Understanding relationships between evolutionary history of Sea Oats (Uniola paniculata) Poaceae, and adaptations to environmental conditions

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Background: A long ribbon of barrier islands, which shelters inland habitats, estuaries, lagoons and sounds, borders the southeastern coast of the United States. Even during normal conditions, the ocean strikes the coastline with substantial force. Oceanfront sand dunes absorb the initial main impact of the ocean’s energy. After beaches, dunes are the second line of defense in protecting the land from the sea. Their effectiveness in the defense of interior terrestrial habitats against waves, winds, tides and storms depends upon their height and stability, which in turn depends on dune vegetation.

The principal native dune-forming vegetation along the southeastern North American coast is sea oaks, Uniola paniculata (Poaceae) (Figure 1 and 2). Sea oats are used in restoration projects because they are one of the most effective native sand-binding and dune-building grasses. However, there is a lack of scientific data regarding which natural populations are most suitable as a source of propagules, and there is considerable disagreement about how to delineate local provenances. Furthermore, a major unresolved issue in evolutionary biology is the relationship between molecular measures of genetic diversity and quantitative variation (Frankham 1999). Our research project addresses this problem by using simultaneous analyses of evolutionary history and the distribution of genetic diversity (measured by neutral genetic markers) and geographic patterns of adaptive variation (measure by morphological and reproductive traits).

Objectives:
The overarching objective is to define Evolutionary Significant Units (ESUs) and Management Units (MUs) based on:

i) Evolutionary history and historical dispersal
ii) Geographic distribution of adaptive traits

Specific objectives:
A. Reconstruct a phylogeographic history of Uniola paniculata based on chloroplast DNA (cpDNA). Phylogeographic structure will provide the basis for the delineation of ESUs.
B. Test congruence between phylogeographic structure and distribution of nuclear genetic diversity.
C. Measure the distribution of adaptive variation across geographic range of U. paniculata.
D. Test for congruence between the distribution of genetic diversity (both cpDNA and nuclear DNA) and adaptive traits. This analysis will provide a basis for delineating MUs and identifying the most suitable propagules for habitat restoration.

Methods:
Laboratory analysis:
We will PCR-amplify specific non-coding cpDNA regions using universal primers and sequence the amplified fragments from 300-350 plants representing the entire contemporary geographic range of sea oats.

Phylogeographic analysis and delineation of ESUs:
We will use cpDNA sequence variation to infer intra-specific phylogeny and to reconstruct sea oats phylogeography. We will consider populations belonging to each cpDNA lineage (i.e., sharing the same haplotype) a separate ESU.

Preliminary results and discussion
Phylogeography:
CpDNA haplotype diversity: We identified seven variable cpDNA fragments resulting in five cpDNA haplotypes clustered into two major groups: Western (TX, MS) and Eastern (SC, FL, GA, NC, VA). Each of the major clades has internal and more shallow subdivisions (sub-clades) separated by fewer mutations (i.e., sequence differences) (Table 1).

CpDNA haplotype geographic distribution: The geographic distribution of haplotypes is clustered in most cases, although there are some unexpected results with haplotypes located outside of their main range. Furthermore, there are unique haplotypes located along the coast from Northern Florida to South Carolina, imbedded in the center of the most common lineage. This unexpected complexity can be explained by human introductions of non-local haplotypes, by homoplasmy, and by long-term isolation of populations along sea oaks’ naturally fragmented range. Seed dispersal mitigated by the Gulf Stream and patterns of tropical storms may contribute to observed haplotype distribution.

Evolutionary significant units and adaptive traits
While cpDNA clades provide information about independent maternal lineages that may have evolved separately from each other, they do not provide any information regarding the evolution of adaptive traits in these populations. We compared the phylogeographic structure of sea oats with a previously published study on the distribution of morphological traits (Seneca 1972). The distribution of these prematurally adaptive traits is only partially congruent with phylogeography (Figures 3 and 4).

We are collecting more extensive data regarding adaptive and reproductive traits and their geographic distribution. This comparison will lead to delineation of MUs taking into account both evolutionary history (based on cpDNA) and adaptive variation shaped by natural selection (based on reproductive and morphological characteristics). Thus, our research will provide new science-based tools for designing restoration and conservation management strategies.

Future directions: evolutionary significant units, adaptations and climate change
A. The outcome of our current investigation will form a foundation for subsequent growth chamber experiments testing the response of U. paniculata to a range of temperatures and CO2 concentrations predicted for the next 100 years. We will measure both reproductive and vegetative traits (e.g., pollen development and fertility, grain filling, above and below ground biomass) and investigate the variation of plant responses within and among populations, MUs and ESUs.
B. We will investigate the variation of sea oats in their mycorrhizal associations across the entire geographic range.

References:

Acknowledgment: