Population Genetic Issues in the Management of Freshwater Mussels

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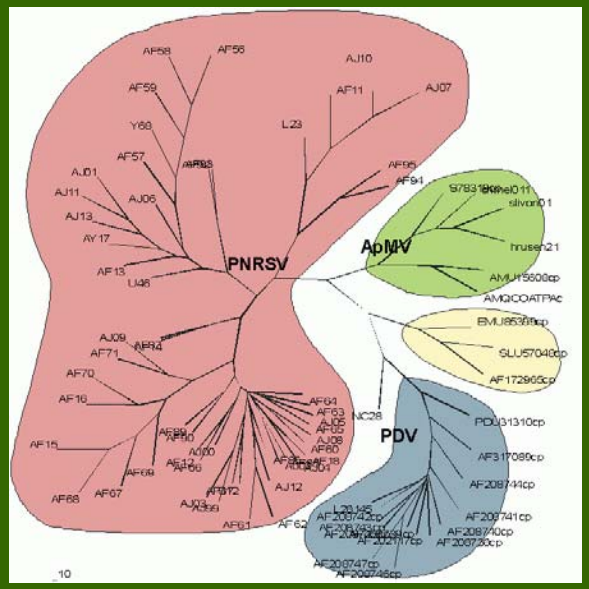
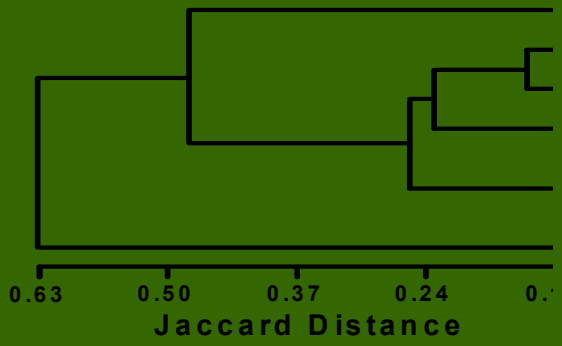
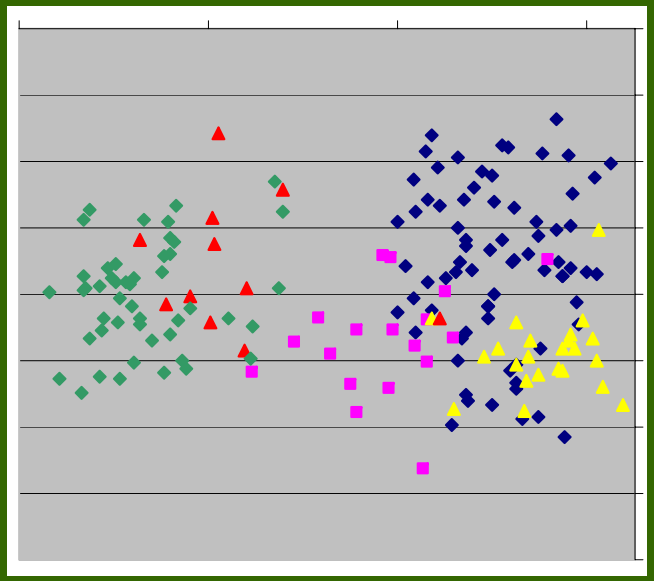






Population Genetic Issues in the Management of Freshwater Mussels

Overview:

1. Scope & Purview of Population Genetics in Conservation
    a. Population Genetics vs. Systematics
    b. Utility of Population Genetics Tools
    c. Limitations of Genetic Markers
2. Conservation Issues
    a. Population Genetic Diversity
    b. Population Genetic Divergence
    c. Hybridization
    d. Reproductive Ecology
3. Restoration Issues
    a. Translocation Issues
    b. Captive Breeding Issues

The Molecular Systematics View

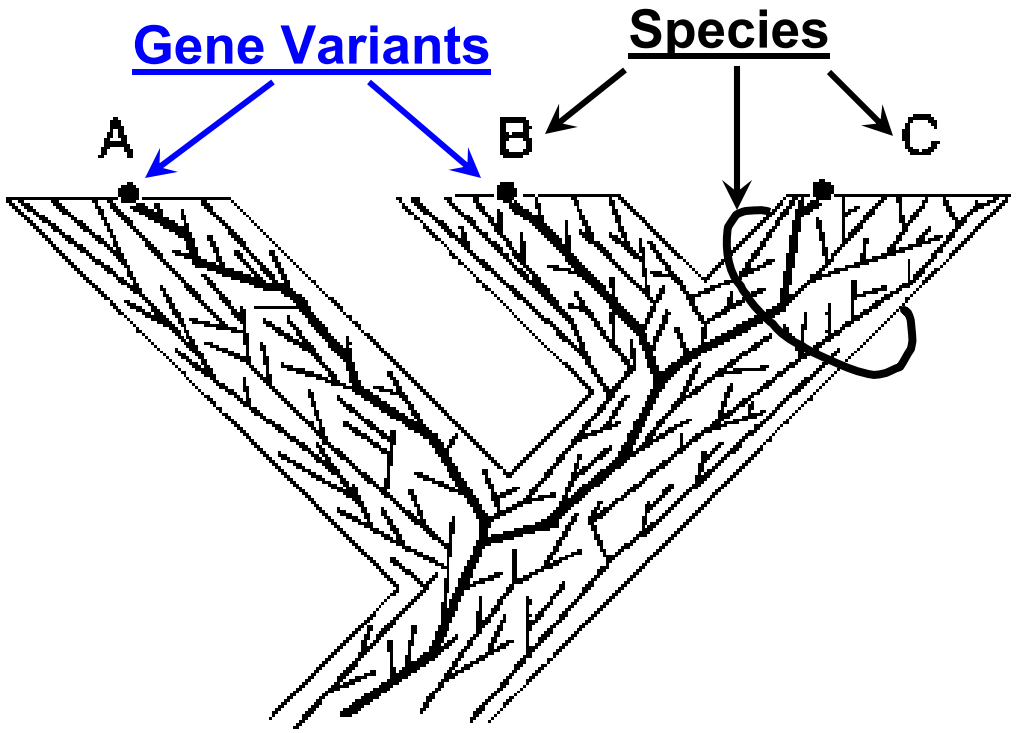


FIGURE 1. A gene tree contained within a species tree leading to three extant species: A, B, and C. Bold branches of gene tree show relationships among the sampled copies of the gene (●). Sampled copies from sister species B and C are sister copies.

(adapted from Maddison 1997)

Goal: Reconstruction of evolutionary history among species

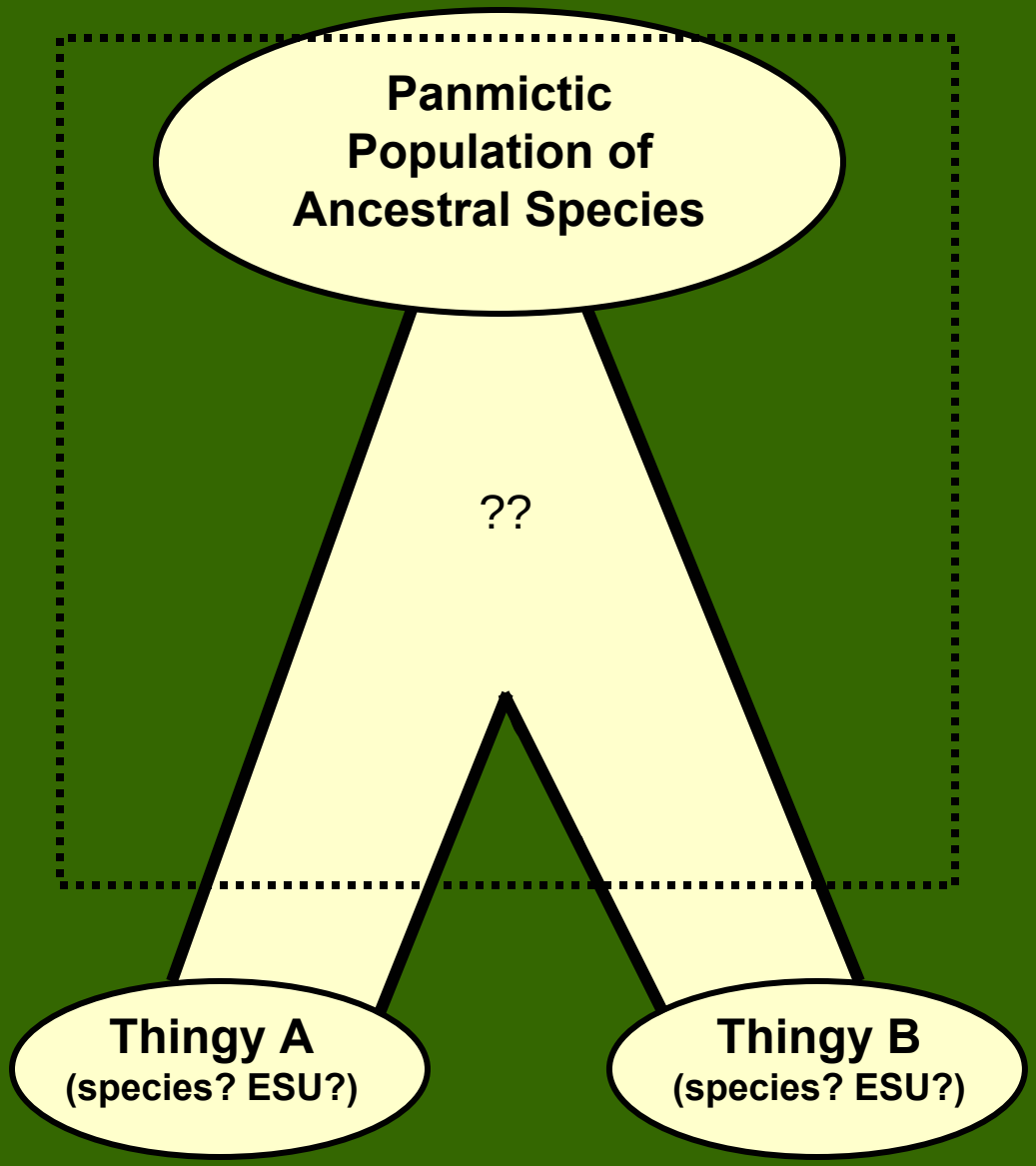
Method: Use genetic sequence changes to infer relation-ships among species

Works well when enough differences have accumulated and sorted among species

Difficulties:

- ***recent speciation***
- ***hybridization***
- ***recombination***

The Population Genetics View



Goal: Reconstruction of evolutionary and demographic history among <u>populations</u>

Goal: Assessment of genetic variation <u>at and below the species level</u>

Method: Use gene variant FREQUENCY differences to assess gene flow between populations

Effective over shorter time frames & shallower genetic distances than in systematics

Population Genetic Processes

Allelic variation within population, but no spatial discontinuities or reproductive isolation

↓

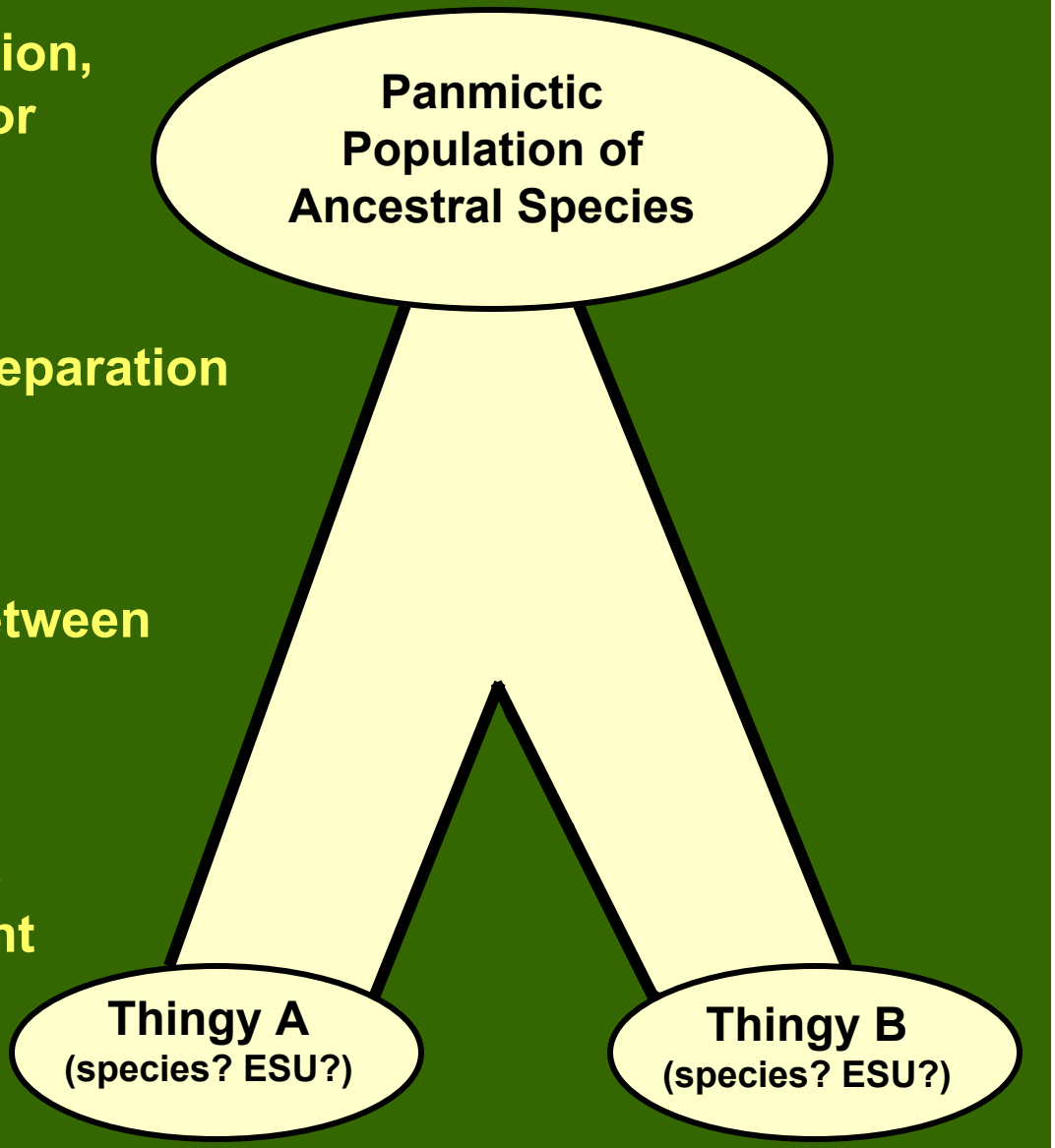
Geographic or reproductive separation without genetic differences

↓

Allele frequency differences between populations in different areas

↓

Allelic composition differences between populations in different areas (eventually reciprocal monphyly)



Data Requirements and Molecular Tools for Population Genetic Assessment

1) Need molecular markers that mutate rapidly (e.g. msats, AFLPs, 3rd codon positions, ITS regions…)

2) Need neutral molecular markers so that differences are a reflection of demographic processes & gene flow, not local selection.

3) Need a large sample from each population (minimum 20) to determine allele frequencies with any accuracy.

4) Need to avoid sampling familial groups if trying to represent a particular population.

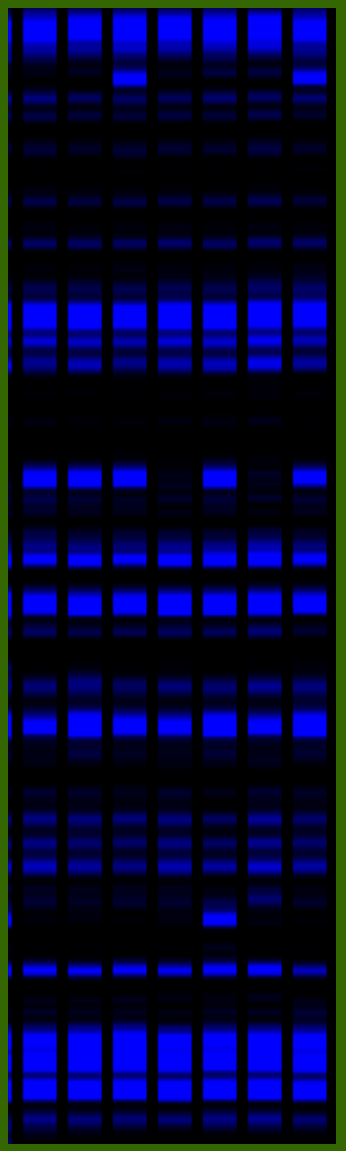
5) Need finer-scale spatial data about landscapes, since looking at the effects of gene flow and geologically recent barriers.

Molecular Markers in Population Genetics

	Microsatellites	AFLPs	Sequences
Type of Marker	Nuclear Tandem repeats Alleles are fragment size variants	Nuclear Restriction & PCR based Alleles are fragment size variants	Nuclear, mito-chondrial, or chloroplast Nucleotide sequence data
Primary Advantages	Codominant High mutation rate Many alleles	Multilocus (>100) No species-specific development required	Historical perspective All variation in gene detectable Comparable across many taxa
Primary Disadvantages	Species-specific dev't required Evolution unclear	Dominant Evolution unclear	Primer dev't Single locus data
Primary Uses	Fine structure Pedigrees Bottleneck IDs Diversity Index	Fine structure Hybridization	Phylogeny reconstruction

Utility of Molecular Markers in Malacology
(more than just phylogeography!)

- Taxonomy (proximal species & below)
- ESU & MU definitions
- Host fish relationships (PCR of glochidia)
- Demographic history of populations
  - bottlenecks
  - range expansions
  - population admixture
  - hybridization
  - effectiveness of barriers/corridors
  - migration rate between specific areas
  - effective population sizes
  - degree of inbreeding
- Pedigree reconstruction
  - Mating systems
    - Gonochoristic vs. hermaphroditic
      (dioecious) (monecious)
    - Selfing vs. outcrossing
- Sources & numbers of invasions by exotics



Limitations of Molecular Markers

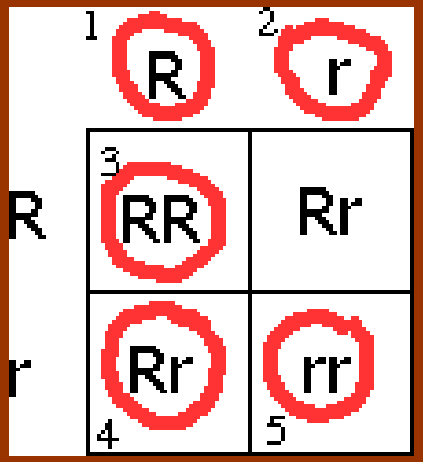
- **Neutral variation ≠ Adaptive variation**
  - **demographic inferences assume marker neutrality**
  - **selection on markers can cause frequency differences to change dramatically**
  - **phylogeographic patterns detected with neutral markers may or may not reflect adaptively important variation among populations !!!**
- **Hybridization can confound results**
- **Recent demographic processes may not be detectable**
- **Marker may not appropriate mutation rate for the question**

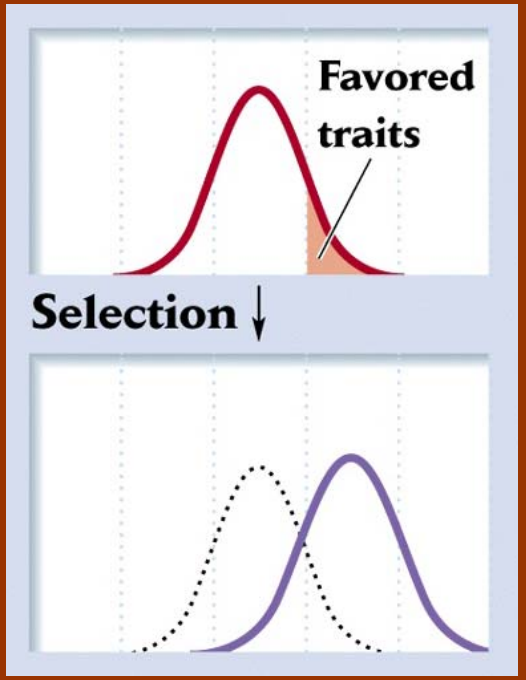
Why conserve WITHIN species genetic diversity?

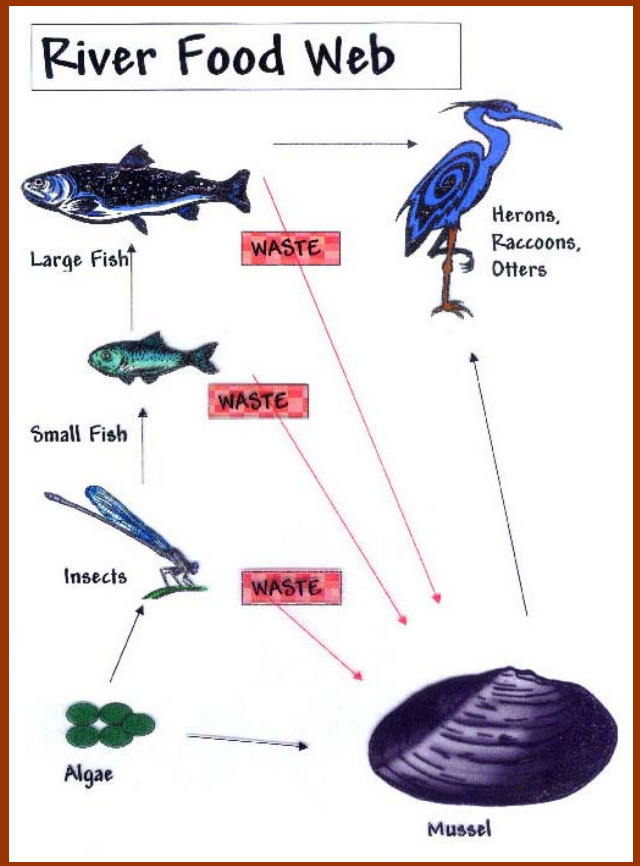
1) To prevent inbreeding depression

2) To prevent the loss of adaptive potential

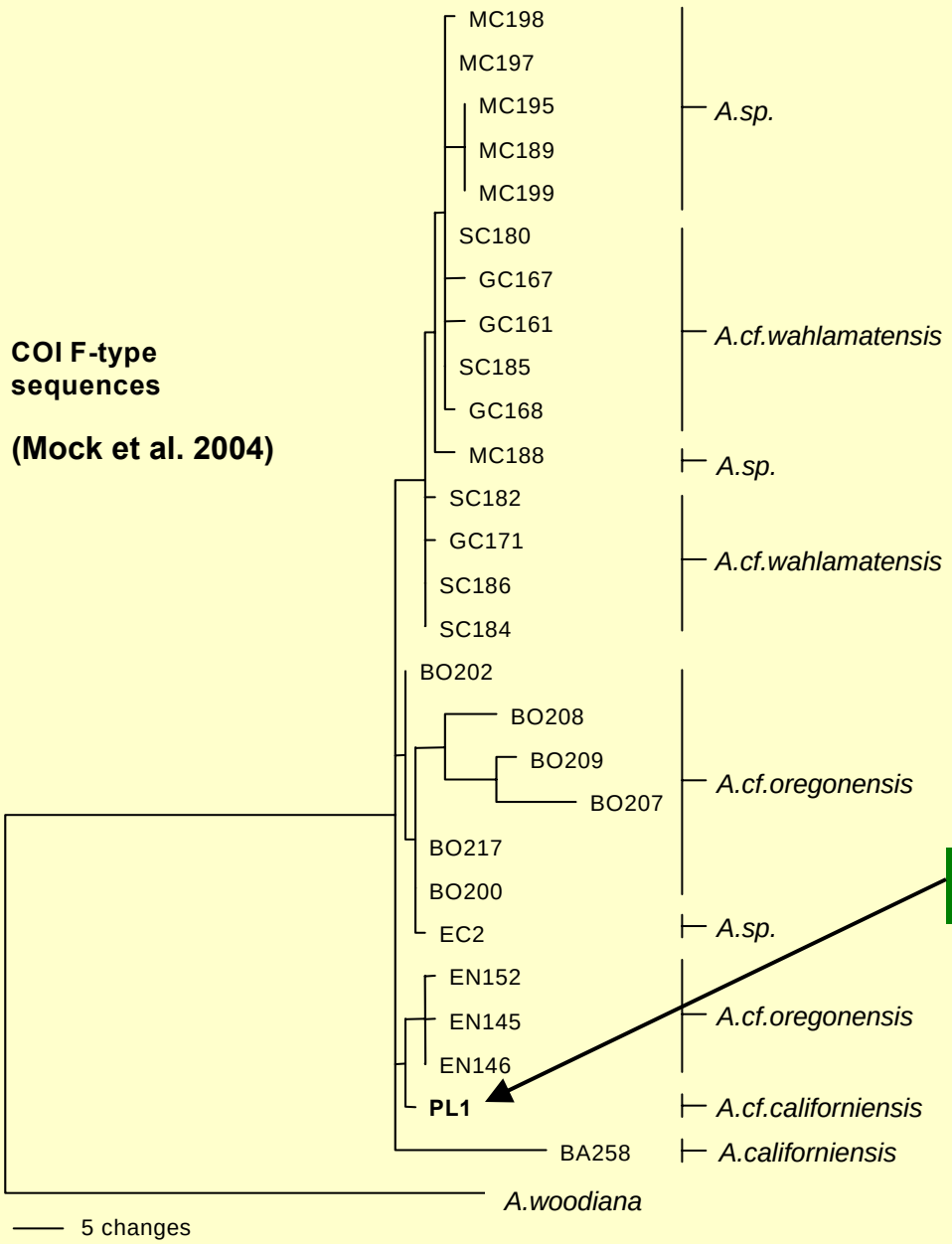
3) To prevent the loss of ecological diversity







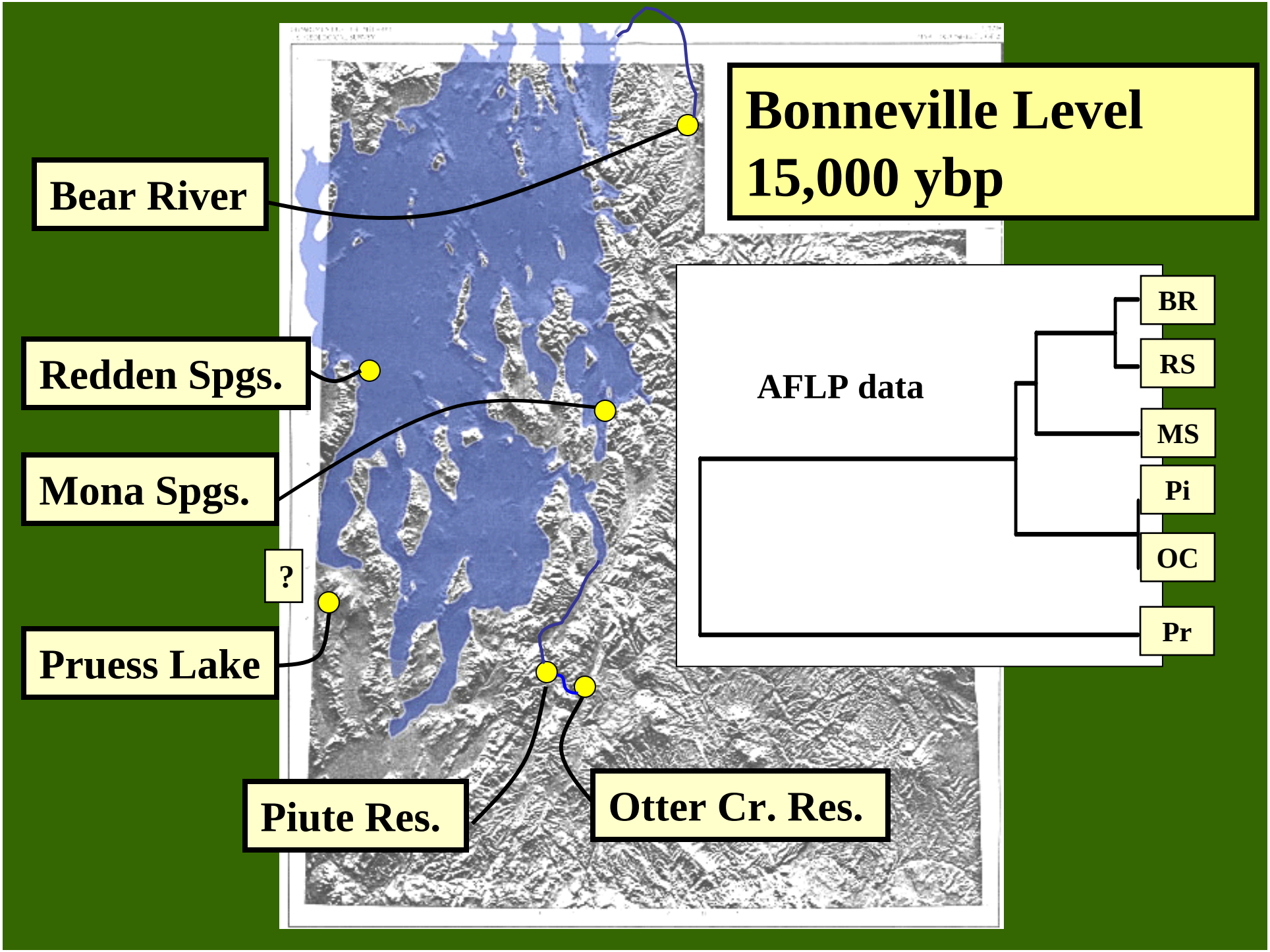
What do we know about genetic diversity in western freshwater mussels?

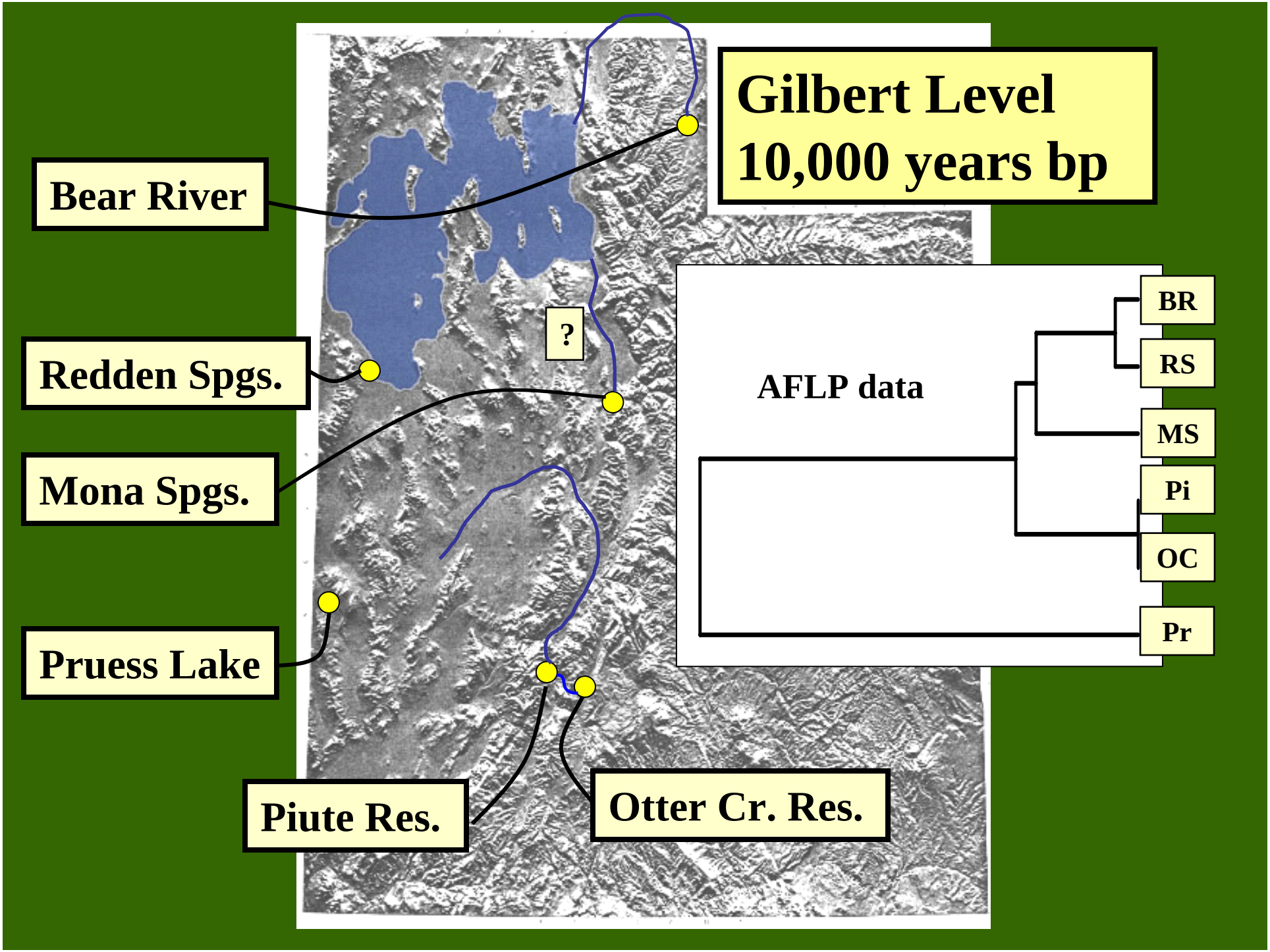


In *Anodonta*:

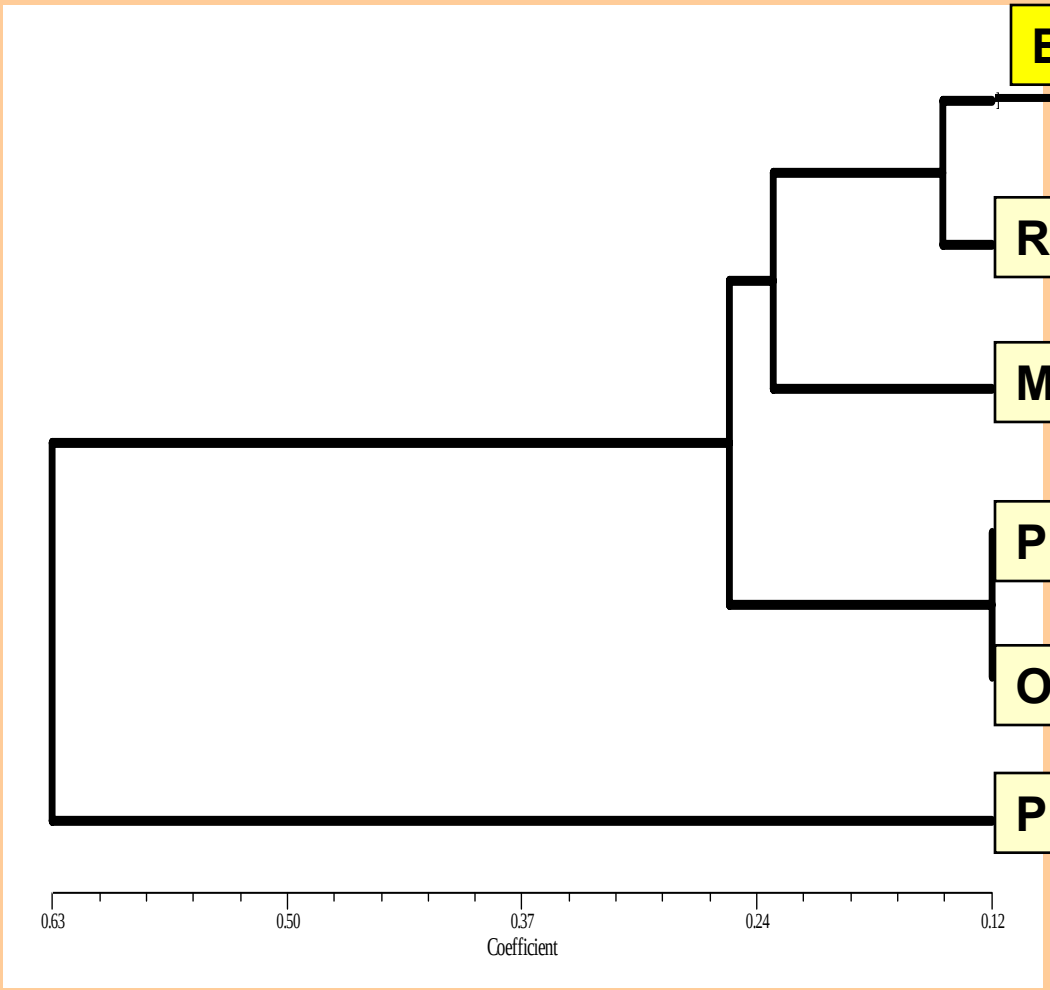
- **Inter-specific distances seem to be small compared to eastern taxa.**
- **Species boundaries are unclear**

Bonneville mitotype


Bonneville Level
15,000 ybp
Bear River
Redden Spgs.
Mona Spgs.
?
Pruess Lake
Piute Res.
Otter Cr. Res.
AFLP data
BR
RS
MS
Pi
OC
Pr

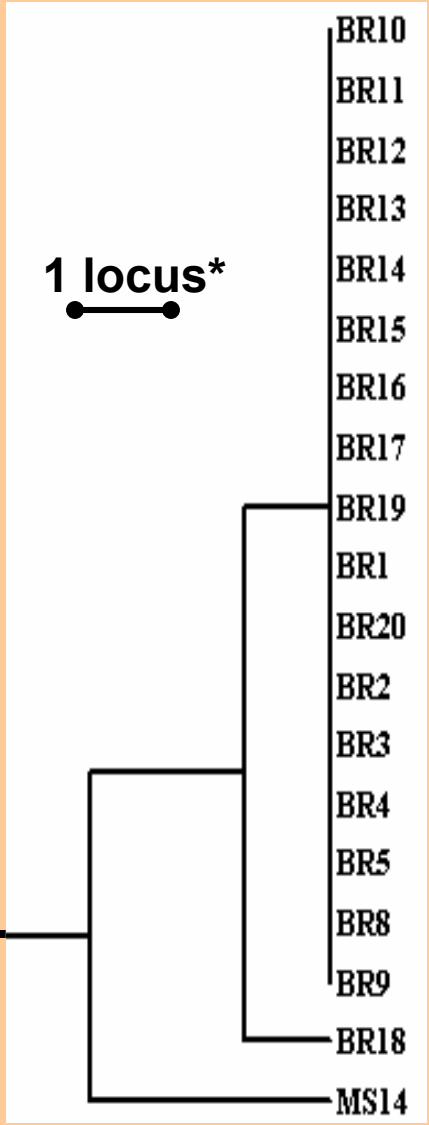

Gilbert Level
10,000 years bp
Bear River
Redden Spgs.
Mona Spgs.
Pruess Lake
Piute Res.
Otter Cr. Res.
?
AFLP data
BR
RS
MS
Pi
OC
Pr

AFLP Population Data



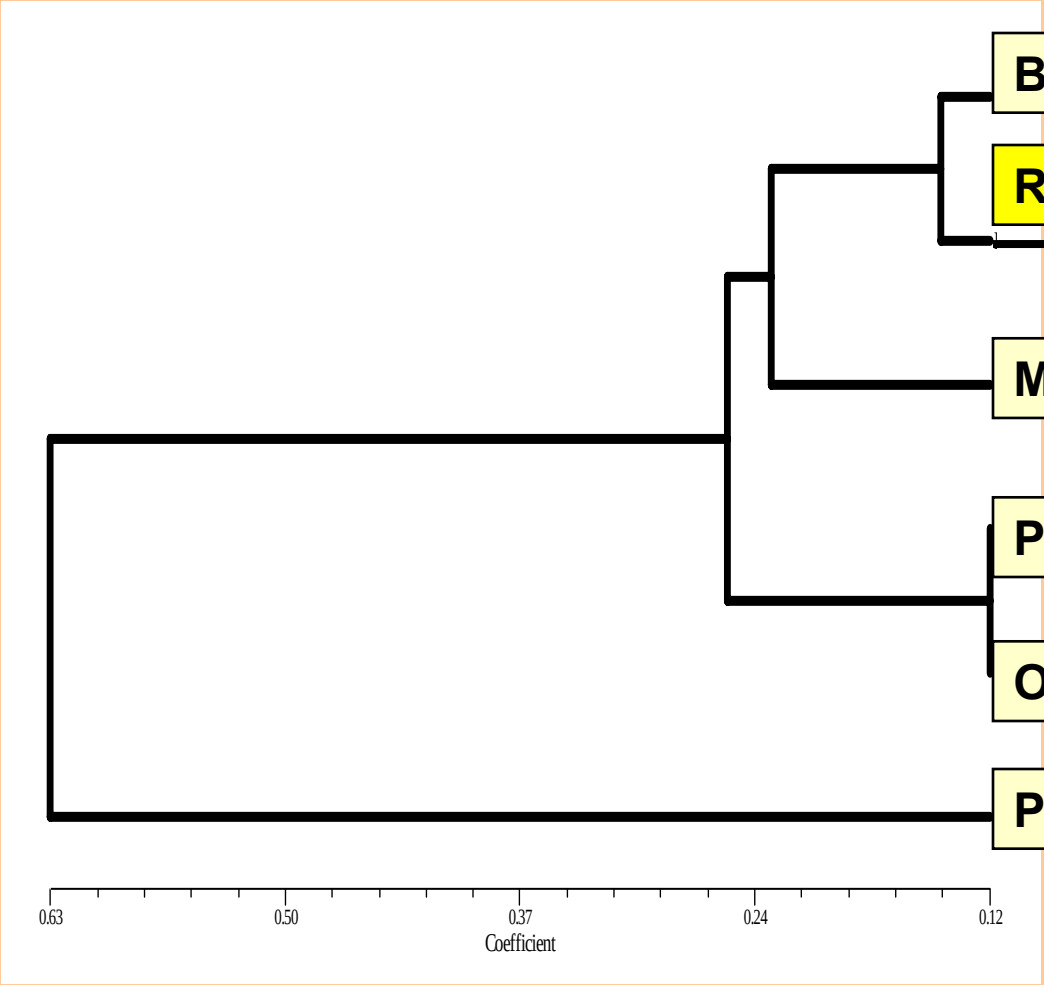
UPGMA Jaccard Distance

AFLP Individual Data



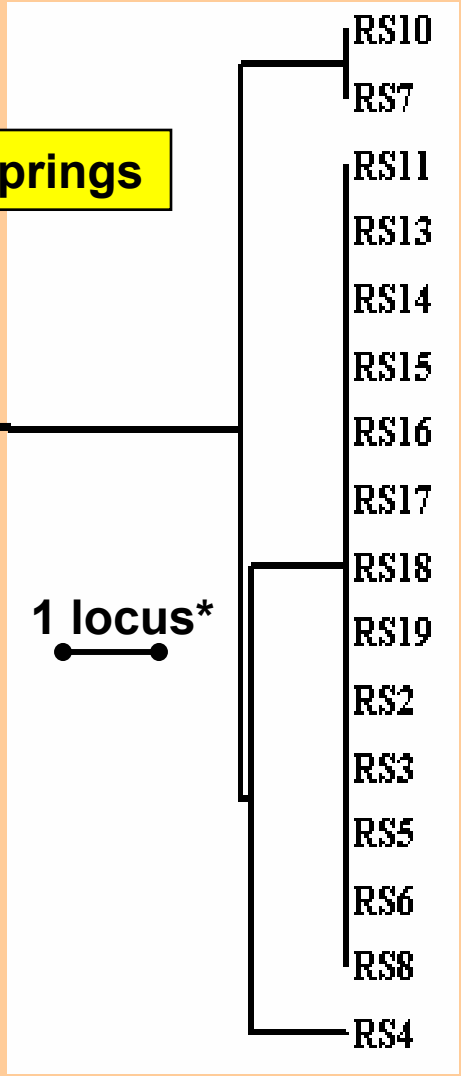
*1 polymorphic locus in BR pop.

AFLP Population Data



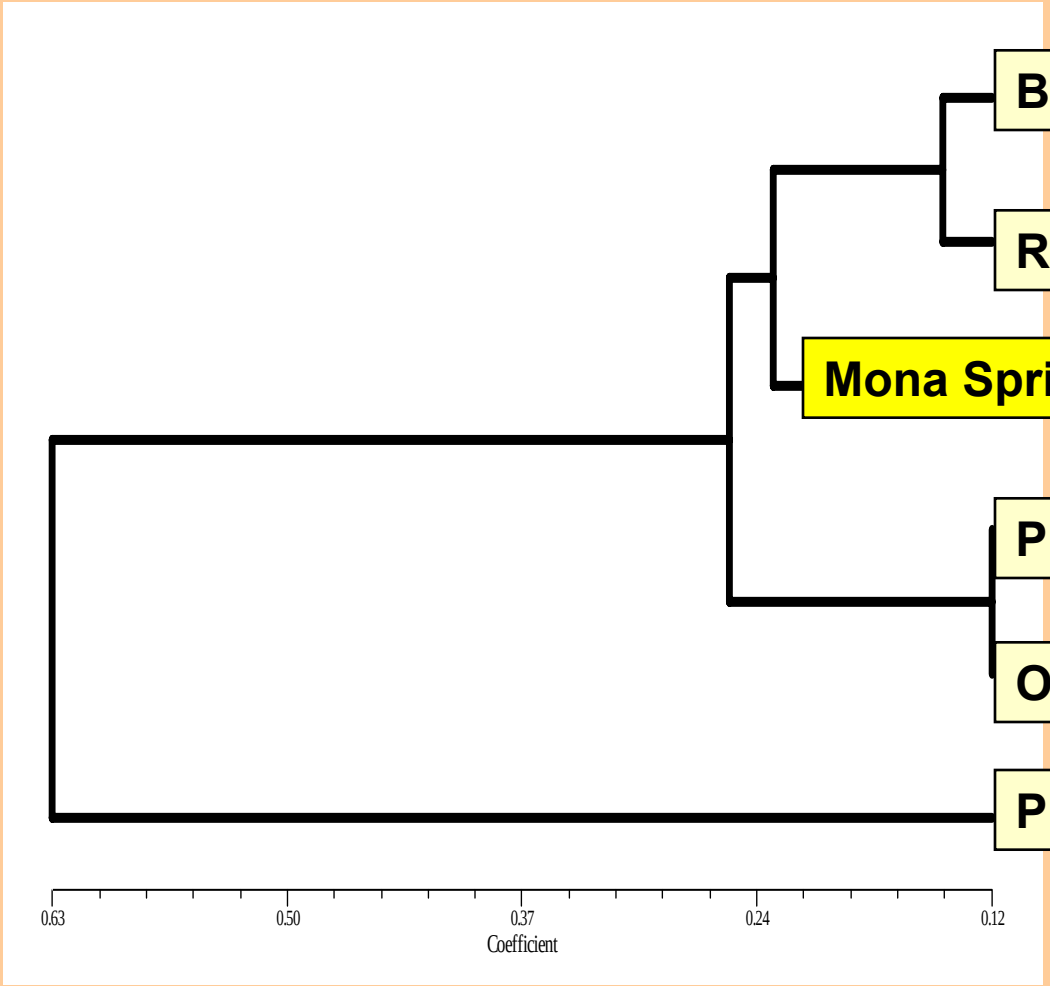
UPGMA Jaccard Distance

AFLP Individual Data



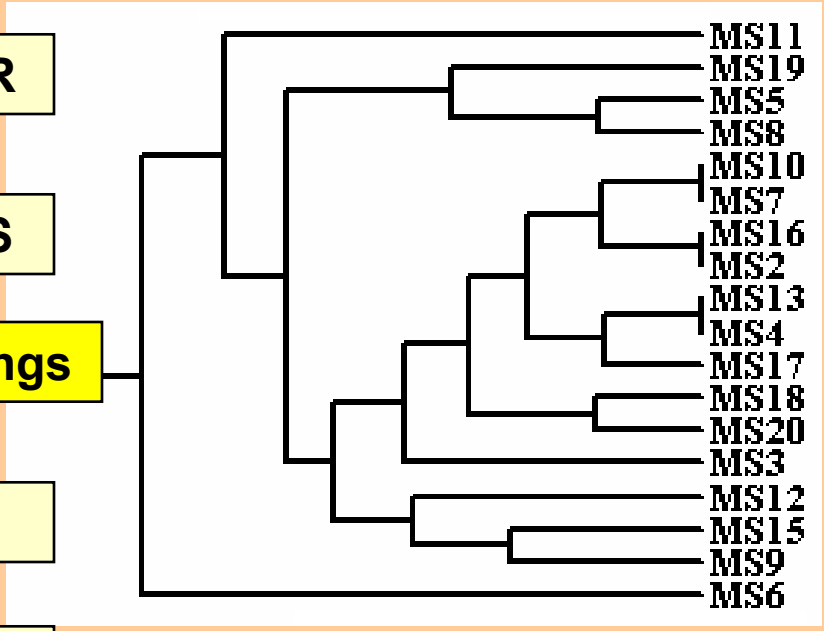
***2 polymorphic loci in RS pop.**

AFLP Population Data



UPGMA Jaccard Distance

AFLP Individual Data

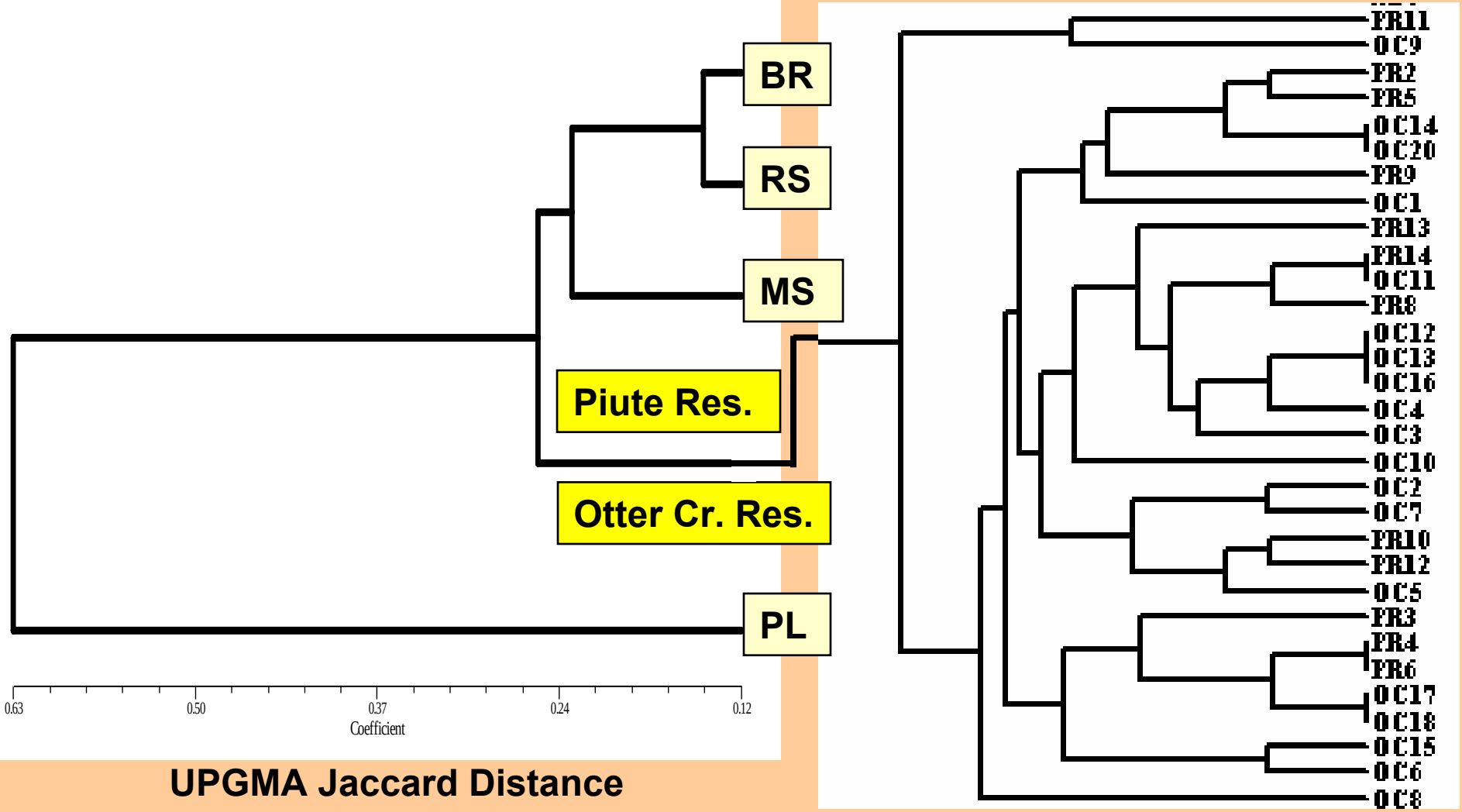


1 locus*

***15 polymorphic loci in MS pop.**

AFLP Population Data

AFLP Individual Data

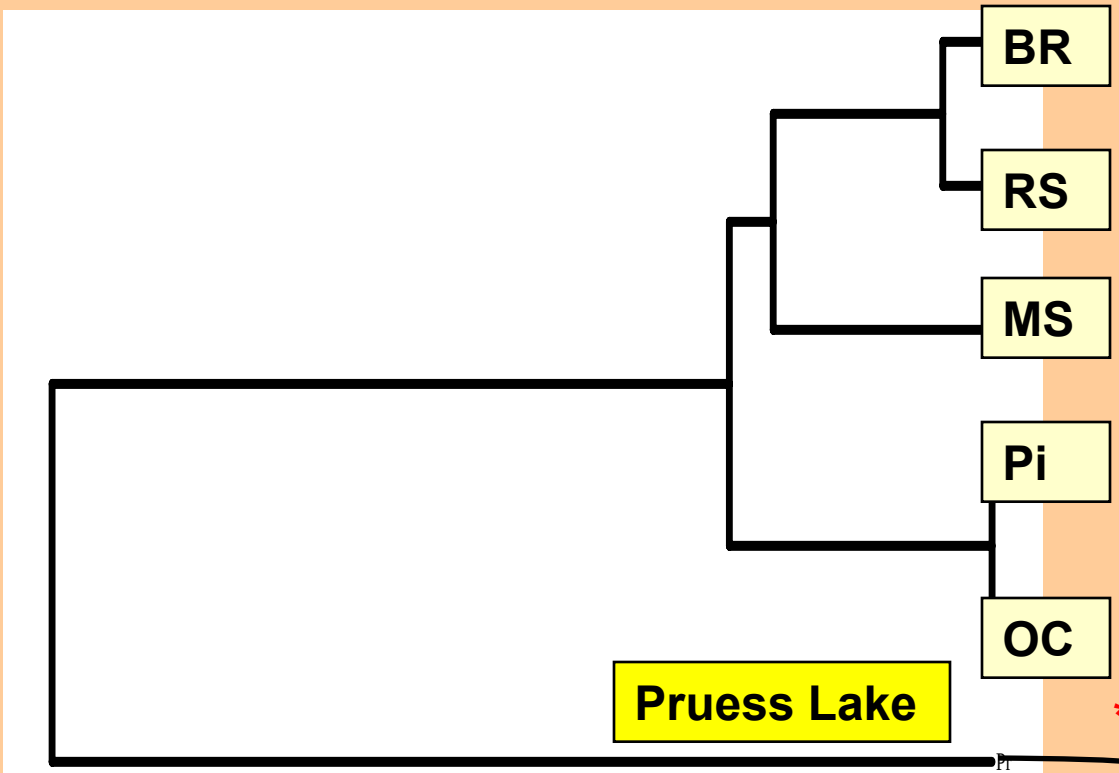


UPGMA Jaccard Distance

***13 polymorphic loci in Pi/OC pop.**

1 locus*

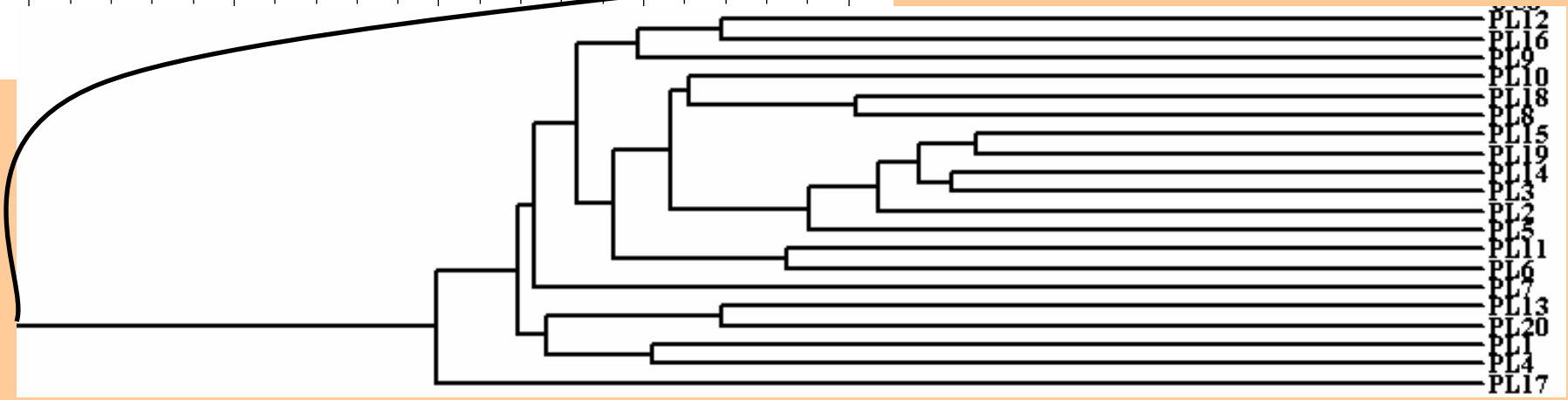
AFLP Population Data



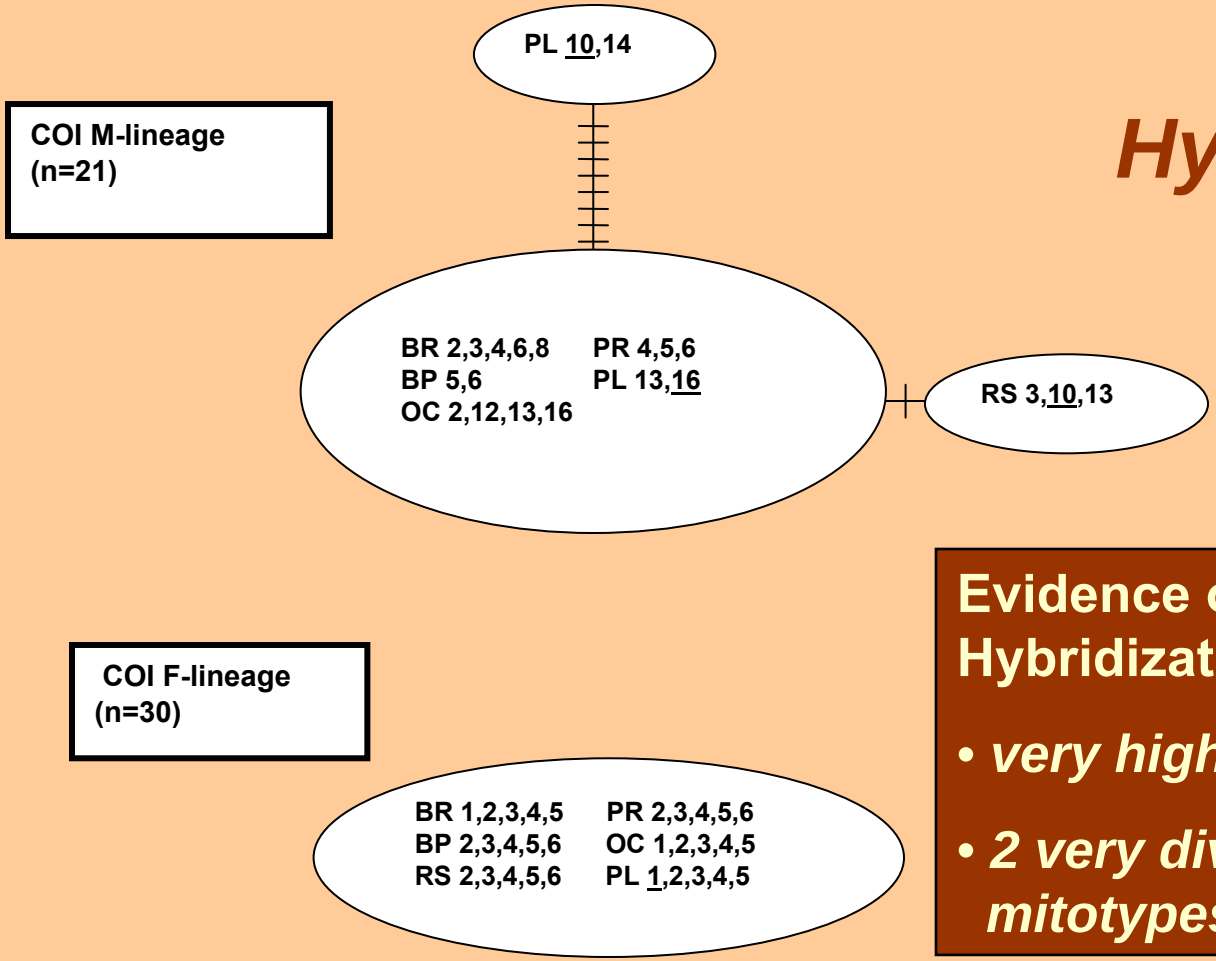
AFLP Individual Data

1 locus

*50 polymorphic loci in PL pop., no identical AFLP profiles



Hybridization



Evidence of Recent Hybridization in Pruess Lake:

- ***very high nuclear diversity***
- ***2 very divergent male mitotypes, no other variants***

Additional conservation questions about western freshwater mussels that can be informed using molecular genetics

Phylogeography:

- How close is the correspondence between species designations and partitioning of genetic variation?
- Where are the centers of diversity for *Anodonta* and other mussel species?
- How is genetic diversity partitioned with respect to fish barriers of different ages?

Reproductive Ecology:

- What fish species/subspecies are serving as hosts?
- How common is selfing vs. outcrossing in different species?
- How genetically different are age-specific cohorts within populations?
- How commonly are populations at risk for inbreeding depression?

Conservation:

- What locations are the highest priorities for conservation?

Genetic issues in the restoration of western freshwater mussels

What are the appropriate sources for translocations?

Source population diversity adequate?

Source population genetically similar to proximal populations?

Consider in conjunction with genetic information:

- geographic/ecological similarity?
- morphological/life history similarity?
- host fish presence?

What are the appropriate sizes for translocations?

- How many adults are contributing to reproduction in the new population or in a captive breeding program?

Captive Breeding Issues:

- Avoid propagating and swamping with low fitness genotypes ("hatchery effects") by:
  - emulating natural selection in captive propagation
  - minimizing the number of generations in captive conditions
  - minimizing the effect of genetic drift in captivity

Photo by Jayne Brim-Box

Pruess Lake, Utah

Jayne Brim-Box

Courtesy of LabLite