

# Defining Conservation Units: ESU's, MU's, and DPS's

Classifying organisms below the species level

Science



Philosophy

Policy



# Conservation Units

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Conservation units are classifications of groups of organisms beneath the species level.

The goal of CU's is to preserve:

- Biodiversity

- Evolutionary processes

- Ecological viability of populations

Consider:

- Adaptive divergence

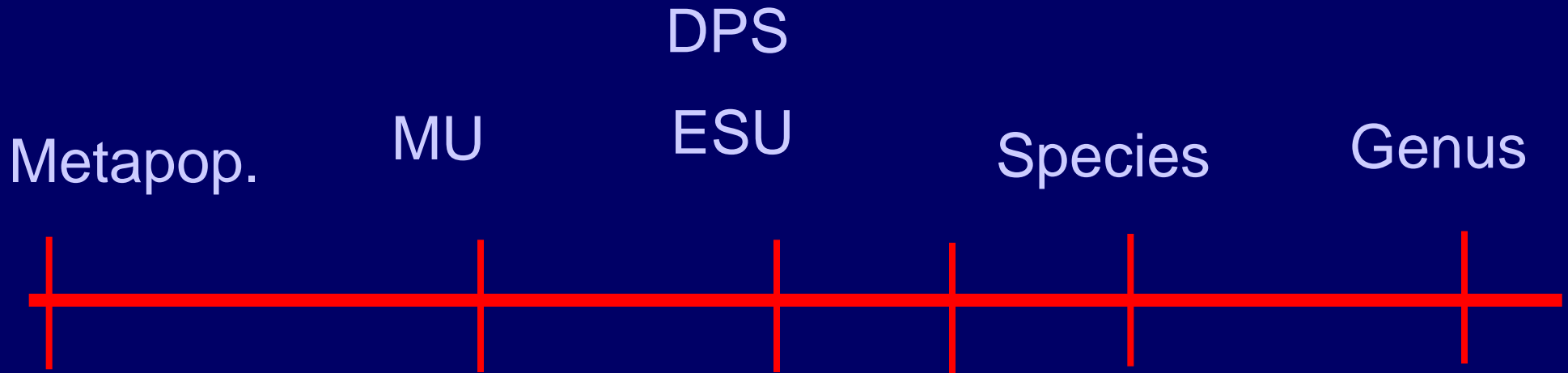
- Historic isolation patterns, Evolutionary history

They can be defined many ways, but are often described as **Evolutionary Significant Units** (ESU's) or **Management Units** (MU's).

# ISSUES TO RESOLVE IN USING CONSERVATION UNITS

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- What criteria will be used to define conservation units?
- How can scientists resolve CU definitions so they are applicable to real world situations?
- How can scientists and agencies bridge the gap between the information that is generated and how it is used in a conservation context?



Adaptive Differences



Gene Flow



“It’s not that evolutionary significance starts at a certain point. Your mother probably thinks that you’re a evolutionary significant unit”

Robin Waples

# Some Conservation Unit Definitions



# Evolutionary Significant Units (ESUs)

Introduced by Ryder 1986 to identify populations  
with significant genetic attributes for present  
and future generations

## Goals

Prioritize species for conservation

Preserve the range of diversity within a species

Provide a guide for transplantation and reintroduction

# Defining ESU's...Ryder (1986) cont.

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- ESU's are “populations possessing genetic attributes significant for present and future generations of the species.”

## Data types:

- Natural history
- Morphometrics
- Distribution and range
- Genetic



**Criteria:** suggested concordance between data sets derived by different techniques





# Conservation Unit Definitions



**Waples (1991, 1995)** An ESU is a population (or group of populations) that is (1) substantially **reproductively isolated** from other conspecific population units, and (2) represents an important component in the **evolutionary legacy** of the species.

**Isolation** does not have to be absolute but gene flow has to be restricted to the point that evolutionarily important differences occur.

Evaluated by genetic data and tagging studies and biogeography

**Evolutionary legacy** is defined as “genetic variability that is the product of past evolutionary events and that represents the reservoir upon which future evolutionary potential depends.” Evaluated using genetic data, ecology, life history traits/adaptive differences

58 DPS/ESUs have been identified in the 7 Pacific Salmon species, and 50% are listed as threatened or endangered under the ESA (Waples 2005)

# The Genetic Approach to ESUs

**Moritz 1994**

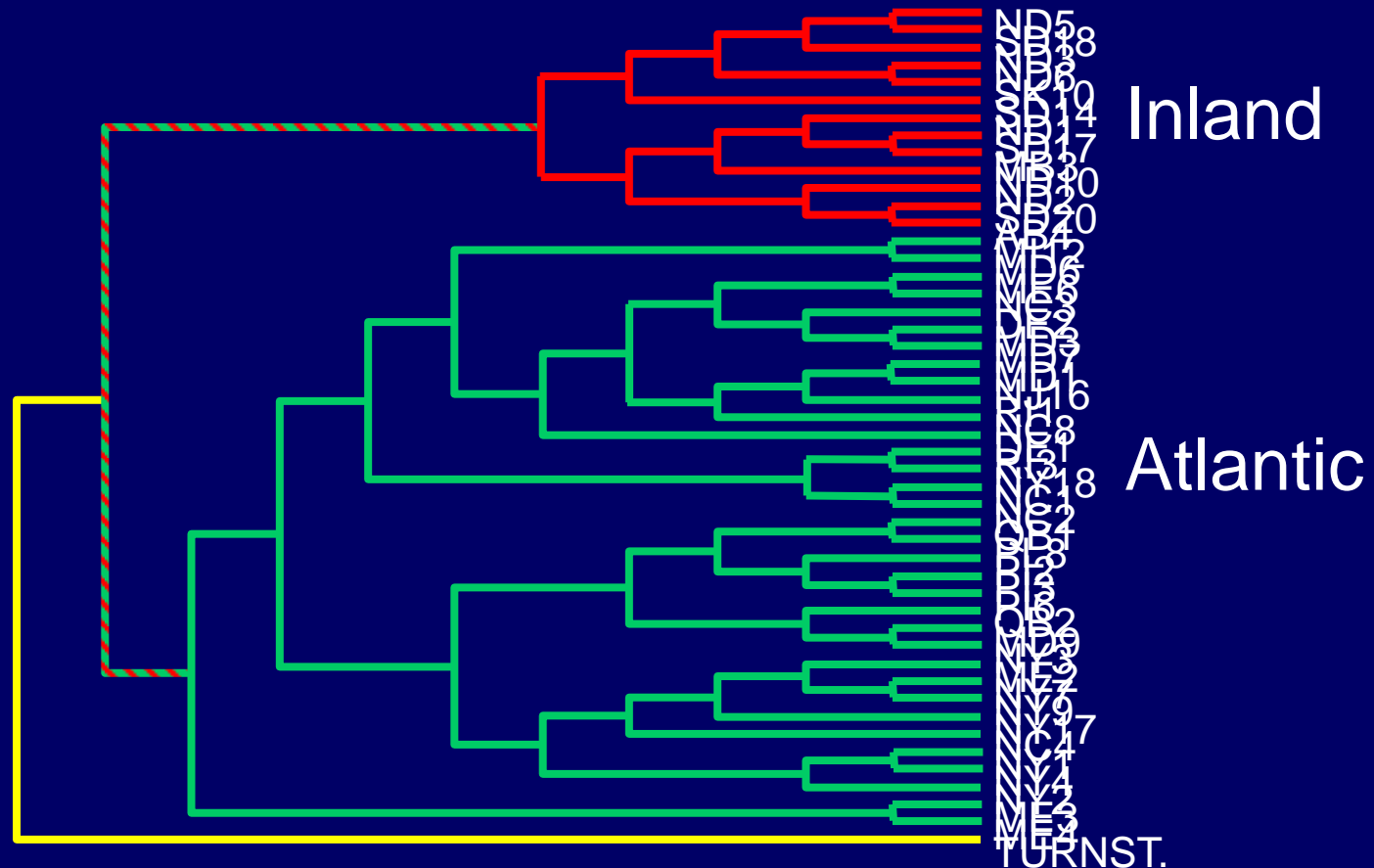
ESUs should be reciprocally monophyletic for mtDNA alleles and show significant divergence of allele frequencies at nuclear loci. - Would give fewer than Waples

MUs are recognized as populations with significant divergence of allele frequencies at nuclear or mitochondrial loci, regardless of the phylogenetic distinctiveness of alleles.

- Would give many more than Waples 100s to 1000s

# Reciprocal Monophyly

Reciprocal monophyly occurs when no individuals in one group are present in another.



# Issues Related to Monophyly

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1. Which phylogenetic/tree method to use?
2. How many bp from what regions of mtDNA?
3. How big a difference among groups is enough?
4. What about taxonomic differences in gene flow?
5. What about differences in the age of taxa/paraphyly?

# Issues Related to Population Differentiation

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Which or how many markers?

How many loci/individuals/populations are enough?

What stats were used to determine differentiation?

What about taxonomic differences?



# Defining ESU's...Crandall et al. (2000)

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- **Populations always in the process of evolving through drift and natural selection**
- **Existing ESU designations: ESU or not**
- **Argue for a broader categorization of population distinctiveness based on genetic and ecological exchangeability**
- **Management recommendations based on category of population distinctiveness**



# Defining ESU's...Crandall et al. (2000) cont.

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**Criteria:** Instead of genetic distinctiveness, emphasize level of genetic and ecological exchangeability on both historical and recent time frames

**Data Types:**

**Ecological exchangeability (shared fundamental adaptations)**

- Life history traits
- Morphology
- Demographic characteristics
- Note: all characteristics must be *demonstrably heritable*



# Defining ESU's...Crandall et al. (2000) cont.

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## Genetic exchangeability (gene flow)

- Various genetic markers to estimate gene flow
- Phylogenetic divergence concordant with geographic barriers

## Historic vs. recent exchangeability

- Historical data (community structure, geographic distribution and associated ecological variables, genetics)
- Genetic markers with resolution at different time scales (microsatellites, mtDNA)
- Phylogenetic relationships using network approaches (nested clade)





# Defining ESU's...Crandall et al. (2000) cont.

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→ Null hypothesis = exchangeability

+ Rejected  
— Fail to reject

	Genetic	Ecological
Recent	+	
Historical		—

\* Esu cutoffs not defined, 8 management recommendations

**Relative strength of evidence**

**Evidence of adaptive distinctiveness**

**Recommended management action**

Case 1

$$\begin{array}{c|c} + & + \\ \hline + & + \end{array}$$

Treat as long separated species

Case 2

$$\begin{array}{c|c} + & + \\ \hline - & + \end{array} \quad \begin{array}{c|c} + & + \\ \hline + & - \end{array}$$

Treat as distinct species

Case 3

$$\begin{array}{c|c} - & + \\ \hline + & + \end{array}$$

Treat as distinct populations  
(recent admixture and loss of genetic distinctiveness)

Case 4

$$\begin{array}{c|c} + & - \\ \hline + & + \end{array}$$

Natural convergence on demographic exchangeability – treat as single population

	(a)	(b)	(c)	
Case 5	$\begin{array}{c c} + & + \\ \hline - & - \end{array}$	$\begin{array}{c c} - & + \\ \hline - & + \end{array}$	$\begin{array}{c c} - & - \\ \hline + & + \end{array}$	Anthropogenic convergence on demographic exchangeability – treat as distinct populations. (a) and (b) Recent ecological distinction, so treat as distinct populations; and (c) allow gene flow consistent with current population structure
Case 6		$\begin{array}{c c} - & + \\ \hline - & - \end{array}$		Allow gene flow consistent with current population structure; treat as distinct populations
Case 7		$\begin{array}{c c} + & - \\ \hline + & - \end{array}$		Allow gene flow consistent with current population structure; treat as a single population
Case 8	$\begin{array}{c c} + & - \\ \hline - & - \end{array}$	$\begin{array}{c c} - & - \\ \hline - & + \end{array}$	$\begin{array}{c c} - & - \\ \hline + & - \end{array}$	Treat as a single population; if inexchangeability is a result of anthropogenic effects, restore to historical condition; if inexchangeability is natural, allow gene flow
	$\begin{array}{c c} + & - \\ \hline - & + \end{array}$	$\begin{array}{c c} - & + \\ \hline + & - \end{array}$	$\begin{array}{c c} - & - \\ \hline - & - \end{array}$	

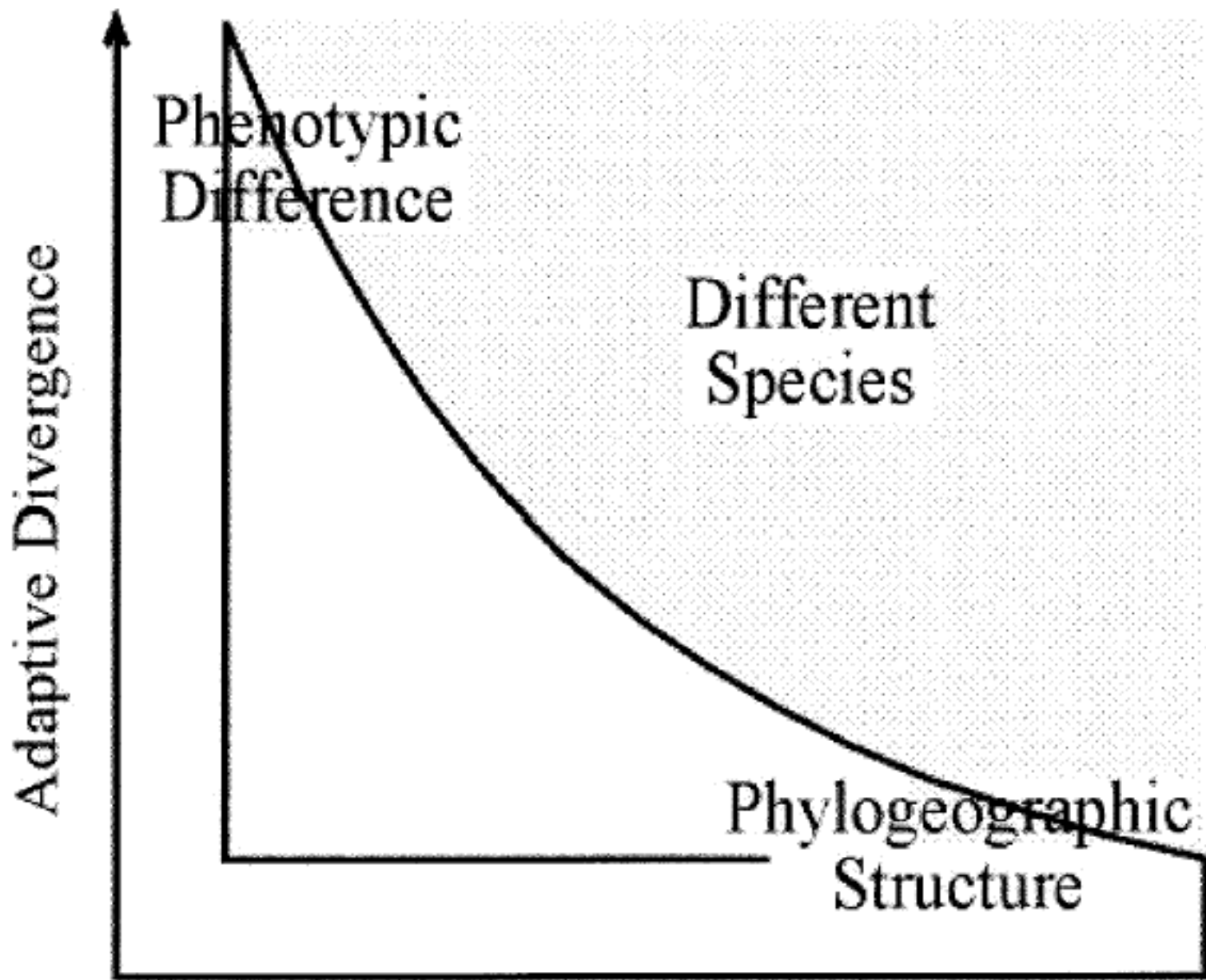
Adaptive Divergence

Phenotypic  
Difference

Different  
Species

Phylogeographic  
Structure

Vicariance



# Management Unit

- Demographically independent
- Birth/death rates depend on local conditions not immigrants
- Important for persistence of ESU
- Long-term independent evolution not required
- Fisheries “stock”
- Harvest quotas

# Defining MU's....Moritz (1994)

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Management Unit (MU) - populations with significant divergence of allele frequencies at nuclear or mitochondrial loci, regardless of the phylogenetic distinctiveness of the alleles

Species → ESU → MU

## ESU

- historical population structure
- mtDNA phylogeny/nDNA
- long term conservation goals

## MU

- current population structure
- allele frequencies
- short term management issues

# Defining MU's....

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- Moritz's MU similar to Dizon et al. (1992) "stock"
- Stock = a group of animals that share a common *space* and *interbreed* (Marine Mammal Protection Act of 1972)
- Dizon et al. (1992) attempted to introduce specific criteria for designation of "stocks"
- 4 stock categories based on level of genetic difference and geographic partitioning
- Moritz (1994) suggested that Dizon et al. (1992) "stock" be
  - restricted to short-term management goals
  - be defined by genetic criteria for designating MU's

# Important Considerations

- Do markers have enough power to detect differences?
- Statistically significant genetic divergence vs biologically important divergence
- $F_{st}$  not appropriate measure – Why?



# Identification of management units using population genetic data 2007

Per J. Palsbøll<sup>1,2</sup>, Martine Bérubé<sup>1</sup> and Fred W. Allendorf<sup>3,4</sup> TREE 22:11

- **Criteria** - Genetic differentiation at level that populations become demographically independent not rejection of panmixia
- Hastings (1993) suggests populations are independent at dispersal rates  $<10\%$
- **Challenging to convert - dispersal  $\neq$  gene flow; and genetics # migrants =  $mN_e$**
- Don't want to rely on measures that incorporate historical gene flow or equilibrium conditions
- Assignment test approaches most valuable - but consider power to detect
- Also NGS has ability to directly evaluate dispersal

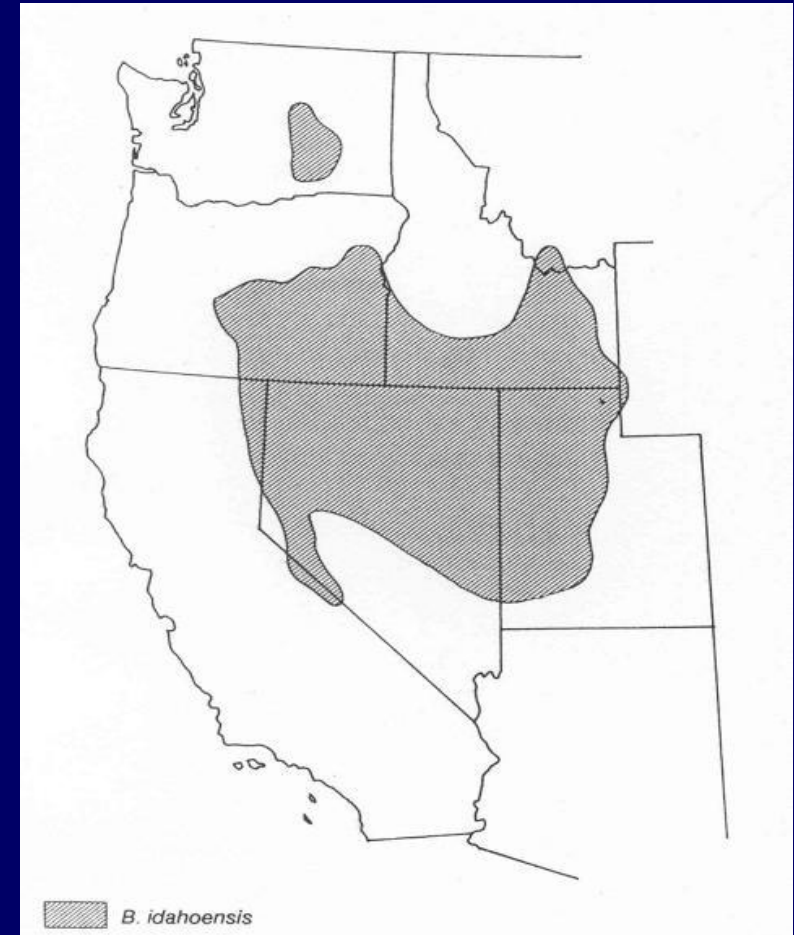
# ESU Case Study

## WA Pygmy Rabbit (*Brachylagus idahoensis*)



# Pygmy Rabbit

- Smallest Rabbit Species in NA
- Historic Range: Great Basin sagebrush habitat ID, WA, NV, UT, MT, CA





# WA Population

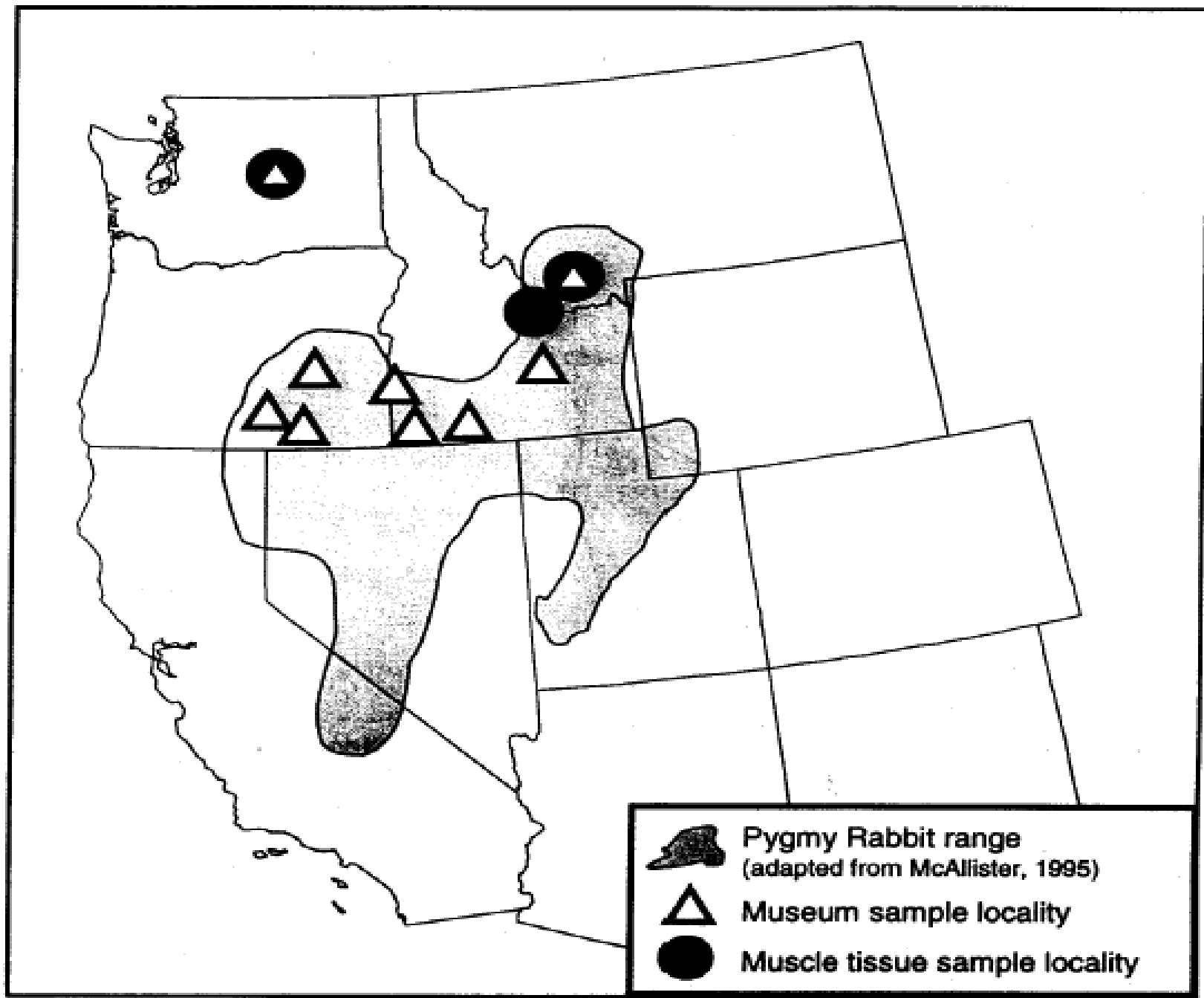
- Disjunct populaton
- Declining population that suffered a severe bottleneck in late 1990s ( $< 30$ )
- Question - Is this population an ESU?



# DataSet

- 307 Base pairs mtDNA cytB region from
- 9 microsatellite loci developed from European rabbit





# 4 CytB Haplotypes

<b>Haplotype</b>	<b>Nucleotide Position in Sequence</b>		
	<b>118</b>	<b>155</b>	<b>241</b>
<b><i>Brachylagus A</i></b>	A	G	C
<b><i>Brachylagus B</i></b>	●	●	T
<b><i>Brachylagus C</i></b>	G	●	T
<b><i>Brachylagus D</i></b>	G	A	T

TABLE 5. Cytochrome *b* haplotype frequencies.

Haplotype	Washington	Idaho	Montana
<i>Brachylagus</i> A	16 <small>≈ 1 mus. sample</small>	-	-
<i>Brachylagus</i> B	-	7	2
<i>Brachylagus</i> C	-	6	3
<i>Brachylagus</i> D	-	2	2
Total	16	15	7

**Molecular Clock Divergence Estimates:  
43 - 115K years**

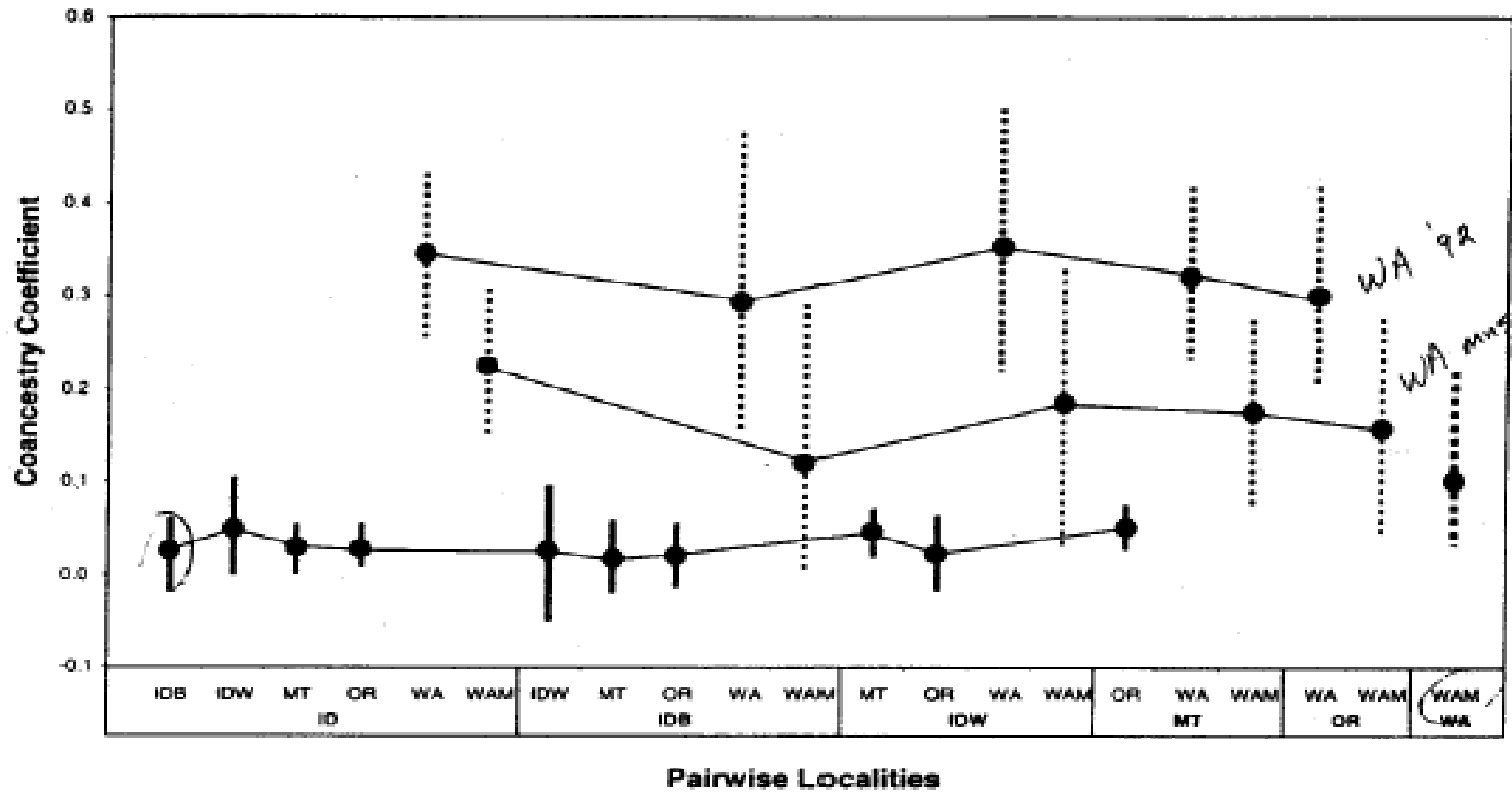


# Avg Diversity Statistics 9 microsatellite loci

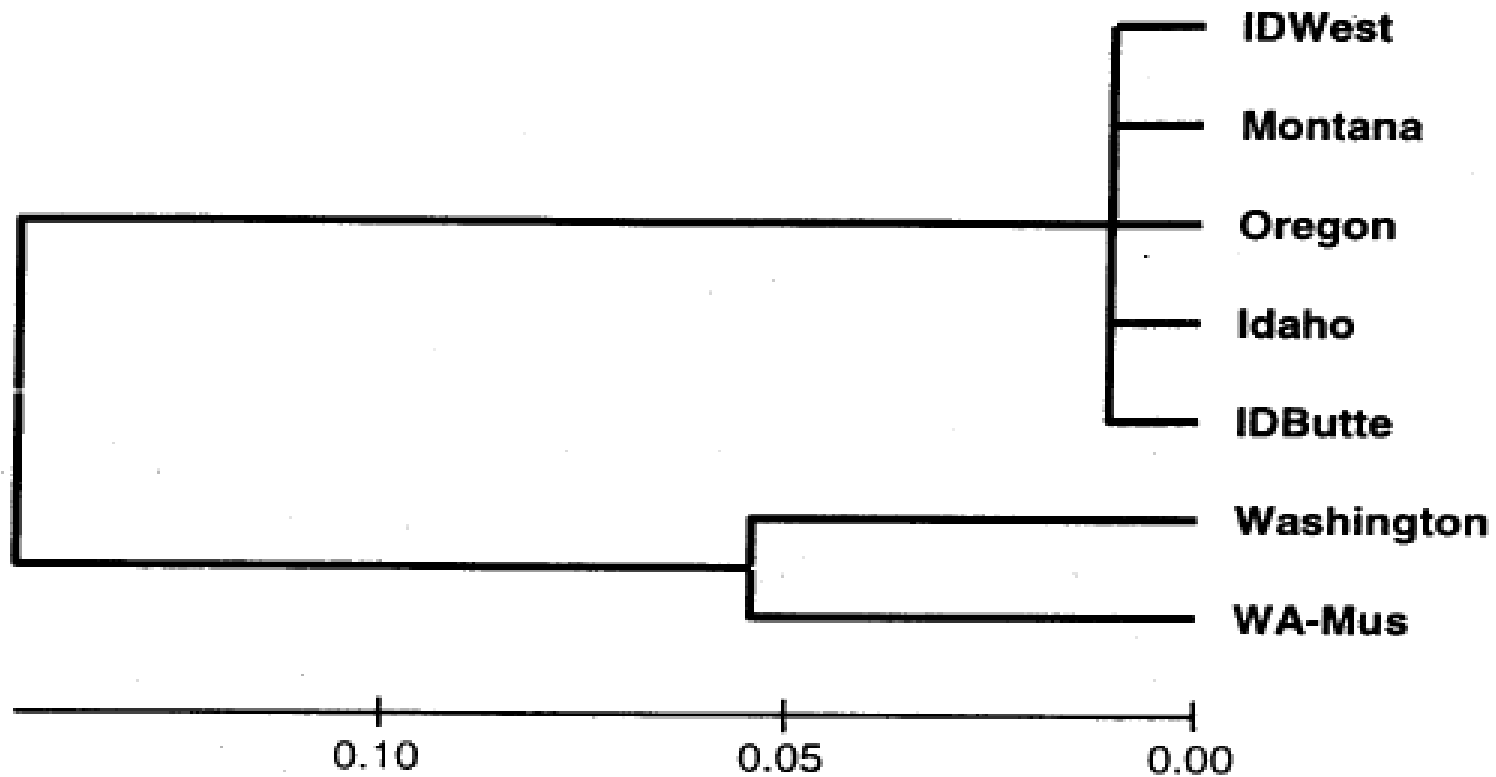
Locality	Private Alleles	$H_o^1$	$H_e$	N
Idaho	3	0.72	0.78	16
IDButte	5	0.85	0.87	3
IDWest	5	0.69*	0.80	8
Montana	3	0.73	0.78	11
Oregon	10	0.83	0.83	16
Washington	0	0.33	0.40	15
WA-MUS	4	0.52*	0.58	15

All pairwise allele frequency distributions were significantly different except Idbutte (IDWest, Montana)

# Pairwise Fst values - 9 microsatellite loci



# Distance Tree based on Fst (microsats)



Does this meet ESU criteria?



J. Witham