

Theory of Natural Selection

Definitions:

Gene: Nucleotide sequence coding for, or regulating the expression of, a phenotypic trait

Genotype: Set of alleles possessed by an individual at a locus (or several loci)

Evolution: Change in allele frequencies over time

allele frequency = proportion of alleles of a given type (e.g., *A* or *a*) at a given locus

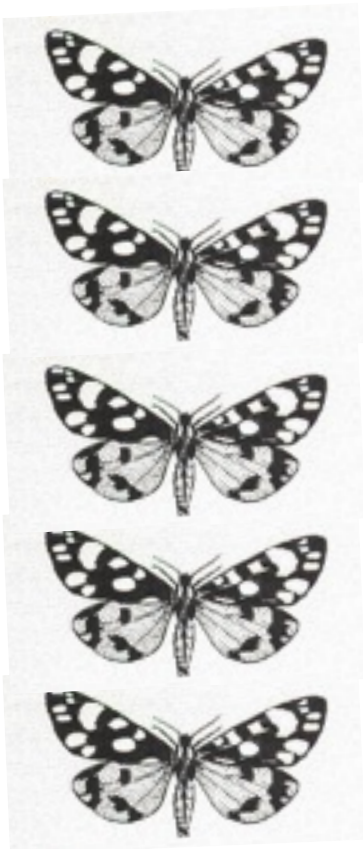
(Note: change in genotype frequency does not define evolution)

what are the allele frequencies?

AA

Aa

aa



Genotype frequencies

$$P(AA) = 5/8 = 0.625 \rightarrow 62.5\%$$

$$Q(Aa) = 2/8 = 0.25 \rightarrow 25.0\%$$

$$R(aa) = 1/8 = 0.125 \rightarrow 12.5\%$$

Allele frequencies

$$p(A) = P + 1/2Q = 0.75 \rightarrow 75\%$$

$$q(a) = R + 1/2Q = 0.25 \rightarrow 25\%$$

Panaxia dominula (Arctiidae)
Scarlet tiger moth

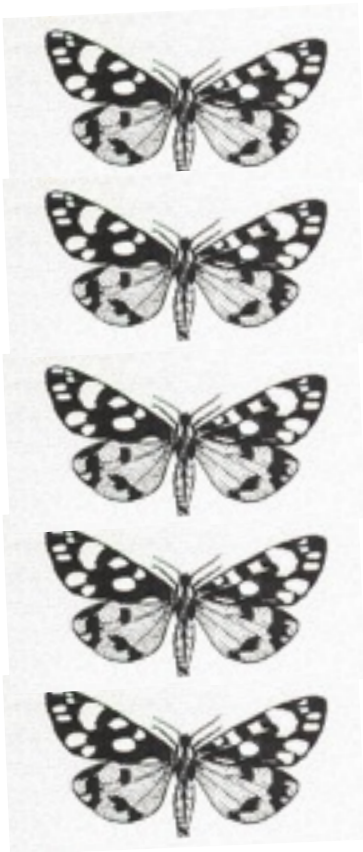
If we define evolution as change in allele frequencies over time, then.....

AA

Aa

aa

... these are the numbers we want to track over time



Genotype frequencies

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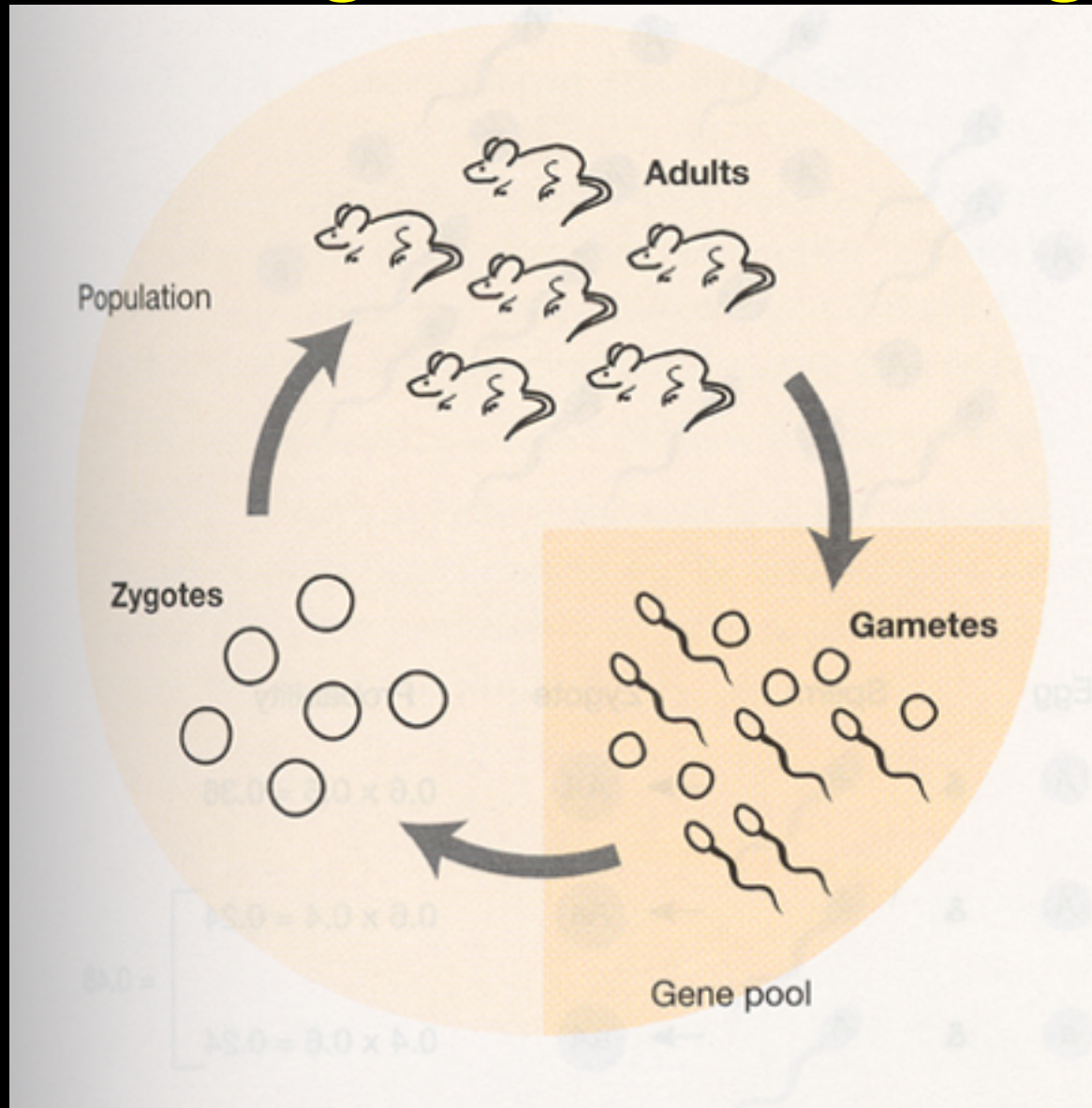
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Allele frequencies

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Evolution as allele frequency change from generation $n \rightarrow$ generation $n+1$



To keep things simple at first, let's look first at a population where allele frequencies don't change
 \rightarrow *Hardy-Weinberg*

Conditions
(= null model of evolution)

Hardy-Weinberg Ratios

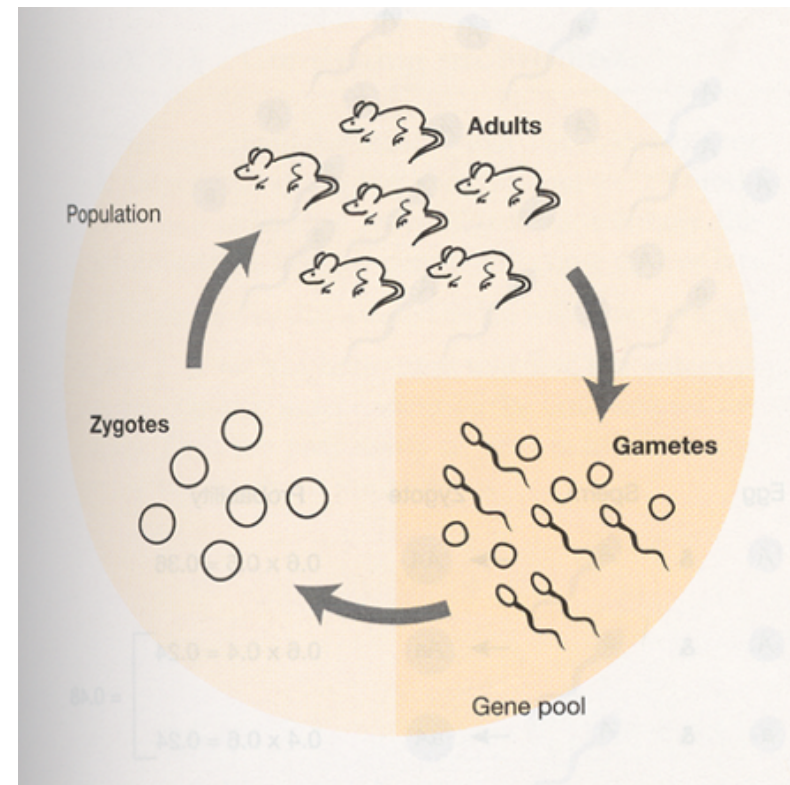
Assuming H-W conditions,
for a diploid organism producing:

“A” bearing gametes at frequency of p
“a” bearing gametes at frequency of q

chance of A + A union	$= p^2$
chance of A + a union	$= pq$
chance of a + A union	$= qp$
<u>chance of a + a union</u>	<u>$= q^2$</u>
total of all unions	$= 1$

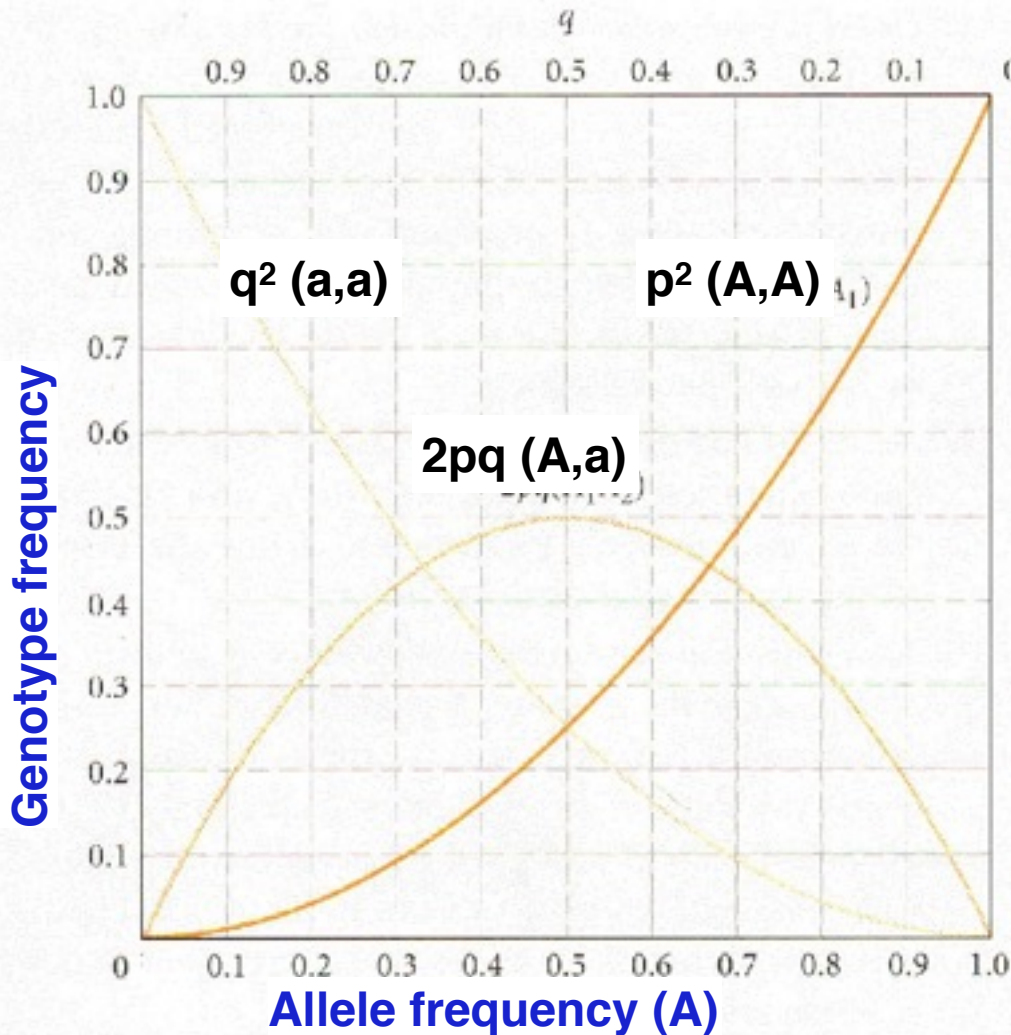
$$\Rightarrow p^2 + 2pq + q^2 = 1$$

Hardy-Weinberg equation



The relationship between

-allele frequencies and -genotype frequencies



Note again:

The predictable relationship between allele and genotype frequency is true only if H-W conditions hold

What if some of the H-W conditions are violated?

- random mating
- no drift
- no gene flow
- no mutation
- no selection

Simple model of selection

<u>Genotype</u>	<u>Chance of Survival (= Fitness)</u>
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AA, Aa	1 (= 100% survival)
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aa	1 - s (= 90% survival)
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Numerical example:

- individuals of genotype “aa” have 10% mortality
from birth to adulthood
- selection coefficient $s = 0.1$
- AA and Aa have no mortality

Simple model of selection

**Change in allele frequency from
time “t” to “t + 1”:**

$$p_{t+1} = p_t / (1 - s q^2)$$

**This equation accomplishes the same as
the detailed step-by-step calculations of
allele frequency changes outline above**

Predicted changes in allele frequency for selection against a recessive gene

Generation	Gene frequency, $s = 0.05$		Gene frequency, $s = 0.01$	
	<i>A</i>	<i>a</i>	<i>A</i>	<i>a</i>
0	0.01	0.99	0.01	0.99
100	0.44	0.56	0.026	0.974
200	0.81	0.19	0.067	0.933
300	0.89	0.11	0.15	0.85
400	0.93	0.07	0.28	0.72
500	0.95	0.05	0.43	0.57
600	0.96	0.04	0.55	0.45
700	0.96	0.04	0.65	0.35
800	0.97	0.03	0.72	0.28
900	0.97	0.03	0.77	0.23
1,000	0.98	0.02	0.80	0.20

Directional Selection

1. Selection Against Dominant Allele

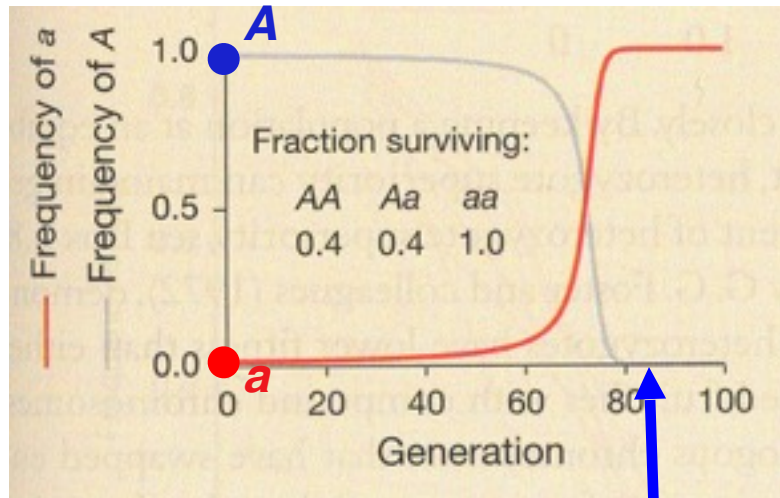
<u>Genotype</u>	<u>Chance of Survival (= relative fitness)</u>	
AA	$1 - s$	
Aa	$1 - s$	(s = selection coefficient)
aa	1	

2. Selection Against Recessive Allele

<u>Genotype</u>	<u>Chance of Survival (= relative fitness)</u>	
AA	1	
Aa	1	
aa	$1 - s$	

(s = selection coefficient)

Selection against dominant allele A

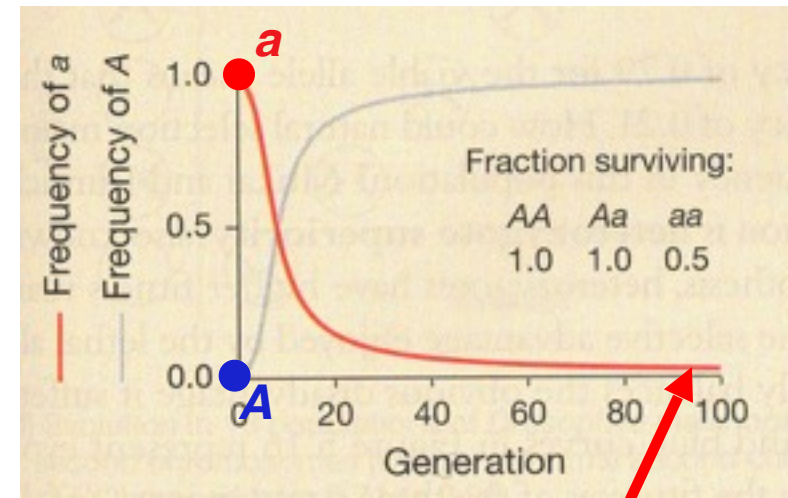


Genotype	Chance of Survival
AA	$1 - s$
Aa	$1 - s$
aa	1

Dominant, deleterious allele A is purged from the population

= population is *rapidly* fixed for a

Selection against recessive allele a

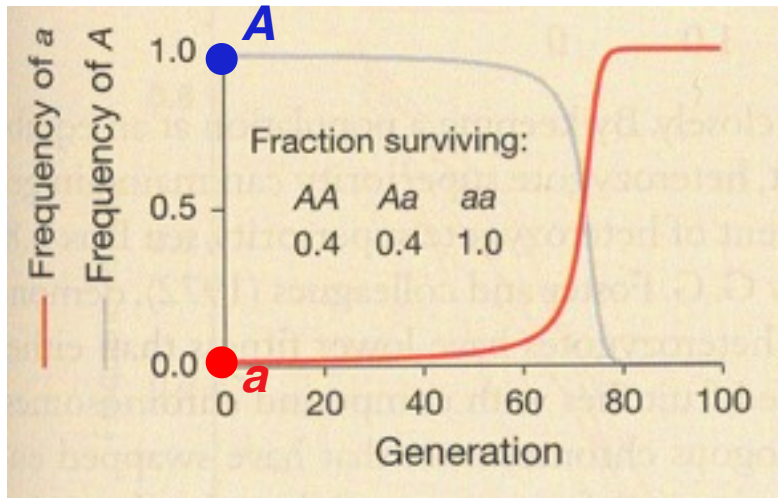


Chance of Survival

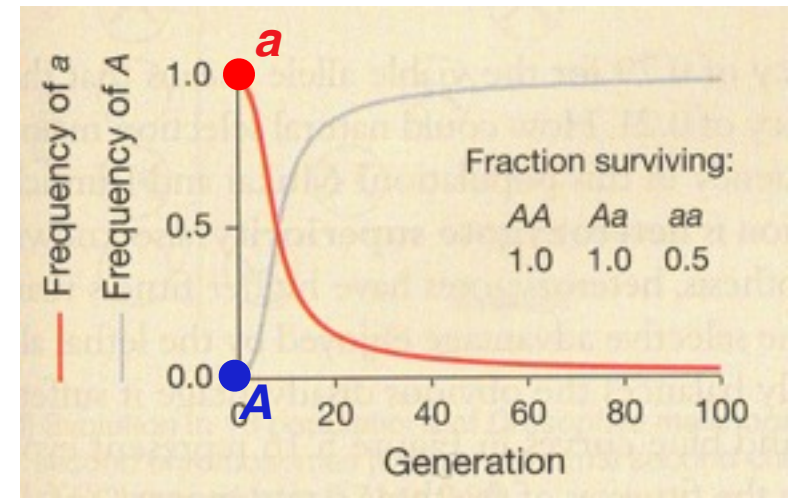
Recessive, deleterious allele a persists for many generations

= population is *slowly* fixed for A

Selection against dominant allele A



Selection against recessive allele a

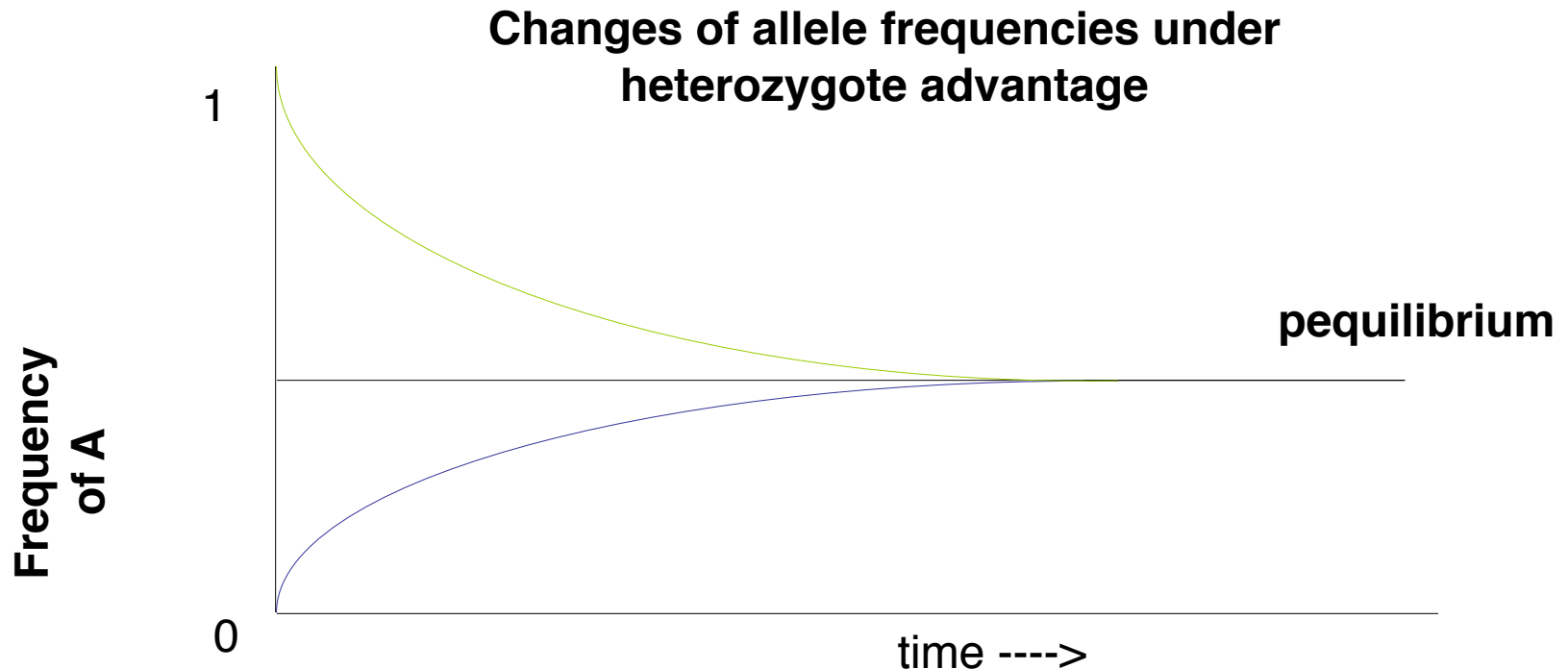


Genotype	Chance of Survival	Chance of Survival
AA	1 - s	1
Aa	1 - s	1
aa	1	1 - s

Most *observed* cases of selection against a deleterious trait involve recessive deleterious alleles (e.g., many human genetic diseases)

Heterozygote advantage

<u>Genotype</u>	<u>Chance of Survival</u>
AA	$1 - s$
Aa	1
aa	$1 - t$



Under heterozygote advantage, allele frequencies stabilize at some intermediate equilibrium frequencies;

=> both alleles will be maintained in the population

Heterozygote advantage

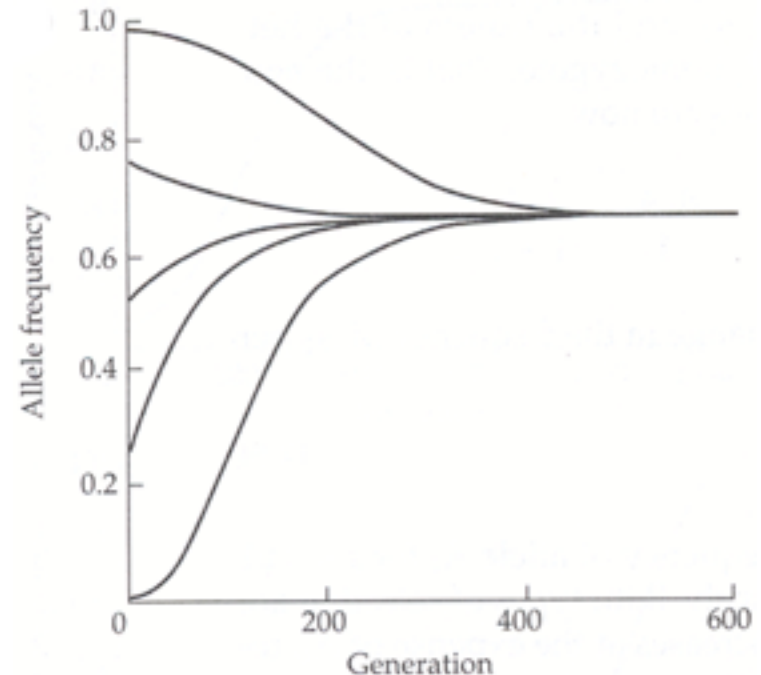
Maintenance of both alleles in population

Equilibrium frequencies:

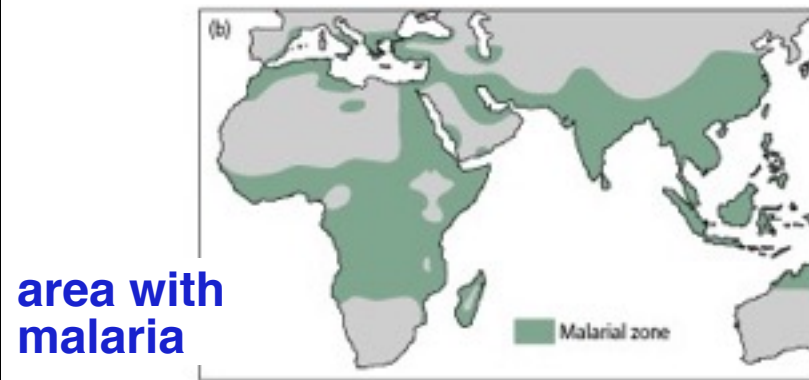
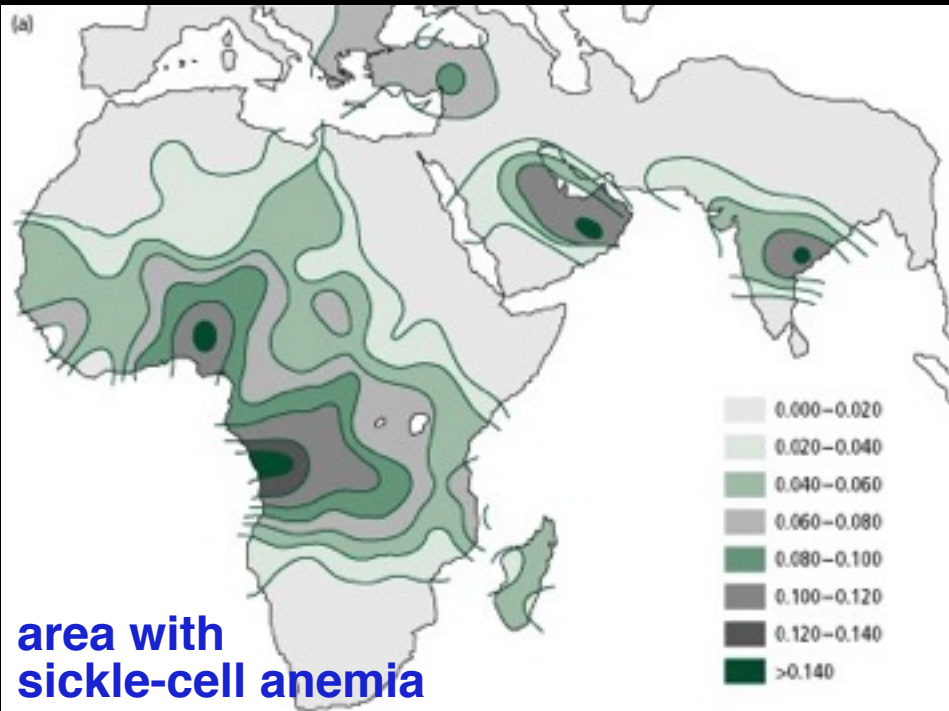
Frequency of A: $p_{\text{equ}} = t / (s + t)$

Frequency of a: $q_{\text{equ}} = s / (s + t)$

- The equilibrium frequency is not necessarily at 50%:50%
- the equilibrium frequency depends on the exact values of s and t



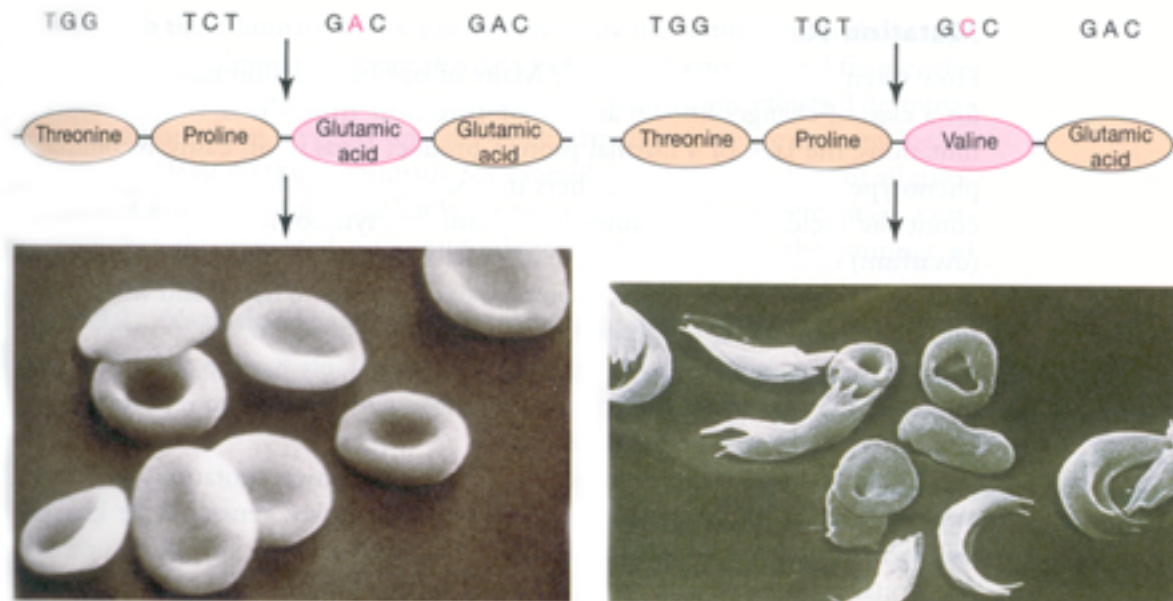
Sickle-Cell Anemia as a result of heterozygote advantage



Global incidence of sickle-cell anemia and malaria coincides

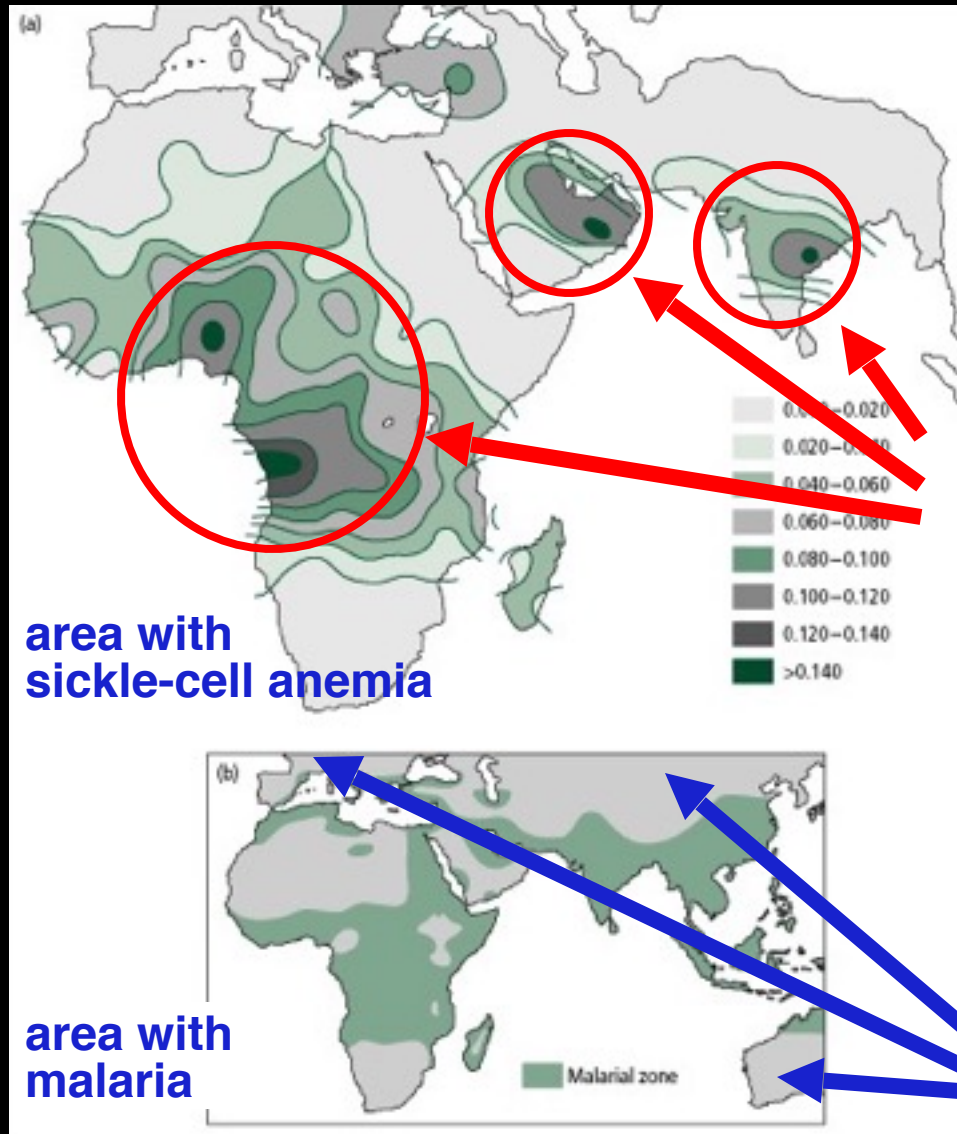
Heterozygote advantage: Sickle-Cell Anemia

<u>Genotype</u>	<u>Phenotype</u>	<u>Chance of Survival</u>	<u>Estimated coefficients</u>
AA	normal red blood cells	$1 - s$	$s = 0.12$
AS	weak anemia	1	
SS	malaria resistance major anemia, 80% mortality	$1 - t$	$t = 0.86$



Definition of Anemia:
Reduction in number of red blood cells in bloodstream, resulting in generalized weakness

Sickle-Cell Anemia as a result of heterozygote advantage



A and S alleles are selectively maintained because of heterozygote advantage

S allele is selected against under directional selection

Frequency-dependent selection

- can also maintain several alleles at a single locus

<u>Genotype</u>	<u>Chance of Survival</u>
AA	$1 - sf(AA)$
Aa	1
aa	$1 - tf(aa)$

$sf(AA)$ = selection coefficient against AA where s is dependent on frequency of AA

Examples of Frequency-Dependent Selection

- Sex-Ratio Selection

The rare sex has a reproductive advantage

- Self-Incompatibility in Plants

to avoid selfing (ensure outcrossing), pollen that has same alleles at incompatibility loci/locus is rejected

=> rare incompatibility alleles are selectively favored