

POSTER ABSTRACTS

USING WHOLE-GENOME SEQUENCING TO BETTER DISTINGUISH THE FEDERALLY ENDANGERED NECHES RIVER ROSE MALLOW (*HIBISCUS DASYCALYX*) FROM ITS CO-OCCURRING CONGENERS

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The protection of biodiversity requires biologically informed criteria to decide what species need protection so that resources can be prudently allocated. Closely related species can co-occur over certain portions of their range, and they can often hybridize with one another, which blurs species boundaries. Endemic, rare species were often defined many decades ago, based on morphology alone, and morphology can be an unreliable predictor of genetic and/or ecological differences among individuals (or lack thereof). Previous work in our lab suggested that the federally threatened species *Hibiscus dasycalyx* (Neches River Rose Mallow) is very closely related to the common species *Hibiscus laevis* (Halberd-Leaved Rose Mallow), and that the two groups are not ecologically different from one another. This suggested that *H. dasycalyx* may not be a separate group from *H. laevis*. However, this work was based on a single gene (GRANULE-BOUND STARCH SYNTHASE I), and single gene phylogenies can be different from whole-organism phylogenies. When we re-ran the phylogenetic analyses using genome wide data, with over 10,000 informative genetic sites, we found that *H. dasycalyx* is actually separate from *H. laevis*, contrary to the single-gene results. Thus while *H. dasycalyx* is very closely related to *H. laevis*, it is genetically distinct after all. Our results show that morphological taxonomy can be a reliable indicator of species boundaries, at least in some cases, and highlight how vitally important it is to use genome-wide data before deciding that the current taxonomy for two species is incorrect. Forthcoming work will examine whether there is evidence of hybridization between *H. dasycalyx* and its co-occurring congeners, as the question moves from whether *H. dasycalyx* is a good species (it is) to what threats to its survival are most urgent.

THE NECHES RIVER ROSE MALLOW (*HIBISCUS DASYCALYX*) IS DEAD, LONG LIVE THE NECHES RIVER ROSE MALLOW? TAXONOMIC CLARIFICATION USING EVOLUTIONARY GENETICS

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The accurate identification of species that are in need of protection is one of the most essential challenges of conservation biology. In a previous study, we combined phylogenetic analysis with ecological niche modeling to help resolve the taxonomic status of the federally threatened East Texas endemic wildflower, *Hibiscus dasycalyx*. *H. dasycalyx* co-occurs with two other closely related congeners that are not rare, and previous work suggests gene flow among them.

In fact, we initially found that *H. dasycalyx* and *H. laevis* were very similar genetically (0.57% diverged at GRANULE-BOUND STARCH SYNTHASE I), and that they were neither reciprocally monophyletic nor significantly diverged ecologically. Our recent work, however, using a Bayesian structuring algorithm (STRUCTURE), revealed that *H. dasycalyx* is distinct from *H. laevis* and *H. moscheutos*, but that our samples contained misidentified specimens as well as recent generation hybrids between *H. dasycalyx* and *H. laevis* that clouded the picture. This recent work potentially revealed a previously unknown population of *H. dasycalyx* as well. We are now re-assessing the genetic similarities of these three species, their phylogenetic relationships, and their ecological niche differentiations from one another, after reclassifying misidentified specimens and removing hybrids from further study. We predict that *H. dasycalyx* will, in fact, be reciprocally monophyletic with *H. laevis* (albeit still closely related) and that they will have distinct ecological niches from one another under this new analytical regime. Our study demonstrates the essential role of evolutionary biology to practical considerations regarding the conservation of biota, and how an integrative approach, synergizing several different approaches (morphological assessment, genetics, evolution, and ecology), can help zero in on what needs protecting and where.

NATIVE SEED DEVELOPMENT FOR RELEASE IN CENTRAL TEXAS

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Texas Native Seeds was formed to provide native seed sources to restore plant communities that have been disturbed in central Texas. Texas Native Seeds is a collaborative effort organized by private landowners, the Caesar Kleberg Wildlife Research Institute (CKWRI)'s South Texas Natives Project, and the Texas Department of Transportation (TxDOT). TNS collects seeds of native plant populations with the purpose of evaluating, selecting, increasing and developing new releases of locally adapted species. The end goal of the project is having commercially available sources of native seeds that can be planted for land restoration. Potential new releases include Hooded windmillgrass, Sand dropseed, White tridens and Purple threeawn. We will present our findings on these three species and discuss the impact they will have in bring back diversity into the Texas landscape.

DEVELOPMENT OF MILKWEED SEED SOURCES FOR SOUTH AND WEST TEXAS

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The potential for monarchs to be listed under the Endangered Species Act has become a great concern in the conservation community. Monarch butterflies almost exclusively lay their eggs on milkweeds, making these plants a high priority for restorationists. Native Texas milkweed seeds are difficult to produce commercially, resulting in available seeds being prohibitively expensive for use in large scale restoration projects. Several species of milkweed are found

throughout Texas that may have merits for large scale seed production, including *zizotes*, broadleaf, slim, green, and antelope horns. In order to identify acceptable populations for seed production, we conducted a common garden study of 40 different accessions of these 5 species. Of the species evaluated, *zizotes* milkweed has been the most successful in yielding large quantities of seed. We have estimated production potential of 244 lbs. of seed per acre per harvest with the potential for multiple harvests annually. Germination tests are currently underway on seed harvested, and early results are very encouraging with seed germination averaging 80%. Even though a significant amount of seed is produced by *zizotes* milkweed, large scale mechanical harvesting of the seed has been difficult because pods ripen indeterminately. Another challenge to production of *zizotes* milkweed is insect damage, especially by aphids, which must be controlled in order to produce seed crops. Results from this project will be used to help improve commercial seed production and availability of affordable native milkweed seeds for Texas restoration efforts.

TEXAS ECOSYSTEMS AND VIRTUAL MAPPING

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Texas Parks and Wildlife's Landscape Ecology Program has developed a Google maps based application, Texas Ecosystem Analytical Mapper (TEAM), to deliver the Ecological Mapping Systems of Texas (EMS) data to Texas citizens. The TEAM application is an interactive mapping tool that will assist users in understanding Texas habitats and integrate vegetation data with land management and resource planning of all types. Wildlife biologists, land managers, naturalists, planners, and conservationists are able to use TEAM to view and print the EMS data in relationship to other natural feature layers such as soils, geology, hydrology and ecoregions. Currently, TEAM allows the user to view and print custom maps and reports of habitat data from uploaded kml and shapefiles, or areas of interest drawn within the application. Other capabilities include: exporting the map and report to a pdf; and calculating the number of acres of each vegetation type within the area of interest. Future updates include improved functionality in addition to a data entry module for crowdsourcing vegetation data and individual profiles for users. TEAM supports land management and conservation approaches incorporating the most current data. It also provides an avenue for community involvement in habitat understanding.

GROUND-TRUTHING POTENTIAL LOCATIONS OF THE FEDERALLY PROTECTED ENDANGERED PLANT SPECIES, HIBISCUS DASICALYX AND ITS CONGENERS

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One of the main challenges to determining whether or not a species is listed under the Endangered Species Act. One is understanding where the target species occurs or is likely to

occur, establishing the rarity of the species, identifying potentially undiscovered populations, and highlighting promising locations for reintroductions. The objective of the project is to create ground-truthed, geo-referenced maps of East Texas, showing the areas of suitable habitat for *Hibiscus dasycalyx* versus its congeners. We have ecological niche models for each species, so we are now going into the field to verify the maps based on them. We are testing whether the species is found in the most suitable habitats and absent from the least suitable habitats, as well as locations in between these two extremes. This will potentially identify new populations of *H. dasycalyx*, as well as quantify how reliable the habitat maps are for each species.

GENETIC DIVERSITY AND STRUCTURE OF A RARE ENDEMIC CACTUS AND AN ASSESSMENT OF ITS GENETIC RELATIONSHIP WITH A MORE COMMON CONGENER

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Endemic plant species with narrow geographic distributions and disjunct populations are prone to loss of genetic diversity especially if they are obligate outcrossing taxa. Simultaneously, delineating clear species boundaries is important in targeted conservation and management efforts. The federally endangered cactus, *Sclerocactus brevihamatus* subsp. *tobuschii*, has a parapatric relationship with *Sclerocactus brevihamatus* subsp. *brevihamatus* but genetic distance between the two taxa is unknown. We 1) developed taxon-specific polymorphic microsatellites, 2) assessed genetic diversity within and among nine populations of *Sclerocactus brevihamatus* subsp. *tobuschii* and within a single population of *Sclerocactus brevihamatus* subsp. *brevihamatus*, and 3) investigated the genetic relationship between the two subspecies. We obtained allelic data from 255 individuals across both taxa using seven self-developed microsatellites. Within-population genetic diversity of subsp. *tobuschii* was moderate to moderately high (mean HE = 0.59; mean HO = 0.37). Indirect estimate of inbreeding (FIS) ranged from 0.15 to 0.63 for subsp. *tobuschii* and was relatively high for subsp. *brevihamatus* (FIS = 0.47). Results from FST and AMOVA showed low genetic differentiation whereas DEST showed elevated genetic differentiation among the sampled populations of subsp. *tobuschii*. A Mantel test and spatial autocorrelation suggested no significant genetic and spatial correlation among nine populations or within each population of subsp. *tobuschii*. The Infinite Allele Model detected significant bottleneck ($p < 0.01$) in three populations of subsp. *tobuschii*. STRUCTURE analysis (K=3), and both rooted and unrooted NJ dendrograms suggested three distinct clusters across the ten populations of the two sub-taxa within *Sclerocactus brevihamatus*. Our results suggest that subsp. *tobuschii* is sufficiently differentiated from subsp. *brevihamatus* to retain its current taxonomic status.

TWENTY YEARS OF MONITORING THE ENDANGERED TEXAS SNOWBELL (*STYRAX PLATANIFOLIUS* SSP. *TEXANUS*)

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The Nature Conservancy, Texas Chapter

A large population of Texas snowbells were discovered at The Nature Conservancy's Dolan Falls Preserve in 1993. A monitoring program was started by Jackie Poole in 1995. Individual snowbells were tagged, measured, and their flowering and fruiting status noted. Monitoring has continued every 1-3 years since then, collecting data on over 1000 plants. We will present basic demographic data for the monitored snowbells and discuss the health of the population.

A ROLE FOR HERBARIA IN PLANT CONSERVATION: THE TEXAS OKLAHOMA CONSORTIUM OF HERBARIA (TORCH)

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Approximately 400 years of plant life on earth are documented through 350,000,000 million plant specimens deposited in approximately 3000 herbaria around the globe (*Index Herbariorum*, 2016). According to a 2010 survey conducted by the Texas Oklahoma Regional Consortium of Herbaria (TORCH), in Texas and Oklahoma alone there are more than 3.5 million specimens deposited across more than 50 herbaria. These herbaria represent unique resources for plant conservation, providing botanist verified records of plant occurrences, phenology, species associations, habitats, and geological associations. TORCH supports the increased access by researchers to herbarium data through a centralized online location, in a standardized format, which acknowledges the contributions of all collections, unique in their emphasis, size, and contents. A history of the TORCH organization is presented, along with a discussion for a continued role for herbaria to play in plant conservation and an invitation to participate and connect.

STATUS AND DISTRIBUTION OF THE FORT WORTH PRAIRIE AND LAMPASAS CUT PLAIN ENDEMIC *PEDIOMELUM REVERCHONII* (FABACEAE)

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Pediomelum reverchonii (S. Watson) Rydb. is a bushy-branched perennial forb in the Fabaceae family with a conservation status of G3S2. There is currently no information on the population size or distribution of *P. reverchonii* in Texas. We compiled a list of potential sites of populations using herbarium specimens, literature searches, iNaturalist, botanist interviews, and Texas Parks and Wildlife Department, and visited each site to record the GPS coordinates and state (fertile, sterile, dead) of each individual plant. We found 16 previously documented sites and 1 new site with sizes from just a few plants to over 500 with an average of 113 plants. The habitat was restricted to relatively shallow limestone prairies and rock outcrops with no specific

limestone formation needed. Roadsides were the most common sites and present many threats to the species including scraping, mowing, herbicide application, and road expansion. The less-than-ideal habitats and old age of the populations suggest that *P. reverchonii* once covered a much larger area, but has been reduced to small, spread-out populations from overgrazing, mowing, construction, and road scraping. We determined the conservation ranking of *P. reverchonii* is accurate considering the number of known sites in Texas and the country, and will conduct habitat surveys and further data collection in the next growing season.