

Does Genetic Diversity in a Dominant Tree Drive Biological Diversity?

Population Genetic Structure and Diversity in a Dominant Riparian Tree

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Abstract

To investigate how genetic diversity affects biodiversity we initiated studies of population genetic variation in cottonwoods. Cottonwoods frequently hybridize along river corridors and the hybrid zones typically harbor considerable genetic variation, which is strongly correlated with arthropod community diversity. To examine how genetic diversity within a single species of cottonwoods affects biodiversity, we are undertaking an analysis of population genetic structure in Fremont cottonwood in natural populations and in a common garden. Our initial analyses indicate differences in population genetic diversity and structure across several sites. Based on these results we choose populations to conduct our studies of within-species biodiversity and selected genotypes to plant in the common garden.

Introduction

Biological diversity is a key feature of riparian ecosystems, and is driven, in part, by species that dominate riparian landscapes. Cottonwoods are dominant riparian tree species found on river corridors throughout the American southwest and frequently hybridize along these corridors, forming extensive hybrid zones. We have genetically characterized a number of these hybrid zones and have found a direct link between host plant genetic variation and arthropod community structure and diversity. A primary remaining question is whether there is sufficient genetic variation within a single species to drive the same patterns of biological diversity as those observed in cottonwood hybrid zones.

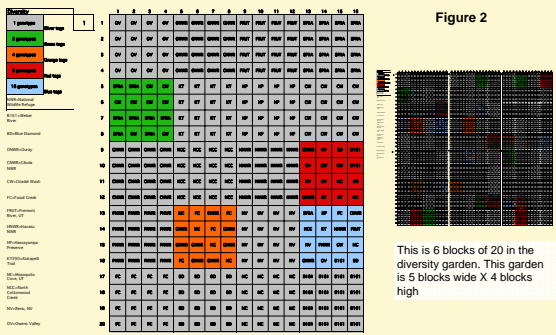
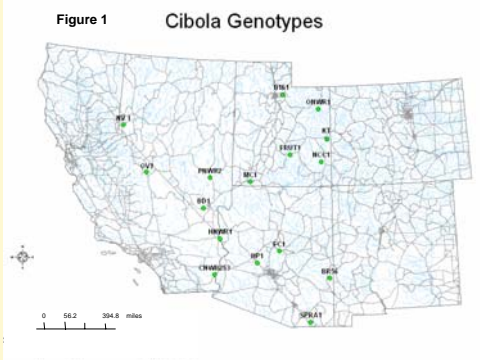
In phase I of this study, we examine how genetic variation within a single cottonwood species (*Populus fremontii*) is partitioned geographically and whether there are significant among population differences in genetic diversity and structure. In particular we ask the following questions:

1. Is genetic variation in *P. fremontii* geographically structured?
2. If genetic variation is geographically structured, are there significant differences in genetic diversity across populations?

If we identify populations that vary in their genetic structure and diversity, we will proceed with Phase II of our study, which is to examine how genetic diversity within a dominant tree species affects biological diversity and structure in dependent arthropod communities. These studies will be performed in natural populations and in common garden settings.

Methods

Leaf samples of *P. fremontii* were taken from natural populations from Arizona, California, Nevada and Utah (figure 1). These sites included the Lower Colorado River, San Pedro River, Verde River, Wupatki National Park, the Dolores River and two sites from Arches National Park. Individual trees were tagged and GPS coordinates were taken at each site. To assess population genetic structure and diversity in *P. fremontii*, we used fluorescent amplified fragment length polymorphism (FAFLP) analysis. Population genetic structure was analyzed using Tools for Population Genetic Analysis (TPPGA; Miller 1997), which included standard diversity estimates, an estimation of among population variation (Fst), and Nei's genetic distance. Population genetic structure and genetic divergence within populations were visualized using the UPGMA clustering algorithm. Among population differentiation was further analyzed using an analysis of similarity (ANOSIM) as implemented in DECODA (Minchin, 2001). From this data, trees with genetically distant genotypes were selected and planted in the common garden in Cibola, AZ (Figure 1 and 2).



This is 6 blocks of 20 in the diversity garden. This garden is 5 blocks wide X 4 blocks high

This is just one block w/ the 5 treatments

Results

- FAFLP analysis of 172 trees resulted in 127 loci, 72 of which were polymorphic (Table 1). Percent polymorphic loci for each population ranged from 20-61%.
- Estimation of heterozygosity of the populations ranged from 0.0329-0.1435.
- The overall Fst value was 0.1164 and the overall R value was 0.1901.
- The analysis of similarity (ANOSIM) showed that 15 out of 21 pairwise comparisons of the populations were statistically significantly different (Table 2).
- Nei's genetic distance ranged from 0.10 - 0.60. Genetic distance trees using the UPGMA algorithm show that genetic divergence is highest in the Lower Colorado River, AZ population and lowest in the Dolores River, UT (Fig. 3).
- 16 distinct genotypes were selected to be planted in the Cibola garden (figure 2).

Genetic Diversity Statistics

	Heterozygosity	% Polymorphic Loci	Total Polymorphic Loci	Monomorphic Loci	Total Loci
Lower Colorado River, AZ	0.1435	61.1111	72	55	127
San Pedro River, AZ	0.0601	33.3333	72	55	127
Verde River, AZ	0.06	33.3333	72	55	127
Wupatki, AZ	0.0606	36.1111	72	55	127
Arches - Courthouse Wash, UT	0.0805	38.8889	72	55	127
Arches - Horseshoe Canyon, UT	0.0661	33.3333	72	55	127
Dolores River, UT	0.0329	20.8333	72	55	127

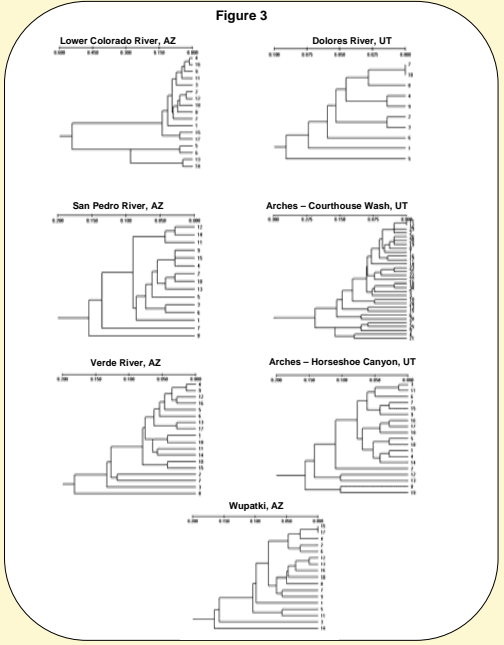
Overall Fst=0.1164

ANOSIM Analysis

	Lower Colorado River, AZ	San Pedro River, AZ	Verde River, AZ	Wupatki, AZ	Arches - Courthouse Wash, UT	Arches - Horseshoe Canyon, UT
San Pedro River, AZ						
Verde River, AZ						
Wupatki, AZ						
Arches - Courthouse Wash, UT						
Arches - Horseshoe Canyon, UT						
Dolores River, UT						

statistically different Overall R = 0.1901

GENETIC DISTANCE AND POPULATION STRUCTURE



Conclusions

Phase I of this study shows that there is both among and within population differentiation in *P. fremontii*. The two most genetically differentiated populations, Lower Colorado river and Dolores river, appear to be good candidates for proceeding with Phase II of our study. In Phase II we will investigate how among population genetic differences in cottonwoods do or do not affect arthropod community diversity. These studies will likely include additional genetic characterization of our candidate populations using codominant microsatellite markers. If our findings support the hypothesis that genetic diversity drives biodiversity, even within a single cottonwood species, we will effectively demonstrate the important role that cottonwood trees play in promoting biodiversity in riparian ecosystems. These studies could also lead to a better understanding of the role that host plant genetics play in shaping plant-animal interactions over evolutionary time.

References

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We gratefully acknowledge funding from E.R.D.E.N.E and the National Science Foundation.
Acknowledgements: special thanks to the National Park Service for collecting permits and assistance and to Mathias Dahner, Melanie Hadlock & Amber Williams for laboratory assistance and Matt Ziegler for creating our map of genotype origins.