Evolutionary Processes

Reading: Chap. 25

I. Introduction - The modern synthesis

II. No evolution: Hardy-Weinberg equilibrium

- A. Population genetics
- B. Assumptions of H-W

III. Causes of microevolution (forces leading to genetic change)

- A. Natural selection
- B. Genetic Drift
- C. Gene flow
- D. Mutation
- E. Nonrandom mating

Terms and Concepts

species, population

population genetics

gene pool, allele frequencies

Hardy-Weinberg equilibrium, non-evolving population

Genetic drift, sampling effect, bottleneck effect, founder effect

Natural selection: directional selection, stabilizing selection, diversifying selection, sexual selection.

What do these things have in common?

Scarlet tanager

"Irish elk"

Homo sapiens – immature male

?

I. Introduction: Where do we go from here?

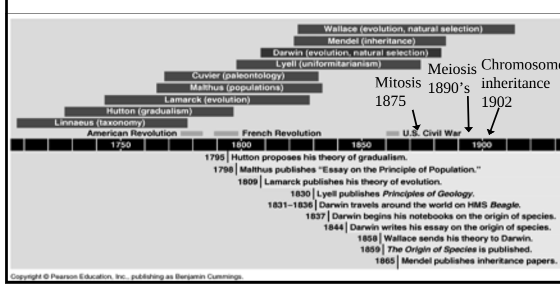


Fig 22.1

The Modern Synthesis: Started in 1930's

Integrates ideas from many different fields:

- Darwinian evolution
- Mendelian genetics
- Population genetics
- Comparative morphology & molecular biology
- Taxonomy – relationships of taxa
- Paleontology – study of fossils
- Biogeography – distribution of species

Applications (to name just a few) :

- Medical microbiology
- Medical genetics
- Forensic science (e.g., DNA evidence)
- Conservation biology
- Agricultural policy (e.g., crop breeding, pest resistance)

The Modern Synthesis

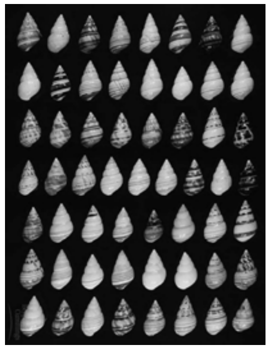
Populations are the units of evolution (changes in allele frequencies from generation to generation)

Natural selection plays an important role in evolution, but is not the only factor

Speciation is at the boundary between microevolution and macroevolution

Microevolution (Ch 25 – Evolutionary processes) - generation-to-generation changes in allele frequencies within populations.
(occurs even if only a single locus in a population changes)

Macroevolution (Ch 26 – Speciation) - development of new species (and higher taxa).



II. Hardy-Weinberg equilibrium:

Bottom line: H-W is what happens when populations are NOT evolving.

A. The genetics of populations

Population = localized, interbreeding group of individuals of one species

Population gene pool = all the alleles of all the individuals in the population

Consider one locus,

- If you could count all alleles in all individuals,
- e.g. in a population of yellow- and green-seeded peas
  - There are **YY**, **Yy** and **yy** individuals
- Of all the alleles, a certain fraction are **Y**, say p is that fraction
- Then the rest of the alleles are **y**; that fraction is q

Hardy-Weinberg Theorem

H-W: In populations with Mendelian transmission of traits (i.e, segregation, independent assortment), in the absence of other forces,

Frequencies of alleles & genotypes in a population's gene pool remain the same for any number of generations.

That is, meiosis and random fertilization do not lead to evolution.

H-W equilibrium relies on certain assumptions (upcoming)

Expressed by the formulas on the next page

Hardy-Weinberg formulas

(for one locus, 2 alleles)

allele frequencies: $p + q = 1.00$
(by definition)

genotype frequencies: $p^2 + 2pq + q^2 = 1.00$
(because of Mendelian inheritance, expressed using laws of probability – multiplication & addition)

Where,
p = frequency of 1 allele
q = frequency of alternate allele
both expressed as decimal fractions of a total of 1.00

and,
p^2 = frequency of **YY**
2pq = frequency of **Yy**
q^2 = frequency of **yy**

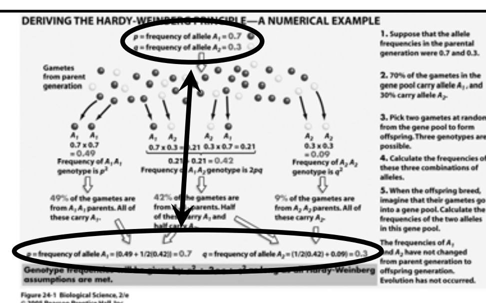


Fig 24.1 The Hardy-Weinberg equilibrium of allele frequencies in non-evolving populations

This equilibrium will hold true no matter what the frequencies of the alleles in the parent population. Try it with p = 0.24 and q = 0.76, for example, in a population of 1000 peas.

B. Assumptions of Hardy-Weinberg equilibrium

1. No selection (natural or artificial)
2. No genetic drift (very large population size, no sampling effect)
3. No migration (no gene flow in or out)
4. No mutations (change in form of an allele – the ultimate source of genetic change)
5. Random mating

Therefore, H-W equilibrium is a <u>null hypothesis</u>.

An example: Is there selection for heterozygotes in HLA genes?

(see pp. 507-8)

2 genes: HLA-A, HLA-B

Code for proteins important in immune system

Co-dominant

Hypothesis: more proteins, greater disease resistance

Havasupai Tribe – People of the Blue-Green Waters

http://www.moon.com/planner/grand_canyon/mustsee/havasupai.html

http://www.cpluhna.nau.edu/People/pais.htm

http://www.grandcanyontreks.org/supai.htm

http://www.cpluhna.nau.edu/People/pais.htm

http://www.americansouthwest.net/arizona/grand_canyon/havasu_canyon.html

HLA genes in the Havasupai People

TABLE 24.2 Do *HLA* Genotype Frequencies of Humans Conform to the Hardy-Weinberg Model?

	Observed Number	Expected Number
HLA-A		
Homozygotes	38	48
Heterozygotes	84	74
HLA-B		
Homozygotes	21	30
Heterozygotes	101	92

Source: T. Markow et al., *HLA* polymorphism in the Havasupai: Evidence for balancing selection. *American Journal of Human Genetics* 53 (1993): 943–952.

Why the difference between H-W and observed genotypes in Havasupai People?

Why is H-W theorem important?

1. Extends Mendelian genetics of individuals to population scale (where evolution works).
2. Shows that if Mendelian genetic processes are working, variation is maintained at the population level.
3. Gives a baseline (NULL HYPOTHESIS) against which to measure evolutionary change.
   (Good examples in your book: MN locus, HLA genes)

III. Causes of microevolution

A. Natural selection
B. Genetic drift
C. Gene flow
D. Mutation
E. Nonrandom mating

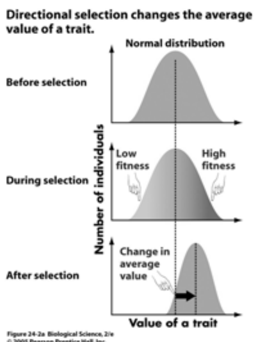
All are departures from the conditions required for the Hardy-Weinberg equilibrium

A. Natural selection

Only factor that generally adapts a population to its environment. The other three factors may effect populations in positive, negative, or neutral ways.

Four types:
1. Directional
2. Stabilizing
3. Disruptive/diversifying
4. Sexual selection

1. Directional selection



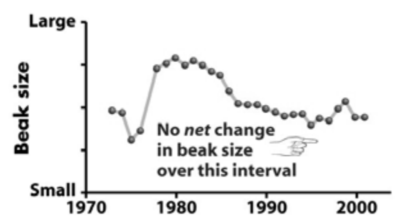
Phenotype moves toward one end of the range;

Ex. Cliff swallows in Great Plains.

During 1996 cold snap, large birds had better survivorship than small birds.

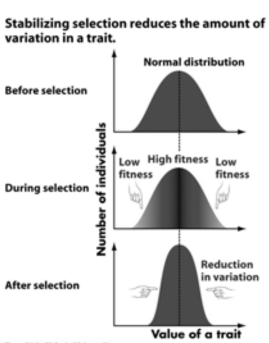
Directional selection tends to reduce genetic diversity within populations, but only if

- selection pressure is constant (environmental change, not just yearly variation)
- no strong counterbalancing selection pressures

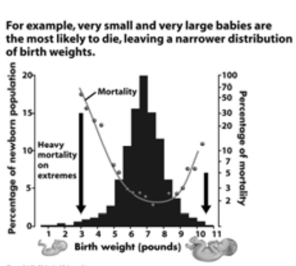


23.13

2. Stabilizing selection



- No change in average value of trait.
- Reduced variation in trait

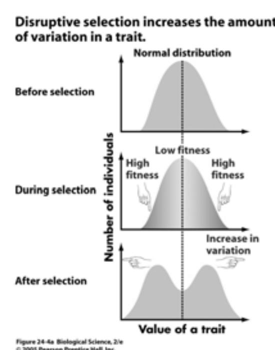


3. Disruptive/diversifying selection

Selects for two ends of a range

Can result in balanced polymorphism

Can result in speciation, IF coupled with sexual selection (reproductive isolation).



Example

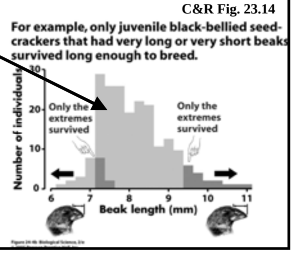
Beak type in black-bellied seedcrackers

West Cameroon, Africa

- Only two types of seeds – small & large
- Intermediate billed birds inefficient at feeding on either type

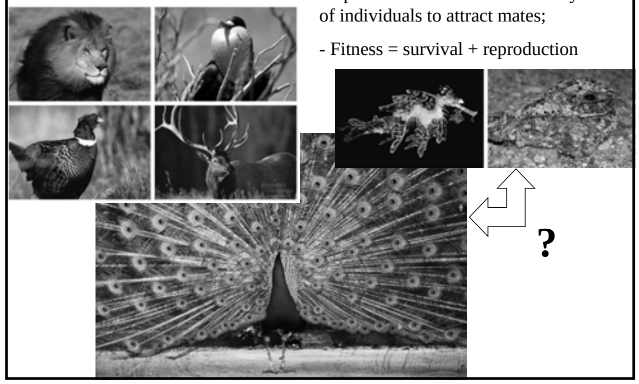
C&R Fig. 23.14

All juveniles



4. Sexual selection

- Operates on differences in ability of individuals to attract mates;
- Fitness = survival + reproduction



Sexual selection

Tends to act more strongly on males than females

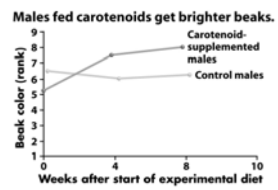
(eggs are expensive, sperm are cheap)

Predictions:

- Females more choosy than males
- Male-male competition for mates

Females more choosy than males?

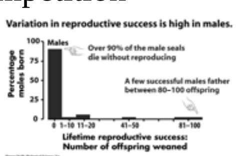
Sexually selected traits should reflect male fitness.

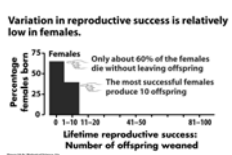


Carotenoids in beaks & feathers
- well-fed
- not fighting diseases

Females chose siblings with brighter beaks

Male-male competition





Elephant seals
- male territories
- Sexual dimorphism

(male/female size difference (4x!))

B. Genetic Drift

Changes in gene frequencies due to chance events (sampling errors) in small populations

Hardy Weinberg assumes reproduction works probabilistically on gene frequencies,

$(p + q = 1)$

Reproduction in small populations may not work this way

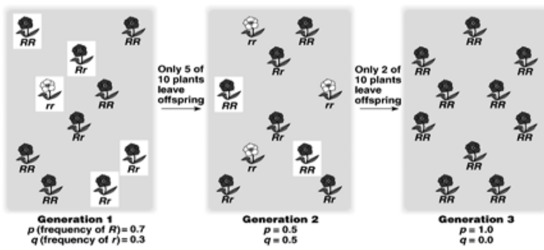
Three similar situations lead to genetic drift
- Sampling effect
- Bottleneck effect
- Founder effect

Genetic drift: sampling effect

Wildflower population with a stable size of only 10 plants

Some alleles could easily be eliminated

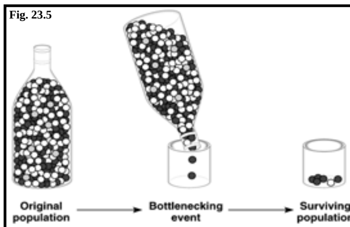
Draw drift



C&R Fig. 23.4

Bottleneck Effect

Fig. 23.5



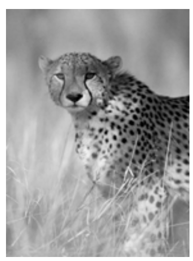
C&R Fig. 23.5

- Large population drastically reduced by a disaster
- By chance, some survivor's alleles may be over- or under-represented, or some alleles may be eliminated
- Genetic drift continues until the population is large enough to minimize sampling errors

Endangered species

- Bottleneck incidents cause loss of some alleles from the gene pool
- This reduces individual variation and adaptability
- Example: cheetah
  - Genetic variation in wild populations is extremely low
  - Similar to highly inbred lab mice!

C&R Fig. 23.5x



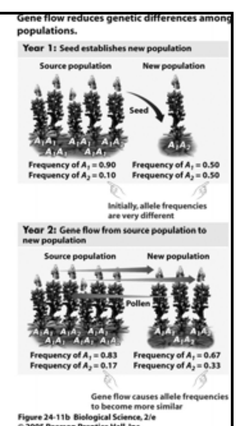
Founder effect

- New population starts with a few individuals not genetically representative of a larger source population.
  - Extreme: single pregnant female or single seed
  - More often larger sample, but small
- Genetic drift continues until the population is large enough to minimize sampling errors

C. Gene flow

- Genetic exchange due to migration of alleles
  - Fertile individuals
  - Gametes or spores
- Example:
  - Wildflower population has white flowered plants only
  - Pollen (with *r* alleles only) could be carried to another nearby population that lacks the allele.
- Gene flow tends to reduce differences between populations

Gene flow: Lupines on Mt. St. Helens



D. Mutation

Change in DNA
- Rare and random
- More likely to be harmful than beneficial

Only mutations in cell lines that produce gametes can be passed along to offspring

One mutation does not affect a large population in a single generation

Very important to evolution over the long term
- The only source of new alleles
- Other causes of microevolution redistribute mutations

What keeps mutations?

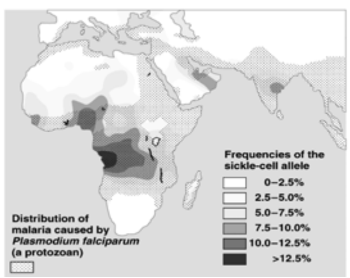
Diploidy – masks recessive alleles

Hardy-Weinberg Equilibrium says that, without natural selection, gene frequencies remain the same

A balance of recessive alleles can be kept even without Hardy-Weinberg
- Heterozygote advantage
- Frequency-dependent selection

Heterozygote advantage

Sickle-cell allele
- Homozygous recessives unhealthy
- Heterozygotes protected from malaria

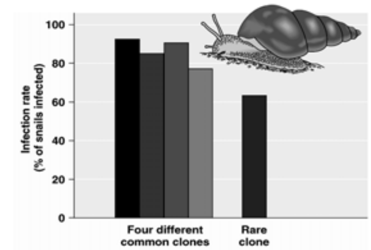


C&R Fig. 23.10 Sickle-cell allele and malaria

Frequency-dependent selection

Common morphs of snails more likely to die from parasites

Rare morph less likely



C&R Fig. 23.11 Infection of snails by parasitic worms

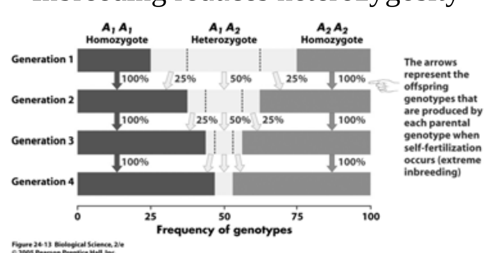
E. Non-random mating

Inbreeding: mating between relatives

How close?

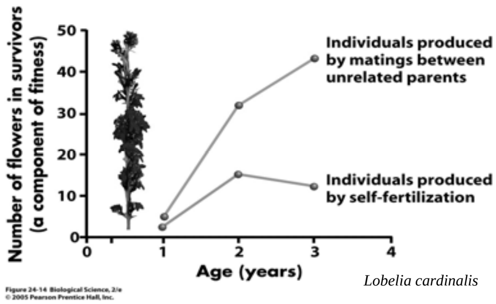
Self fert	Within family (parents, sibs)	Within extended family	Within local population	Across local populations
Extreme inbreeding	High inbreeding			Low inbreeding

Inbreeding reduces heterozygosity



No change in ALLELE frequencies, but change in GENOTYPE frequencies.

Inbreeding reduces fitness of offspring = inbreeding depression



Lobelia cardinalis

1. Loss of function mutations.
2. Heterozygote advantage (e.g., immune system genes)

Inbreeding effects

Inbreeding doesn't directly change allele frequencies – so not exactly evolution.

But contributes to evolution when there is selection against homozygotes.

Sexual selection is also non-random mating, but DOES change allele frequencies.