The Role of Genetics and Genomics in Riparian Restoration and Management: Insights from Research in Foundation Cottonwood Trees

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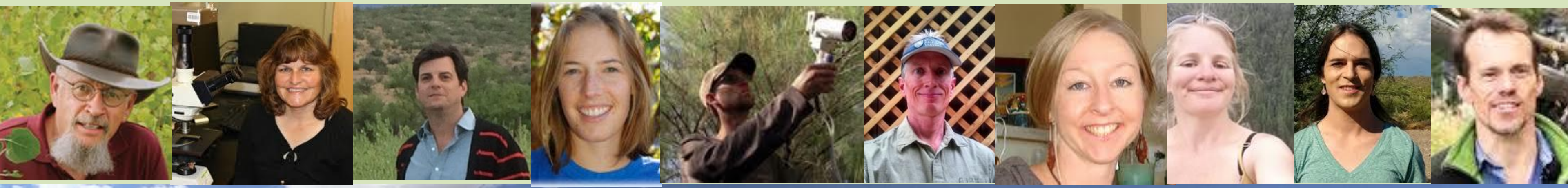

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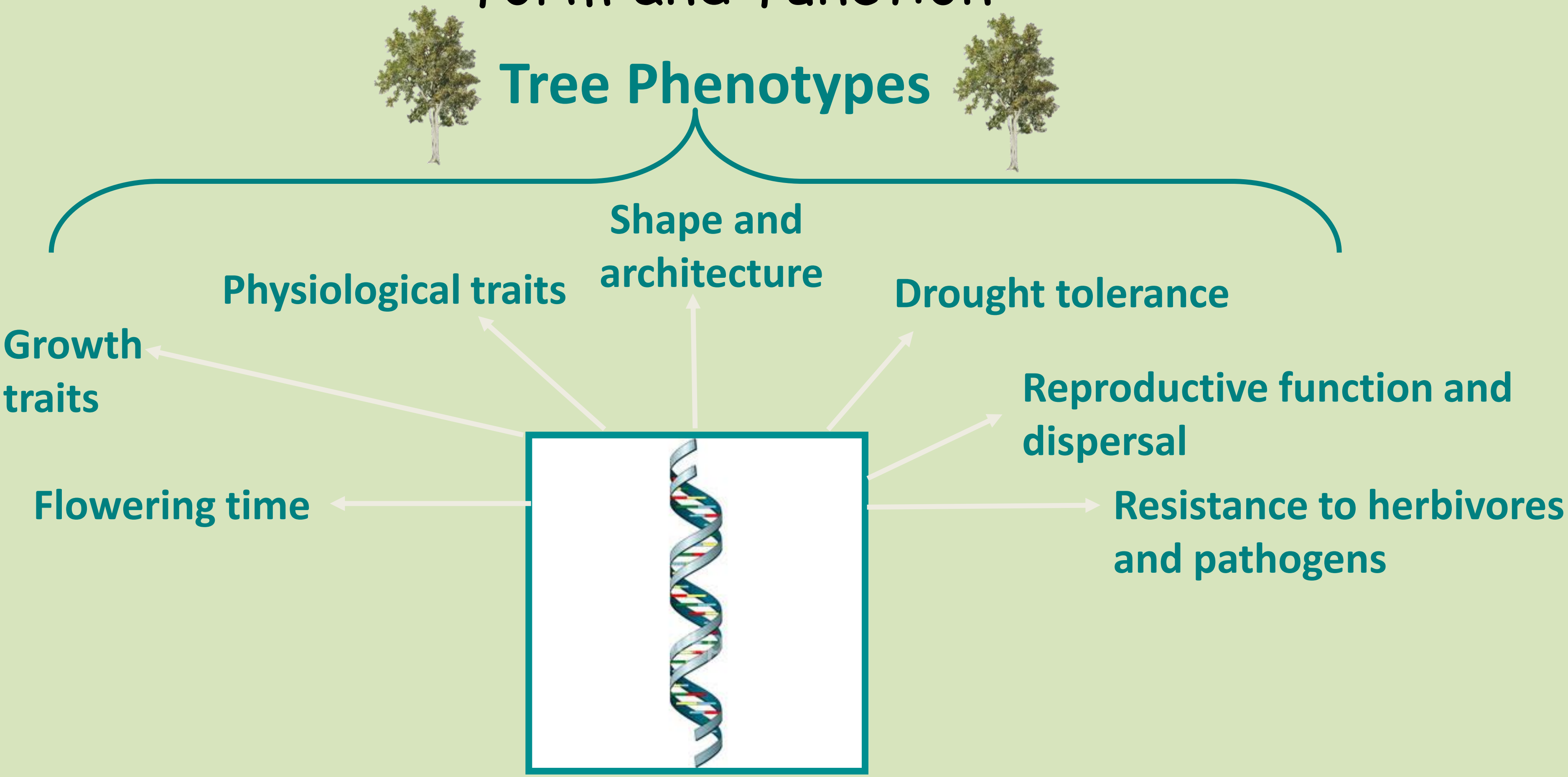
Fremont cottonwood "Ribbon of Green"
Boulder Creek, Utah
Photo by Tom Whitham

Why use genetic tools?

Genes and genetic variability determine form and function



Tree Phenotypes

Growth traits

Physiological traits

Shape and architecture

Drought tolerance

Reproductive function and dispersal

Flowering time

Resistance to herbivores and pathogens

Tree Genotype

Genetic and genomic information

- Genetic and genomic information
  - Molecular markers
    - AFLPs (many 1000s of loci; easy to generate)
    - SSRs (100s-1000s of loci; less easy to generate)
    - SNPs (1000s of loci;requires partial/whole genome sequencing)
  - Genomic sequences
    - Partial sequence data (e.g., individual genes, a few 1000bp)
    - Whole genome data (entire genomes; millions of bps)
- Both provide direct insight into the role genetics may play in restoration management

Allan, G. J. & Max, T. L. (2010) Molecular Genetic Techniques and Markers for Ecological Research. Nature Education Knowledge 3(10):2

Issues in restoration ecology

- Restoring with local vs. non-local genotypes
  - How well-adapted are local genotypes?
  - Will novel genotypes succeed in a new restoration site?
- Genetic variation
  - How much is known about genetic variation across a species' range?
  - How much of this variation is adaptive (i.e., able to respond to environmental change)?
- Sampling of collection sites
  - Should we be maximizing ecological distance? Genetic distance? Both?
- Preservation of ecological interactions
  - Do dependent communities respond to genetic variation in their hosts?

Investigating genetic variation in 3 riparian species

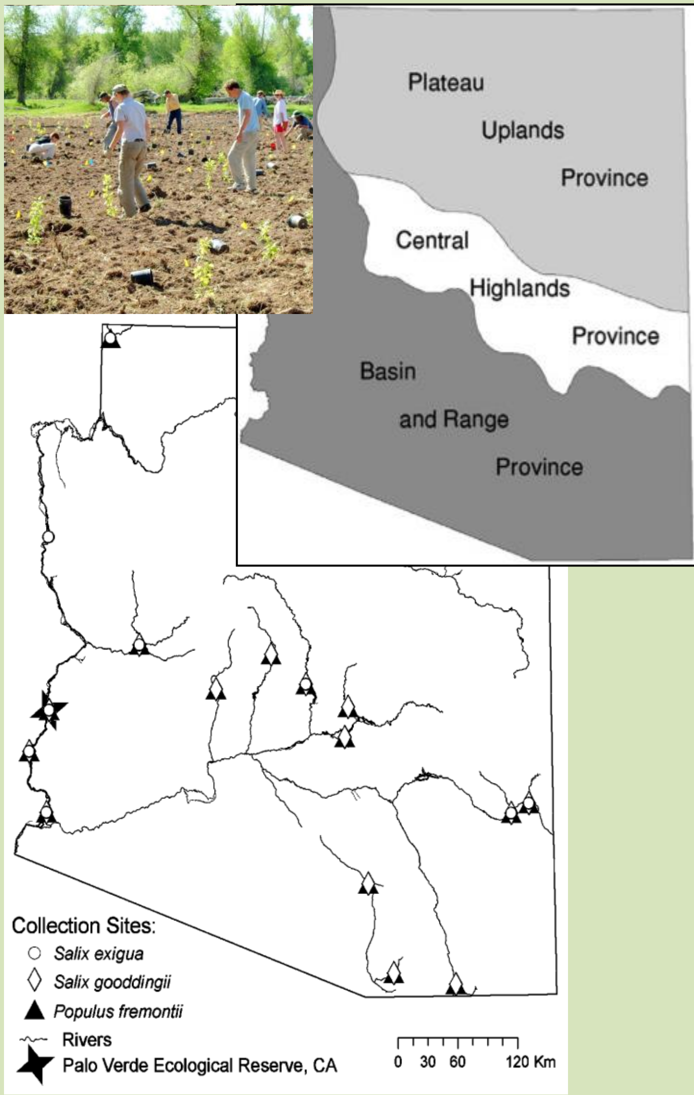
Fremont cottonwood *(Populus fremontii*)

Gooddings willow *(Salix gooddingii*)

Coyote willow (*Salix exigua*)

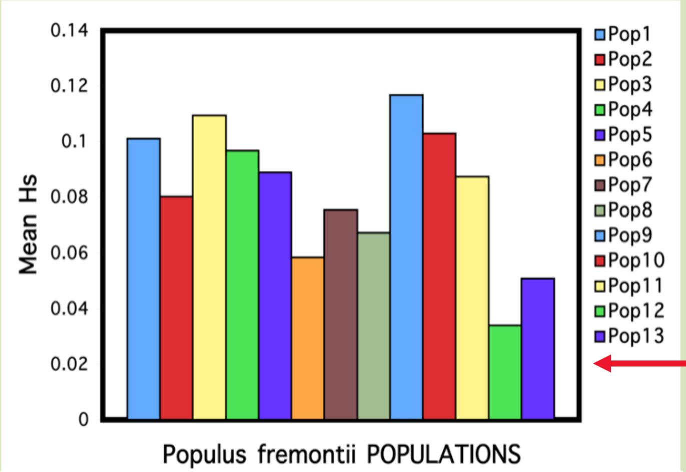
Restoration Experiment

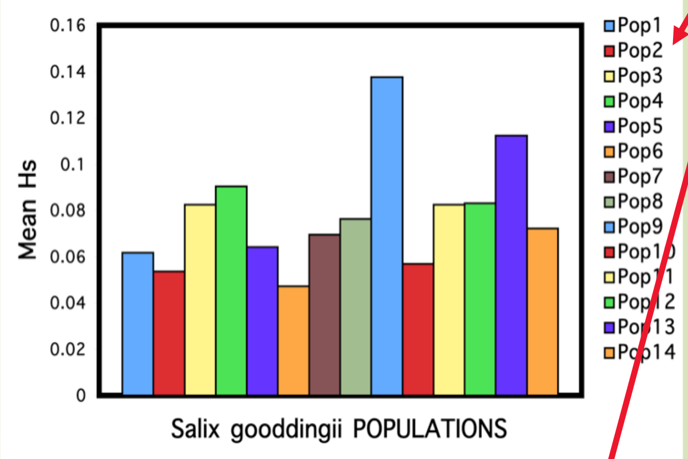
- Restoration of approximately 5,940 acres of riparian habitat along the LCR
- Propagation and planting of 3 riparian species:
  - Fremont cottonwood, Gooding's willow, and Coyote willow
  - 16 collection locations
  - 10 genotypes/ species/ location
  - 400 total genotypes
- Experimental design: randomized blocks of genetic diversity and structure
- Assessment of dependent community structure and composition

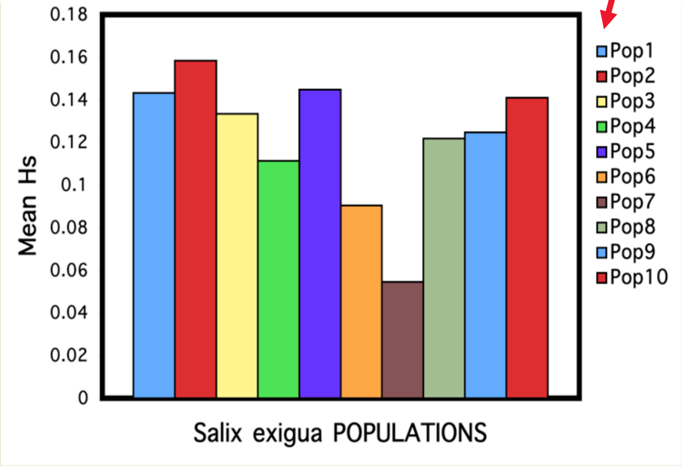


Populations of each species are variable in their genetic diversity and structure

H_s : Within population diversity

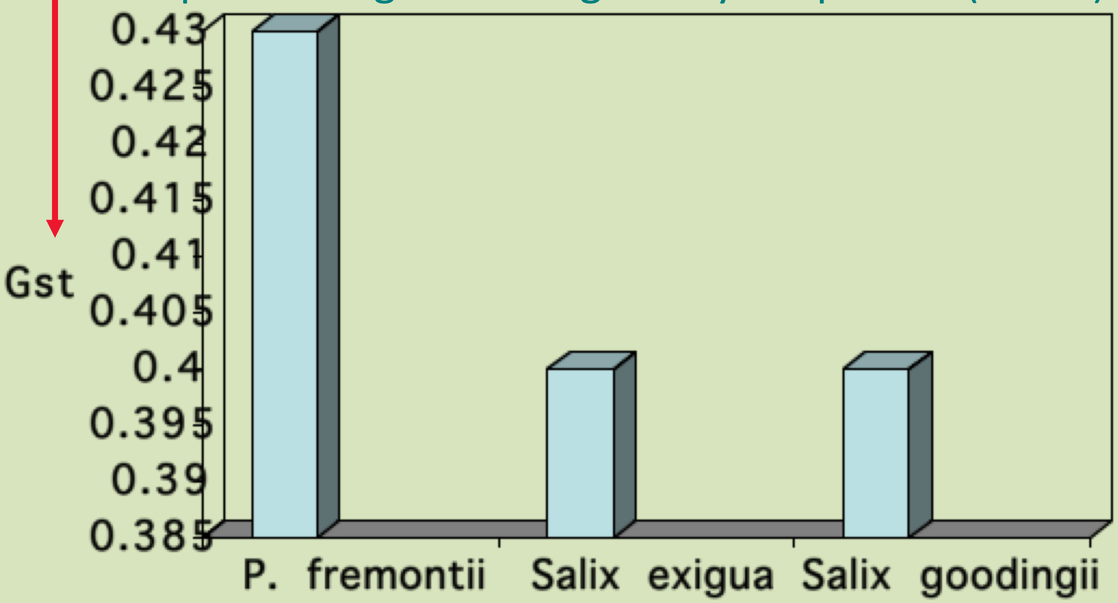




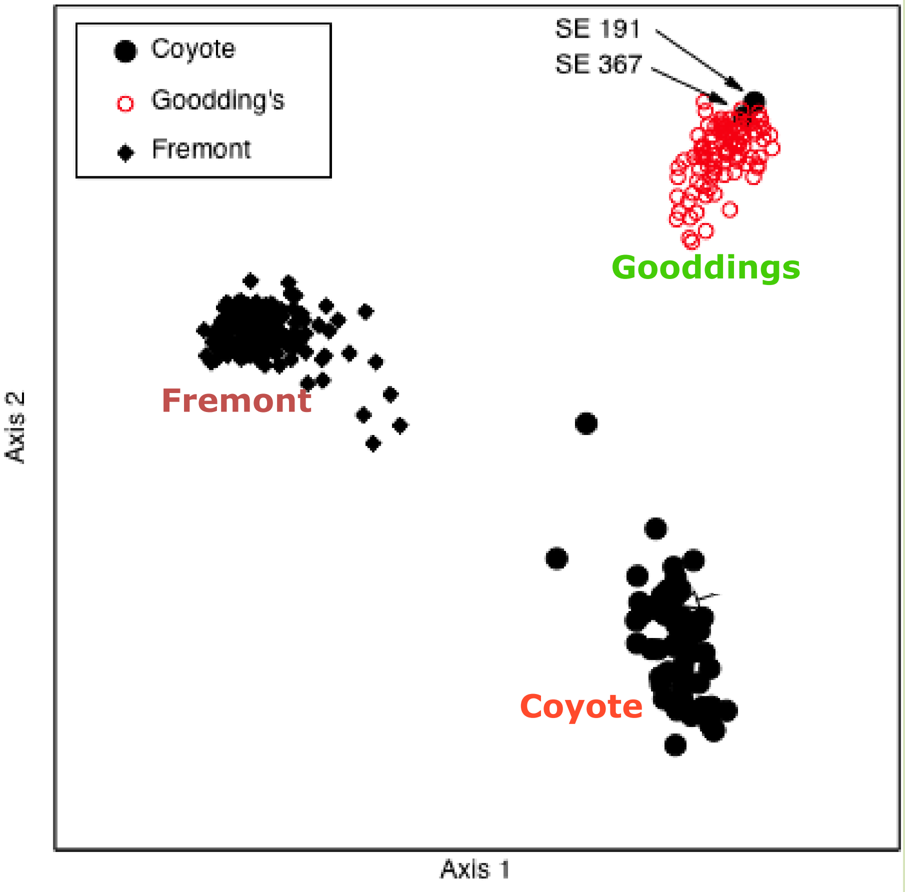


D_{ST}: Among population diversity

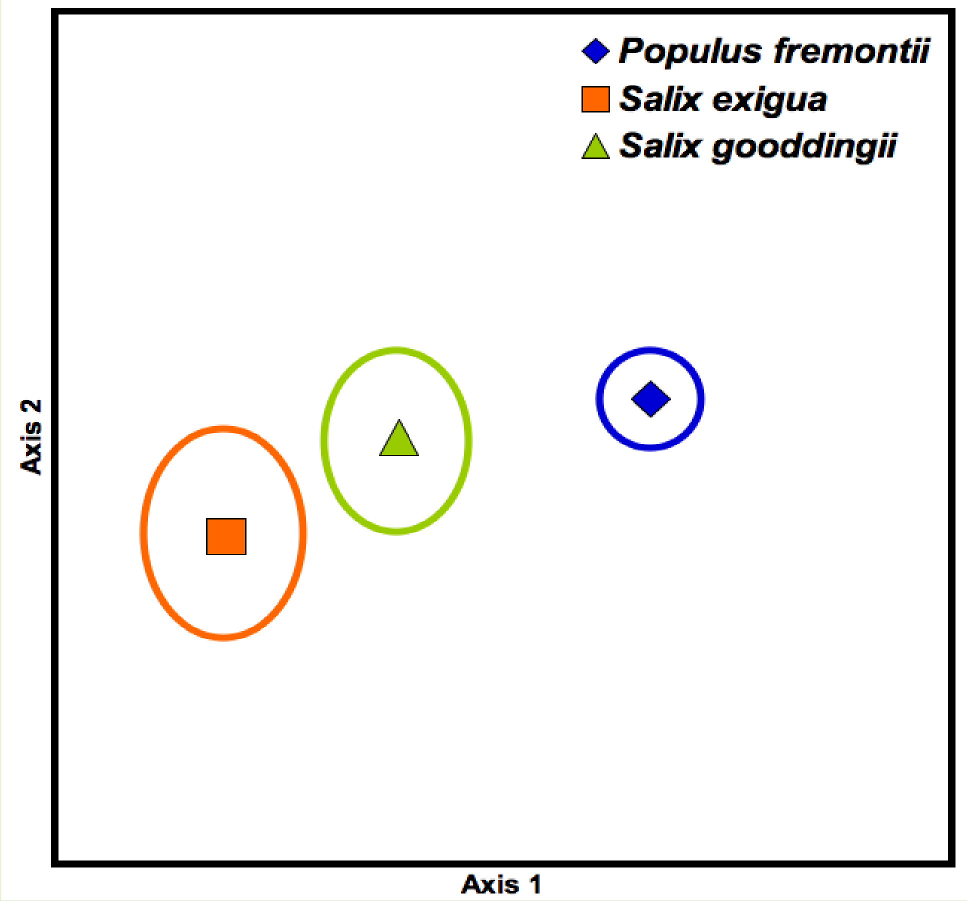
Amplified Fragment Length Polymorphisms (AFLPs)



Genetic differentiation of riparian species coincides with arthropod community differentiation



Species Genetic Differentiation based on AFLP markers

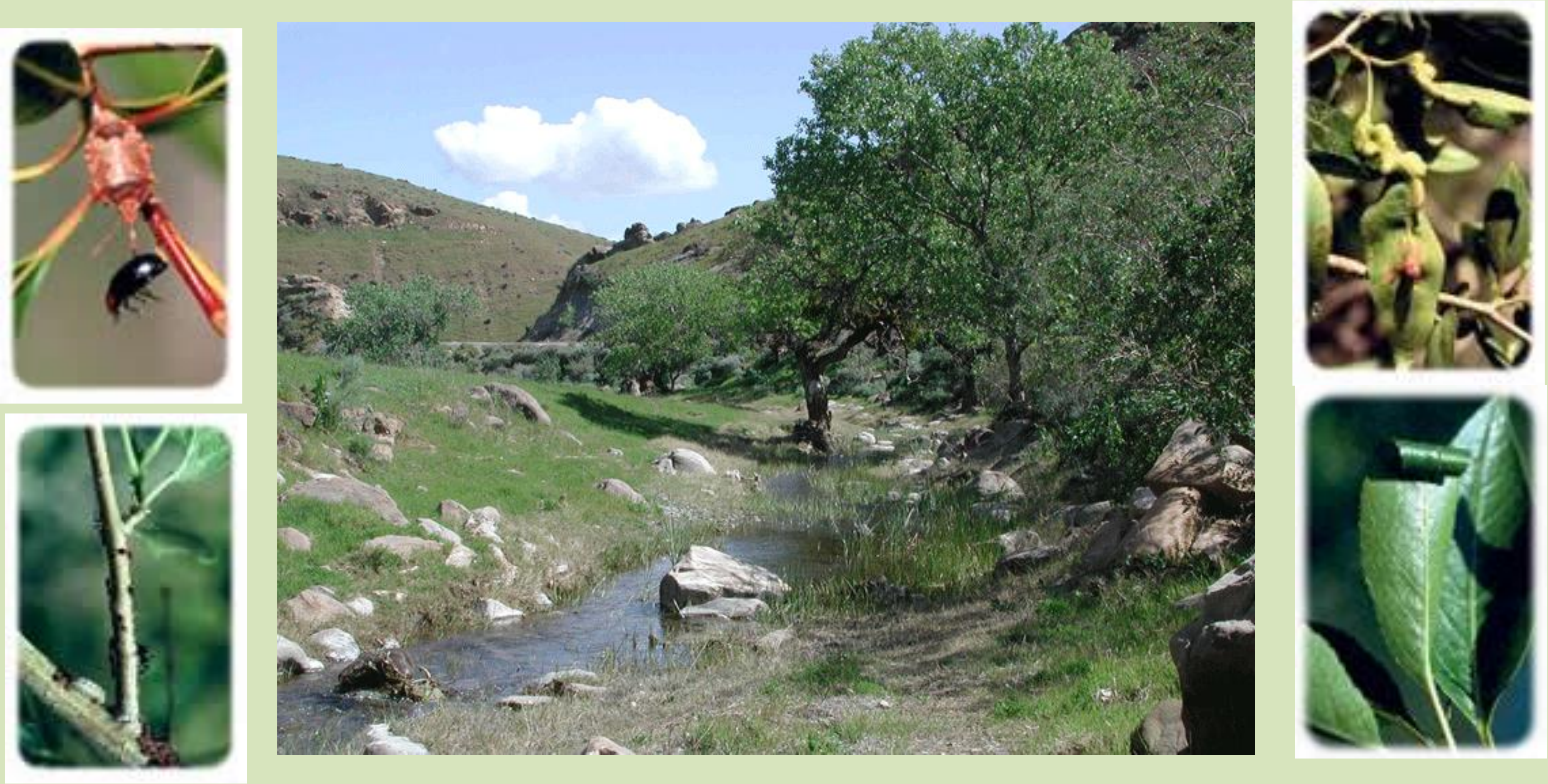


Arthropod communities on related riparian plant species are also differentiated

A genetic similarity rule determines arthropod community composition

(Bangert et al. Molecular Ecology 2006)

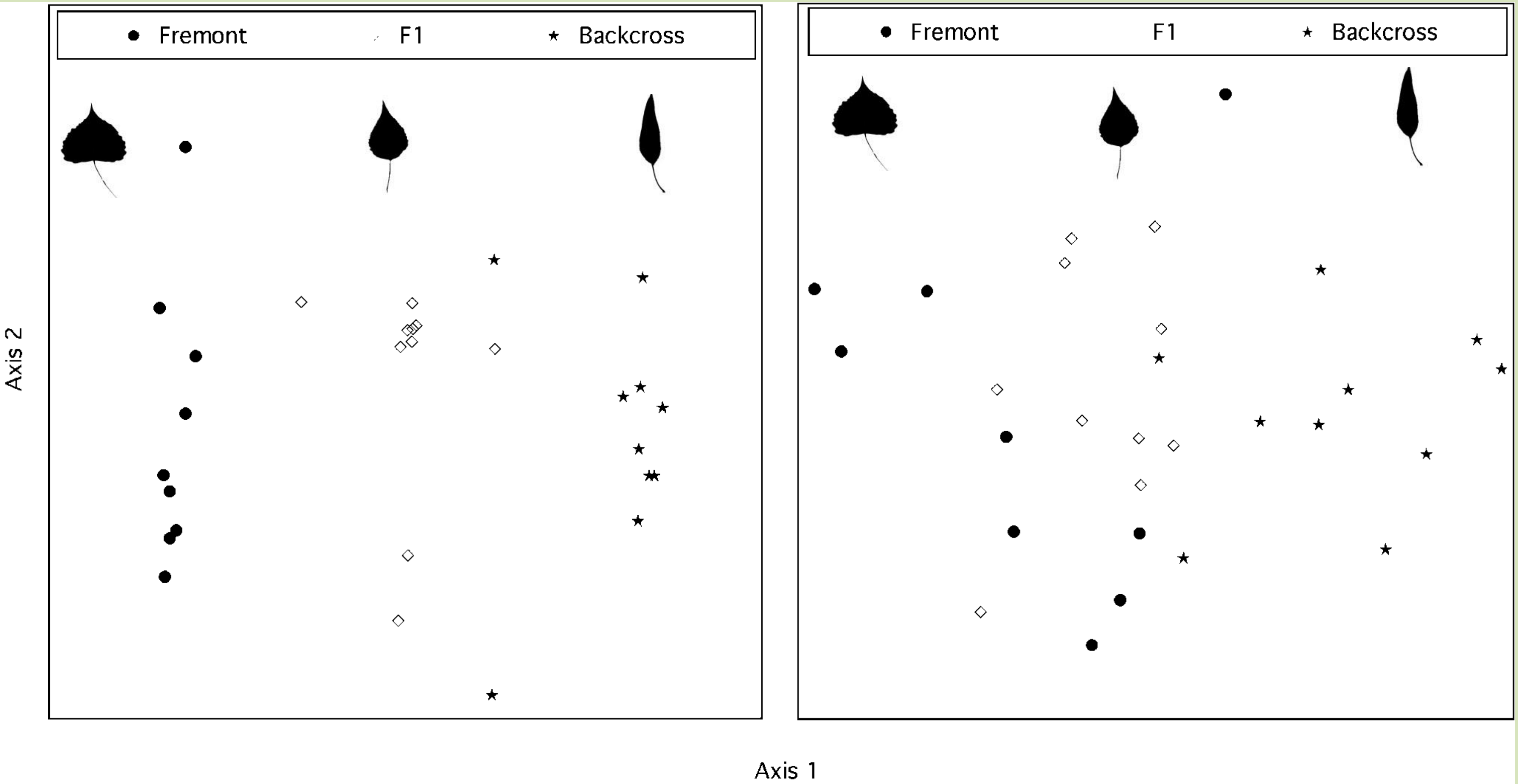
- Can we distinguish between hybrid hosts and their parent species?
- Does genetic variation in these hosts predict arthropod community composition?



Blue River, AZ: Fremont x Narrowleaf system

AFLP composition: Cottonwoods
all pairwise $p \leq 0.0001$

Arthropod Community composition:
all pairwise $p \leq 0.007$

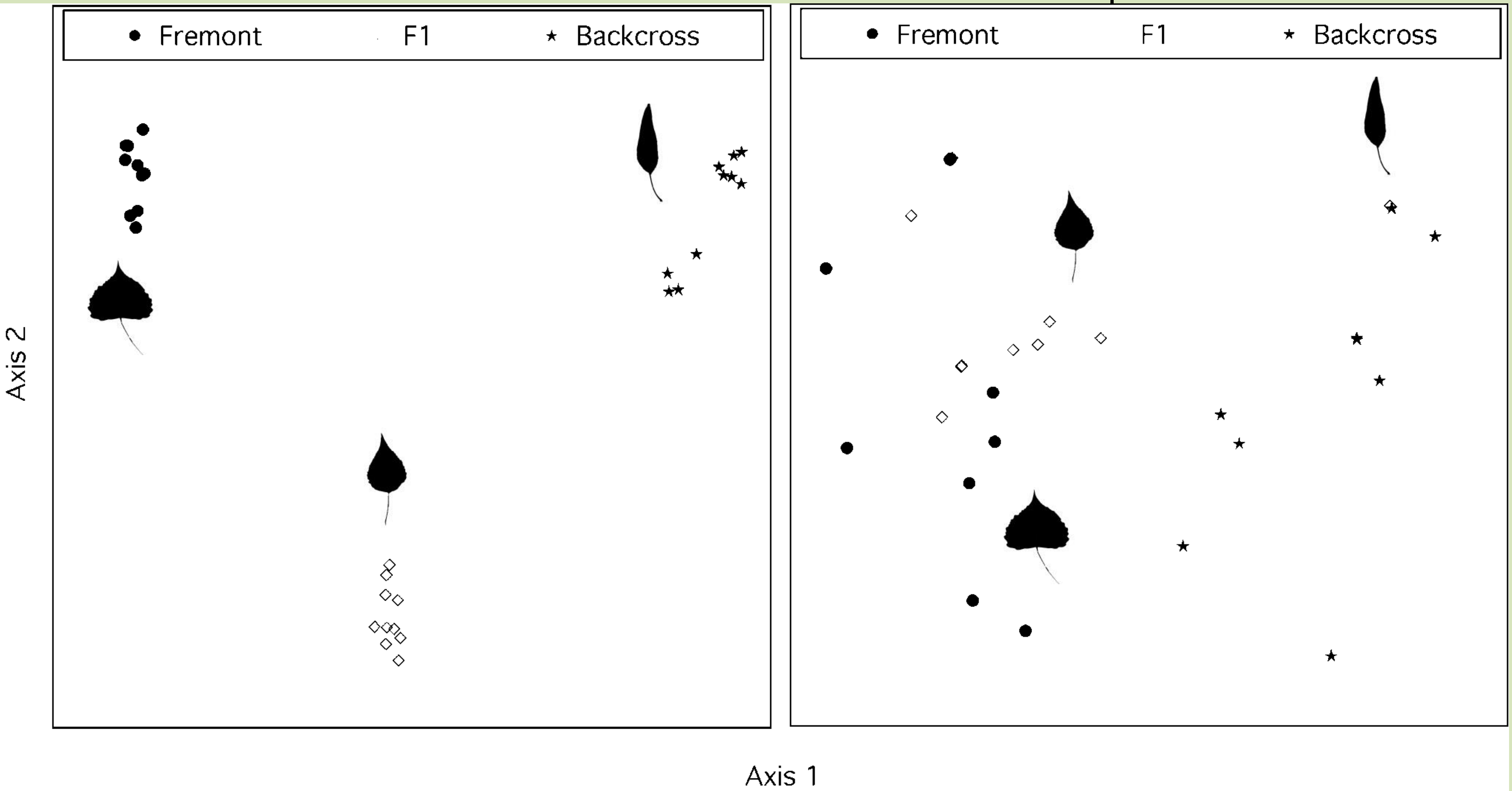


Bangert et al. 2006

Indian Creek, UT: Fremont x Narrowleaf system

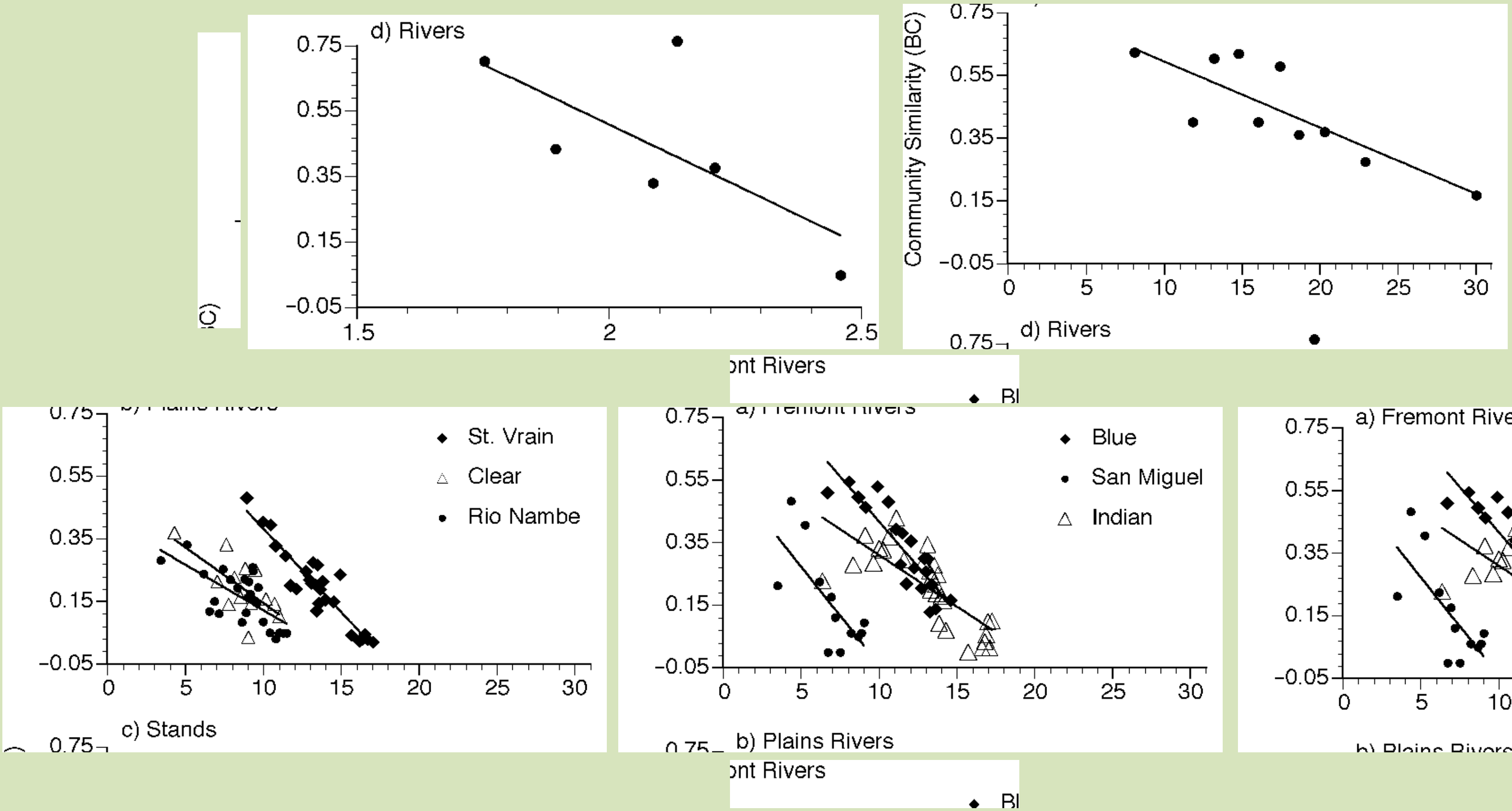
AFLP composition: Cottonwoods
all pairwise p ≤ 0.0001

Arthropod Community composition :
Fremont vs. F1 p = 0.04
other p < 0.0001



Bangert et al. 2006

Genetic variability matters:
Genetic variation and arthropod communities scale together from rivers to regions



Genetically similar trees have similar arthropod communities

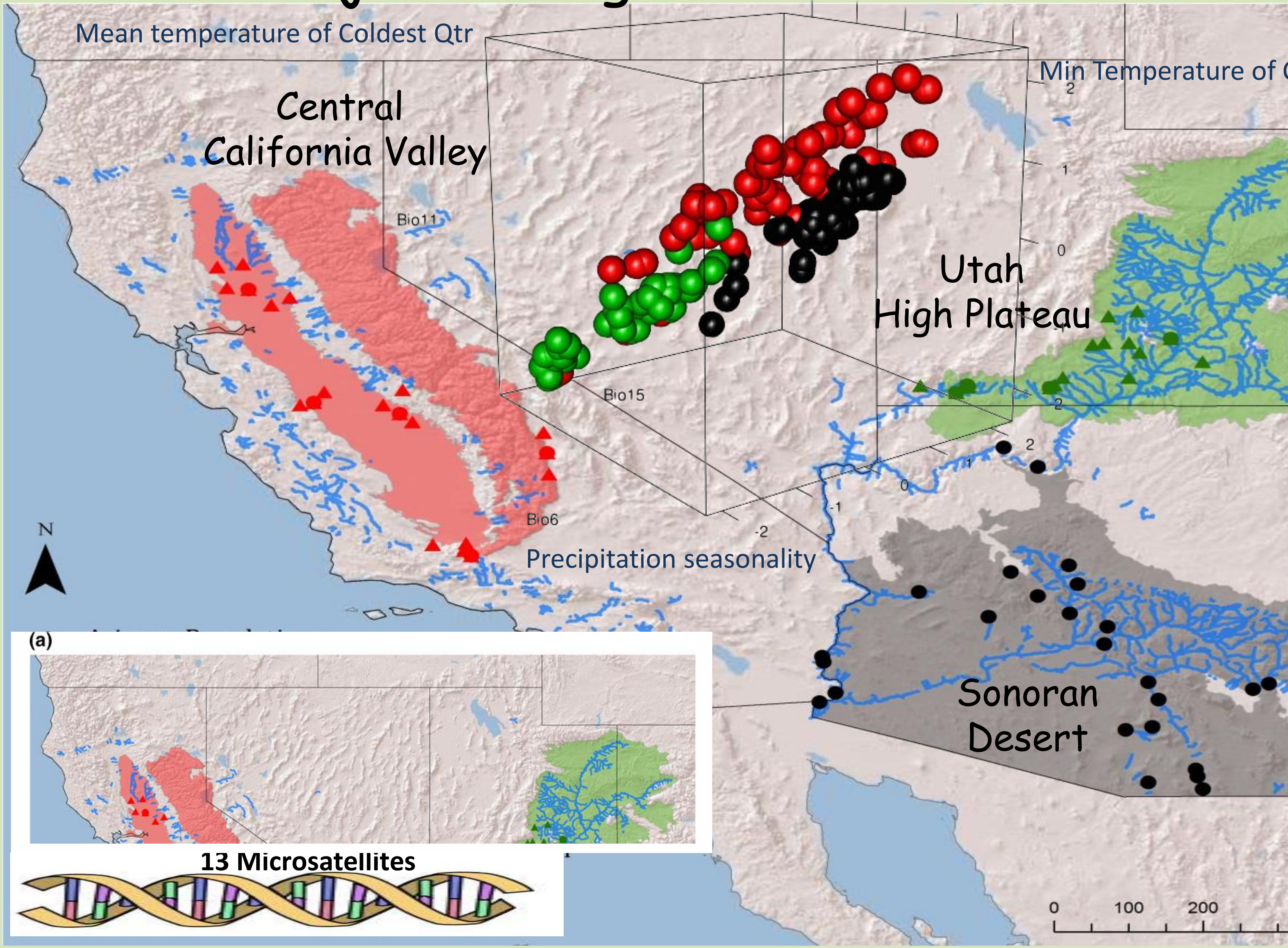
Bangert et al. 2006

Genetics & Environmental Variation

- To what extent is genetic variation shaped by environmental variation?
- Can we use genetic and genomic data to guide management and restoration of riparian ecosystems?

Fremont cottonwood "Ribbon of Green"
Boulder Creek, Utah
Photo by Tom Whitham

Genetic data aligns with climate niche data to define major ecoregions in Fremont cottonwood

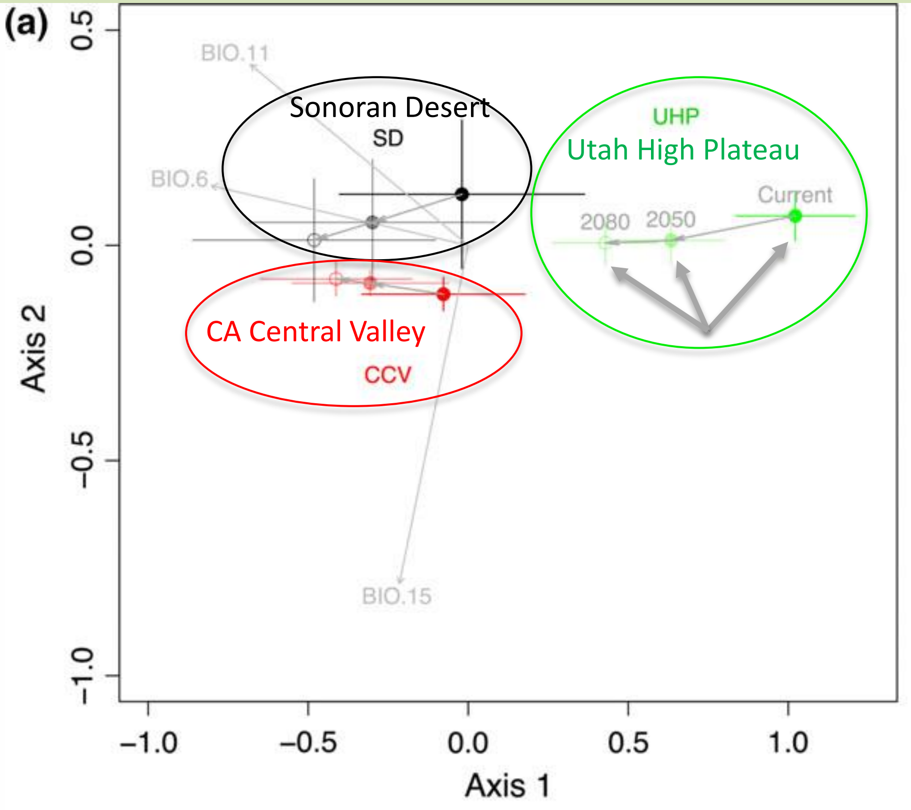


Ikeda et al. 2017, Global Change Biology

Dana Ikeda

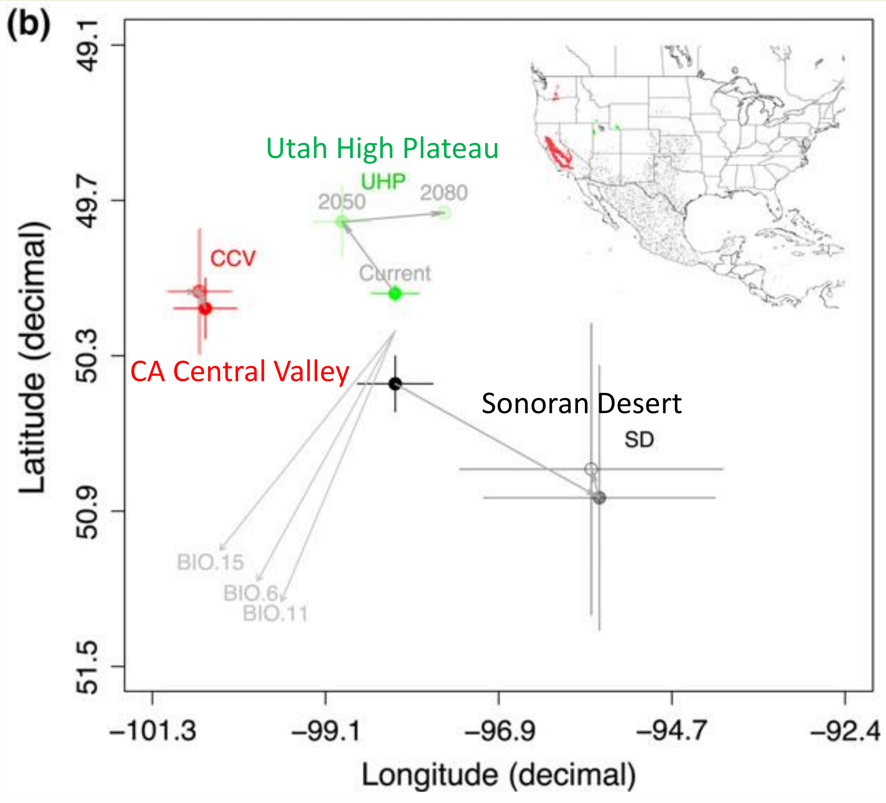
Genetically informed ecological niche models improve climate change predictions

DANA H. IKEDA[1,2], TAMARA L. MAX[3], GERARD J. ALLAN[1], MATTHEW K. LAU[4], STEPHEN M. SHUSTER[1] and THOMAS G. WHITHAM[1,2]



Ecotypes from each ecoregion occupy climatically distinct niche space

($p < 0.0001$)



Ecoregion niche space shifts with climate change resulting in greater niche divergence

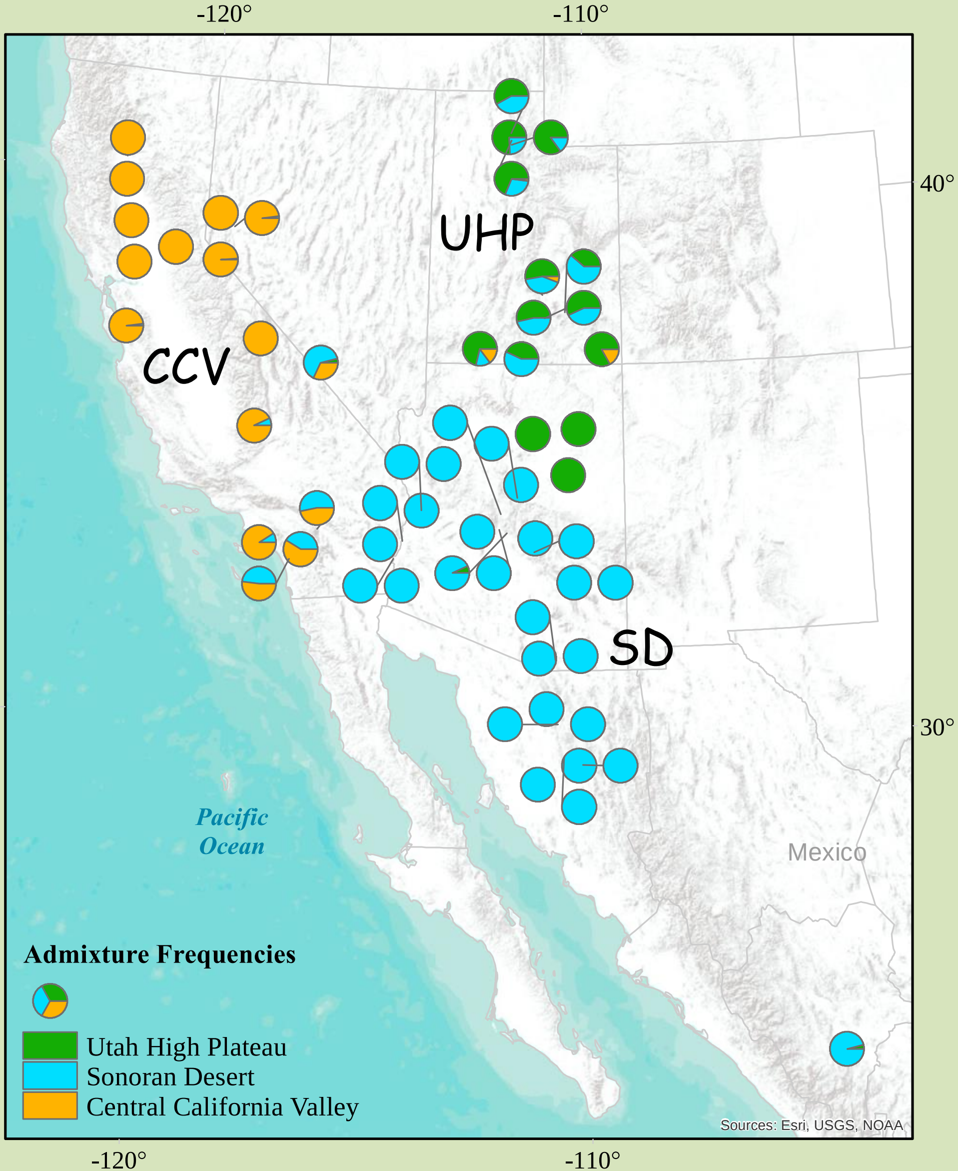
($p < 0.0001$)

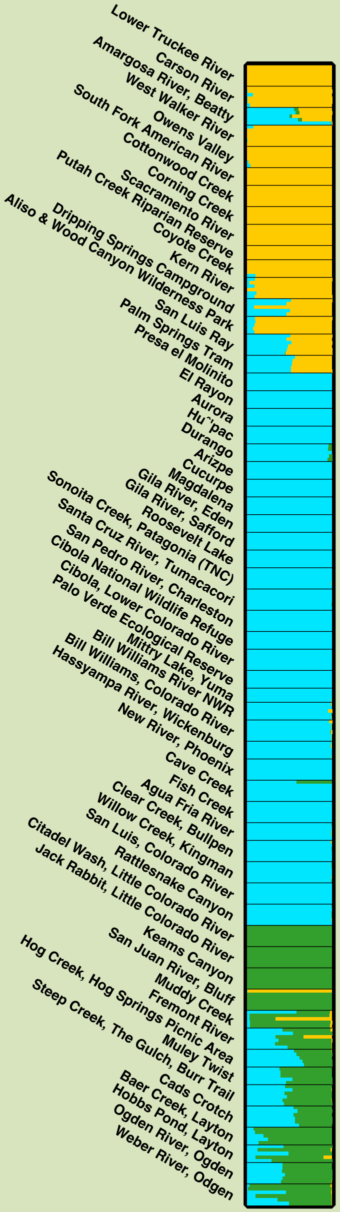
Global Change Biology (2017) **23**, 164–176,

Genomic SNP variation co-identifies 3 ecoregions and reveals landscape-level connectivity and admixture

(9000 SNP loci)

256 trees from 48 source populations across the species range genotype for 9000 SNP loci



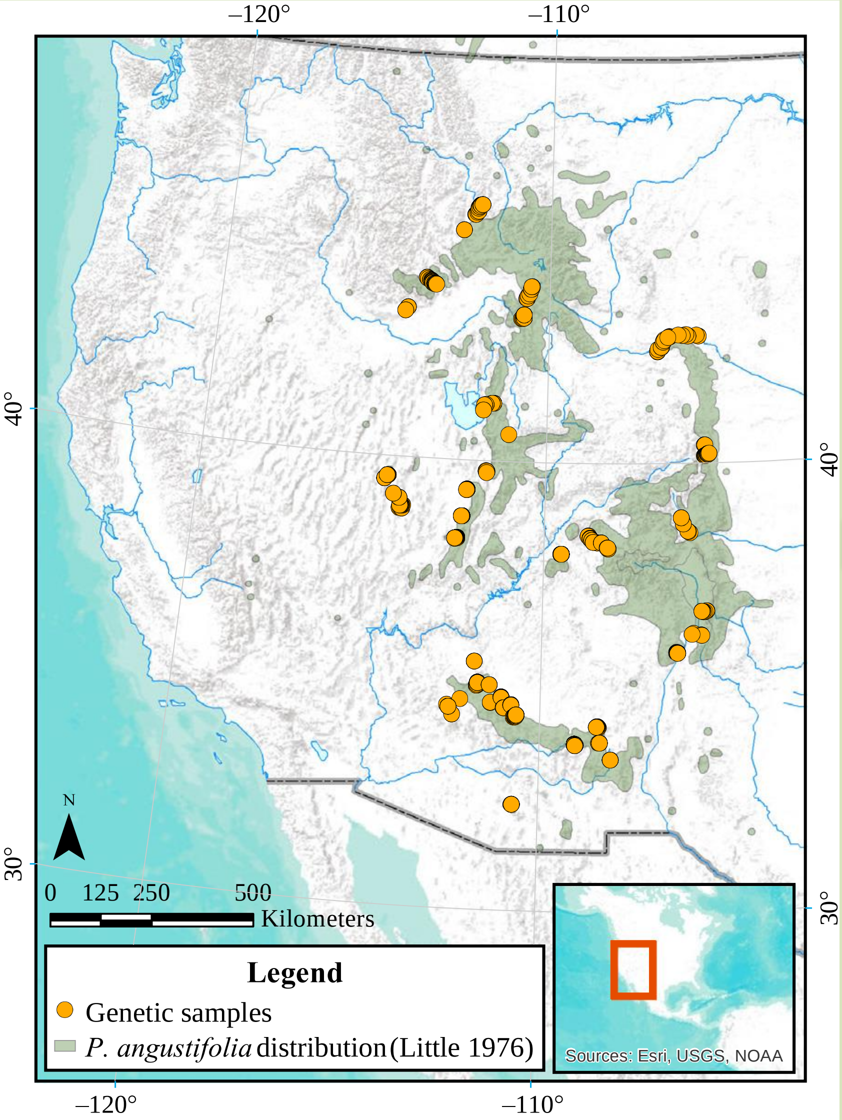


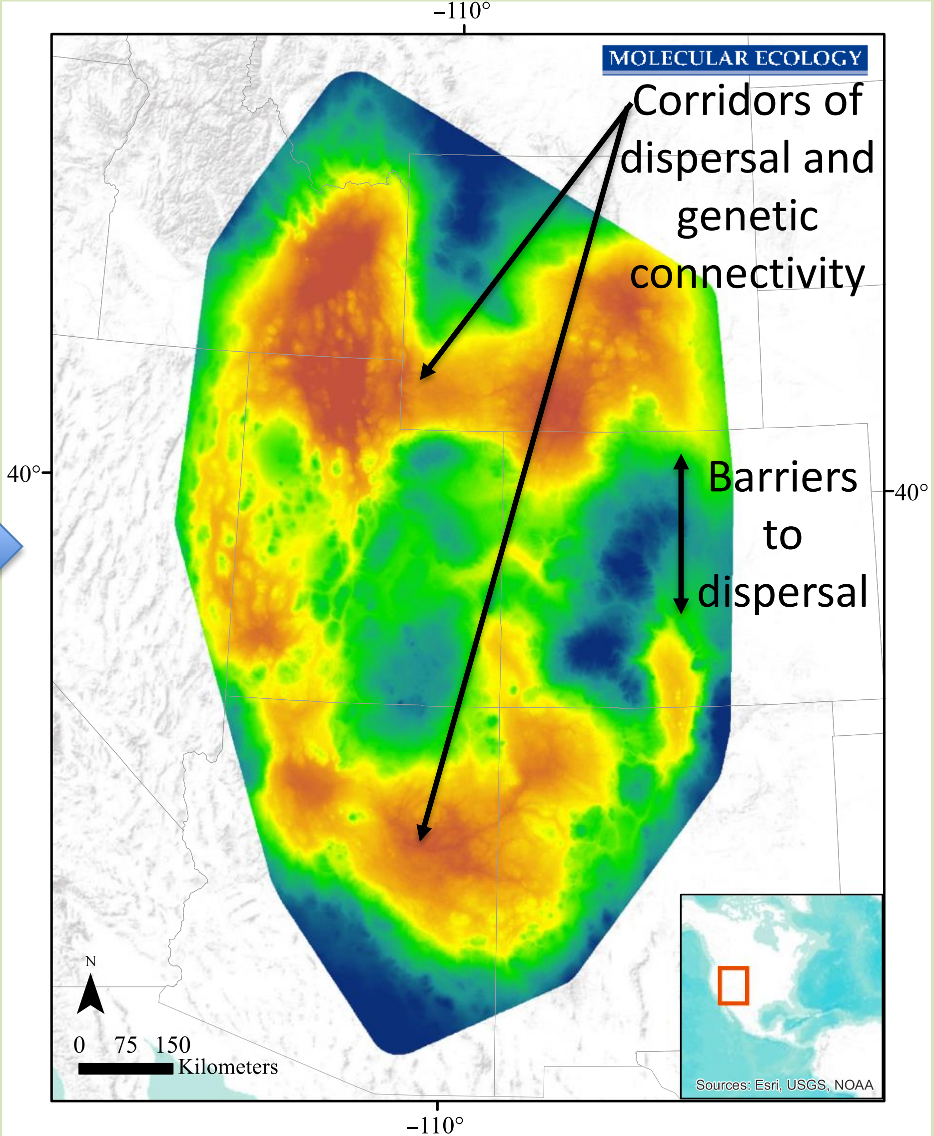
Helen Bothwell

Conserving threatened riparian ecosystems in the American West: Precipitation gradients and river networks drive genetic connectivity and diversity in a foundation riparian tree (Populus angustifolia)

Helen M. Bothwell[1] | Samuel A. Cushman[2] | Scott A. Woolbright[3] | Erika I. Hersch-Green[4] | Luke M. Evans[5] | Thomas G. Whitham[1,6] | Gerard J. Allan[1,6]

Molecular Ecology 2017: 1-19





Corridors of dispersal and genetic connectivity

Barriers to dispersal

What's the message for restoration management?

- Genetic and genomic methods can help us:
  - Better **understand** genetic variation and relatedness of focal species
  - Investigate how dependent communities **respond** to genetic variation in foundation species
  - Determine how genetic variation is **structured** across complex landscapes
  - **Link** genetic variation to environmental variation to reveal factors that shape genetic variation
  - More accurately **model** shifts in species distributions and dispersal by incorporating genetic information