PRESENTATION ABSTRACTS

Why an evolutionary view of biodiversity matters

Brent D. Mishler

It is all too common, even among biologists, to take a typological view of species and simply assume that species are the way biodiversity comes packaged, period. On the contrary, as explained most compellingly by Charles Darwin, the species level is an arbitrary human construct. What really matters are lineages splitting from each other, and sometimes coming back together again, at many nested levels in the tree of life. There is nothing special about the particular level called species. There are important lineages below the traditional species level, and above that level as well. Organisms given the same species name are not interchangeable in their traits or their ecology. This truism has obvious implications for conservation biology. Biodiversity can't be assessed or evaluated looking only at species, nor can its future be predicted. We need to examine the whole tree of life. In restoration, we can't assume that just because a plant from a nursery bears the same species name as a plant that used to grow at a site, that it has the same properties or is a good replacement. Particularly in plants, a considerable amount of fine-scale variation within named species is correlated with geography. Thus, geography is a pretty decent proxy for relationships if genetic studies are lacking. Furthermore, geography plays a part in evolutionary processes affecting biodiversity; plants are often locally adapted. For these reasons it is important to conserve distinct geographic populations, even if they do not bear a taxonomic name, and to avoid introducing plants from distant populations into them because of the risk of diluting local adaptations.

Recognition and conservation of cryptic diversity in the California flora

Bruce Baldwin

The rise of molecular and computational tools for analyzing plant relationships and of online access and querying capability for California herbaria have contributed significantly to floristic and systematic progress and have revealed additional diversity that still awaits formal description or recognition. The undescribed or otherwise unrecognized component of California's plant diversity includes lineages that may be challenging or impossible to identify reliably based on morphology but are evolutionarily distinct based on multiple lines of evidence, including molecular (DNA) and biochemical findings. Inferred ecological differences between closely related cryptic lineages often underscore that such diversity warrants conservation attention and should be anticipated in plant groups that are geographically widespread or occur across steep ecological gradients. A major challenge of systematic botany is resolution of fine-scale phylogenetic structure and refinement of taxonomy to reflect natural groups that have largely evaded detection but may have irreplaceable ecological properties, including tolerances to physical environmental extremes or herbivory, or host status for other endemic organisms. The preservation of cryptic diversity, not just genetic variation, needs to be considered in conservation strategies for responding to climate change and other human-caused habitat degradation and fragmentation. Otherwise, an untold number of endemic plants may become extinct through inadvertent neglect or from well-intended but irreversible actions. Such extinction would represent not only a loss of biodiversity, with associated loss of ecological function and evolutionary potential, but also a loss of access to evolutionary information that could prove critical to understanding the past and present flora, including the ability to secure its future.

Population-level sampling illuminates near-cryptic species diversity in *Navarretia* (Polemoniaceae)

Leigh Johnson

California is the center of diversity for many genera. For *Navarretia* (Polemoniaceae), 91% of the recognized species and subspecies occur within California's borders, and 57% are endemic to this state. With 47 species currently recognized, *Navarretia* has increased greatly in number from the 28 that were recognized in the first edition of The Jepson Manual. Four species were added as the result of molecular work that placed former members of *Gilia* within *Navarretia,* along with resurrecting a cryptic species long lost in synonymy. Molecular data also contributed to one subspecies being returned to species status and another elevated to species status. Thirteen additional species (10 of these found only in California) have been described as new. These species have come to light largely through field work purposefully conducted to sample species broadly across their geographic range. Continued field work combined with herbarium studies indicates additional diversity exists in several species-groups still being investigated. Some of the taxonomic novelties enumerated above are geographically widespread while others are narrowly distributed; some are edaphic specialists while others are more generalists. Most, however, are at least somewhat superficially similar to previously recognized species such that their taxonomic recognition has been previously overlooked.

Two cryptic species of California mustard within *Caulanthus lasiophyllus*

Justen Whittall

The pace of morphological, ecological and genetic divergence rarely coincides. At one extreme, we have explosive lineages with spectacular morphological variation associated with ecological adaptations and very little underlying genetic divergence (i.e. recent adaptive radiations). At the other extreme, we have genetically distinct lineages that lack differentiating morphological characteristics. Although both extremes are important targets for conservation efforts, charismatic adaptive radiations often overshadow cryptic species. Focusing on the latter, we know hidden diversity can be found lurking in widespread species whose distributions span phylogeographic barriers. Herein, we investigate the molecular and morphological variation among 52 populations of the widely distributed California mustard, *Caulanthus lasiophyllus* (Brassicaceae) and compare it to its closest relatives in the "Guillenia Clade" (*C. anceps* and *C. flavescens*). Genetically, we compare sequences from the nuclear ribosomal ITS region and two chloroplast loci (*trn*L-F and *ndh*F). All 52 individuals were also scored for 13 morphological traits, as well as monthly and annual climate conditions at each collection locality. The molecular data clearly indicate that *C. lasiophyllus* consists of two distinct lineages separated by eight ITS differences - eight times more variation than what distinguishes *C. anceps* and *C. flavescens*. Fewer variable sites were detected in the *trn*L-F and *ndh*F regions, yet these data are also consistent with cryptic division within *C. lasiophyllus*. These two cryptic lineages are geographically and climatically distinct; yet nearly indistinguishable morphologically (however, an ephemeral basal leaf character discovered during the course of this study may help distinguish these lineages early in development). These results for a relatively common California native highlight the potential for cryptic genetic divergence in presumed singular, widespread species that span biogeographic barriers. The relationship between neutral genetic divergence and ecological adaptations is an important next step. Regardless, the potential for cryptic genetic divergence underlying species that span biogeographic barriers, should be considered when translocating germplasm.

Look again: hidden diversity in California jewelflowers

Kyle Christie

California supports more endemic plant taxa than any other comparably sized area in North America, and is one of the world's most species-rich biodiversity hotspots. It hosts more floristic diversity than any other state in the United States, yet is also the second most at-risk to species loss. Recent estimates suggest that over two million, and potentially up to eight million species occur on Earth, however such assessments often fail to identify cryptic species, or those hidden to traditional taxonomic approaches. Accurately identifying species has major implications for conservation and management, particularly in the face of global climate change and habitat loss. The jewelflowers (*Streptanthus*, s.l.) are notable for their recent diversification in California and propensity for occurring on harsh serpentine soils. Despite substantial previous work in this group, additional diversity may still be undiscovered. An integrative taxonomic approach – one combining morphology, biological factors, and molecular evidence – suggests that multiple species have remained hidden in plain sight within the *Streptanthus breweri* complex. This finding illustrates how a better understanding of species and ecotype diversity may inform restoration efforts, and ultimately foster California's unique plant diversity.

Poppy Puzzles: Clarifying a couple cryptics

Shannon Still

Currently there are 18 taxa recognized in the genus *Eschscholzia*. However, due to morphological variation, there have been nearly 200 named taxa and >160 type specimens for the genus, of which more than 100 are recognized as synonyms for the California poppy (*E. californica*). While this was excessive as many of these taxa were described by overzealous botanists, there are still many mysteries to solve in the genus. This talk will discuss how a couple of new species were described, and where current and future work could help resolve some of the cryptic mess in the group.

Monterey pine colonization in northern California: Implications for species introductions in a changing climate

Robert Steers, Susan Fritzke, Jen Rogers, James Cartan, and Kaitlyn Hacker*

Monterey pine (*Pinus radiata*) has been planted throughout the world and is known to colonize native vegetation types. To determine the impact of pine colonization on northern coastal scrub, floristic surveys were conducted in 20 blocks that consisted of occupied and unoccupied plots. An occupied plot contained two subplots located under the canopy of an isolated pine tree, whereas a paired, unoccupied plot contained two subplots located in coastal scrub adjacent to each pine. Pine trees sampled ranged in size from 2.8 to 119 cm (1.1 to 46.9 in) basal diameter. The results demonstrate that understory native cover and species richness are negatively correlated with tree size. This study also shows that type-conversion from shrub to tree dominance will result in fundamental impacts, and that the earlier trees are controlled, the lower those impacts will be. Whether to accept these vegetation changes as desirable or not requires consideration given the natural resource management objectives of the colonized area, the special status designation of this species (CDFW G1/S1, CNPS 1B.1), the commercial importance of *in situ* genetic conservation, and the overall conservation challenges of P. radiata, a fire dependent species with only five, disjunct natural populations.

Amplifying within-population resilience to drought and disease in the Lake Tahoe Basin

Patricia Maloney

Recovery from drought, pest-outbreaks, and fire often requires restoration efforts. Using trait-based approaches to estimate quantitative genetic parameters and utilizing comprehensive environmental datasets allows one to assess the ability of natural populations to respond to selection pressures. Plant populations can adjust to changing environmental conditions through a number of processes including local adaptation, demographic (e.g., episodic mortality), physiological, and effective dispersal. Natural resource managers are at a critical moment in how to best manage resources for adaptation and uncertainty. Selection of seed/source material, either local or non-local, for restoration has become much debated and is a fundamental decision for land-managers. Using trait-based approaches to estimate quantitative genetic parameters, including heritability and population differentiation allows one to assess the ability of natural "local" populations to respond to selection pressures. Maloney and others find that traits are correlated not only with climate but soil and geography, such correlations are one type of evidence for local adaptation. Trait-based approaches linked with comprehensive environmental databases can provide a perspective on evolutionary potential that can better inform gene conservation activities (e.g., cone collection strategies, seed-banking, reforestation). A case study will be presented in which this approach and information was utilized to guide restoration strategies for sugar pine reforestation for mountain pine beetle outbreak recovery to facilitate regeneration and assist in gene flow in high MPB-impacted areas in the Lake Tahoe Basin.

The genetic consequences of hybridization between California native plant species with closely related taxa

Kristina Schierenbeck

When non-native genotypes or species are introduced, hybridization with native populations may erode the genetic composition of local species, perhaps even resulting in extinction. When hybridization is accompanied by introgression, or repeated backcrossing to local, parental species via hybrids, there will be a loss of genetic distinctiveness in the local population. Genotypes within native populations or species have evolved *in situ* for multiple generations. Gene flow from non-native introductions into native populations will alter the genetic structure of long stable populations that evolved via natural selection. These native populations may then no longer be adapted to the local environment and unable to respond to local conditions. Well-documented examples of non-native genotypes hybridizing intra- and interspecifically with native California plant taxa and that have resulted in changing the genetic composition of native populations and species will be provided.

Lessons from provenance tests- real trees on the ground

Jessica Wright

Seed transfer in tree species in California is guided by the California Seed Zone map. Seeds are considered safely transferred within a 500-foot elevation band within a seed zone. However, given the fact that the climate is changing, how can we most efficiently use this map going forward? One of the best sources of information on how trees respond to being moved are provenance tests. These tests contain a number of different sources of trees, growing in one or more common gardens. Data from these tests can shed light on how trees perform in a novel climate, both in terms of growth but also traits that may be important for the success of trees. Here I will discuss results from a provenance test in valley oak, *Quercus lobata,* as well as a number of tests in conifers. We have found associations with the climate of origin of the trees, and their performance in the tests, including growth as well as the timing of leaf emergence in the spring. These results could be important for informing seed transfer in California.

Consideration of a Paradigm Shift in the Genetic Management of Fragmented Populations

Michele Dudash

Thousands of small isolated populations or species are threatened from a lack of gene flow that has resulted in inbreeding depression, lower genetic diversity, and ultimately an increased risk of extinction. We offer an alternative management strategy with clear guidelines that incorporates both genetics and evolutionary biology and advocate for this approach rather than inaction. Augmentation of gene flow as a management strategy has been overly conservative owing to concerns surrounding outbreeding depression. Our collective body of work demonstrates that the risks of outbreeding depression can be predicted, inbreeding depression is ubiquitous, and taxa (populations or species) with lower genetic diversity will experience even greater challenges with ongoing global climate shifts. The essential steps of a scientific-based genetic management plan for diploid plants and animal populations policy is reviewed in the context of current policy, which we believe is woefully inadequate.

Regional genetic distinctiveness among remaining populations of an endangered salt marsh plant in California and conservation strategies

Amy Vandergast, Elizabeth Milano, Margie Mulligan and Jon Rebman*

Salt marsh systems in California have been highly modified and many marsh obligate species have undergone range reductions and habitat loss with concomitant losses of genetic diversity and connectivity. Remaining salt marshes are threatened by rising sea levels, and so these habitats will likely require active restoration and re-establishment efforts. We used flow cytometry and single nucleotide polymorphic markers (SNPs), to assess relative ploidy, and estimate genetic diversity and population structure across remaining populations of an endangered annual plant, salt marsh bird's-beak (*Chloropyron maritimum* subsp. *maritimum*), in southern California and Baja California, Mexico. Overall, we found five distinct genetic clusters that coincide with geographic regions. Genetic diversity was greatest in the southern part of the range including Baja California and San Diego. Our results highlight that each geographic cluster represents a unique subset of the taxon's genetic diversity that should be protected, and regional structure can provide guidance for future restoration.

Considerations when mixing source populations to restore rare plants

*Adrienne Basey St. Clair, Peter Dunwiddie, Jeremie Fant, Tom Kaye, Andrea Kramer**

Abstract: Mixing source populations for reintroduction efforts is increasingly recommended for rare species, either because available source populations don't match the ecology of the reintroduction site, or because they have low genetic diversity and/or may be experiencing inbreeding depression or mate limitation. But to-date very little information is available on whether mixing source populations leads to desired changes in reintroduced populations, and whether the approach used to mix populations impacts outcomes. We tracked metrics of genetic diversity after four wild-collected source populations were mixed in a nursery production setting and used to reintroduce multiple populations of *Castilleja levisecta*, a rare species extirpated from Oregon and experiencing inbreeding depression in remnant populations in Washington. We found that genetic diversity, inbreeding, and relatedness changed during the production and use of material with mixed source populations. Additionally, the step at which source populations were mixed (before or after nursery production), and the type of plant material used (seed or seedling), influencing whether source populations were equally represented. Genetic diversity increased throughout the production process, while inbreeding and relatedness increased in nursery production beds but decreased in reintroductions. Populations restored using seeds had lower inbreeding and relatedness relative to those restored using plugs. The results illustrate the value of taking a long-term, integrated approach informed by research when planning and implementing reintroductions with mixed-source germplasm.

The ghosts of translocations past, present, and yet to come: Applying inexact molecular tools to rare plants on shifting landscapes

Loraine Washburn

Many rare plants we see on the southern California landscape today are the unlikely survivors of past demographic circumstances which are generally unknown to us. In undertaking the snapshot glimpse that molecular tools allow of the present moment, we then hope to use this insight to inform translocations of plants into circumstances and settings whose future state we can view through the lens of future climate predictions, but without a clear view of what this future may actually offer from the plant's perspective. The cases of Orcutt's hazardia and Nevin's and the island barberries exemplify such attempts to make good choices for informed propagation and planting, in hopes of allowing these species a time yet to come.

Topoclimatic variability and seed collection strategies

Stu Weis

Seed zones provide an important coarse scale filtering of climatic adaptations, but topoclimates within seed zones should be considered in designing sampling strategies to capture a wide range of genetic variability. Topoclismates include insolation differences (I.e. north versus south-facing slopes) which drive maximum temperatures and water balance. Topographic position determines cold air pooling, which drives minimum temperatures and frost frequency. These gradients can be on the order of 5-10ºC and occur over tens of meters. Phenological variation across topoclimatic gradients can be several weeks. Seed collection and production strategies need to increase the probability climatic suitability by explicitly sampling across the entire available topoclimatic and phenological range.

Production of Native Seed of Known Genetic Origin at Hedgerow Farms

Pat Reynolds

Hedgerow Farms has been producing native seed of known genetic origin for habitat restoration projects for more than 30 years. The farm has approximately 350 acres in seed production with more than 120 different species grown out. For many species, Hedgerow Farms produces several different ecotypes that cover wide geographic areas in central and northern California so best-fit ecotypes can be used for specific habitat restoration projects. Ecotype seed production starts with wildland stock seed collection and moves through field planting, maintenance, harvest, drying, cleaning, testing, bagging, labelling, storage and distribution. Each step in the process requires specialized equipment and in-depth knowledge gained through trial and error and experimentation. Numerous best management practices are incorporated into farming practices to maintain the genetic integrity of the species and ecotypes produced. These include crop rotation, appropriate spacing between plots, consideration of species breeding systems and thorough cleaning of equipment and machinery between uses. Hedgerow Farms also implements numerous seed increase contract grows yearly for clients that are seeking local ecotypes that are not commercially available. Hedgerow Farms' operation includes a native plant nursery with capabilities to grow out all of the ecotypes produced from seed and contract grows of special items from wildland collected seed.

A landscape genomics framework for native plant restoration in the Mojave Desert

Daniel F. Shryock, Lesley A. DeFalco, and Todd C. Esque*

Local adaptation is pervasive across plant taxa and shapes how populations respond to changing environments, including when seeds are transferred for ecological restoration. Consequently, understanding the environmental drivers of local adaptation is fundamental to predicting species responses to climate change and effectively applying seed treatments to restore degraded ecosystems. Seed sourcing strategies are increasingly designed to promote both climate change resilience and long-term population stability. While substantial challenges remain in obtaining genetic information necessary to inform restoration strategies for native species, the availability of high-throughput sequencing has made landscape genomics a cost-efficient approach for rapid development of seed transfer guidelines. In this approach, genome scans are used to characterize associations between genotypes and climate regimes and to predict spatial patterns in local adaptation. In support of the National Seed Strategy, the U.S. Geological Survey (USGS), Western Ecological Research Center is working in partnership with the BLM Mojave Desert Native Plant Program to develop landscape-genomics based seed-transfer guidelines for multiple native species of restoration importance. Thus far, we have developed seed transfer zones for three Mojave Desert species – *Ephedra nevadensis*, *Sphaeralcea ambigua*, and *Plantago ovata* – with several other species currently in genotyping. We present a brief overview of this approach and describe how landscape genomics can promote effective, resilient restoration designs in a time of rapid environmental change.

Vegetation refugia and climate-adaptive land management

Jim Thorne, Joseph Stewart, Ryan Boynton, Jessica Wright, Hyeyeong Choe, Steve Ostoja*

This talk presents three concepts related to climate change and vegetation. After a few definitions, we present an overview of: (1) Using analogous climates to anticipate future conditions at a restoration site to ask where should seed source come from for planting?; (2) The need for a spatial triage approach to collection of seeds for use in future restoration work; and,
(3) How climate shifts within a network of protected areas can be used to anticipate future species suitability.These basic concepts can be used with varying levels of detail in helping conservationists plan and implement conservation, restoration, and climate adaptation.

The right seed in the right place at the right time: National Seed Strategy & Seeds of Success

Peggy Olwell

The loss of biological diversity, the lack of commercially available, locally adapted native seed, and the increasing rate of extreme weather events such as wildfires, hurricanes, floods and drought are taxing our ability to restore healthy native plant communities and functioning ecosystems, globally. In 2001, Congress recognized the lack of commercially available native seed and directed the BLM to develop a native plant materials development program and Seeds of Success is the first step in developing native seed for restoration. Over the past 20 years, BLM and its SOS partners have made over 25,000 native seed collections of over 5,000 taxa from 43 states. In California, alone, SOS made more than 3,900 seed collections of 922 unique taxa covering 430 genera from 15 different ecoregions. In 2014, the BLM and 11 other federal agencies recognized the necessity to highlight the issue and need for native seed and developed a National Seed Strategy (Strategy). The Strategy includes four goals, with associated objectives and actions to improve seed supplies for restoring healthy and productive native plant communities. The Strategy fosters collaboration between private, tribal, state, local, and federal partners to guide the development, availability, and use of seed needed for timely and effective restoration. With almost 4 million acres of land burned this year and with 5 of the 6 largest wildfires in California history occurring in 2020, the need for commercially available, locally adapted native seed is even more imperative. I encourage California to join the Seeds of Success partnership and work with us to implement the National Seed Strategy in California to address these urgent needs.