

Background

The order Malpighiales contains one of the largest collection of angiosperms, comprising almost 16,000 species. Many well-known families exist within Florida, including Passifloraceae, the passionflower family, Rhizophoraceae, the mangrove family, and Salicaceae, the willow family. Considering the distribution of species within Malpighiales throughout Florida and the southeastern United States, I chose to focus my study on a phylogenetic analysis of this order. Polyploidy describes an organism that has greater than two homologous sets of chromosomes. Although the exact role of polyploidy in the evolution of species is still being investigated, there exists evidence that polyploidy was a significant factor in the evolution of plant species, especially angiosperms. My research attempts to determine the correlation between polyploidy and geographical distribution of Malpighiales within Florida.

Hypothesis

The group of species within the order Malpighiales that has descended from a species that has undergone whole genome duplication will exist in more diverse niches, indicated by a more widespread distribution, due to an increased likelihood of adaptation to environmental changes.

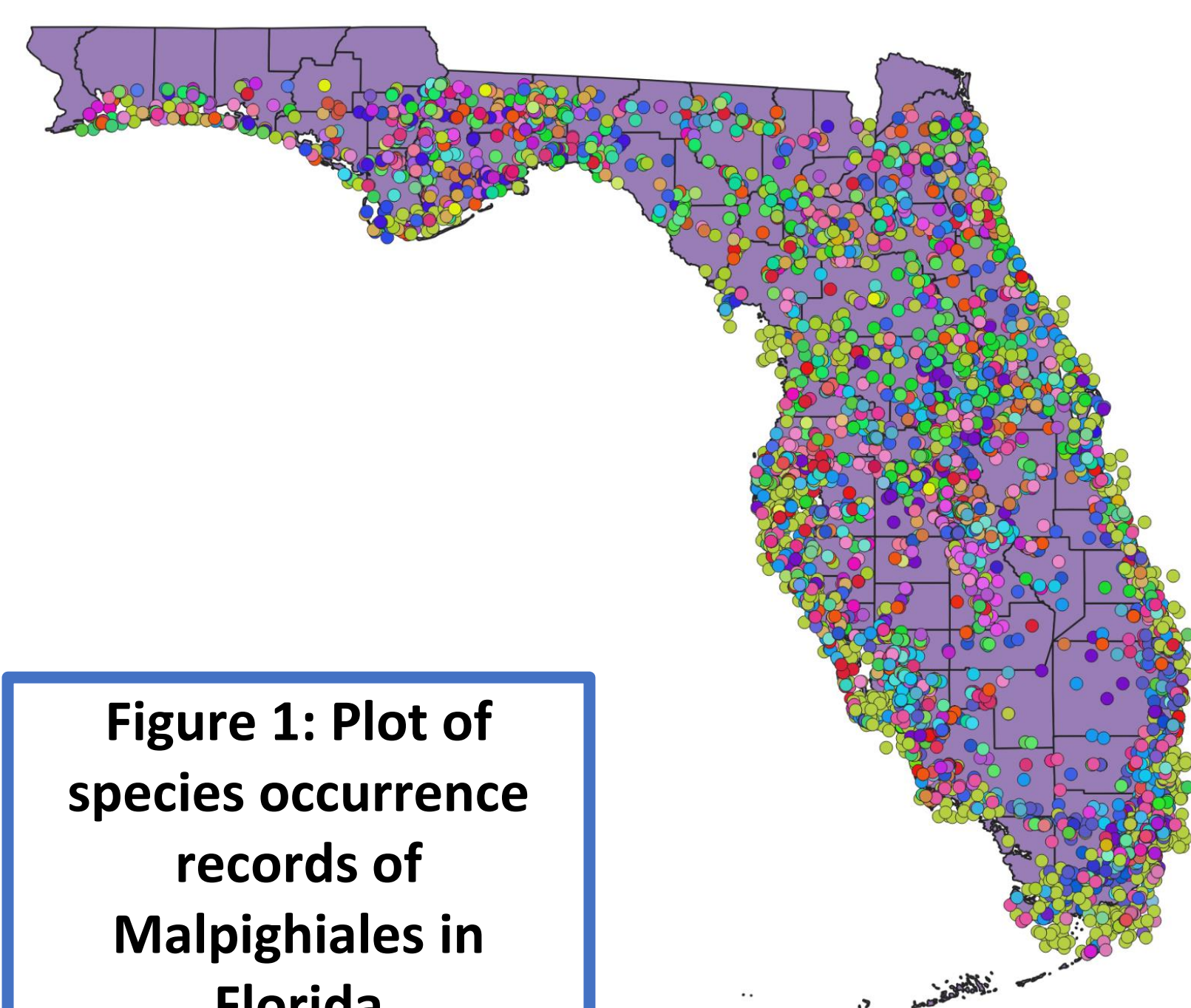
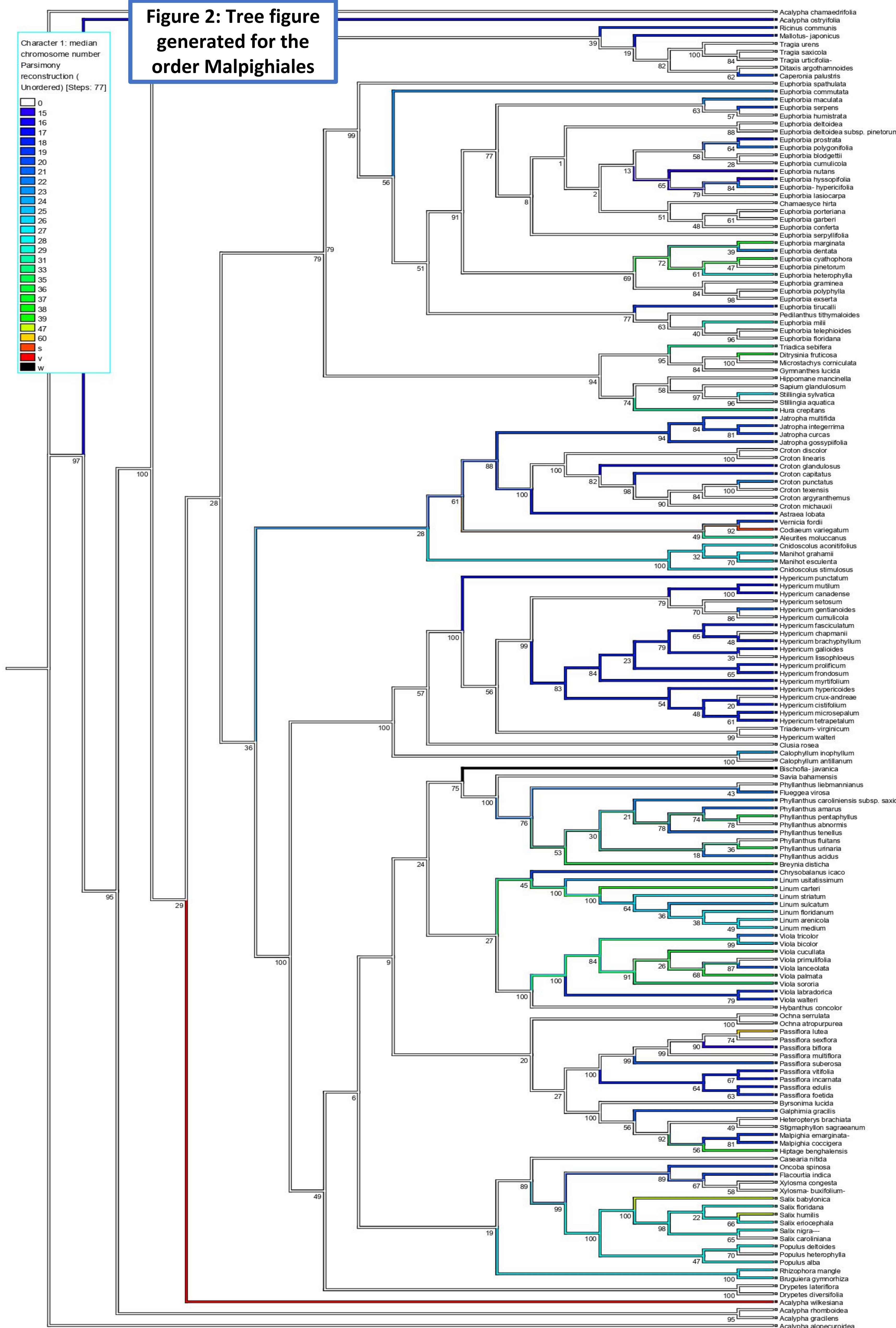


Figure 1: Plot of species occurrence records of Malpighiales in Florida

Methods

In an effort to resolve plant phylogeny of Malpighiales within Florida, I downloaded genetic sequences for two barcoding loci, rbcL and matK, from GenBank. I aligned the sequences using MAFFT, and, using RAxML software, created a maximum-likelihood phylogenetic tree Malpighiales. I then obtained species occurrence records from the Global Biodiversity Information Facility and plotted the data in QGIS to obtain range measurements. I compared this with data collected from the Chromosome Counts Database, determining if a species was polyploid based on the median chromosome number. I predicted that there would be a positive correlation between median chromosome number and range size.

Figure 2: Tree figure generated for the order Malpighiales



Results

After gathering chromosome count data and analyzing the range size of each species within Florida, I calculated the correlation coefficient between the range size and polyploidy, which was -0.14. Based on the analysis, the correlation between range size and polyploidy is not significant. The figure below indicates the mean range size for species that are diploid and species that are polyploid. The results suggest that diploid species within Malpighiales have a greater mean range size than polyploid species.

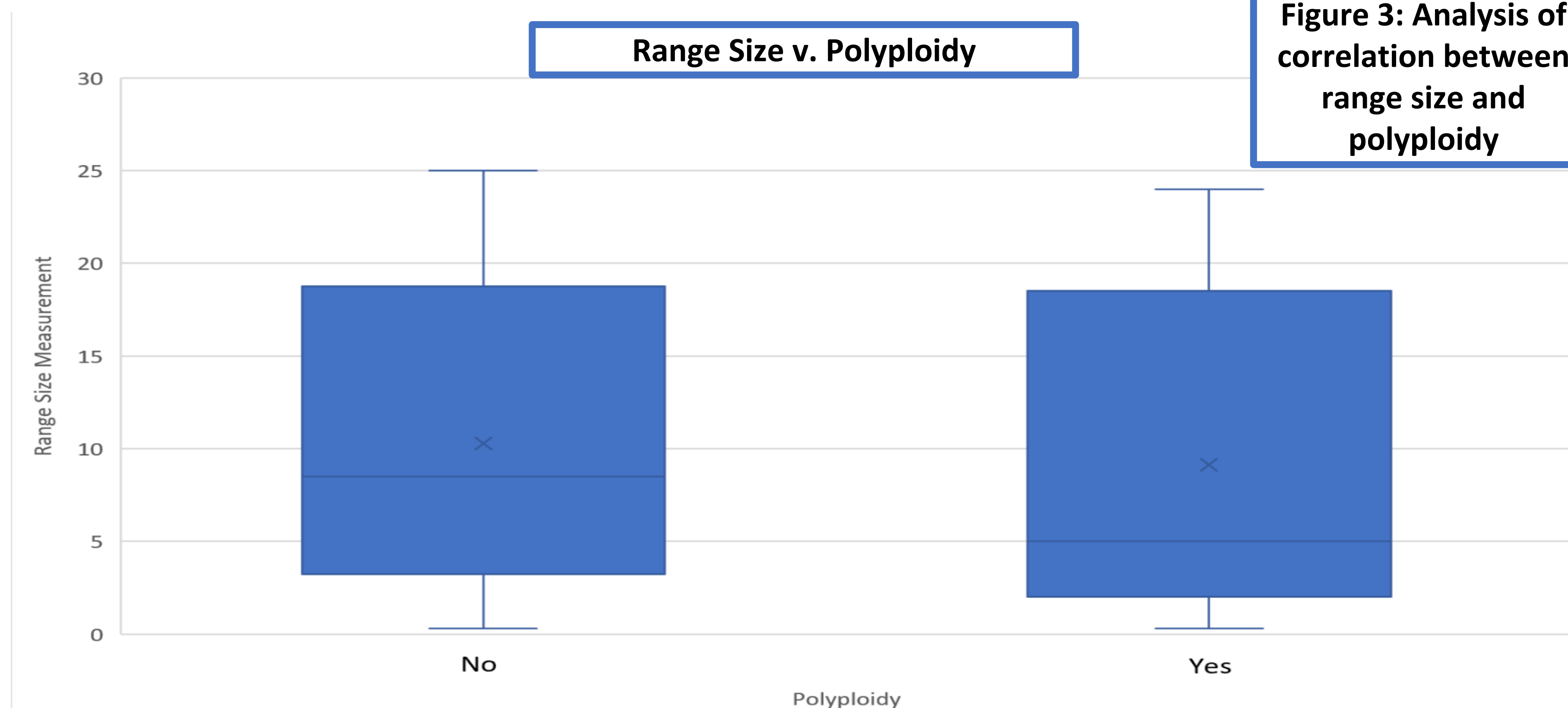


Figure 3: Analysis of correlation between range size and polyploidy

Conclusion

After gathering chromosome count data and analyzing the range size of each species within Florida, I did not find a significant positive correlation as predicted, but a statistically nonsignificant negative correlation between the median chromosome number and range size. In continuing the research, I will investigate models using the median chromosome number as a categorical variable, as well as studying the negative correlation between range size and polyploidy in Malpighiales.

References

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