

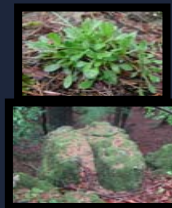
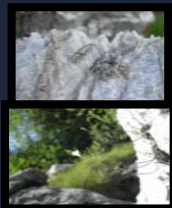
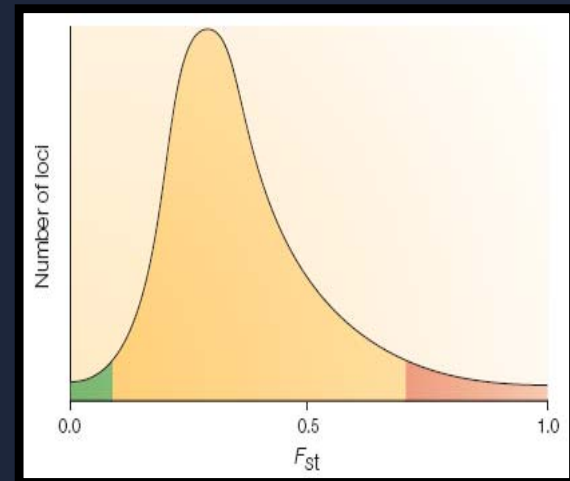
# Research in the Lawton-Rauh Lab: Plant Population Genetics

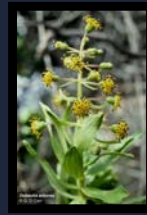
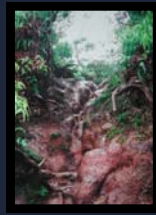
*Arabidopsis* sister species and the Hawaiian silversword alliance

## Brief overview:

**‘Comparative Molecular Population Genetics & Molecular Evolution’**  
*...tools to investigate population dynamics and gene-specific processes*

Amy Lawton-Rauh  
Dept. Genetics & Biochemistry  
Clemson University  
AmyLR@clemson.edu  
www.clemson.edu/~amylr



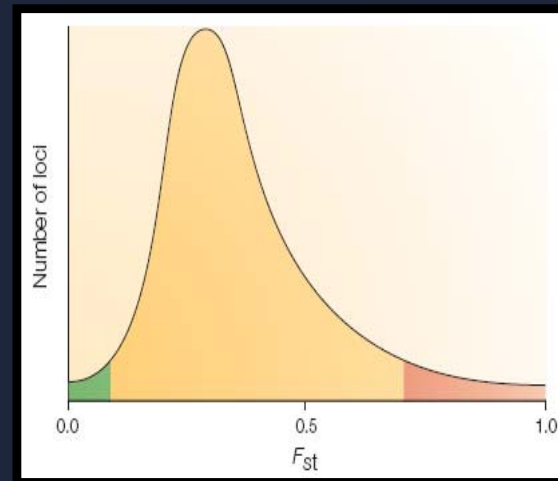
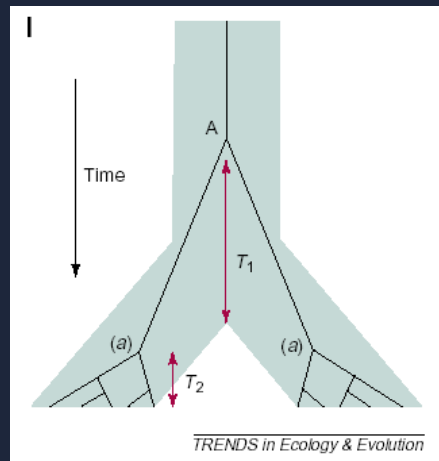


# Research in the Lawton-Rauh Lab: Plant Population Genetics

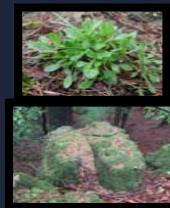
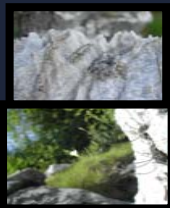
## *Arabidopsis* sister species and the Hawaiian silversword alliance

Brief overview:

‘Comparative Molecular Population Genetics & Molecular Evolution’  
*...tools to investigate population dynamics and gene-specific processes*



Luikart et al. Nature Genetics. 2003





# European *Arabidopsis lyrata* (*A. petraea*):

glacial tills  
in Scandinavia

Vatnajokull glacier  
Iceland  
(photo by Ramos-Onsins)



on isolated Dolomitic rock outcrops  
in Central Europe

Harz Mtns, Germany



Franconian Alps, Germany





# European *Arabidopsis lyrata* (*A. petraea*):

glacial tills  
in Scandinavia

Vatnajokull glacier  
Iceland  
(photo by Ramos-Onsins)

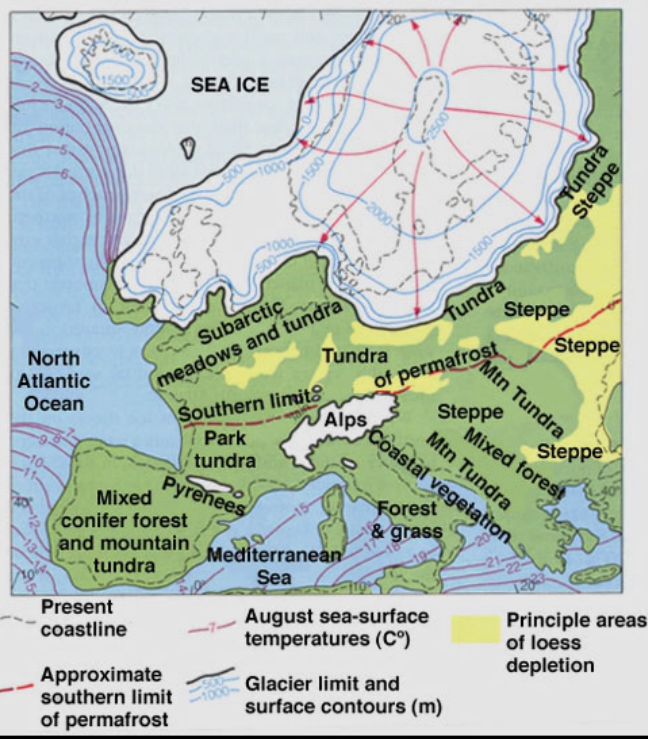


on isolated Dolomitic rock outcrops  
in Central Europe

Harz Mtns, Germany



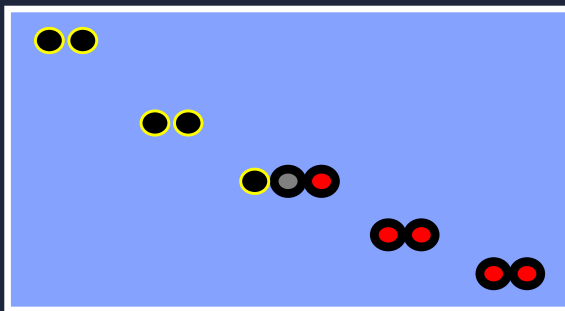
Franconian Alps, Germany



# Relative Roles of Demography vs. Selection

*in shaping genetic variation: Arabidopsis petraea & Arabidopsis arenosa*

- 1.) Frequency of unique polymorphisms increases with geographical distance between populations
- 2.) Frequency distributions of sequence diversity differ between populations with different postglacial histories
- 3.) Between-species isolation by distance is correlated with higher levels of linkage disequilibrium than within-species isolation by distance



○ Population, *A. petraea*

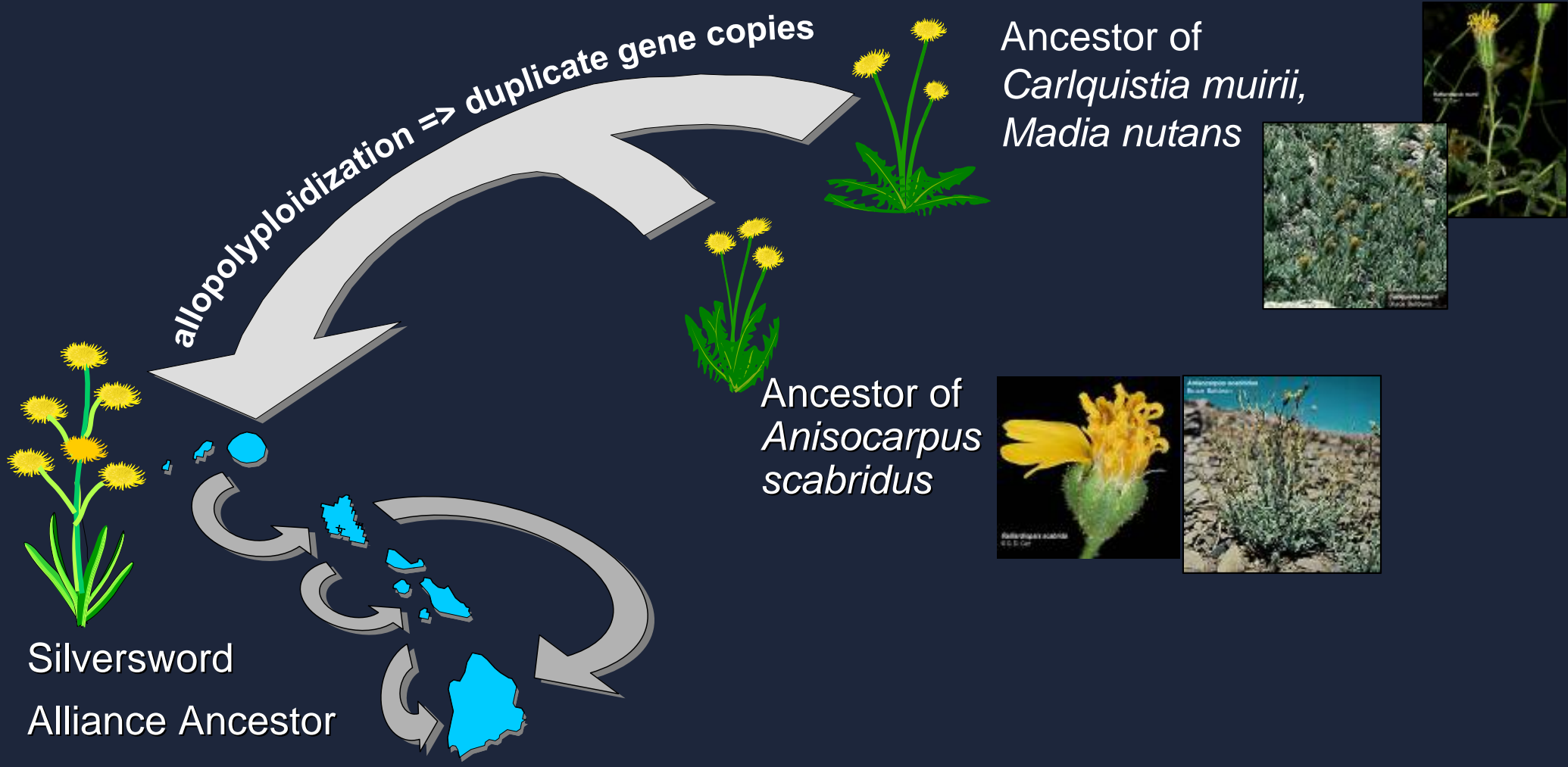
● Population, *A. arenosa*

● Population, hybrids of *A. petraea* & *A. arenosa*

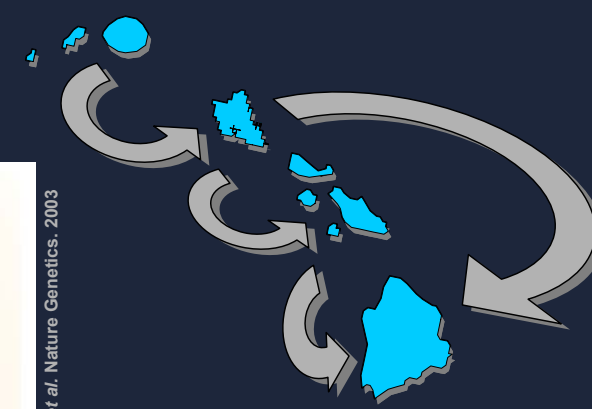
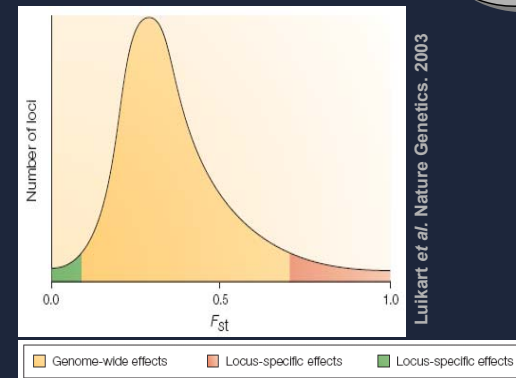




# Hawaiian Silversword Alliance: origin & radiation



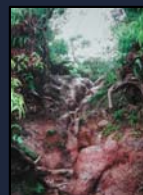
What are the relative roles of  
 genome dynamics (heredity)  
 morphology (form)  
 physiology (function)  
 in shaping the adaptive evolution  
 in the Hawaiian silversword alliance?



What are the relative contributions of:  
 demography & selection  
 in shaping genetic and genomic variation?



How many genes are involved in the morphological and physiological  
 differentiation among Hawaiian silversword alliance species?





# ***Mahalo nui loa (und Danke schön)!***

## **Lawton-Rauh Lab Folks:**

**Cindy Climer, Ph.D. Student**

**HSA, *Arabidopsis petraea*-*A.arenosa***

**Brad Rauh, Research Associate, Manager**

**HSA, Madia, *Arabidopsis petraea***

**Margaret Beaudrot**

**Clemson, HHMI/SCLife Honors Intern**

**Katie Horton**

**Clemson, Research Assistant**

**Chelsea Reighard**

**Clemson, HHMI/SCLife & Calhoun Intern**

**Jennifer Smith**

**Francis Marion Uni, NSF-REU Intern, S '07**

**Sarah Walker**

**Clemson, GEN-491 Intern 2006-07**

## **Collaborators, HSA:**

**Bruce Baldwin**

**UC-Berkeley**

**Elizabeth Friar**

**Rancho Santa Ana Botanic Garden**

**David Remington**

**UNC-Greensboro**

**Rob Robichaux**

**University of Arizona**

## **Collaborators, *Arabidopsis* sp.:**

**Juliette deMeaux**

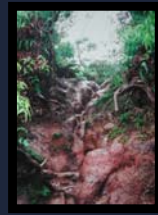
**Max Planck Institute, Cologne**

**Marcus Koch**

**Universität Heidelberg**





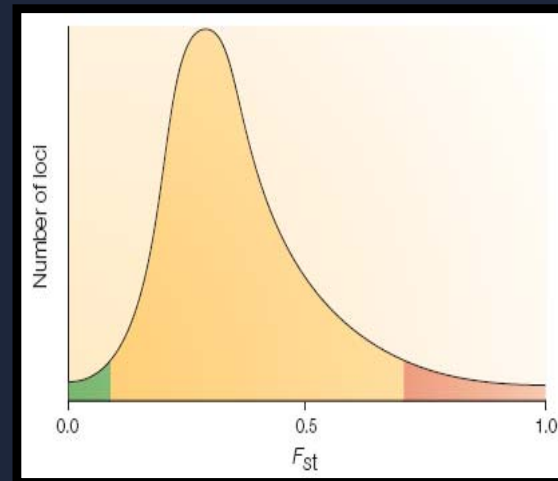
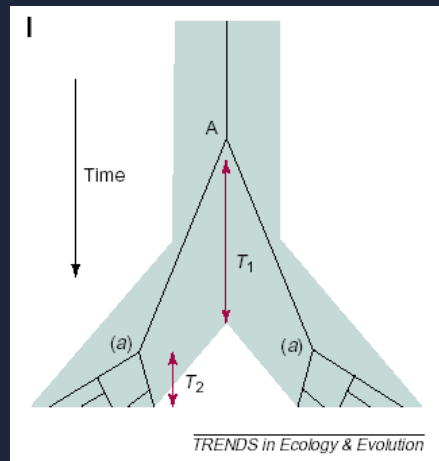


# Research in the Lawton-Rauh Lab: Plant Population Genetics

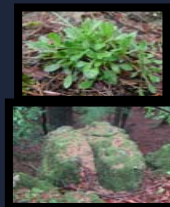
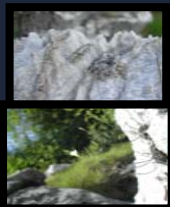
*Arabidopsis* sister species and the Hawaiian silversword alliance

## Brief overview:

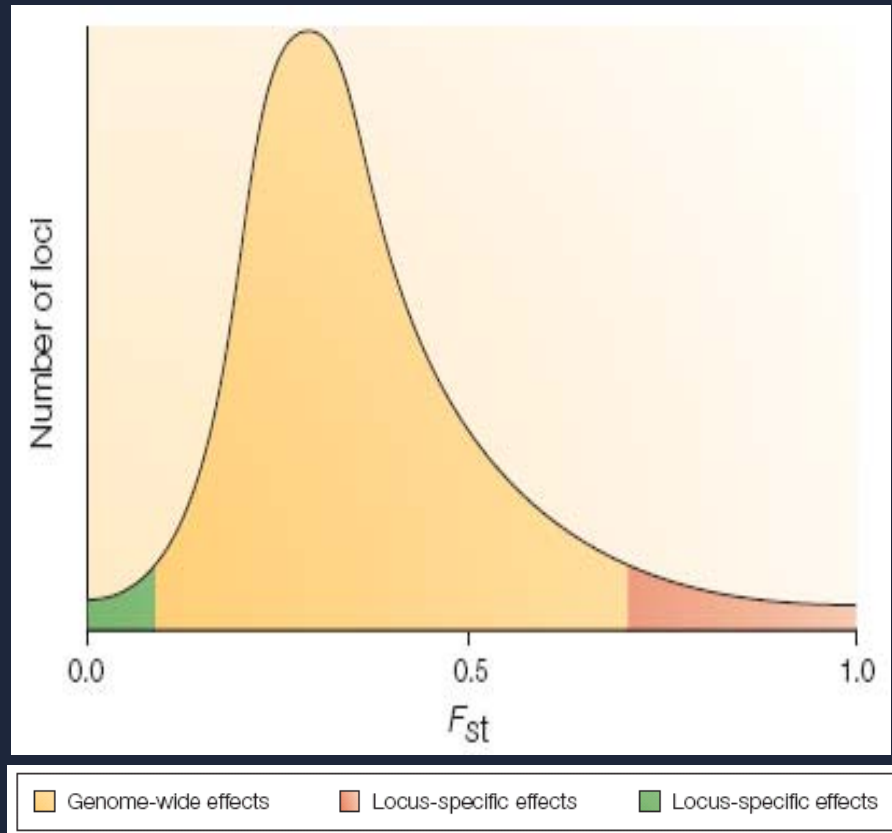
**‘Comparative Molecular Population Genetics & Molecular Evolution’**  
**...tools to investigate population dynamics and gene-specific processes**



Luikart et al. Nature Genetics. 2003



# 'Population Genomics': Brief Introduction



*relevant to:*

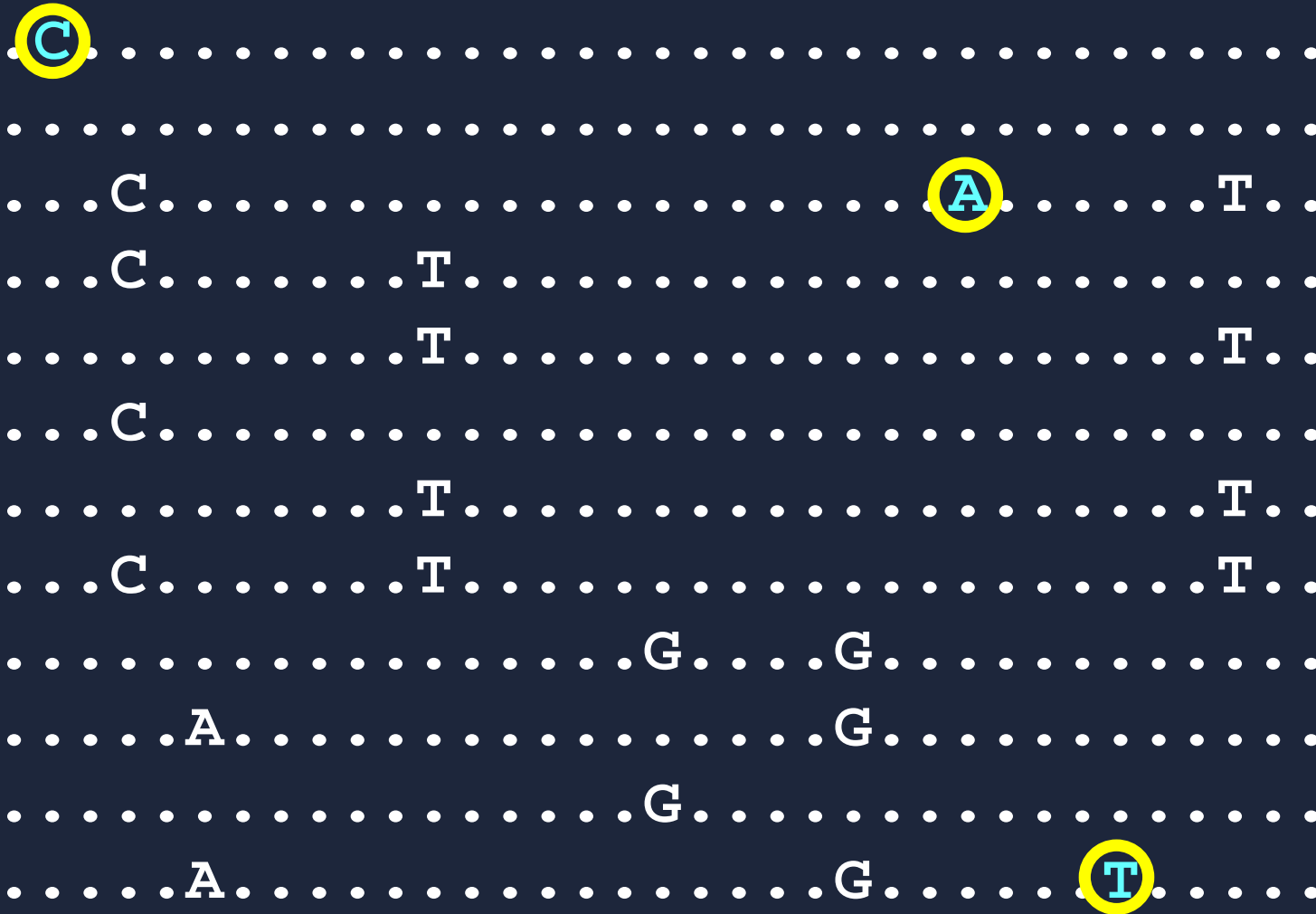
association genetics  
functional genomics

(human) disease mapping  
crop science, breeding  
conservation genetics



# Nucleotide Sequence Diversity

ATCGTGTGCCCATAAACCCTTTACTCCTTACGGGC

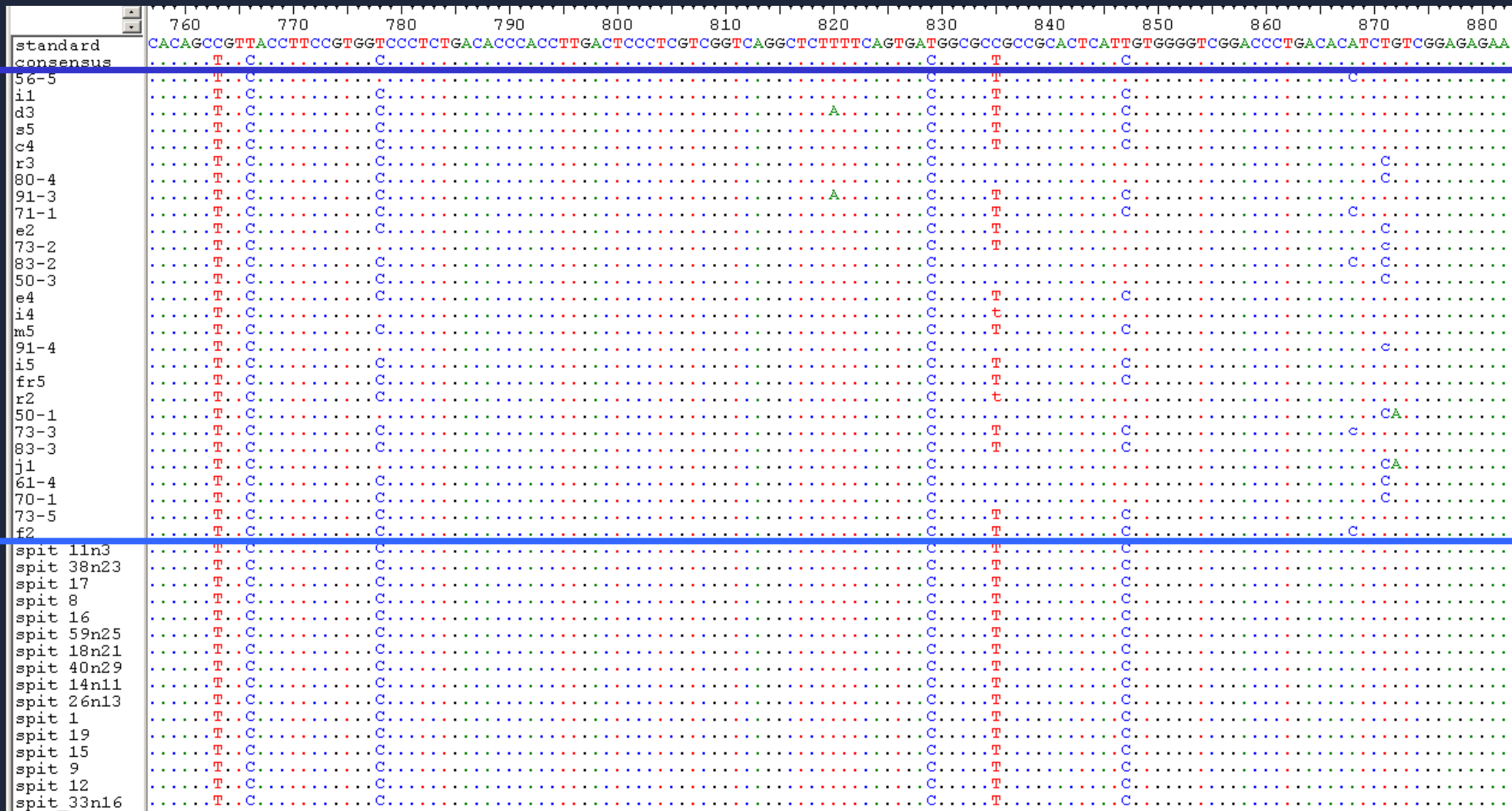


*Expect some rare polymorphisms, some singletons*

*“singleton”:*

 *single nucleotide polymorphisms found in 1 individual*

# Allele/haplotype segregation patterns differ among populations





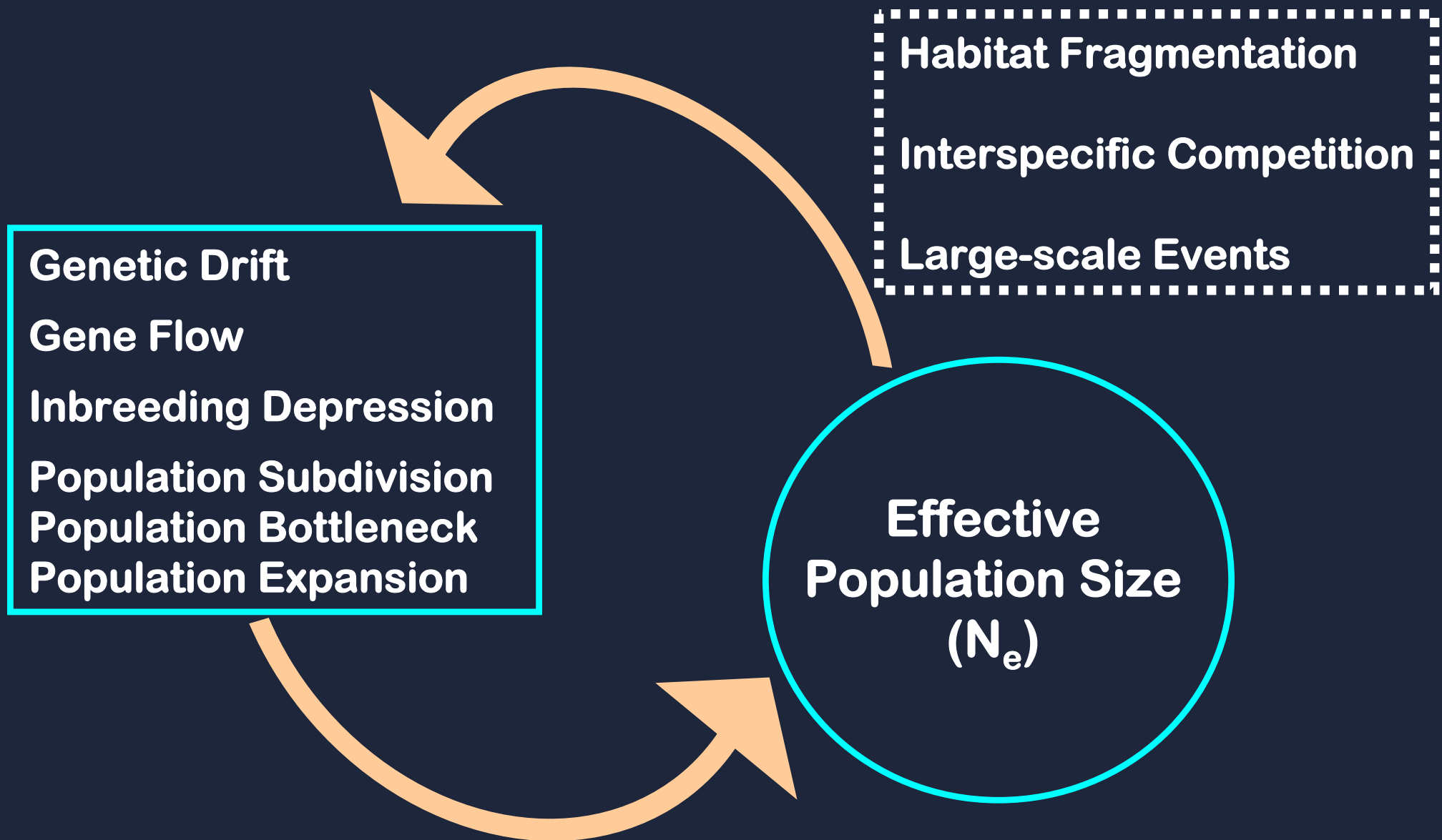
# Demography

- Population expansion
- Population contraction (bottleneck)
- Population subdivision
- Gene flow, migration

**...affects the entire genome  
(all loci at the same time)**

# Genetic variation is shaped by many factors

$$\text{Nucleotide Diversity } (\theta) = 4 N_e \mu$$



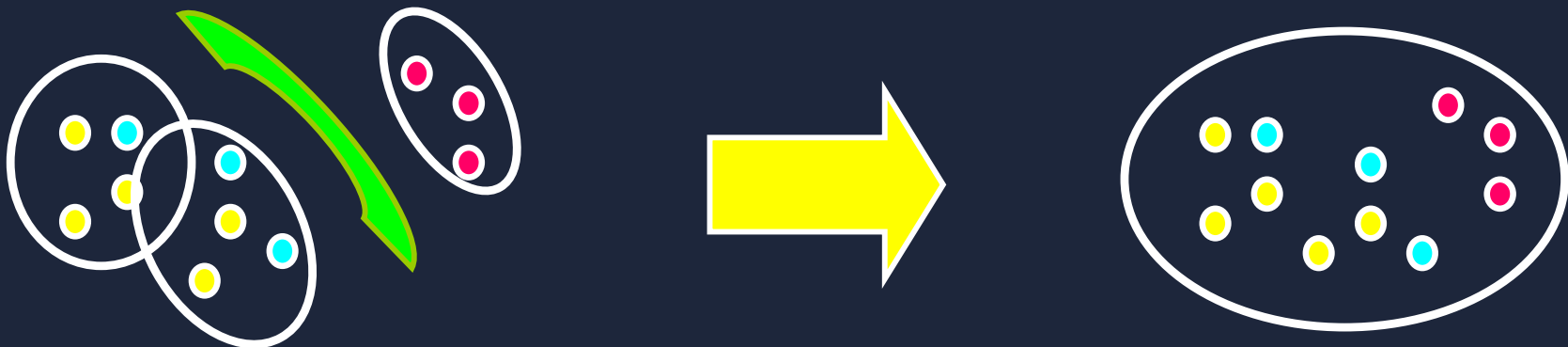


# Non random association of alleles...

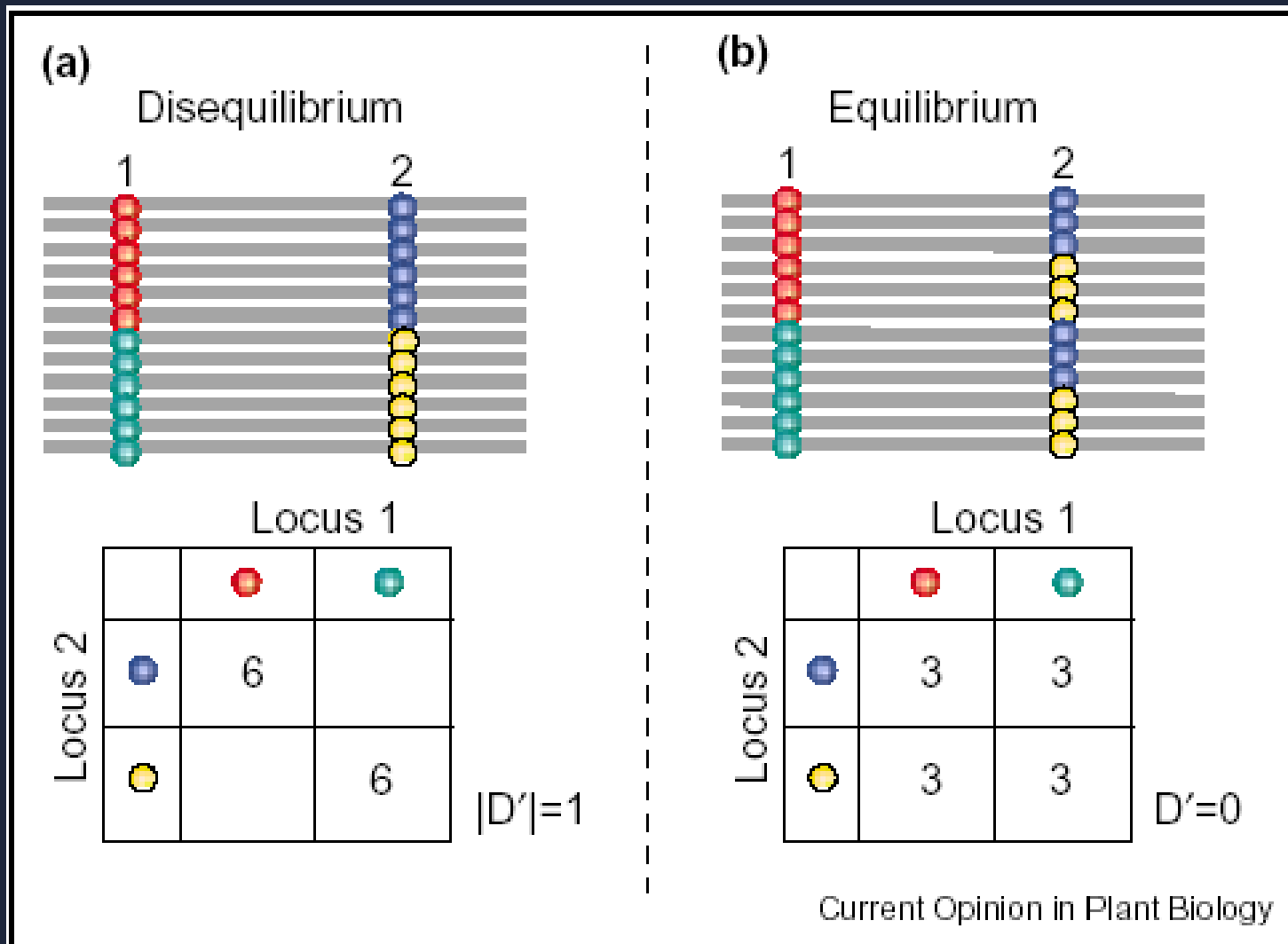
Linkage disequilibrium and selection for linked loci?



Migration of unique alleles that appear to be linked (via gene flow)?



# Linkage Disequilibrium (LD): Non-random association among alleles



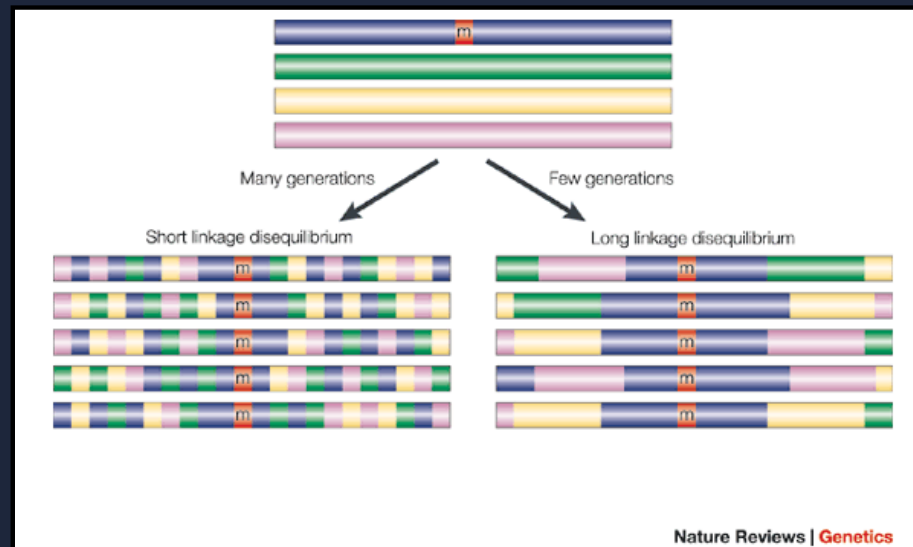
Rafalski A. (2002) Applications of single nucleotide polymorphisms in crop genetics. *Curr. Opin. Plant Bio.* 5:94-100.

# Linkage Disequilibrium Influences Nucleotide Sequence Diversity

Linkage Disequilibrium:

Non-random association among loci/sites

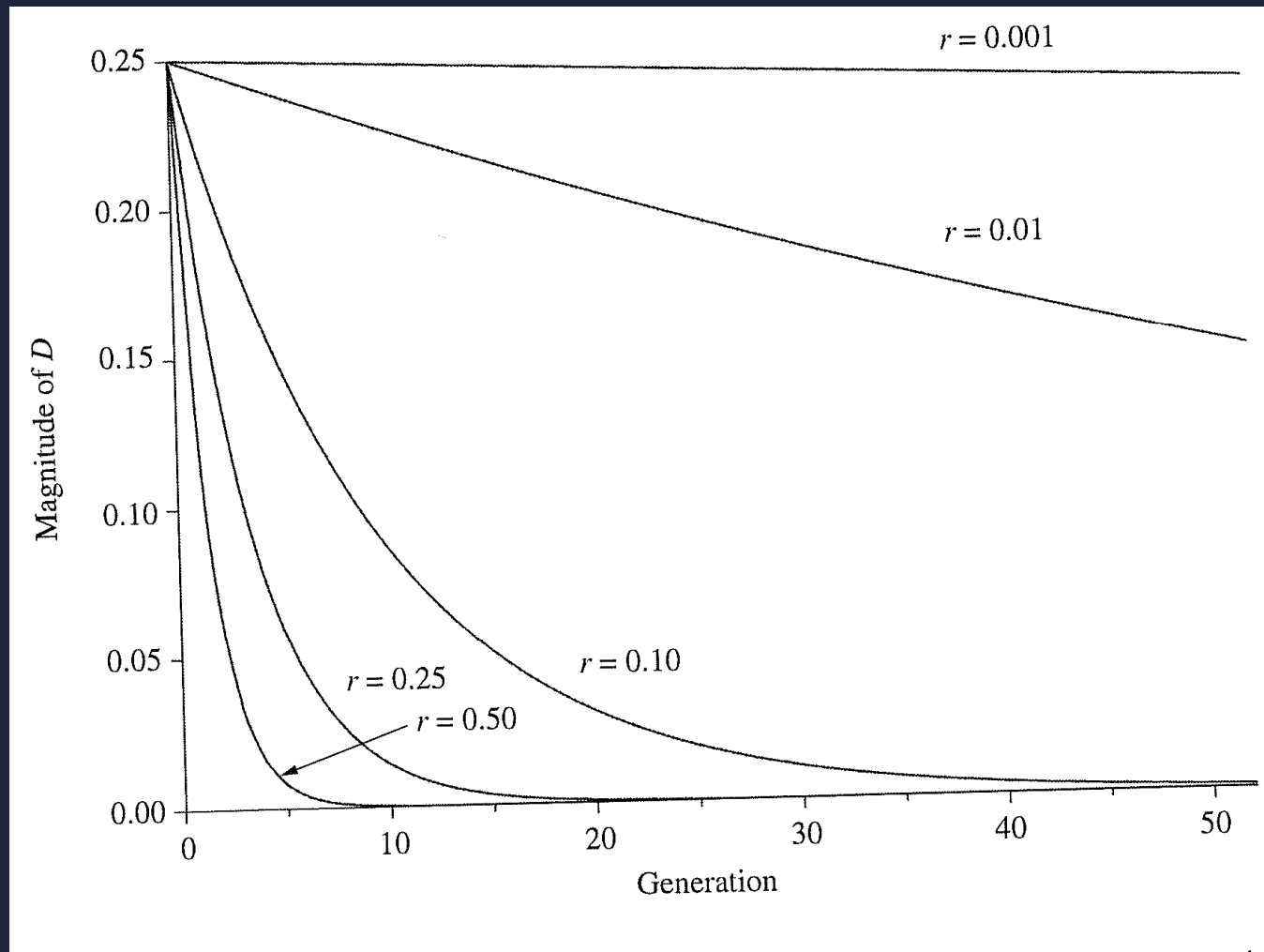
Depends on recombination rates & distance between loci/sites





# Linkage disequilibrium

breaks down at different rates,  
correlated with recombination rate ( $c$ )



# Recombination Rate Impacts LD and Nucleotide Sequence Diversity

When a mutation arises,  
it is in complete linkage (LD) with entire genome.

Over generations, recombination breaks up LD in  
proportion to genetic distance between loci.

# Recombination Rate Impacts LD and Nucleotide Sequence Diversity

When a mutation arises,  
it is in complete linkage (LD) with entire genome.

Over generations, recombination breaks up LD in  
proportion to genetic distance between loci.



Other factors 'interrupt' linkage breakdown

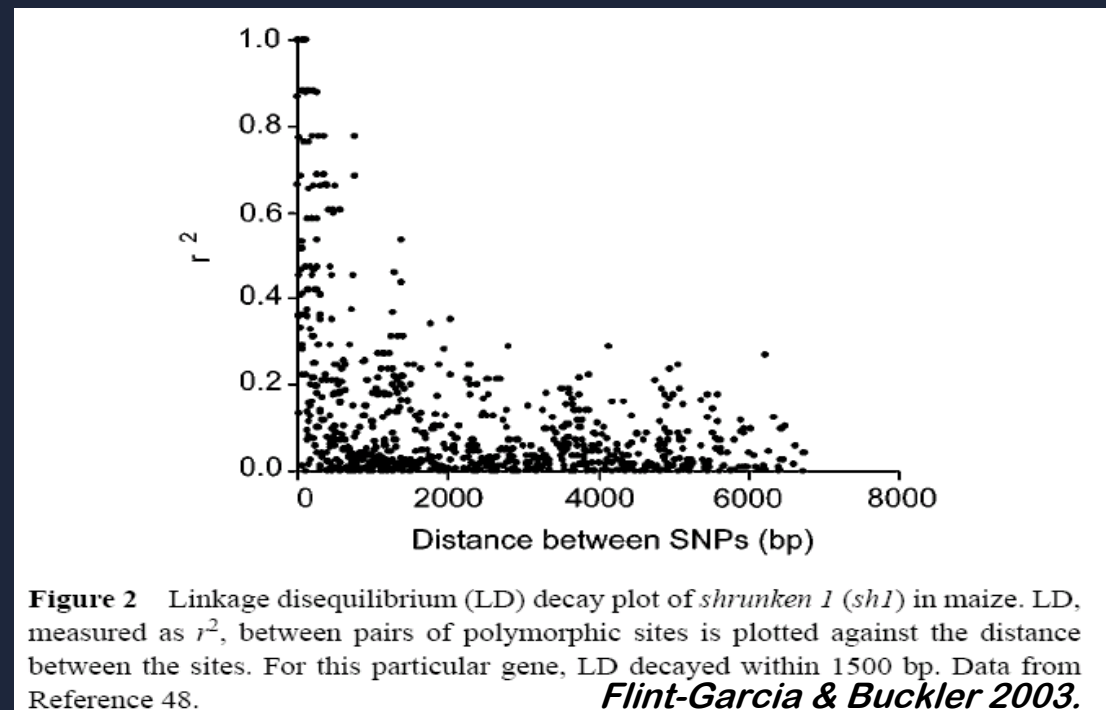
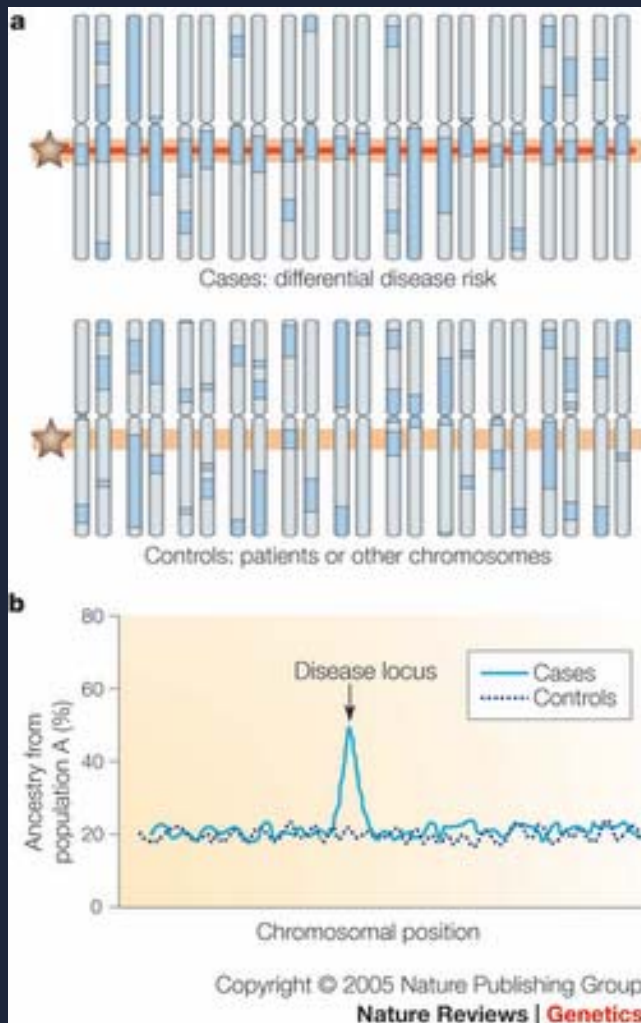
*Selection*

*Demography*



# Linkage Disequilibrium (LD)

breaks down in regions outside selection



# Molecular population genetics

## Genetic scales to consider:

Single gene: selection or neutrality at 'favorite/candidate' locus (YFG)

Genomic neighborhood: selection or neutrality in region containing YFG,  
related to effective recombination rate (linkage disequilibrium)

Entire genome: changes in population size, gene flow, population structure

...all relate to timeframe and organismal life history;  
scope of hypothesis determines analysis tools used



Molecular evolution, phylogenetics, population genetics

# Molecular population genetics:

Different ways to estimate and compare levels of genetic variation

## Different genetic markers:

AFLP

Microsatellites

Organelle Loci (cpDNA, mtDNA)

Nuclear Loci (Coding regions, Introns)

General loci

Candidate genes and 'your favorite gene (YFG)'

## Must consider:

Levels of genetic variation/polymorphism

Mutational model limitations

Analytical power for detecting specific processes

Allele/haplotype age

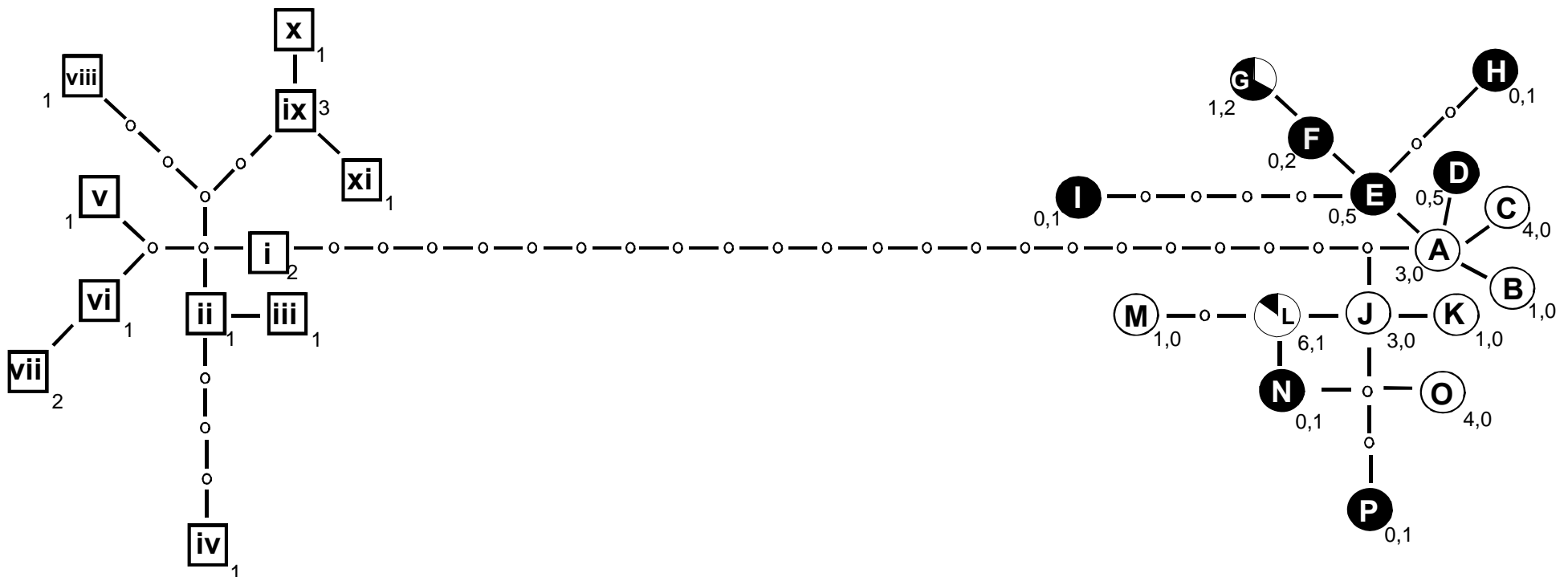
Gene divergence times (for molecular evolution studies)



# Phylogenetic trees for the population level: haplotype network analysis

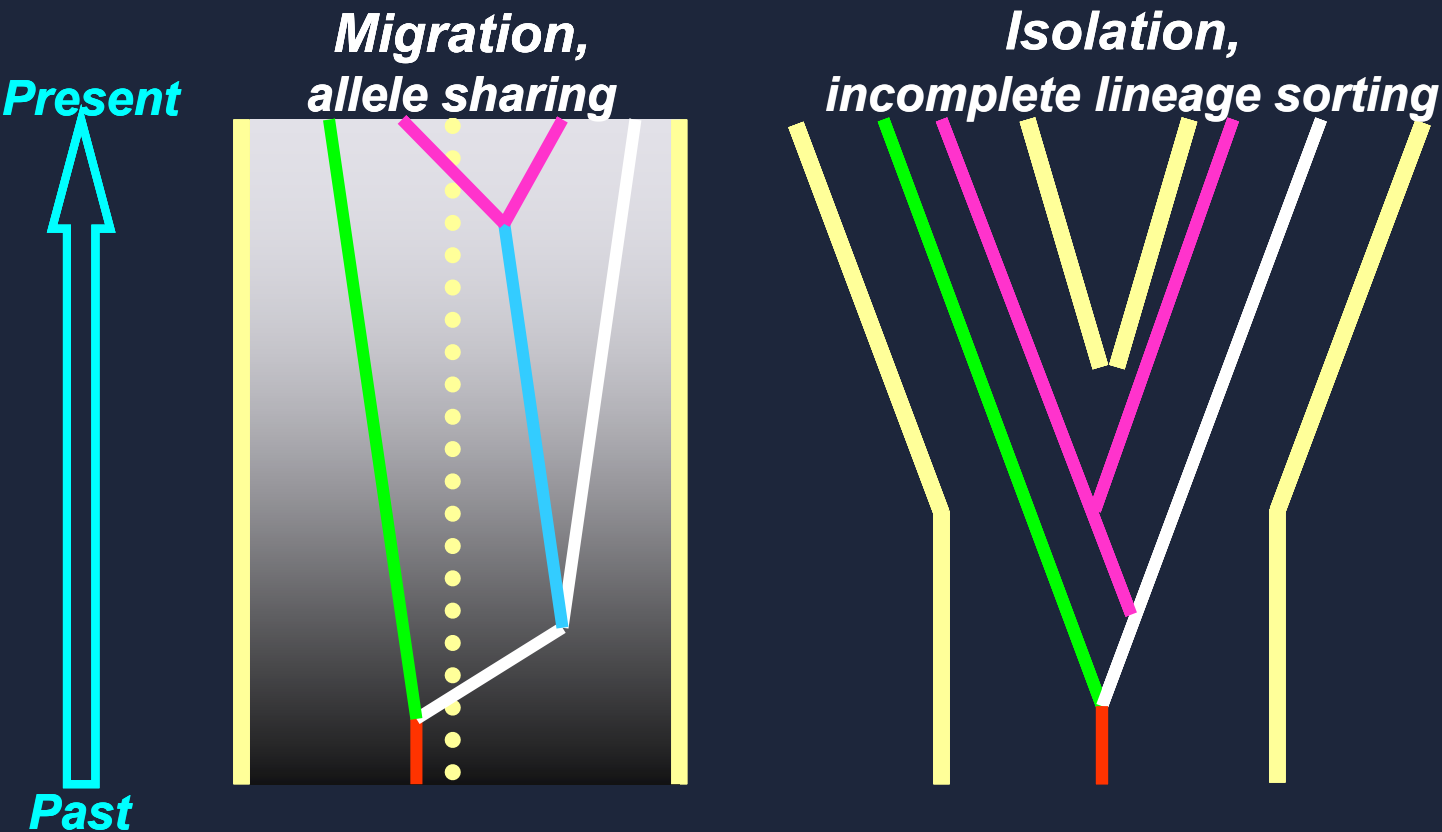
Statistical parsimony-based haplotype network: *ASAPETALA1-B*

□ *A. sandwicense*    ● *D. arborea*    ○ *D. ciliolata*



# Shared alleles between taxon 1 and taxon 2:

## Testing *Isolation vs. Migration* using the coalescent & Bayesian statistics



# Shared alleles between taxon 1 and taxon 2:

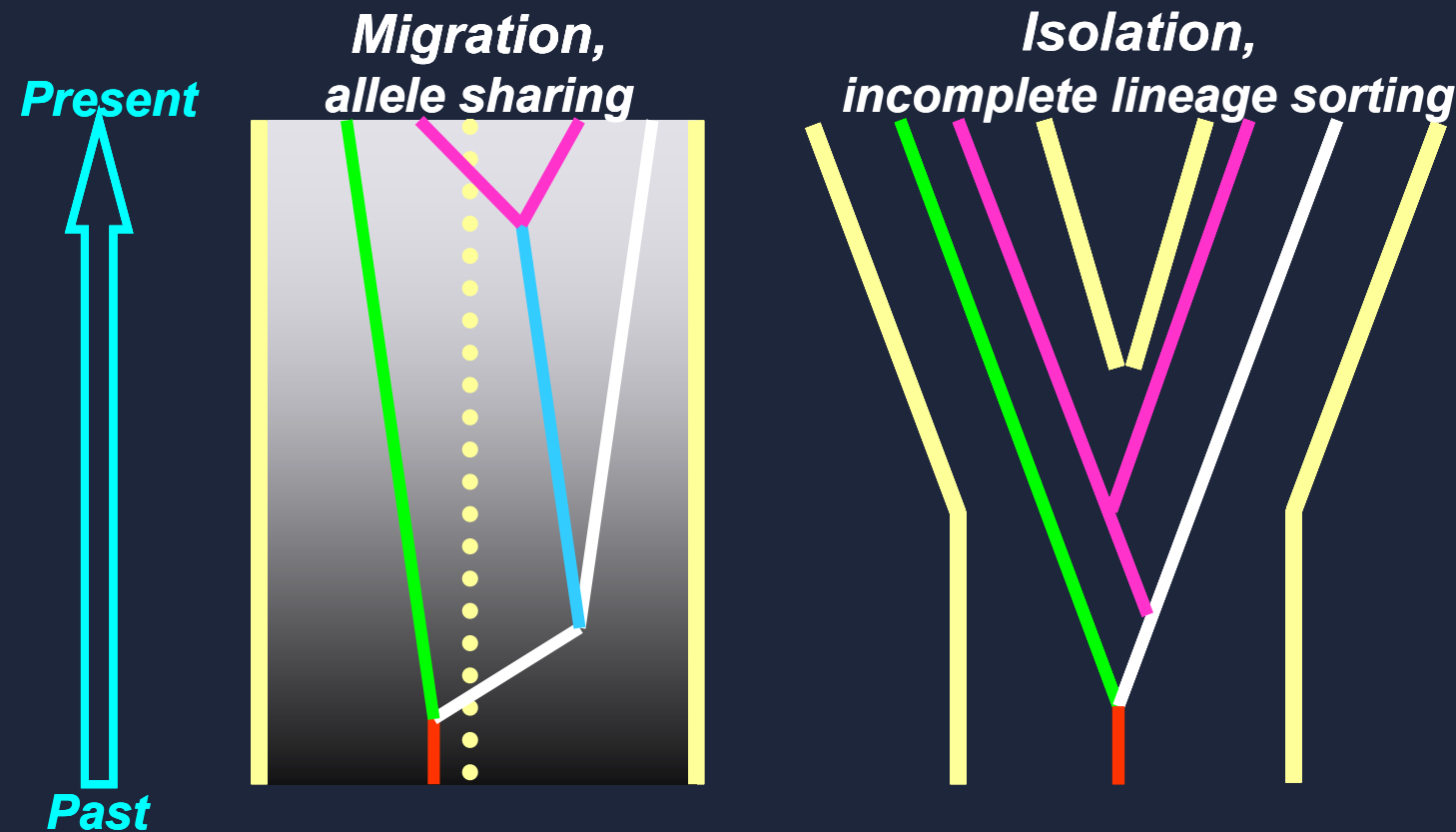
## Testing *Isolation vs. Migration* using the coalescent & Bayesian statistics



$$\text{TMRCA} = t / (2 N_e)$$

$$M = 2N_e m$$

Gene divergence  
Species divergence  
Migration rate



# Testing “Isolation” vs. “Migration” using the coalescent & Bayesian statistics

Nielsen R and Wakeley J (2001) *Genetics* 158, 885-896

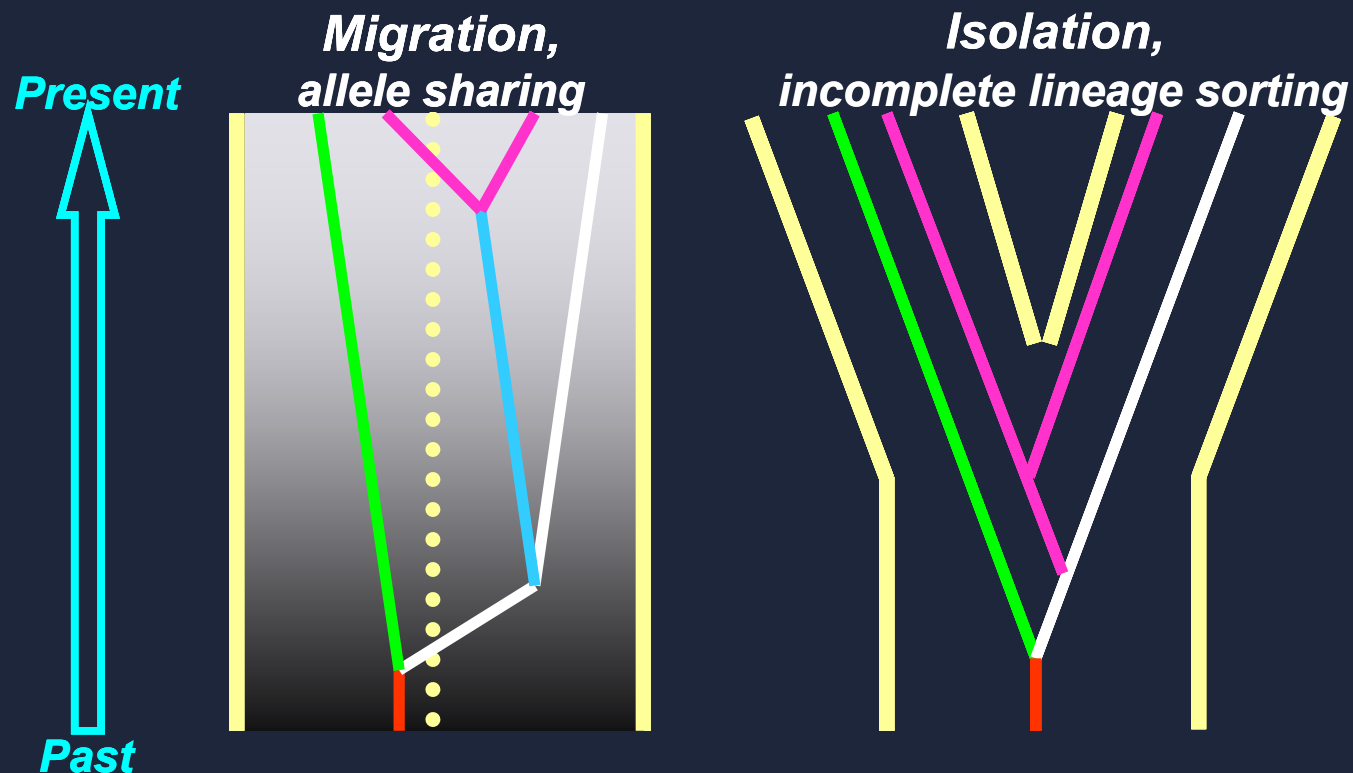
$$\text{TMRCA} = t / (2 N_e)$$

Gene divergence

Species divergence  
(credibility interval)

$$M = 2N_e m$$

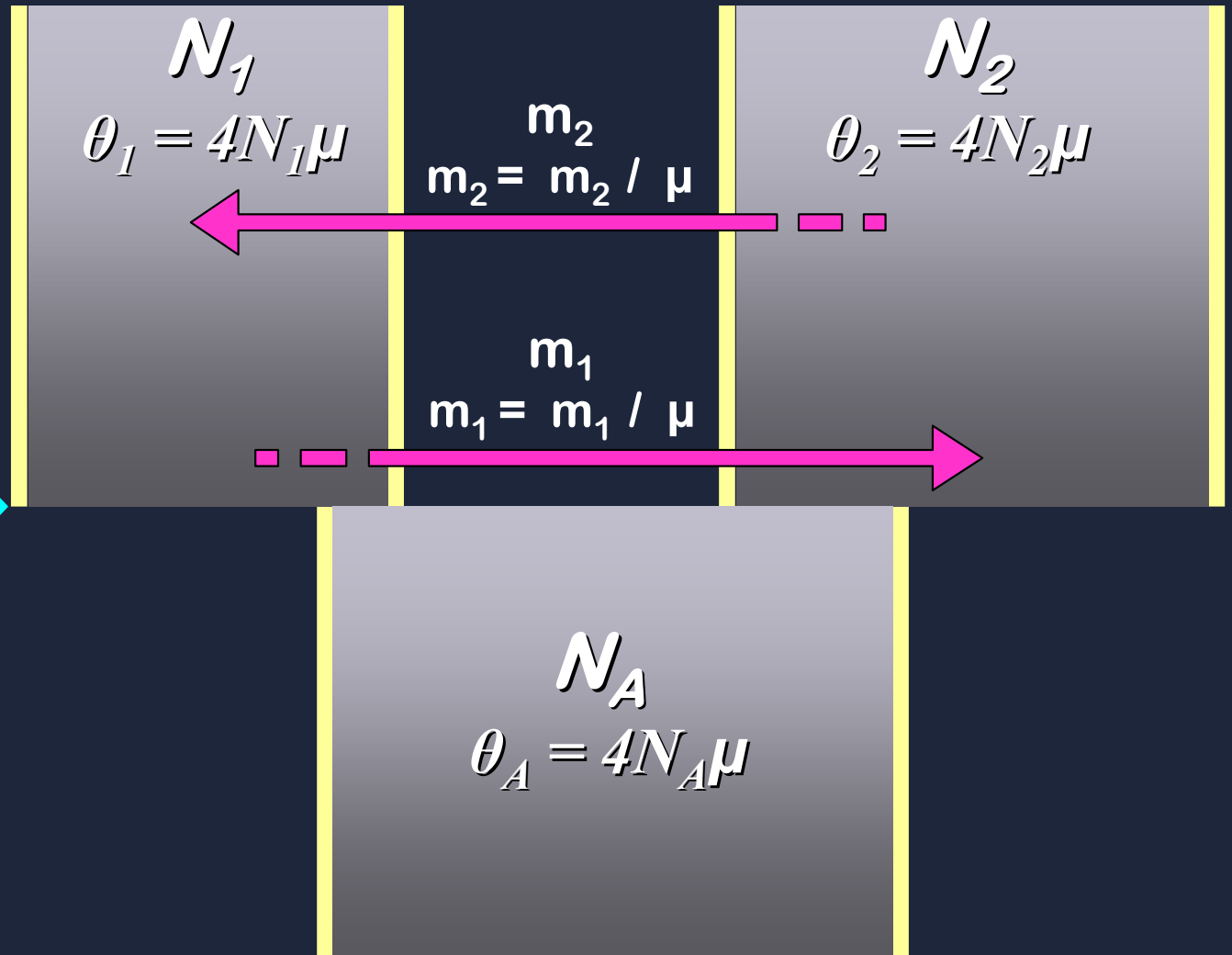
Migration rate  
(credibility interval)



# Isolation with migration model: gene flow directionality

(Hey *et al.* 2004)

Present



$t$

$t = t\mu$

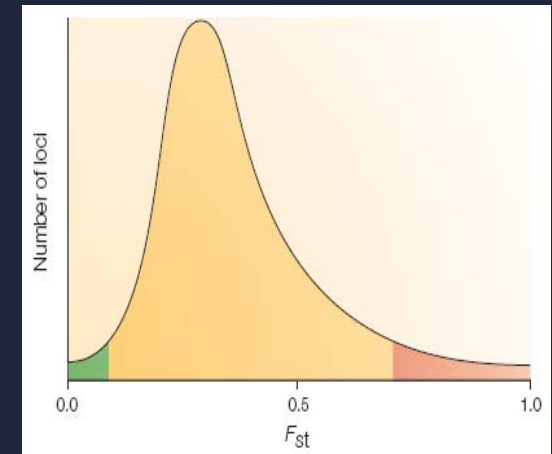
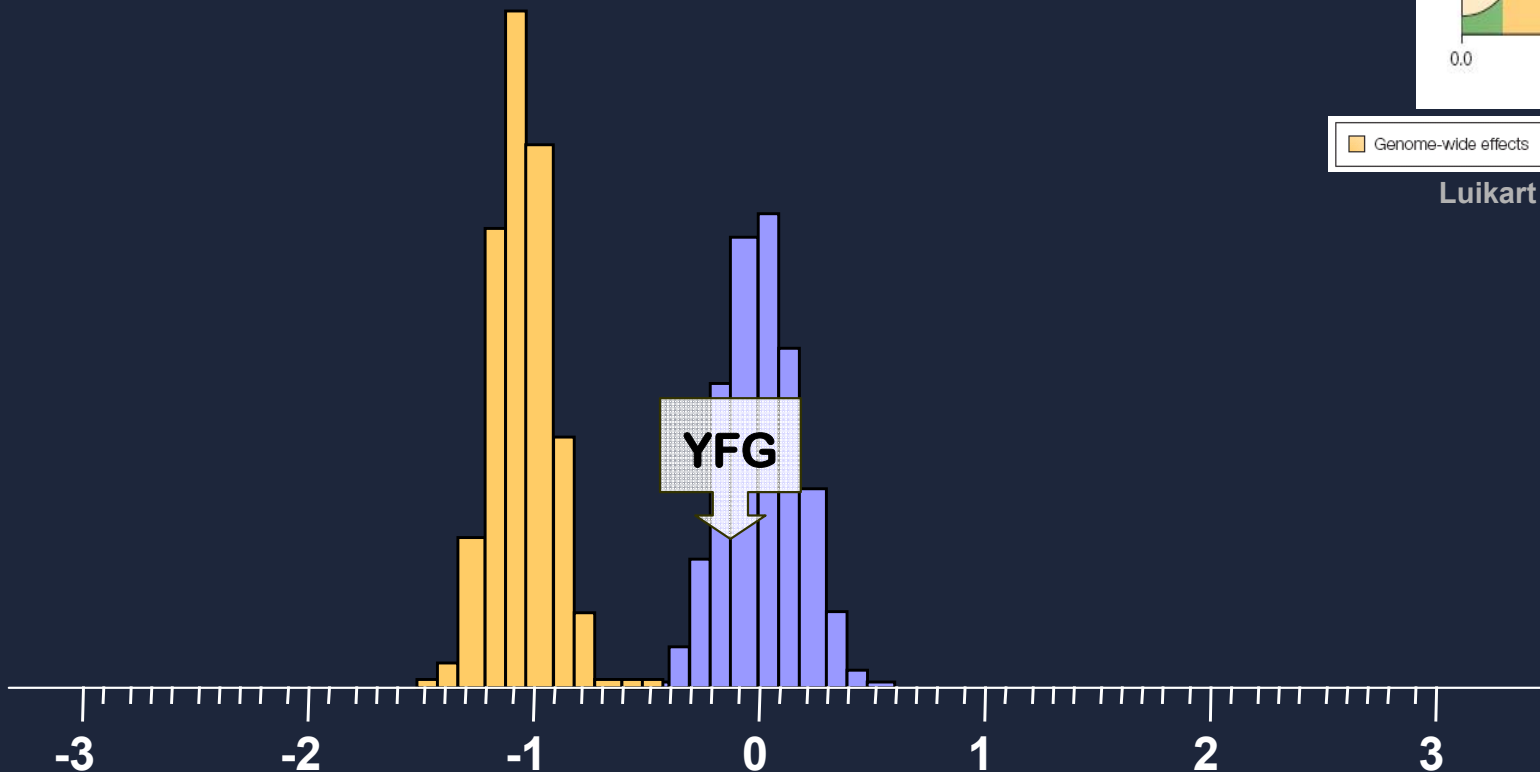
Past



# Distribution of estimates across loci:

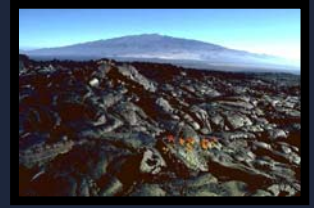
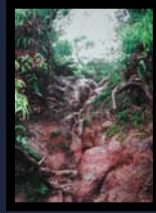
coordinates of 'favorite/candidate' genes?

Population expansion    Demography-equilibrium



Genome-wide effects    Locus-specific effects    Locus-specific effects

Luikart *et al.* Nature Genetics. 2003



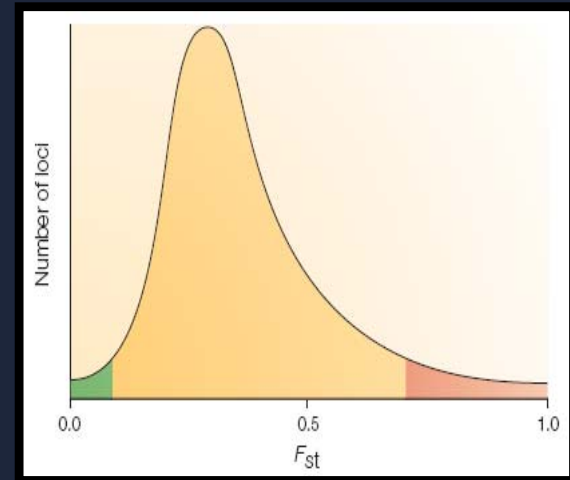
# Research in the Lawton-Rauh Lab: Plant Population Genetics

## *Arabidopsis* sister species and the Hawaiian silversword alliance

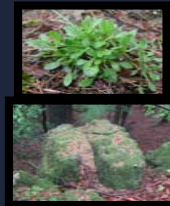
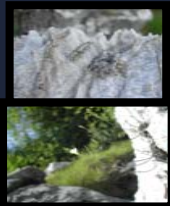
### Brief overview:

**‘Comparative Molecular Population Genetics & Molecular Evolution’**  
*...tools to investigate population dynamics and gene-specific processes*

**Amy Lawton-Rauh**  
 Dept. Genetics & Biochemistry  
 Clemson University  
 AmyLR@clemson.edu  
 www.clemson.edu/~amylr

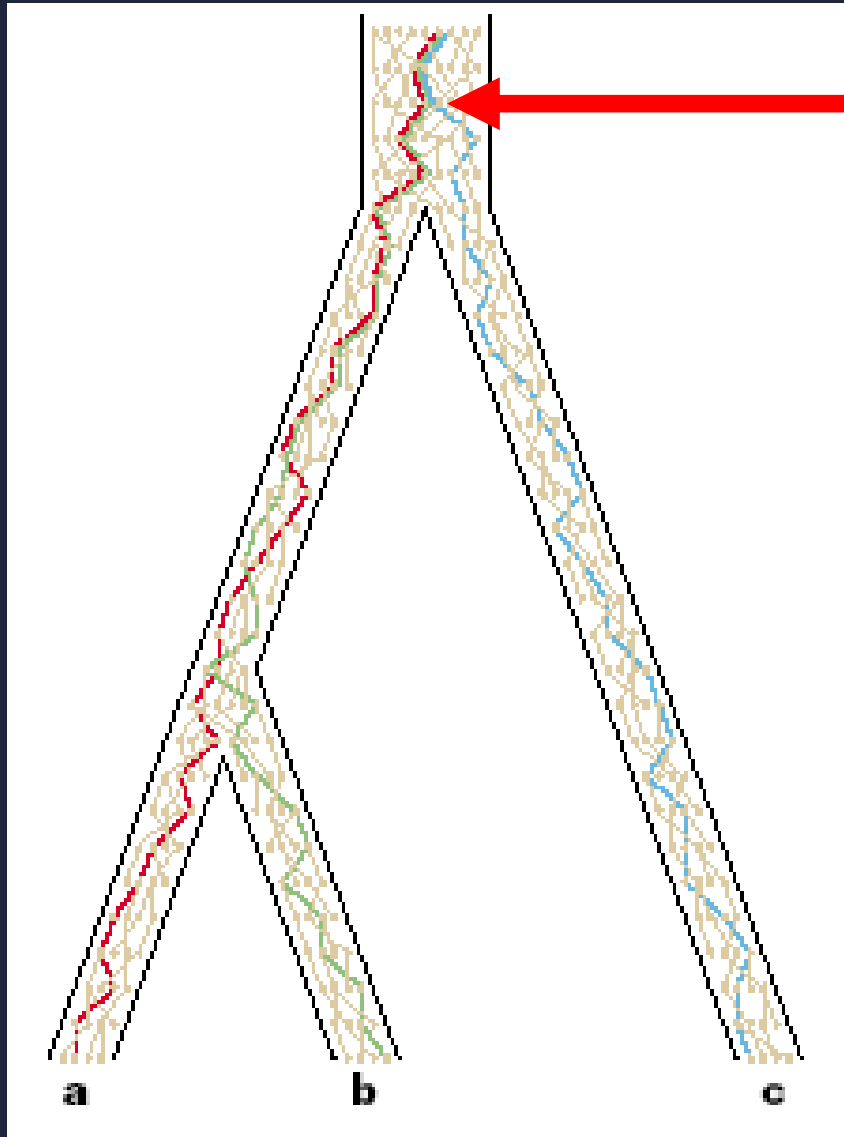


Luikart et al. Nature Genetics. 2003

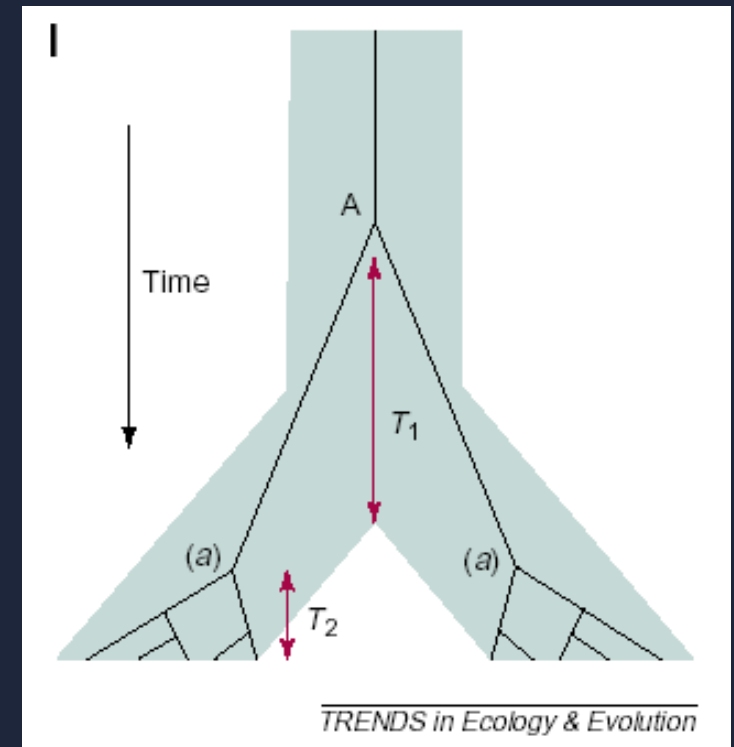


# Estimating Migration depends upon $T$

( $T$  = time to most recent common ancestor)



coalescence @ common ancestor  
species (entire genome)  
alleles @ specific locus



*TRENDS in Ecology & Evolution*