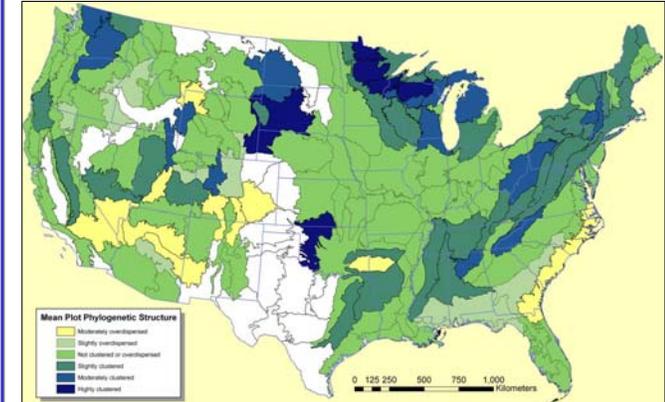


Figure 4: Sections with significant phylogenetic overdispersion are confined to the Interior West and the Southeast. Sections with the greatest clustering are in the Upper Midwest and the Great Plains. Phylogenetically overdispersed communities are expected to be more genetically resilient to change.

Future Work

- ❖ Investigation of the relationship between phylogenetic community structure and small- and large-scale ecological variables.
- ❖ Quantification of the impact of non-native tree species on phylogenetic diversity and community structure.
- ❖ Assessment of the evolutionary history of invasiveness in non-native tree species, and of invasion susceptibility in native trees.

References

- Webb, C.O., Ackerly, D.D., and Kembel, S.W. 2007. Phylocom: Software for the Analysis of Community Phylogenetic Structure and Character Evolution. Version 3.41.
- Wikström, N., Savolainen, V., and Chase, M.W. 2001. Evolution of the angiosperms: Calibrating the family tree. *Proc. R. Soc. Lond. Ser. B-Biol. Sci.* 268(1482): 2211-2220.



This research was supported in part through Research Joint Venture Agreement 06-JV-11330146-124 between the USDA Forest Service and North Carolina State University.