A Phylogenetic Analysis of Biodiversity in an Oak Dominated Forest of the Chicago Region

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INTRODUCTION

The Morton Arboretum's East Woods is an abundantly diverse ecosystem and a model forest restoration for other oak dominated forests across the Midwest. Consistent monitoring, including two extensive surveys, have been conducted on the East Woods over the last 11 years. We analyzed survey data collected in 2007 and 2018 for 529 plots across the woods. In evaluating the biodiversity in these plots, we adopted a phylogenetic approach for determining the distribution of species based on their traits. Previous work has shown that accounting for this phylogenetic diversity better explains environmental gradients and patterns of species distribution than species richness metrics.[1,2,3,4] Classifying species within plots on a phylogenetic basis allows for considerations of niche, community dynamics, and ecosystem function to be incorporated into the analyses based on the traits represented by species.[5,6]

HYPOTHESES & OVERARCHING QUESTIONS

We wanted to determine: What are the changes in biodiversity to the East Woods over the past 11 years? And what are the main drivers of these changes?

1. Plots with denser invasive cover will have a less phylogenetically diverse understory.
2. Plots with median canopy openness will have higher diversity relative to low or high canopy openness levels.
3. Moisture and light levels in plots will have limiting effects on phylogenetic diversity within plots.
4. Dissimilarity among plots quantified using pairwise phylogenetic beta-diversity will be more responsive to environmental differences than dissimilarity quantified using species comparisons

METHODS

1. Survey plots containing species previously unreported in Morton Arboretum's East Woods were selected for resurvey and vouchers obtained of new species
2. Cleaned/verified species list was then used to generate a phylogeny using a supertree approach[7]
3. Community dissimilarity matrices were generated using both phylogenetic and non phylogenetic metrics
4. Environmental distances were computed for plot environmental dataset collected in 2007[8]
5. Additionally, correlation between species and variation among environmental data were quantified

RESULTS

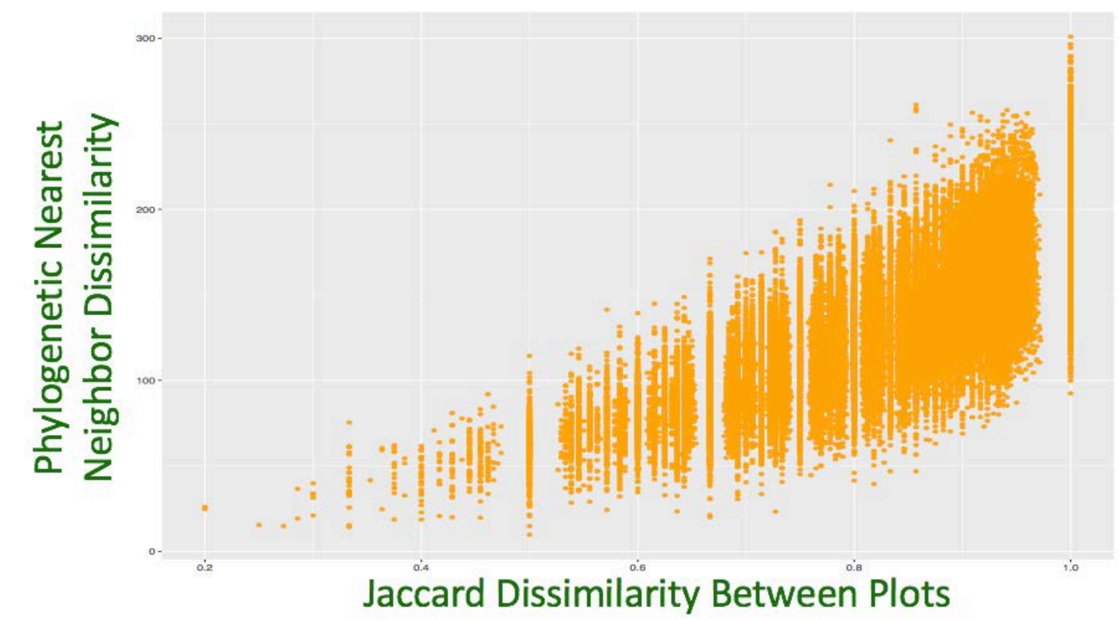


Figure 1: Both Jaccard distances and phylogenetic nearest neighbor (taxa) distances were computed on community data. The phylogenetic metrics were more sensitive to dissimilarity among plots where Jaccard distances tended to group phylogenetically distinct communities as similar.

- None of the environmental variables observed (canopy, elevation, slope, aspect, or invasives ratio) related to phylogenetic diversity (Figure 4)
- In addition, the phylogenetic diversity of the tree layer did not predict the diversity of the understory
- Phylogenetic metrics were more sensitive to effects on diversity by canopy and slope, but not elevation or aspect among plots than the Jaccard distances (Figure 1)
- Individual species have varying responses to each of the environmental variables (Figure 3)

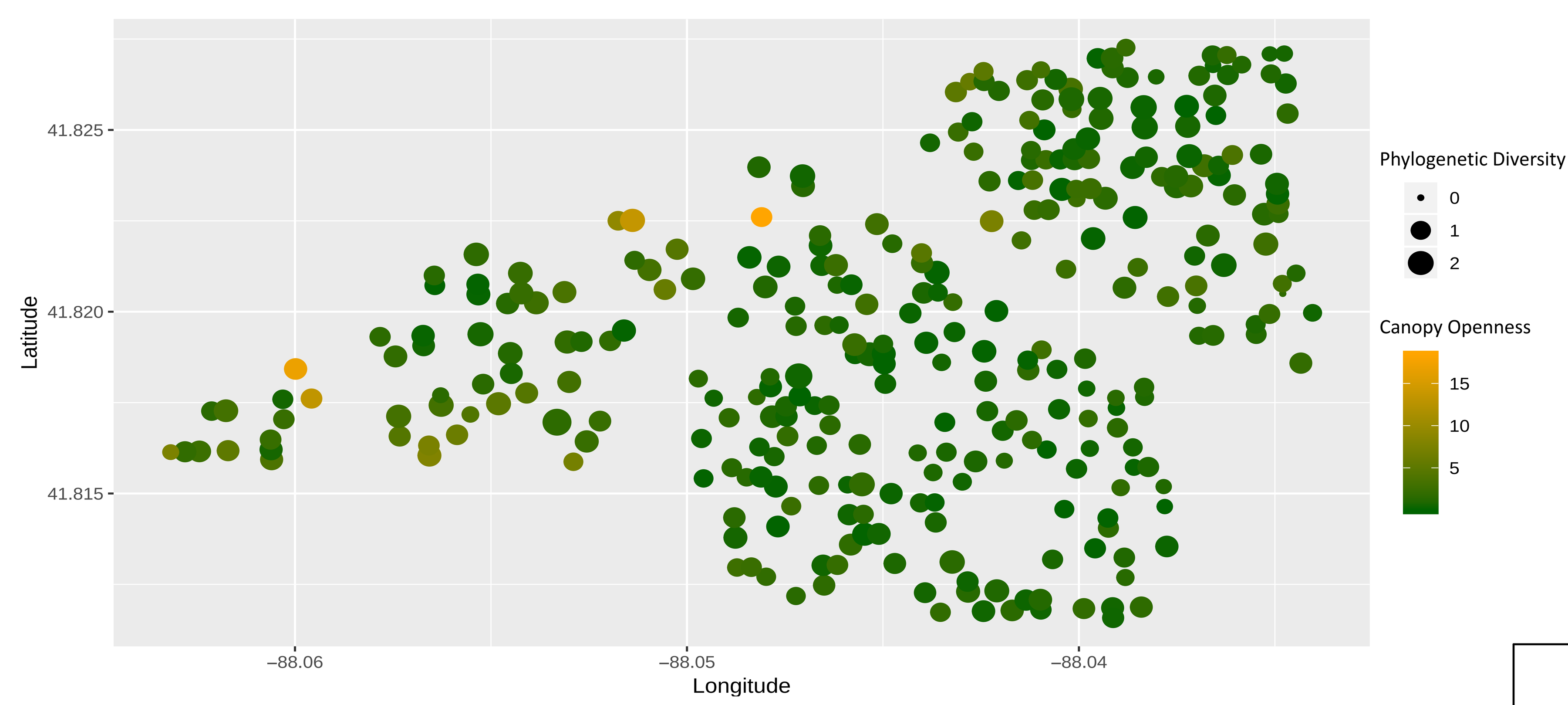
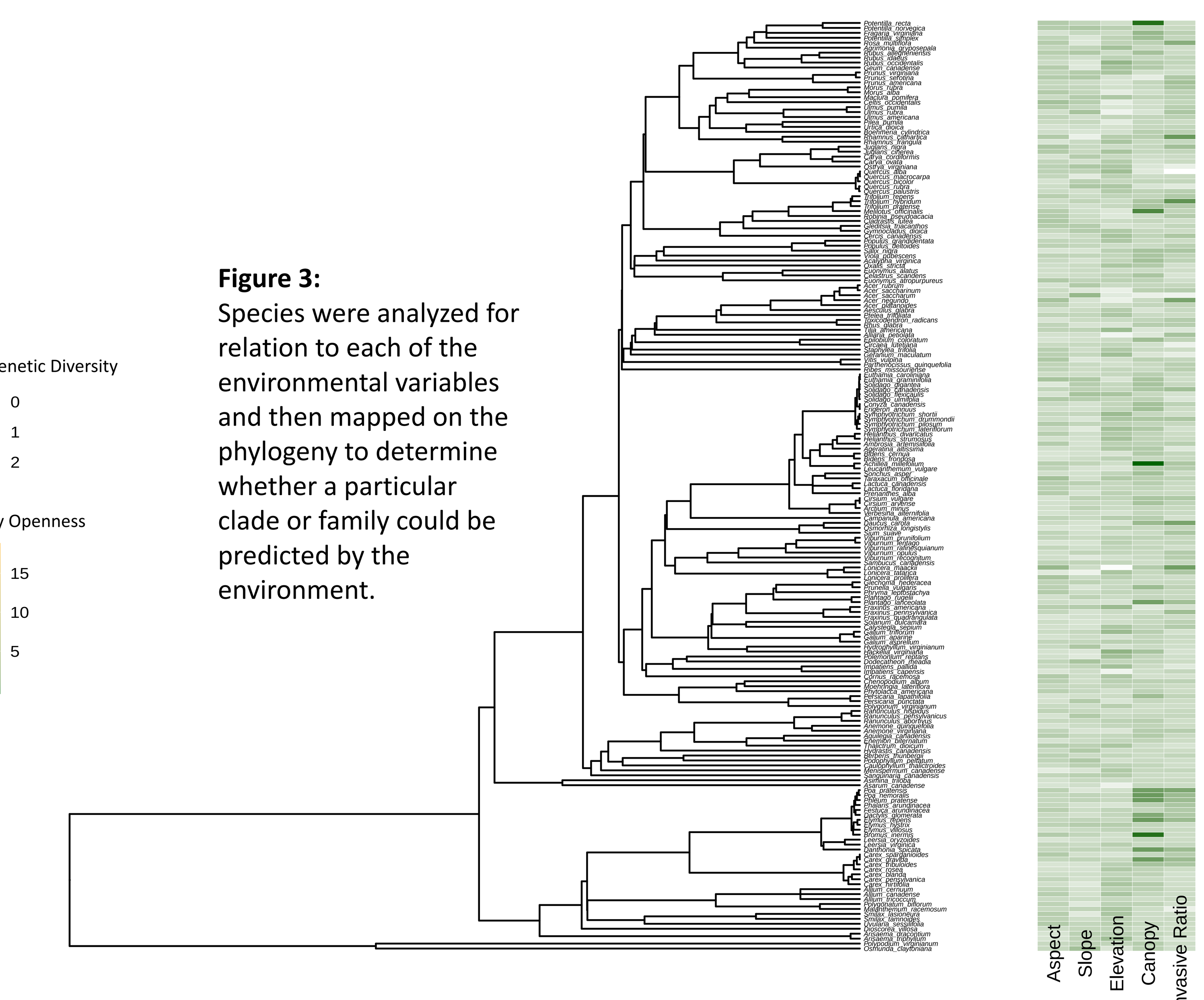


Figure 2: Mapping of survey plots across arboretum's East Woods. Plot size is indicator of phylogenetic diversity. Larger plots correspond to more diverse plots. Plot color indicates how open the canopy is at that particular plot. Orange plots correspond to more open plots.

Figure 3: Species were analyzed for relation to each of the environmental variables and then mapped on the phylogeny to determine whether a particular clade or family could be predicted by the environment.



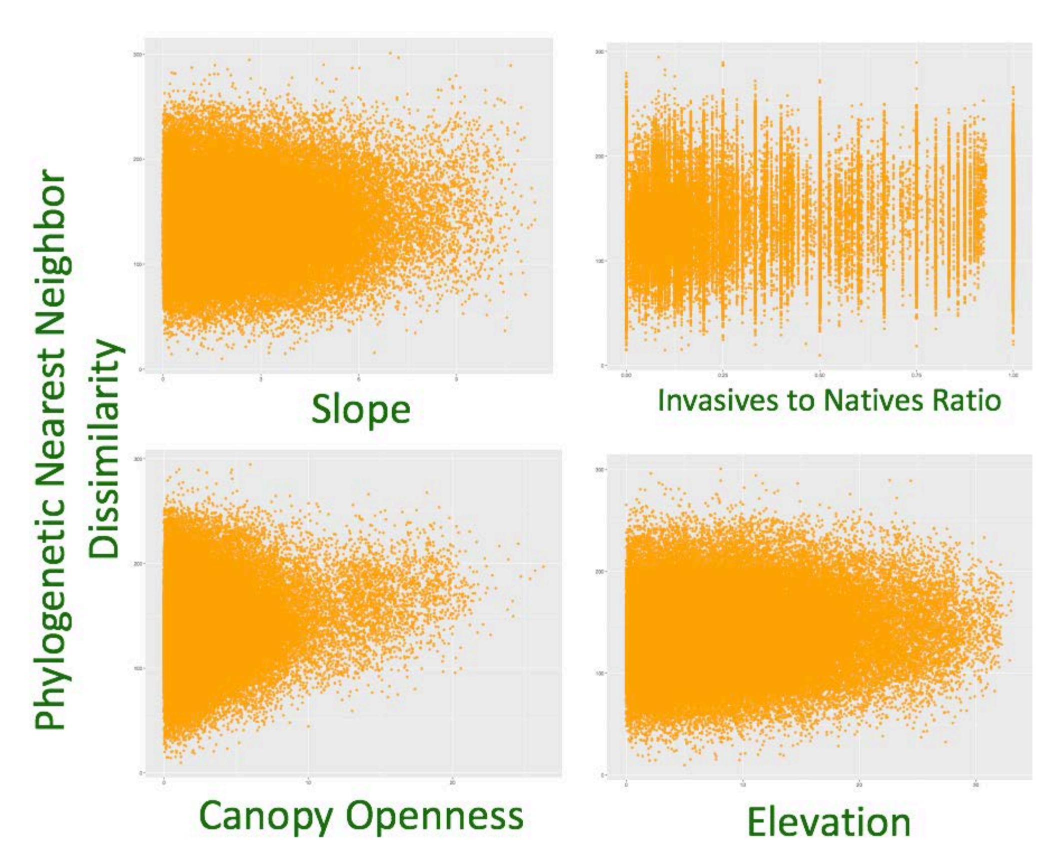


Figure 4: Relationships between environmental data (clockwise: slope, invasives ratio, canopy, and elevation). While none of the variables displayed a linear relationship with diversity levels, canopy distinctly shows a pattern in diversity distribution that likely accounts for particular trait groups.

CONCLUSIONS

- It is plausible that the geographic scale of the study was not broad enough to detect significant variability among plots
- Additional environmental and management variables will be included to better model all predictors of biodiversity changes in this ecosystem
- Based on our results, phylogenetic analysis is more sensitive to diversity differences than Jaccard distances
- Species correlations with environmental variables could be a consequence of specific traits and should be further investigated with trait or genetic data

FUTURE WORK

- Incorporating up to date GIS data on slope, aspect, and elevation
- Incorporating soils and biogeochemical data into analysis
- Inclusion of farmland use history data from DuPage County records
- Management data on canopy thinning and burn history over the last 30 years

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