

Lecture 7: Population genetics III

Migration, Population structure, inbreeding & genetic linkage

HS 2017, 701-0245-00L

Dr. Sébastien Wielgoss

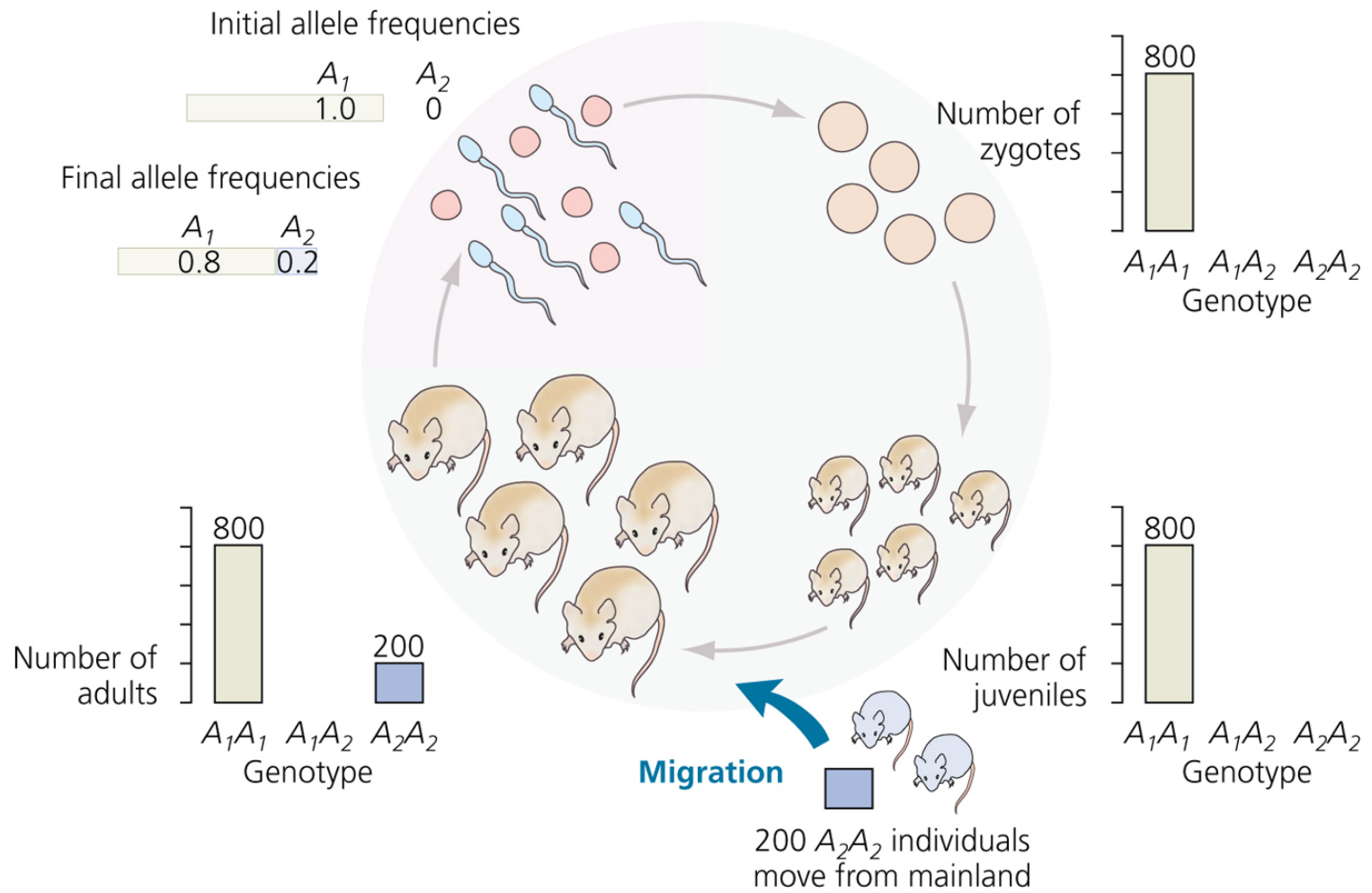


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Population Genetics:

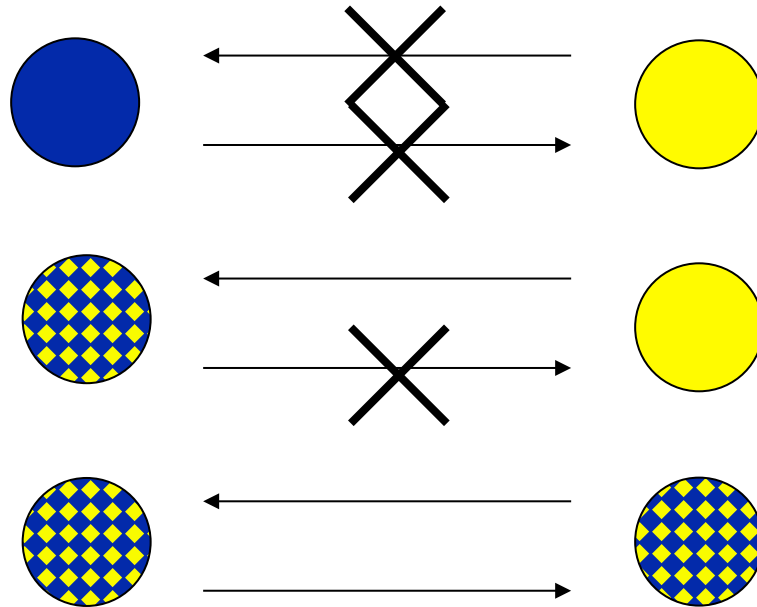
Migration

Figure 7-2



Migration homogenizes allele frequencies across subpopulations

... if not opposed by other forces of evolution such as selection.

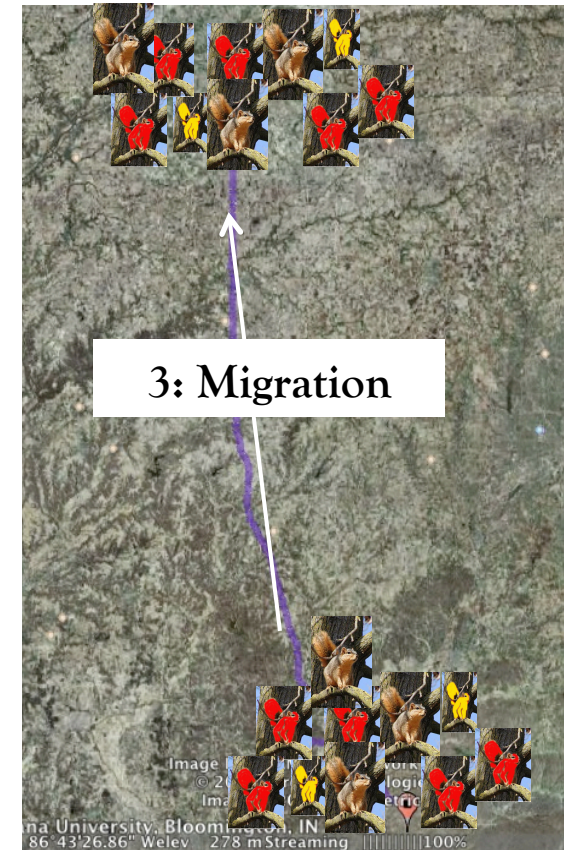
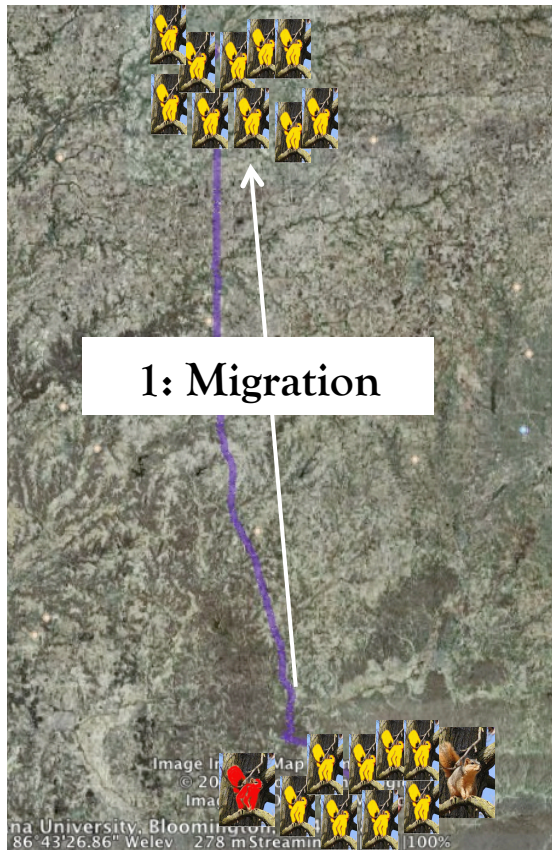


Genetic differentiation across populations

Genotypes



F_{ST} values measure the degree to which separate populations are genetically distinct due to absence of gene flow.

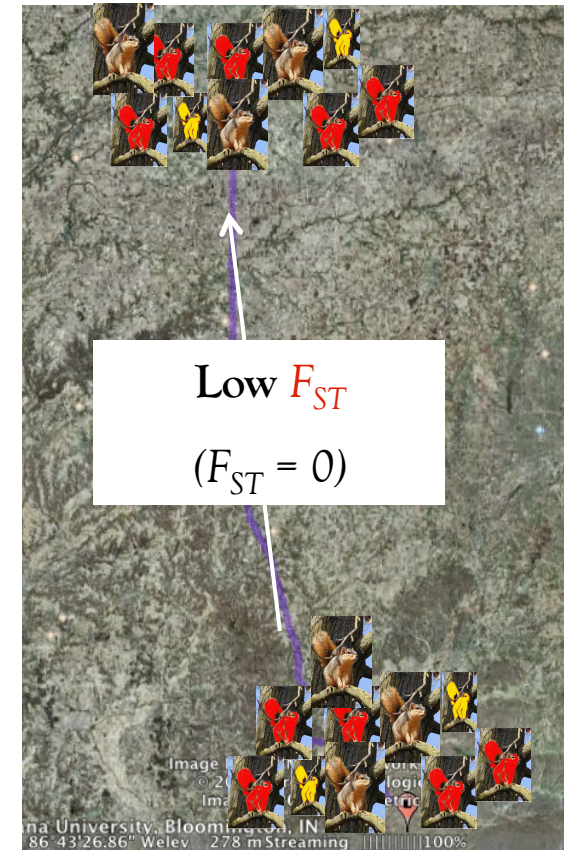
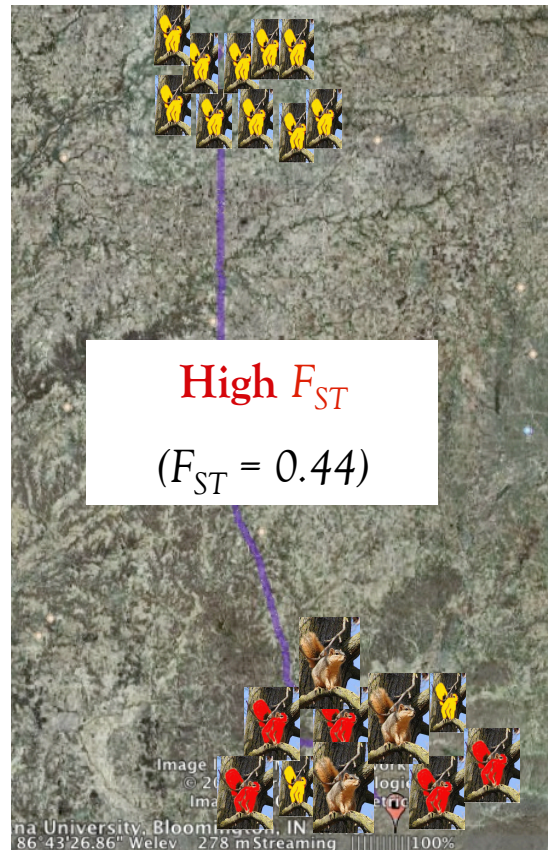
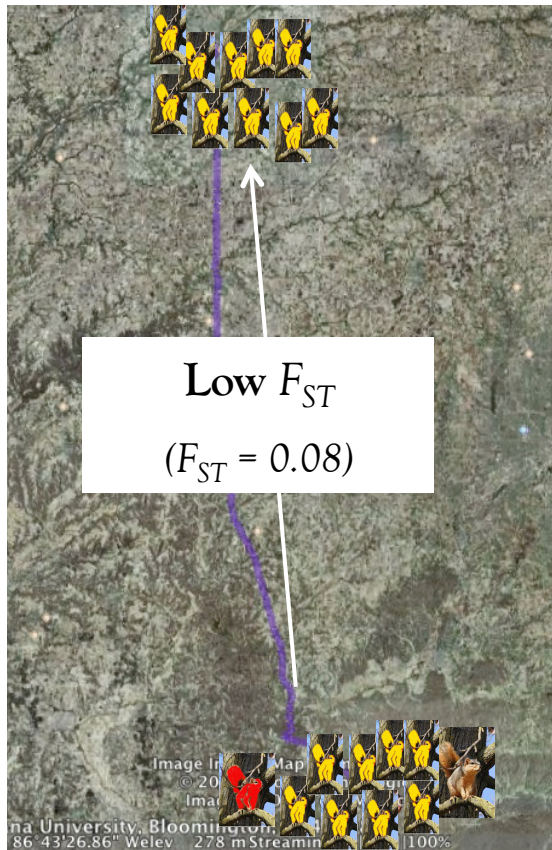


Genetic differentiation across populations

Genotypes



F_{ST} values measure the degree to which separate populations are genetically distinct due to absence of gene flow.



Continent-Island model of migration

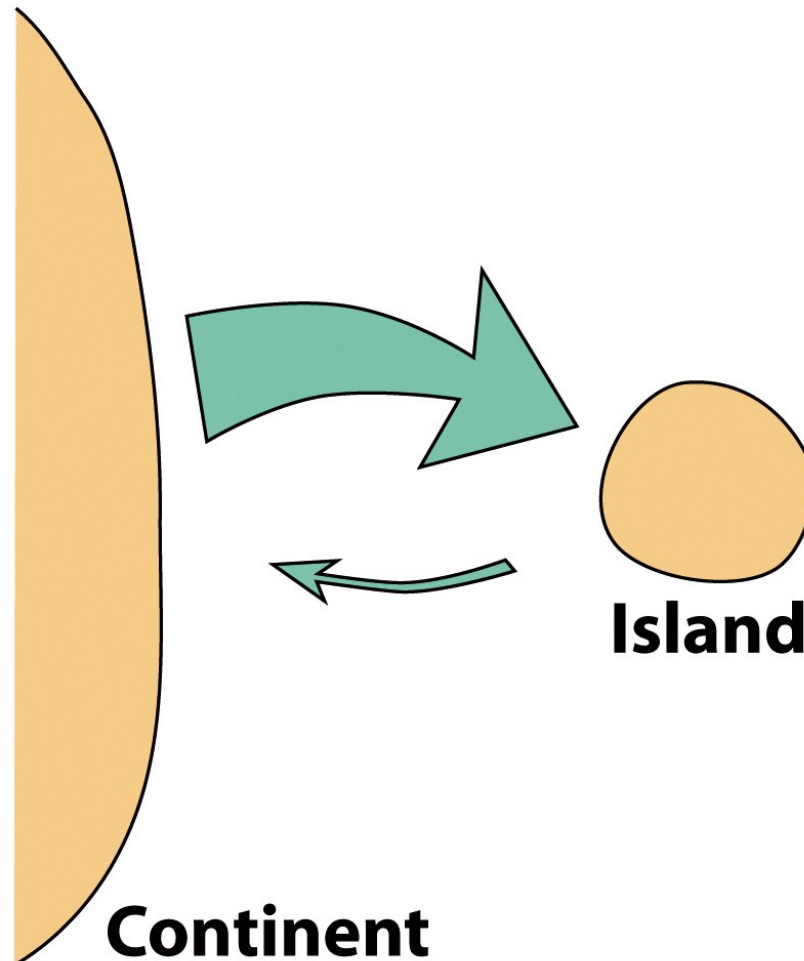
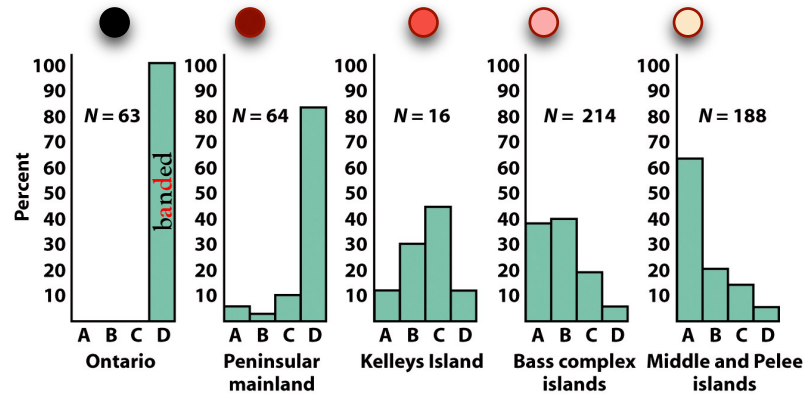
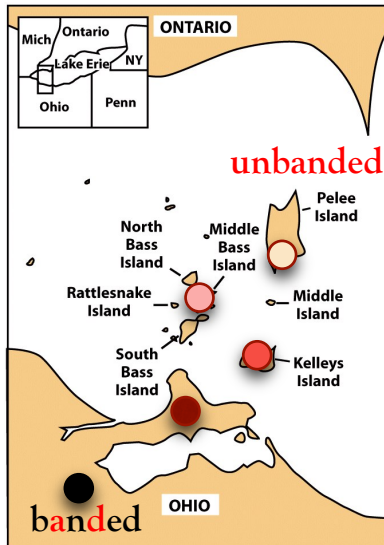


Figure 7-4 Evolutionary Analysis, 4/e
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Migration-selection balance in Lake Erie water snakes



Banded snakes disfavored by selection on islands

But:

input of banded phenotypes

due to migration from the mainland.

The forces that cause evolutionary change

Forces that **create variation** in evolving populations:

- mutation,
- recombination.

Forces that **determine the fate** of variation:

- selection,
- genetic drift,
- migration,

(indirectly: non-random mating, NRM)

Selfing reduces Heterozygote Frequency

- (a) Each individual produces offspring by selfing:

A_1A_1 individuals produce A_1A_1 offspring

A_1A_2 individuals produce A_1A_1 , A_1A_2 , and A_2A_2 offspring in a 1:2:1 ratio

A_2A_2 individuals produce A_2A_2 offspring

“Selfing”

A_1A_1	A_1A_2	A_2A_2
375	250	375



- (b)

Genotype:	A_1A_1	A_1A_2	A_2A_2	
# of individuals:	250	500	250	Generation 0
	375	250	375	Generation 1
	437.5	125	437.5	Generation 2
	468.75	62.5	468.75	Generation 3

Figure 7-25 Evolutionary Analysis, 4/e
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$$f(\text{Heterozygotes}) = 2pq/(2^3) = 0.5/(2^3) \sim 0.0625$$

Inbreeding Can Depress Average Fitness

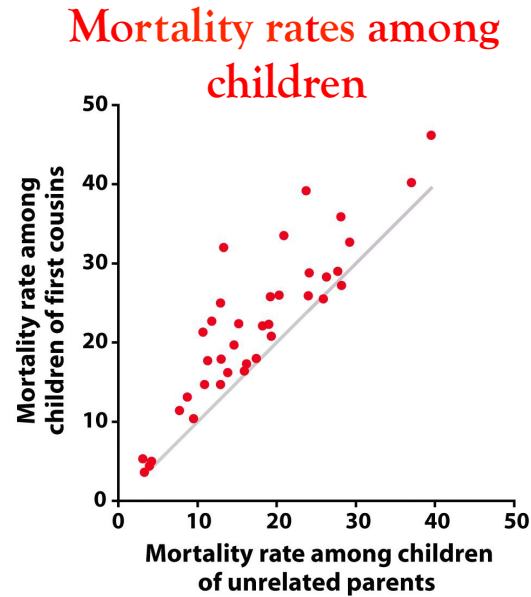


Figure 7-28 Evolutionary Analysis, 4/e
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Evolution at Multiple Loci:

Linkage disequilibrium

Evolution at Multiple Loci: Linkage

Extension of Hardy-Weinberg analysis to two loci

Two-locus version of HWE

We will not only be concerned with tracking:
allele frequencies, but also with
chromosome frequencies

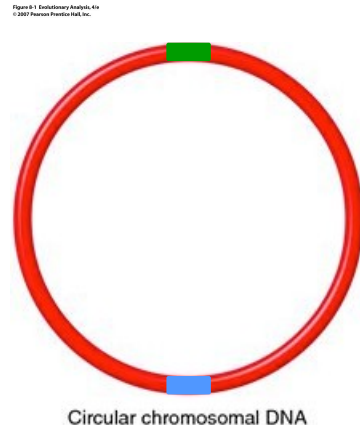
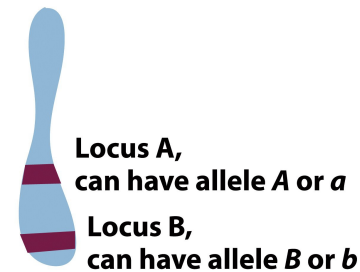
We will learn how evolution at one locus can affect
evolution at another locus

Linkage

There is **genetic linkage** between two loci if:

→ they are on the same non-recombining stretch of a chromosome

- a) In nuclear chromosomes of sexual diploids
loci remain together after meiotic crossing
- b) In non-recombining organisms/ organelles
(e.g., clonal bacteria/ mitochondria):
loci are on the same single chromosome



Linkage and Selection

If two loci are **linked**, selection on one locus can affect the evolutionary fate of the other (= a hitchhiking effect).

→ Do you remember mutational events that lead to linkage?

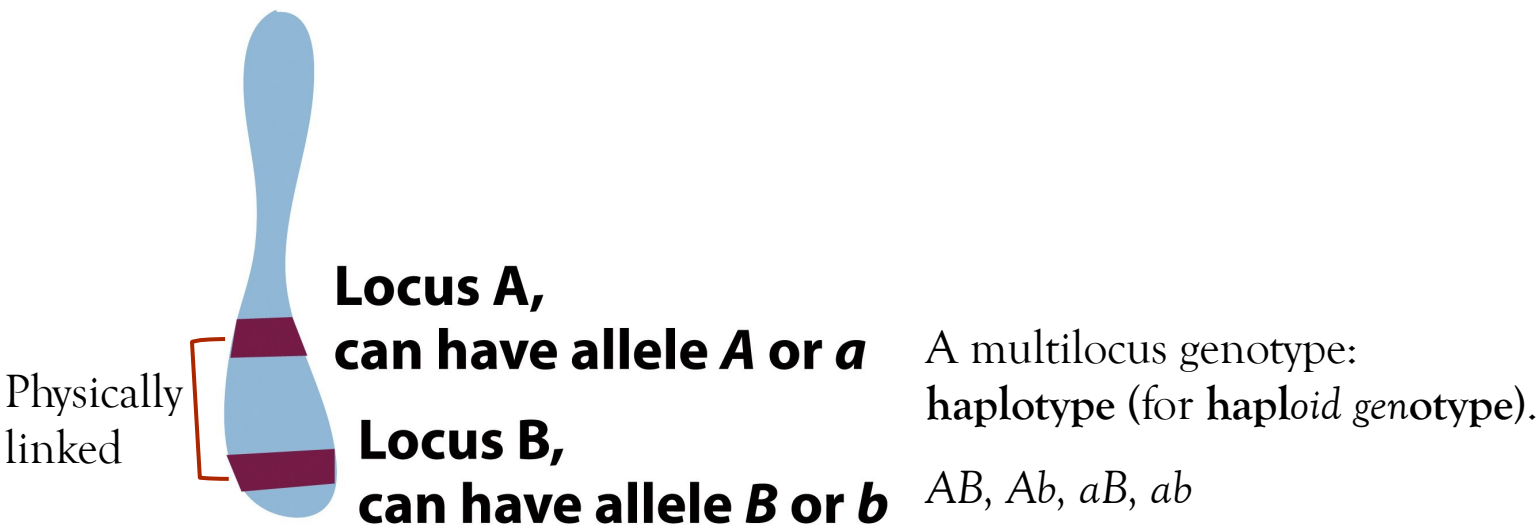


Figure 8-1 Evolutionary Analysis, 4/e
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A population in Linkage Equilibrium:

The frequency of any haplotype can be calculated by multiplying the frequencies of the constituent alleles.

$$g_{AB} = f(AB) = f(A) \times f(B) \quad g_{Ab} = f(Ab) = f(A) \times f(b)$$

$$g_{aB} = f(aB) = f(a) \times f(B) \quad g_{ab} = f(ab) = f(a) \times f(b)$$

g , *genotype frequency*

=> The coefficient of linkage disequilibrium, D , where

$$D = g_{AB}g_{ab} - g_{Ab}g_{aB}$$

Linkage (Dis)Equilibrium

Linkage happens due to relative physical location on **chromosomes**,
but *linkage equilibrium & disequilibrium*
are characteristics of **populations**.

A Population in Linkage Equilibrium

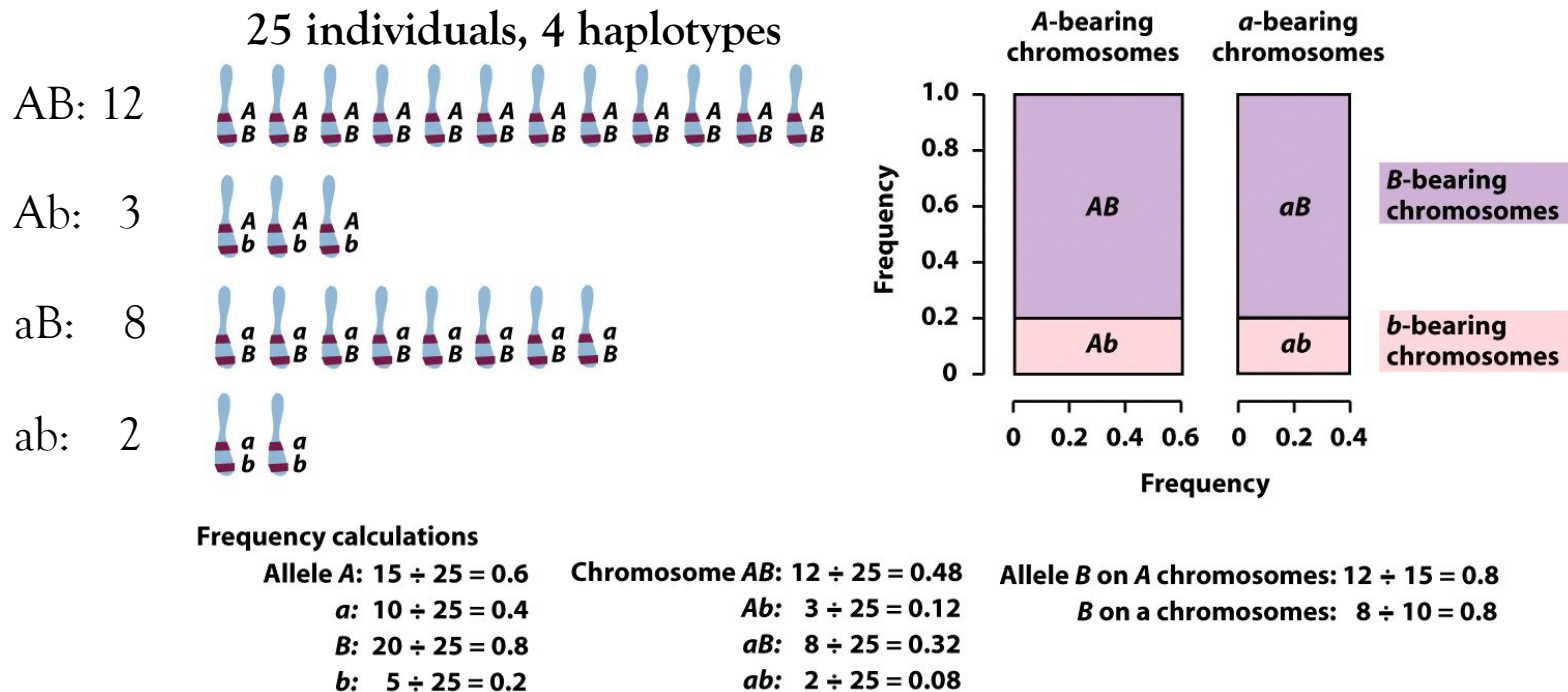


Figure 8-2a Evolutionary Analysis, 4/e
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The frequencies of *B* and *b* alleles are **the same** on *A*- and *a*-bearing chromosomes (and vice versa).

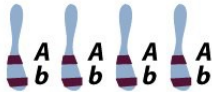
A Population in Linkage Disequilibrium

A population in linkage disequilibrium

AB: 11



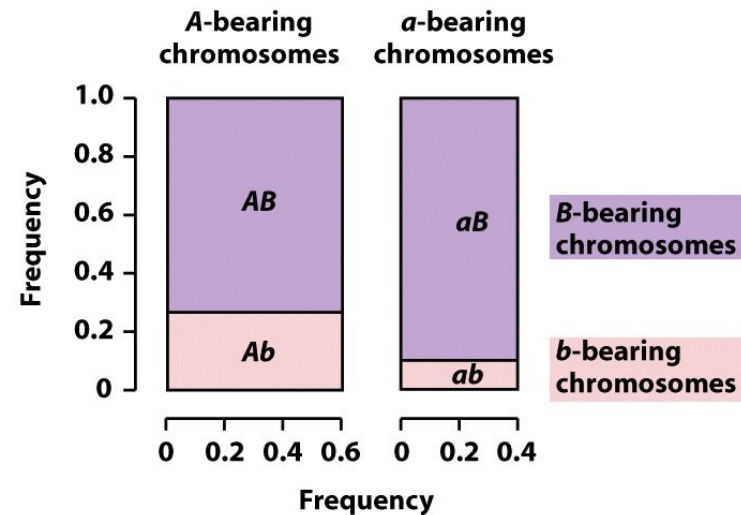
Ab: 4



aB: 9



ab: 1



Frequency calculations

Allele A: $15 \div 25 = 0.6$

a: $10 \div 25 = 0.4$

B: $20 \div 25 = 0.8$

b: $5 \div 25 = 0.2$

Chromosome AB: $11 \div 25 = 0.44$

Ab: $4 \div 25 = 0.16$

aB: $9 \div 25 = 0.36$

ab: $1 \div 25 = 0.04$

Allele B on A chromosomes: $11 \div 15 = 0.73$

B on a chromosomes: $9 \div 10 = 0.9$

Figure 8-2b Evolutionary Analysis, 4/e
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The frequencies of B and b alleles are **different** on A- vs. a-bearing chromosomes (and vice versa).

Let's calculate D for the respective examples:

$$D = g_{AB}g_{ab} - g_{Ab}g_{aB}$$

Under LE

Chromosome AB : $12 \div 25 = 0.48$

Ab : $3 \div 25 = 0.12$

aB : $8 \div 25 = 0.32$

ab : $2 \div 25 = 0.08$

$$D = 0.48 \cdot 0.08 - 0.12 \cdot 0.32$$

$$D = 0.0384 - 0.0384 = 0$$

Under LD

Chromosome AB : $11 \div 25 = 0.44$

Ab : $4 \div 25 = 0.16$

aB : $9 \div 25 = 0.36$

ab : $1 \div 25 = 0.04$

$$D = 0.44 \cdot 0.04 - 0.16 \cdot 0.36$$

$$D = 0.0176 - 0.0576 = -0.04 (\neq 0)$$

Evolutionary forces that increase LD

Under Hardy-Weinberg and linkage equilibrium
haplotype frequencies do not change over generations.

Deviations from HW expectations suggests that one of three mechanisms causing linkage disequilibrium is at work:

1. Selection on multi-locus genotypes
2. Genetic drift
3. Population admixture (i.e. migration)

Concepts for today's class

- 1) Migration homogenizes allele frequencies across different subpopulations.
- 2) Deleterious alleles can be kept at migration-drift-balance.
- 3) Decreasing gene flow (i.e., migration) between subpopulations will often lead to increasing genetic differentiation amongst them (increased population structure)
- 4) Inbreeding (sex between close relatives) leads to loss of heterozygosity within populations
- 5) When two genes are genetically linked, selection on one locus can interfere with the expected haplotype frequencies under Hardy-Weinberg expectations, thereby causing linkage disequilibrium (LD) in the population.

Thanks for your attention!

... and don't forget about next lecture:

Date: Wednesday, 15 Nov 2017

Location: HG F 3

Time: 8:00 - 10:00