

Goal I: Conserving species

What is needed for long-term persistence of populations?

Populations/
species

How do populations work?

Population genetics

Population dynamics

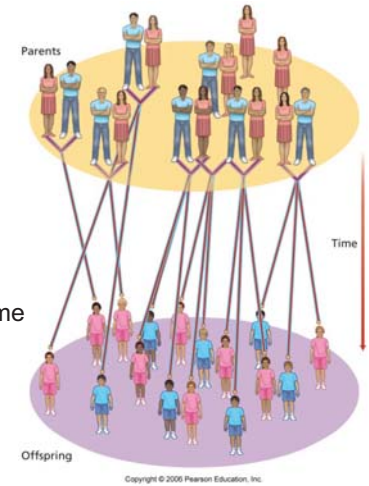
Population genetics

- Why is genetic diversity important for population persistence?
- What processes affect population genetic diversity?

Population dynamics

- How and why do populations change in size?
- Why are some populations more vulnerable to extinction?

Population - a group of individuals of one species in a specified area
- continuous through time



Population genetics - change in allele frequencies through time

Population dynamics - change in number of individuals through time

Q: What exactly is continuous through time?

Basics: calculating genotype frequencies and allele frequencies in a population

genotype frequencies:

allele frequencies:

frequency of R?

- A) 0.3
- B) 0.4
- C) 0.6
- D) 0.9
- E) 1.8



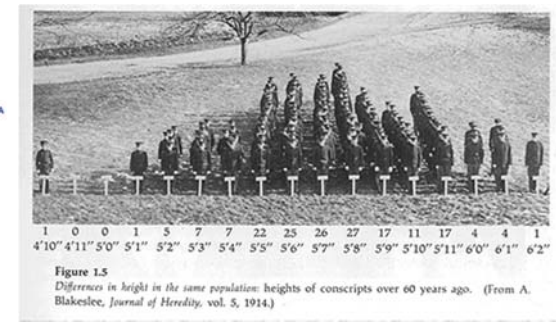
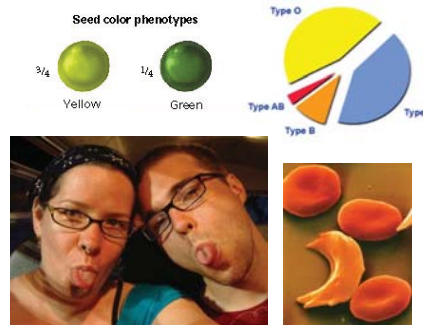
100 white (rr)
300 red (RR)
600 pink (Rr)

total = 1000 individuals

Types of phenotypic variation

Discrete (= qualitative)

Continuous (= quantitative)



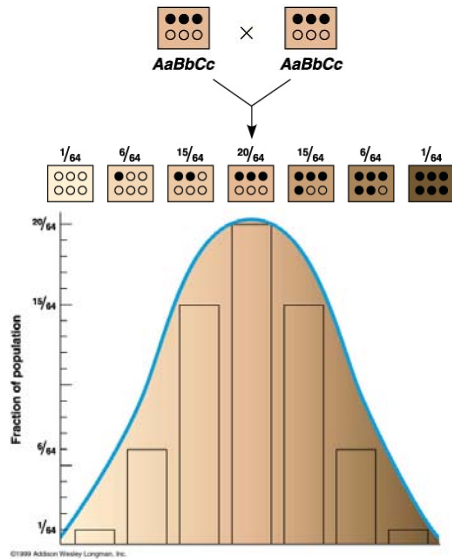
➤ Often based on possession of allele at a single locus (gene)

➤ Based on multiple loci
➤ ...but **continuous** variation still results from **discrete** alleles...

Q: What two things are unusual about this example?

Q: How does quantitative variation arise from discrete alleles?

Ex. Human skin color - at least 3 loci affect melanin production



“polygenic (=multilocus) trait”
→ depends on more than one locus

“additive effect”
→ each ● allele “adds” pigment

plus...an environmental contribution
– diet, allergens, disease, etc.
– sun exposure
“phenotypic plasticity”

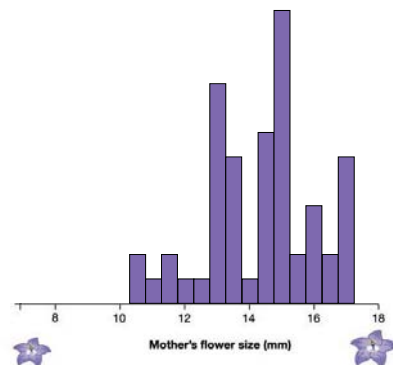


Genetic variation is essential for evolution

1. **variation**: flower size varies in a natural population



Ex: flower size in Alpine Sky Pilots



Q: Why is genetic variation important?



Darwin's simple insight:
Only 3 conditions needed for **evolution**
to occur in response to **natural selection**

- IF: 1) a trait (“X”) **varies** among individuals → phenotypic variation
2) some of the variation in X is **heritable** → genetic variation
3) survival/reproduction wrt X is **non-random** → natural selection

THEN: **Evolution will occur!** → genetic change *between* generations phenotypic change *within* a generation

“individuals that survive & reproduce better will leave more offspring, and more of their alleles, and more of their heritable phenotypic traits, in the next generation, and so on...”

A: Genetic variation is essential for adaptive evolution!

Q: What's wrong with Darwin's photo?

Genetic variation is essential for evolution

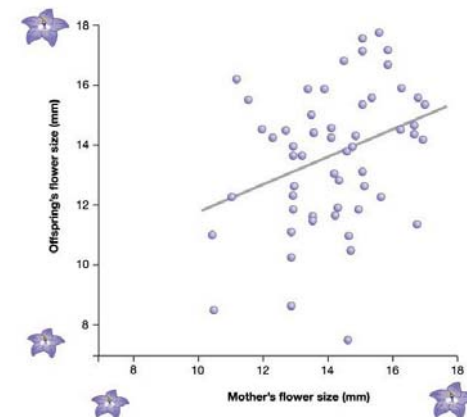
1. **variation**: flower size varies in a natural population
2. **variation is heritable**: mother's flower size predicts offspring's flower size

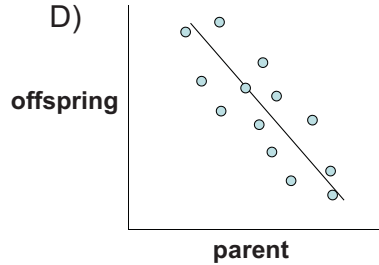
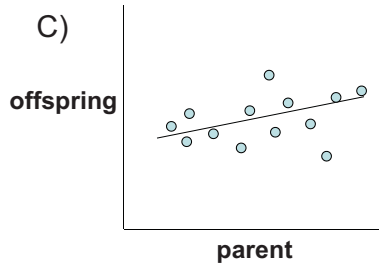
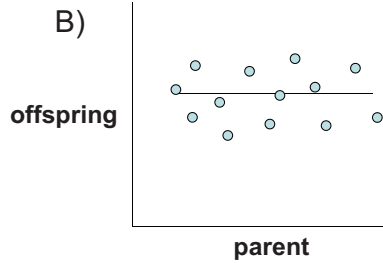
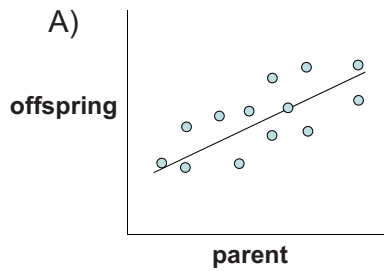


Ex: flower size in Alpine Sky Pilots

heritability (h^2): proportion of phenotypic variation that is explained by genetic variation

Q: How would you measure it?





A
B
C
D

Q: Which trait shows the greatest heritability?
Q: What do each of these relationships mean?

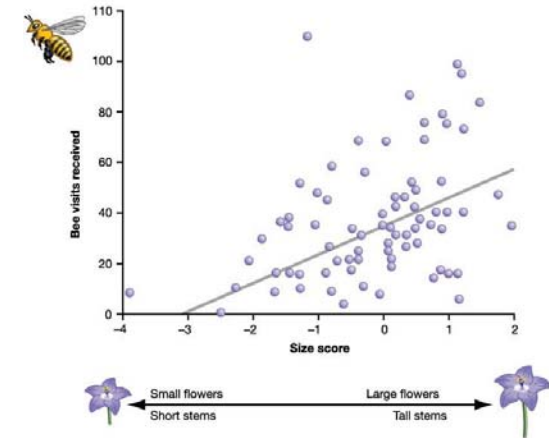
Genetic variation is essential for evolution

- 1) **variation**: flower size varies in a natural population
- 2) **variation is heritable**: mother's flower size predicts offspring's flower size
- 3) **non-random reproduction**: flower size influences pollinator visitation/seed set



Ex: flower size in Alpine Sky Pilots

larger flowers
received more
bee visits



Genetic variation is essential for evolution

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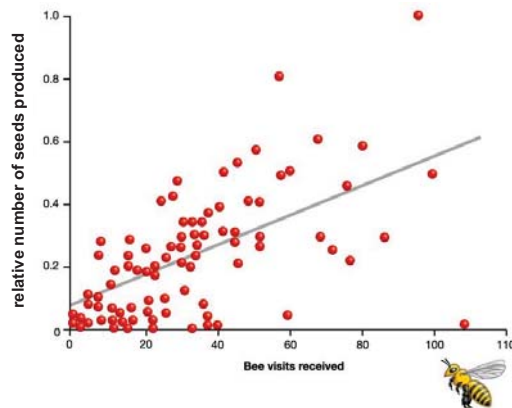


Ex: flower size in Alpine Sky Pilots

larger flowers
received more
bee visits

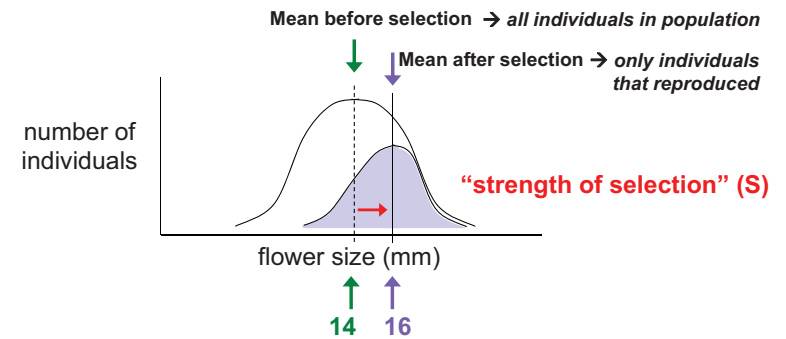
&
more bee visits
led to higher
seed production

↓
plants with larger
flowers will
produce more seeds



Q: Has natural selection happened? A)YES B)NO C) Cannot tell
Q: Will evolution happen? A)YES B)NO C) Cannot tell

How "strong" is natural selection?



$$S = \text{mean after selection} - \text{mean before selection}$$

Q: Does selection happen within or between generations?

natural selection – differential success in *this* generation

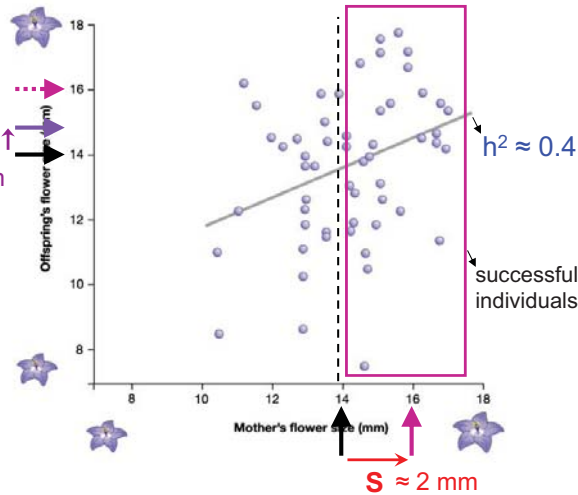
evolutionary response – apparent change in *next* generation

$$R = S \times h^2$$

evolutionary response strength of selection heritability

Q: What will the mean flower size be in the next generation?

- A) 14 mm
- B) 14.4 mm
- C) 14.8 mm
- D) 16 mm
- E) 18 mm



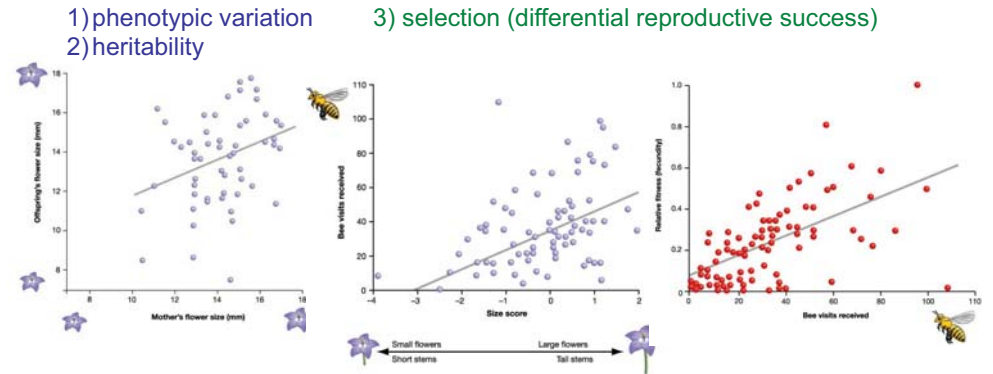
Q: So, why is heritable genetic variation critical for populations?



Ex. Alpine Sky Pilot

- evidence of **microevolution**
= change in **allele frequencies**
- mechanism: **natural selection**

Q: What other mechanisms can cause changes in allele frequencies?



What can change population genetic structure?

(allele and genotype frequencies)
A a AA Aa aa

In the absence of these 4 processes

- no change in **allele** frequencies between generations (no evolution)

In the absence of these 5 processes

- **genotype** frequencies as predicted from random pairing of **alleles**

Hardy-Weinberg Equilibrium (HWE)

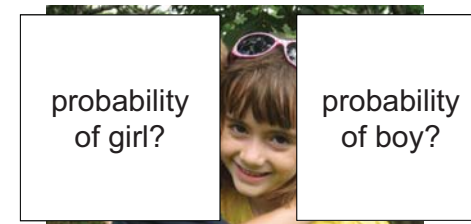
- a **null model** of what is expected in the absence of the 5 processes
- the presence of any of the 5 will cause deviation from HWE:

genotype frequencies *not* as predicted from **allele** frequencies

- will change **allele** frequencies
 - **selection**
 - **mutation**
 - **migration** (→ gene flow)
- will change **genotype** frequencies
 - **genetic drift**
 - **non-random mating**

aside: calculating combined probabilities

- Probability of having a girl **and** then a boy?
(assume probability of X from dad is 50%)

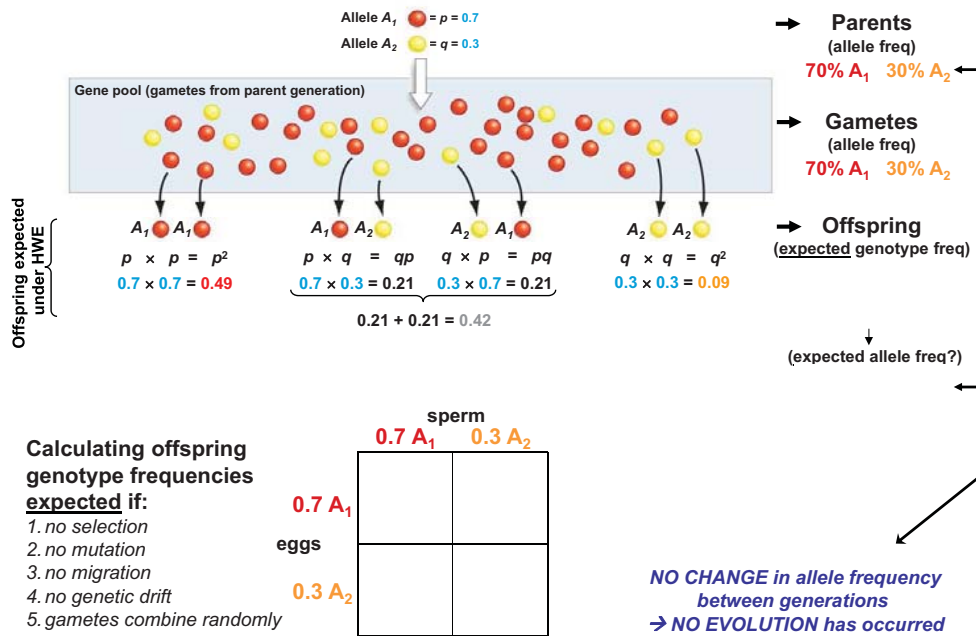


probability of girl?

probability of boy?

- Probability that a random date will be rainy **and** a Tuesday?
(assume probability of rain is 70%)
 - The combined probability of two independent events happening together ("and") is their **product**.
- What is probability that a random date will be Tues **or** Fri?
 - The probability of either of two independent events happening ("or") is their **sum**.

A NUMERICAL EXAMPLE OF THE HARDY-WEINBERG PRINCIPLE



Q1: Is it possible to have allele frequencies of A₁ = 0.7 and A₂ = 0.3 if the genotype frequencies are

A ₁ A ₁	A ₁ A ₂	A ₂ A ₂	
0.5	0.4	0.1	?
0.6	0.2	0.2	?
0.2	0.6	0.2	?
0.7	0.1	0.1	?

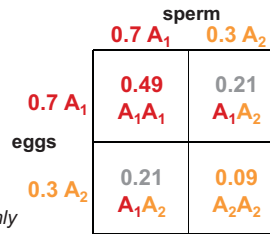
For a population in Hardy-Weinberg equilibrium:

- allele frequencies stay the same from generation to generation
- genotype frequencies are as predicted from random mating

For any allele frequencies (whether or not in HWE!):

- genotype frequencies *always* sum to 1 (check on your math)

Calculating offspring genotype frequencies **expected** if:
1. no selection
2. no mutation
3. no migration
4. no genetic drift
5. gametes combine randomly



A₁A₁ A₁A₂ A₂A₂
0.49 + 0.42 + 0.09 = 1!

Imagine that allele frequencies are A₁ = 0.7 and A₂ = 0.3

Q2: Are these genotype frequencies in HWE? (null hypothesis)

A ₁ A ₁	A ₁ A ₂	A ₂ A ₂	
0.5	0.4	0.1	?
0.6	0.2	0.2	?

A: Use χ^2 -test to test for deviations from the expected genotype frequencies

Test statistic
 $\chi^2 = \sum \frac{(Obs-Exp)^2}{Exp}$

Expected frequencies 0.49 0.42 0.09 (assuming gametes combine randomly)

Exp and Obs are numbers, not frequencies

Imagine that you have measured genotypes for 100 individuals

EX 1

	A ₁ A ₁	A ₁ A ₂	A ₂ A ₂
Observed	50	40	10
Expected	49	42	9
$\frac{(O-E)^2}{E}$	1/49	4/42	1/9

$\chi^2 = 0.23 < 3.84$ threshold value!
✓ HWE

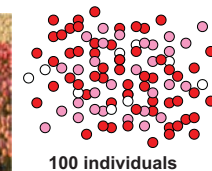
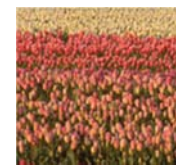
EX 2

	A ₁ A ₁	A ₁ A ₂	A ₂ A ₂
Observed	60	20	20
Expected	49	42	9
$\frac{(O-E)^2}{E}$	121/49	484/42	121/9

$\chi^2 = 27.44 > 3.84$
✗ HWE

Q3: Suppose you measure genotype frequencies in a population of plants. Are these genotypes in HWE?

Step 1: Calculate observed genotype frequencies



red	pink	white
A ₁ A ₁	A ₁ A ₂	A ₂ A ₂
0.6	0.3	0.1

Step 2: Calculate observed allele frequencies from observed genotype frequencies

p = frequency of A₁ =
q = frequency of A₂ =
p + q = ?

Step 3: Calculate genotype frequencies expected under HWE from the observed allele frequencies

p² = frequency of A₁A₁ =
2pq = frequency of A₁A₂ =
q² = frequency of A₂A₂ =
p² + 2pq + q² = ?

Step 4: Compare observed to expected genotype numbers using χ^2 -test.

$\chi^2 = \text{input} ?$

Is test statistic less than threshold? ✓ → population is in HWE
✗ → some assumption of HW is violated

What can change population genetic structure?

(allele and genotype frequencies)

- selection
 - mutation
 - migration
(→ gene flow)
 - genetic drift
 - non-random mating
- will change allele frequencies (p & q)
- will cause deviations from "HWE" (genotype freq not $p^2, 2pq, q^2$)

How does selection cause change in allele frequencies?

Parental allele freq:
0.5 A 0.5 a

	sperm	
	0.5 A	0.5 a
eggs	0.5 A	0.25 AA 0.25 Aa
	0.5 a	0.25 Aa 0.25 aa

10000 zygotes: 250 AA, 500 Aa, 250 aa

Survival to repro: 1.0 for AA, 0.85 for Aa, 0.5 for aa

Survivors: 250 AA, 425 Aa, 125 aa
800 indiv's

Offspring allele freq:
 $250 \times 2 + 425 = 925 / 1600 = 0.578 A$
 $125 \times 2 + 425 = 675 / 1600 = 0.422 a$

Is this population in HWE?
 $\chi^2 =$

How does selection cause change in allele frequencies?

Parental allele freq:
0.5 A 0.5 a

	sperm	
	0.5 A	0.5 a
eggs	0.5 A	0.25 AA 0.25 Aa
	0.5 a	0.25 Aa 0.25 aa

10000 zygotes: 2500 AA, 5000 Aa, 2500 aa

Survival to repro: 1.0 for AA, 0.75 for Aa, 0.5 for aa

Survivors: 2500 AA, 3750 Aa, 1250 aa
7500 indiv's

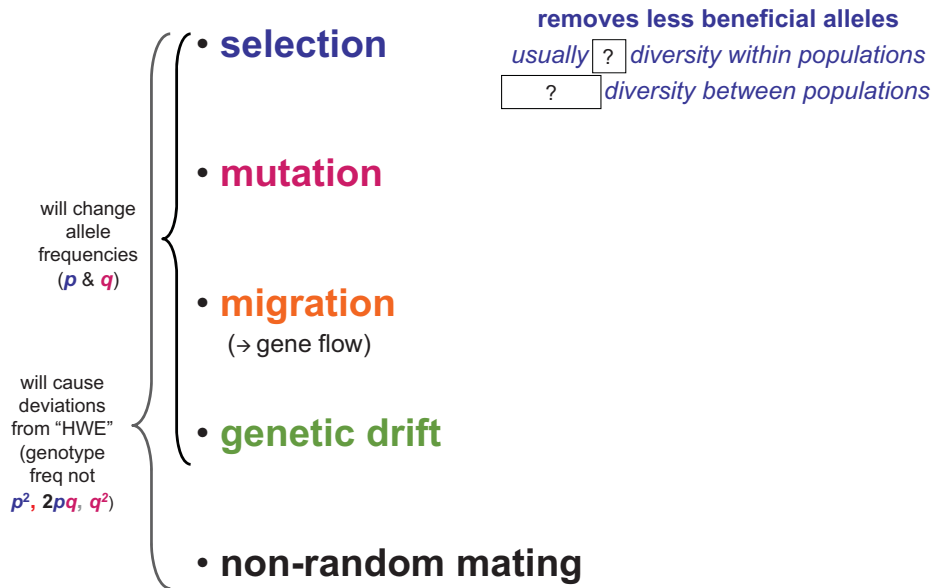
Offspring allele freq:
 $2500 \times 2 + 3750 = 8750 / 15000 = 0.583 A$
 $1250 \times 2 + 3750 = 6250 / 15000 = 0.417 a$

Is this population in HWE?
 $\chi^2 = 6.12 > 3.84$ X

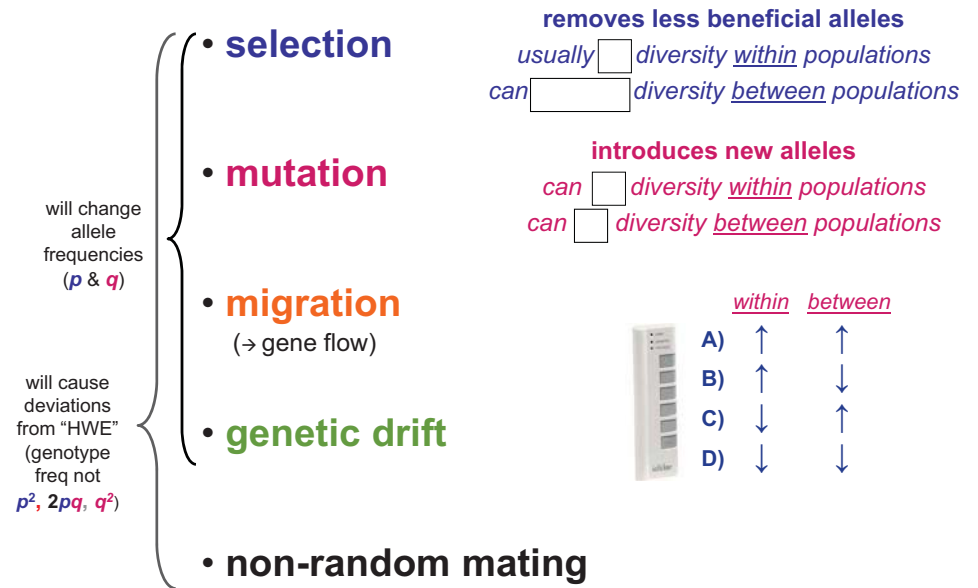
What are the consequences for genetic diversity? Within vs. between populations?



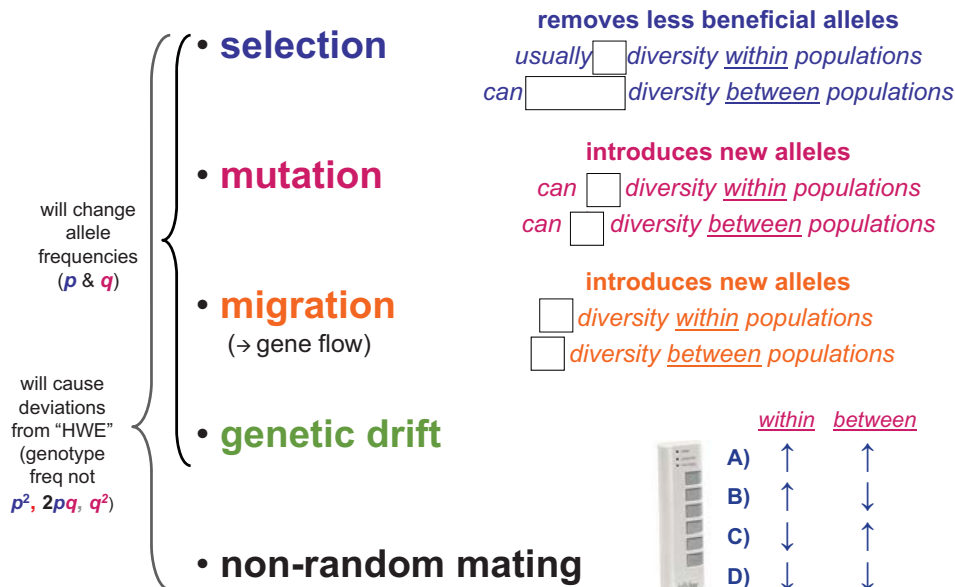
What are the consequences for genetic diversity?



What are the consequences for genetic diversity?



What are the consequences for genetic diversity?



What is genetic drift??

➤ random change in allele frequencies due to **sampling error**

random difference between **expected** and **observed** results

all alleles in gene pool will be included

by chance, only some alleles are included in next generation

Example 1: Toss a coin 10 times--how many heads? how about 1000 times?

➤ Would you be more suspicious to get 7/10 heads or 700/1000 heads?

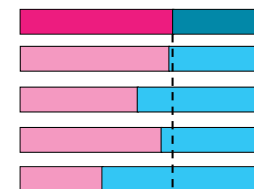
Example 2: CofC student body: 65% f, 35% m

➤ **2011:** 78 students: 63% female, 37% male

➤ **2010:** 40 students: 50% female, 50% male

➤ **2009:** 30 students: 60% female, 40% male

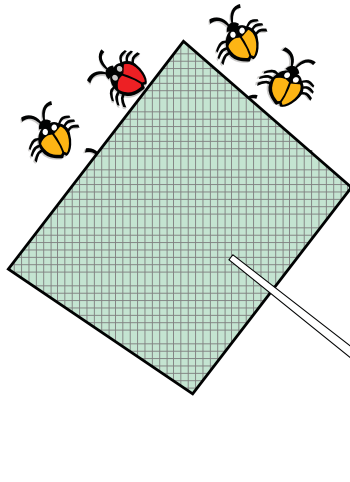
➤ **2008:** 17 students: 35% female, 65% male



→ smaller samples have on average a greater **sampling error**

Genetic drift – survival is **unrelated to trait of interest**

alleles that increase in next generation based purely on chance



Before:

8 RR → 0.50 R

8 rr → 0.50 r

After:

1 RR → 0.25 R

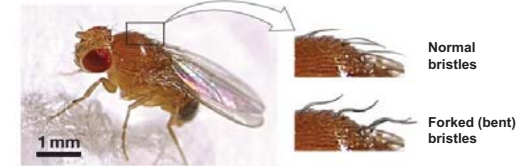
3 rr → 0.75 r

“Bottleneck”—sampling error in time

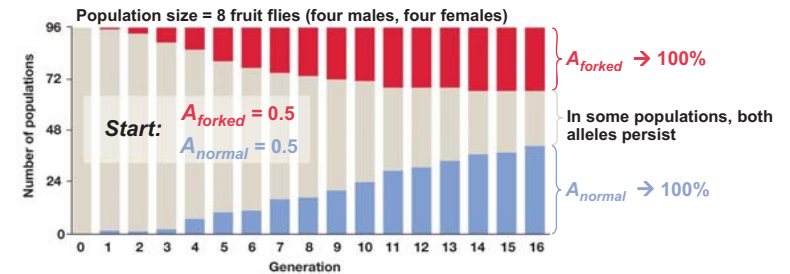
Why is genetic drift most pronounced in small populations?

Effects of Genetic Drift in Small Populations

Ex 1: bristle shape in laboratory flies



In most experimental populations, one or the other bristle type became fixed

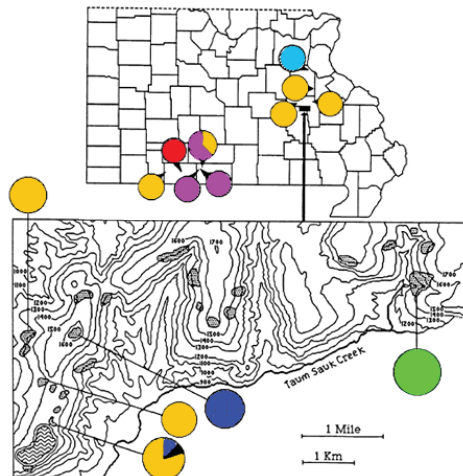


Effects of Genetic Drift in Small Populations

1. Each population will have a **unique, unpredictable trajectory**
2. Will more strongly influence **small populations**
3. Causes **changes in allele frequencies** or **loss of alleles** over time

Ex 2: Collared lizard, *Crotaphytus collaris*

isolated “glade” habitats



different alleles are fixed even in very close populations

Effects of Genetic Drift in Small Populations

→ Unlike selection, does not lead to adaptation

Ex 3: Porphyria

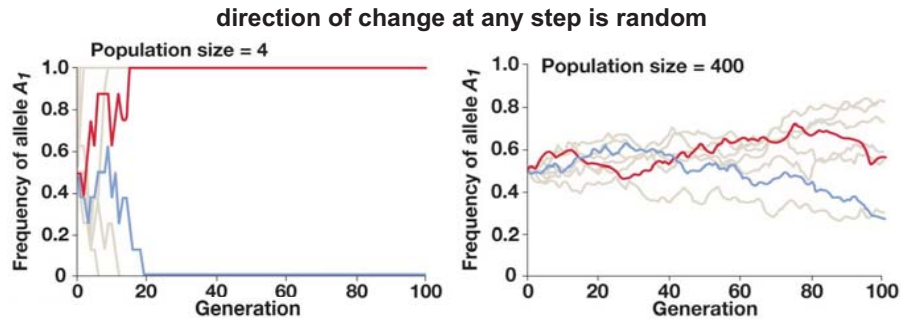
- rare autosomal dominant disorder
- extreme sensitivity to light, skin lesions, neurological complications, excess hair



- in the 1600's, **80 Dutch immigrants** settled in South Africa
→ have left **over 1 million descendants**
- one immigrant couple had the gene for **porphyria**
- **now 3 out of every 1,000** Dutch S. Africans have the gene for porphyria
(compare to general population: 3 : 1,000,000)

Founder effect = sampling error “in space”

Genetic Drift Is More Pronounced in Small Populations



Q: In what two ways do the lines for large and small populations differ?

- smaller populations have bigger jumps at each step
- smaller populations go to fixation at a faster rate (slope of line)

Q: Can an allele "come back" once lost?

Q: Are any populations immune from genetic drift?

Q: What are the consequences for genetic diversity?

What are the consequences for genetic diversity?

- **selection**
 - removes less beneficial alleles
 - usually diversity within populations
 - can diversity between populations
- **mutation**
 - introduces "new" alleles
 - can diversity within populations
 - can diversity between populations
- **migration**
 - (→ gene flow)
 - introduces "new" alleles
 - diversity within populations
 - diversity between populations
- **genetic drift**
 - random loss of alleles
 - diversity within populations
 - diversity between populations
- **non-random mating**

will change allele frequencies (p & q)

will cause deviations from "HWE" (genotype freq not $p^2, 2pq, q^2$)

Expected consequences of genetic drift vs. gene flow

random change in allele frequencies movement of alleles between populations

genetic diversity within populations:

genetic diversity between populations:

as each population becomes smaller:
as each becomes more isolated:



What can change population **genetic structure**?

(allele and genotype frequencies)

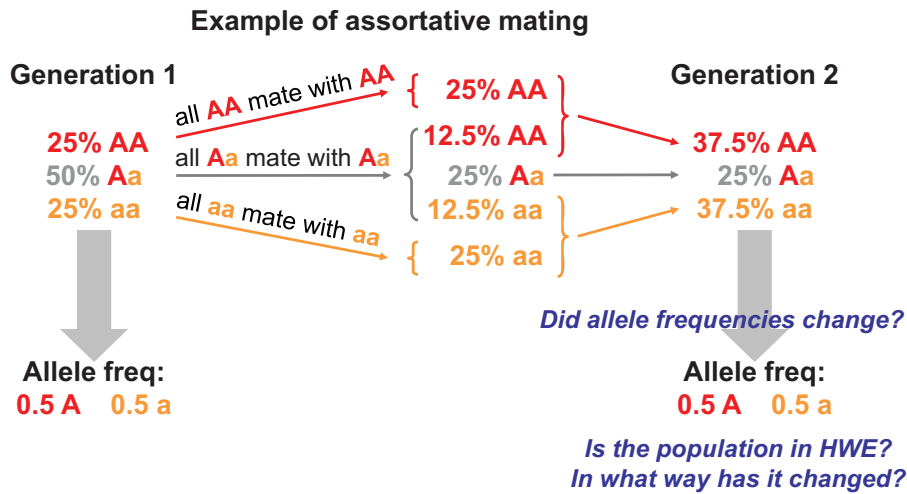
- **selection**
- **mutation**
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will change allele frequencies (p & q)

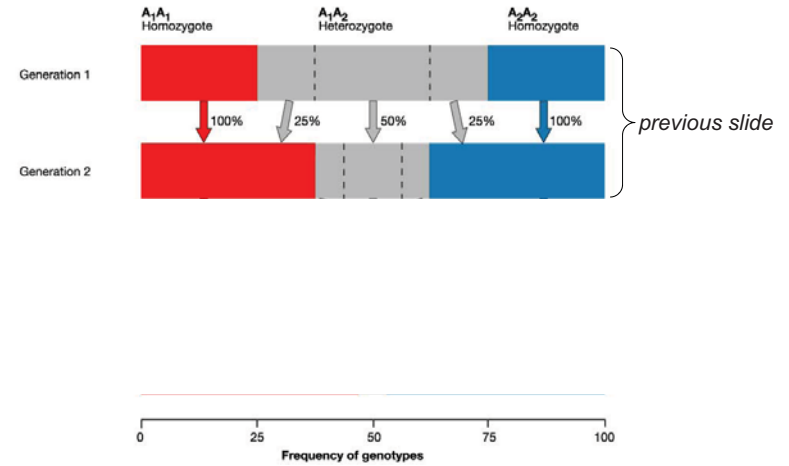
will cause deviations from "HWE" (genotype freq not $p^2, 2pq, q^2$)

How does **non-random mating** affect pop'n genetic structure?

How does **non-random mating** affect pop'n genetic structure?



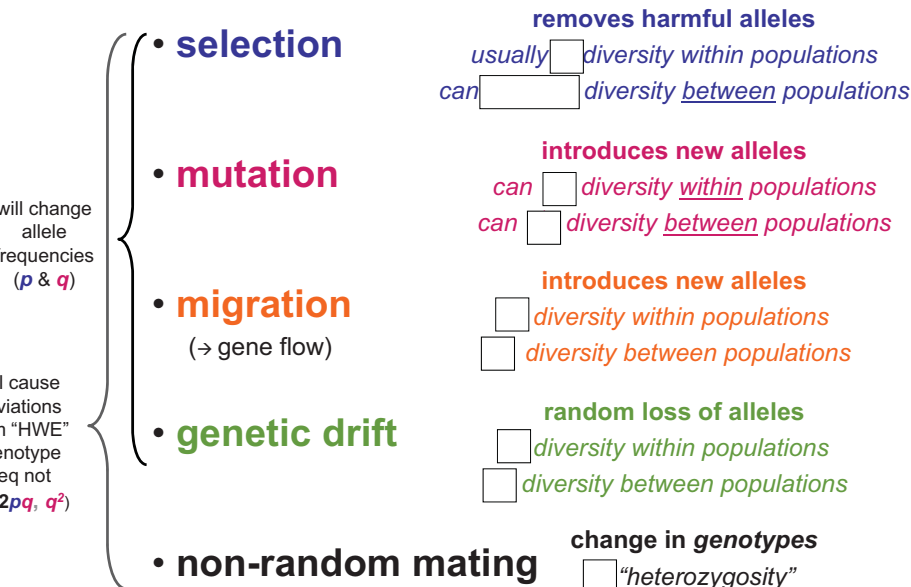
Over many generations...



➤ Assortative mating always leads to excess homozygotes

Q: How does assortative (non-random) mating differ from sexual selection?

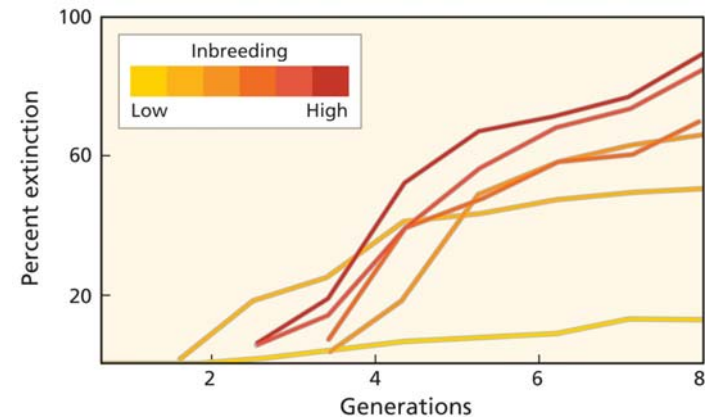
What are the consequences for genetic diversity?



Inbreeding depression

Ex. *Drosophila* with different degrees of inbreeding enforced

- inbreeding leads to greater homozygosity
- greater homozygosity leads to decreased fitness
 - unmasking of deleterious recessive alleles in homozygotes
- more likely in small, isolated populations



Inbreeding depression

- more likely in small, isolated populations



Ex. Florida panther

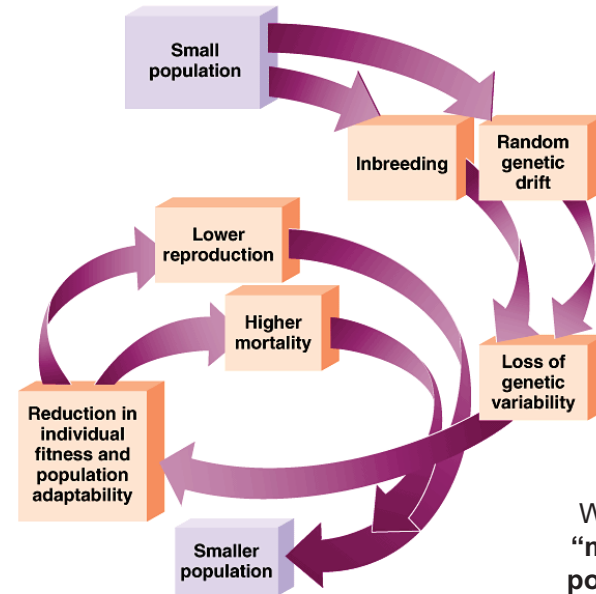
Puma concolor coryii

- subspecies (mountain lion, cougar)
- fragments of south Florida
- federally endangered species
- 80-100 remain

Major threats

- habitat loss & fragmentation
- inbreeding depression
 - heart defects
 - undescended testes
 - defective sperm
- recent introduction of 8 females from Texas subpopulation

Isolation → small population size → **extinction vortex**

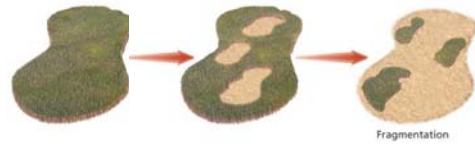


What would be a “minimum viable population size”?

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d. What are the biggest threats?

- habitat fragmentation



↓ **population size** ↓ **gene flow** ↓ **genetic diversity**
 ↑ **local extinction** ↓ **recolonization**

- conservation approach: reduce fragmentation

↑ **connectivity**
 ↑ **gene flow**



Panther corridor