**INTRODUCTION**

With approximately 160 species, Mexico is one of the primary centers of species diversification of the genus *Quercus* (Nixon, 1993). It has been postulated that varying physical factors and multiple complex orogenies, the interface of north temperate and subtropical climates and range shifts from glaciation have combined with the propensity for interspecific gene exchange resulting in the complex patterns of biodiversity seen today (Bacon & Spellenberg, 1996).

If these processes are acting on oak species there should be contemporary evidence supporting this. Outside of speciation studies focusing on hybridizing species pairs there have been no studies focusing on speciation in a phylogeographic context within the group in Mexico.

To better understand the patterns of historical phylogeography in the genus we examined the genetic structure of a wide-ranging complex of four taxa endemic to the Sierra Madre Occidental and Southern Cordillera of Mexico. The *Racemiflorae* is a natural lineage of Red Oaks united by the characteristic of producing acorns on racemose inflorescences (Trelease, 1921; Spellenberg & Bacon, 1996). Additionally the group shows varied patterns of disjunction and sympatry and is thus likely to be representative of the processes of gene exchange and habitat isolation that ultimately lead to speciation.

**SPECIFIC AIMS**

- Contrast patterns of chloroplast and nuclear DNA structure across the range of the four taxa.
- Relate observed patterns of genetic structure to proposed processes leading to species diversification.

**METHODS**

- Sampling of 490 individuals in 49 populations across the range of the four species.
- Genotyping by amplification of 7 mono- and dinucleotide cpSSR and 7 dinucleotide nuclear SSR loci.
- Determination of haplotype (chlorotype) diversity and structuring using Spatial Analysis of Molecular Variance (SAMOVA).
- Panbiogeographical track analysis to depict haplotype migration and infer centers of origin.
- Clustering of populations using UPGMA, Bayesian STRUCTURE analysis, and SAMOVA of nuclear SSR data at differing spatial scales to investigate species distinctions in regions of both sympathy and allopatry.

**RESULTS**

- cpSSR results depicted 29 haplotypes which were shared by multiple species across regions (Fig. 1). Two divergent chloroplast groups were identified. The first and larger group included most northern and southern species and populations while a second was centered in the north of the range and consisted of haplotype 24 and its direct derivatives in *Q. taraumara*, *Q. radiata* and two populations of *Q. conzattii* (Fig. 2).

**DISCUSSION**

Chloroplast and nuclear markers give distinctly different insights into evolutionary history. The independent patterns of history have been identified previously in *Quercus* (Whitemore & Schoal, 1991) and appear to be ubiquitous across the group. They both however show that gene exchange, either long-term or short-term, allows phylogeographic structure and genetic homogenization in geographic regions is a common trait.

In *Racemiflorae* the pattern of shared common chloroplast haplotypes across the Trans-Mexican volcanic belt disjunct suggests a one time mass extinction event and an ancestral *Racemiflorae*. The sharing and frequency of haplotypes however obscures the region of origin.

The occurrence of haplotype 24 in the north of the range indicates the evolutionary recent incorporation of a lineage from outside the group. The common occurrence of this lineage within two of the more restricted specialist species, *Q. taraumara* and *Q. radiata* suggests that their evolution may be more recent and in part a result of introduced evolutionary novelty (Arnold, 1997) through hybridization. While more is needed to prove the relationship we propose that this supports a general hypothesis of cyclic hybridization (Rattenbury, 1962) and generation of evolutionary novelty over time leading to the high levels of *Quercus* species diversity in Mexico.

**LITERATURE CITED**


**ACKNOWLEDGMENTS**

Financial support for this project was provided by CONACYT, SEMARNAP (grant 199280 COI-97 to K. Oyama), DOGAP-PAPIIT, UNAM (grant IN229803 to K. Oyama), and a DGAPA, UNAM Postdoctoral Fellowship to R. McCauley and A. Cortés-Palomino. The authors would like to thank Maria Luisa Herrera Arroyo for providing selected population samples and Renan G. Moreira for laboratory assistance.

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