

EVOLUTION / PHYLOGENETICS

Abstracts

PHYLOGENY AND POPULATION ANALYSIS OF AN ENDANGERED TROPICAL TREE (*GUAIAECUM* SPP.)

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Lignum-vitae or guayacán (*Guaiaecum* spp., Zygophyllaceae) are trees and shrubs endemic to the New World dry tropics. Regarded for their unique wood and various medicinal properties, they are of increasing conservation concern due to historical exploitation, active trade, and reduced habitat. Previous morphological studies have failed to adequately resolve key taxonomic questions or establish clear geographic boundaries for species or populations. The goal of this research is to use comparative DNA sequence analysis to understand the taxonomic boundaries, genetic structure, and geographical distribution of *Guaiaecum*. This information is important for the proper management of remnant populations, effective trade regulation, and future restoration and reintroduction efforts. In addition to its direct application to conservation, this study engages an inadequately studied and poorly understood area of plant evolution. The establishment of distinct evolutionary lineages in plants can be complicated given their capacity for hybridization and introgression; which often poses problems to the traditional separations of systematics, population genetics, and phylogeography. These problems may be overcome; and analysis of multiple loci of highly variable DNA sequences may elucidate the roles of both historic and contemporary genetic exchange among *Guaiaecum* species and populations, thereby identifying distinct genetic lineages of conservation concern as well as providing insight into their evolution.

Keywords: *Plant Evolution, Phylogenetics, Population Genetics, Conservation*

MOLECULAR PHYLOGENY AND CLASSIFICATION OF SANTALACEAE

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Santalaceae is a cosmopolitan family of root and stem hemiparasitic plants in the Sandalwood order (Santalales). The family is paraphyletic with respect to Viscaceae and previous classifications recognize 38 genera (ca. 450 spp.) in four tribes: Amphorogyneae, Anthoboleae, Santaleae, and Thesieae. A molecular phylogeny is presented here based on nuclear SSU rDNA and chloroplast *rbcl* and *matK* DNA sequence data with nearly complete generic-level sampling. These data were analyzed using parsimony, likelihood and Bayesian methods. Five well-supported clades are resolved, but deep-level relationships among these clades remain ambiguous. Tribe Santaleae is polyphyletic and the mistletoe family Eremolepidaceae is monophyletic, but embedded within one clade of Santaleae. Tribe Amphorogyneae is sister to Viscaceae and contains both root parasites and mistletoes. *Anthobolus* is excluded from Santalaceae and allied with Opiliaceae. The mistletoe habit has evolved independently twice in Santalaceae and in three other families in Santalales (Misodendraceae, Loranthaceae, and

Viscaceae). Preliminary work on other genes show promise for resolving deep-level nodes, at which time main clades will be recognized as a formal family-level classification.

Keywords: *Santalaceae*, *Santalales*, *molecular phylogeny*, *classification*

FUNCTIONAL CONSTRAINT UNDERLIES 60 MILLION YEAR STASIS OF DROSOPHILID TESTIS-SPECIFIC BETA TUBULIN

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How do proteins evolve while maintaining their function? Previous studies find a highly stringent structure/function relationship between the *Drosophila melanogaster* testis-specific tubulin b2 and the spermtail axoneme, such that small changes in the b2 protein render it unable to generate a motile axoneme. This raises the question, How does b2 evolve while maintaining its function? To answer, we cloned full and partial-length b2 sequences from 17 species of Drosophilids spanning 60my of evolution. Not a single amino acid difference is coded among them – b2 maintains its function by not evolving. We also performed phylogenetic analyses to determine ortholog/paralog relationships among insect tubulins. We find that the Lepidopteran and Dipteran testis-specific b-tubulins are orthologs, and surprisingly, despite functioning in the same structure, the Lepidopteran orthologs are evolving rapidly. We argue that differences in tubulin isoform use in the testes cause the Dipteran axoneme to be less evolvable, which has facilitated the evolution of a unique amino acid synergism in Drosophilid b2 that is resistant to change, resulting in its evolutionary stasis.

Keywords: *tubulin*, *Drosophila*, *axoneme*, *constraint*

THE INFLUENCE OF GENOTYPE ON ATLANTIC SALMON SURVIVORSHIP

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Atlantic salmon were introduced into Lake Huron from a variety of source populations in the early 1980s. Since then 1.5 year old salmon have been stocked annually, into the St. Marys River in Michigan. Although salmon returning to the St. Marys River comprise a large portion of the adults used for broodstock each year, strains from other locations (e.g., Maine) are often used to supplement the "natural" broodstock. We quantified the influence of genome-wide relatedness and major histocompatibility complex (MHC) genotype on the mortality of young Atlantic salmon. Eggs from a single female were fertilized with milt from a single male to produce full-sib embryos; 32 families were created in this manner. We monitored embryo survivorship in each family and found that hatching success averaged 72%, but the variance was high—some families had survivorship near 100% and others were near 0%. A suite of 10 microsatellite loci was used to estimate relatedness between parents. We found a significant negative relationship between parental relatedness and juvenile survivorship. Thus, our data are consistent with outbreeding depression, the reduction in fitness due to the mating of two dissimilar individuals. This is intriguing given the recent discovery of outbreeding depression in crosses between wild and farmed Atlantic salmon.

Keywords: *MHC, relatedness, Atlantic salmon*

CROSSING BARRIERS: WHAT CAN WE LEARN FROM THE MULTIPLE HYBRIDIZATIONS
WITHIN THE *PHRYNOCEPHALUS PRZEWALSKII* COMPLEX?

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The central Asian desert has a variety of habitats and topological features that provide an assortment of selection regimes and physical barriers. As might be expected this diverse terrain offers several opportunities to study speciation and hybridization. One such system of isolation and secondary contact is the Toad-Headed Lizards *Phrynocephalus przewalskii* complex. Hybridization is common in at least four lineages. The source of hybridization is currently unknown. It could be that a few individuals cross barriers such as the Yellow River or new connections have been made between populations due to the past 300 years of desertification. Microsatellite analyses will allow us to examine allele and genotype distributions. This information will provide evidence with which competing theories of the consequences of hybridization can be tested. To date we have already designed and optimized 13 microsatellite primers for the next phase of our research.

Keywords:

POST-PLEISTOCENE GLACIAL RETREAT, COLONIZATION ROUTES,
AND GEOGRAPHIC VARIATION OF THE NORTHERN WATERSNAKE,
NERODIA SIPEDON, IN THE GREAT LAKES REGION

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Post-Pleistocene glacial retreat and formation of the Great Lakes in North America had a profound impact on the colonization routes of extant reptiles and amphibians. These colonization routes shaped the current distribution of reptiles and amphibians, resulting in intraspecific geographic variation. This research focuses on phylogeographic patterns of the northern watersnake, *Nerodia sipedon*, in the Great Lakes region resulting from post-Pleistocene glacial retreat. Specifically, this study tests the hypothesis that formation of Lake Michigan acted as a geographic barrier, forcing a two-front colonization into Wisconsin and Michigan. The northern watersnake is widely distributed in eastern North America, making it an ideal species in which to test this hypothesis. Currently, complete mitochondrial DNA (mtDNA) sequences for the gene ND2 have been obtained from 38 individuals. From these sequences, 19 unique haplotypes were identified from a total of 20 sites across Illinois, Wisconsin, Michigan, Indiana, Kentucky, Ohio and Ontario, Canada. Statistical parsimony analysis of mtDNA sequences resulted in two genetically distinct networks that could not be connected at the 95% significance level. These clades represent a separation of eastern and western groups, supporting a hypothesis of two-front colonization. Maximum parsimony analysis, including three congeneric outgroup sequences resulted in two clades. These two clades are exactly analogous to the two previously identified

haplotype networks, with bootstrap values for eastern and western clades of 84 and 100, respectively.

Keywords: *Great Lakes*, *Nerodia sipedon*, *phylogeography*, *mitochondrial DNA*