OVERVIEW

Female gametes (frequency)

Male gametes (frequency)

$A_1(p)$ — $A_2(q)$

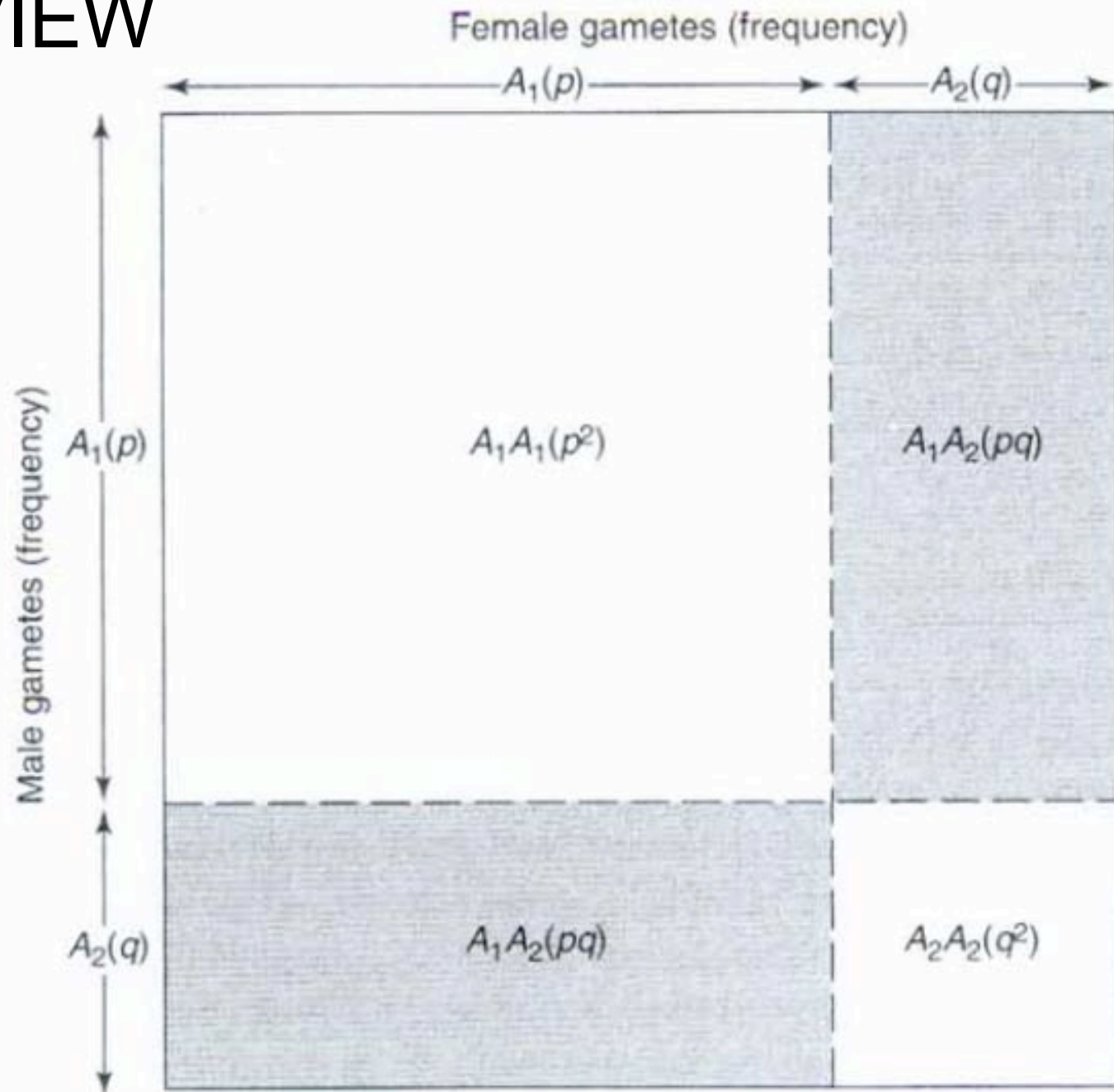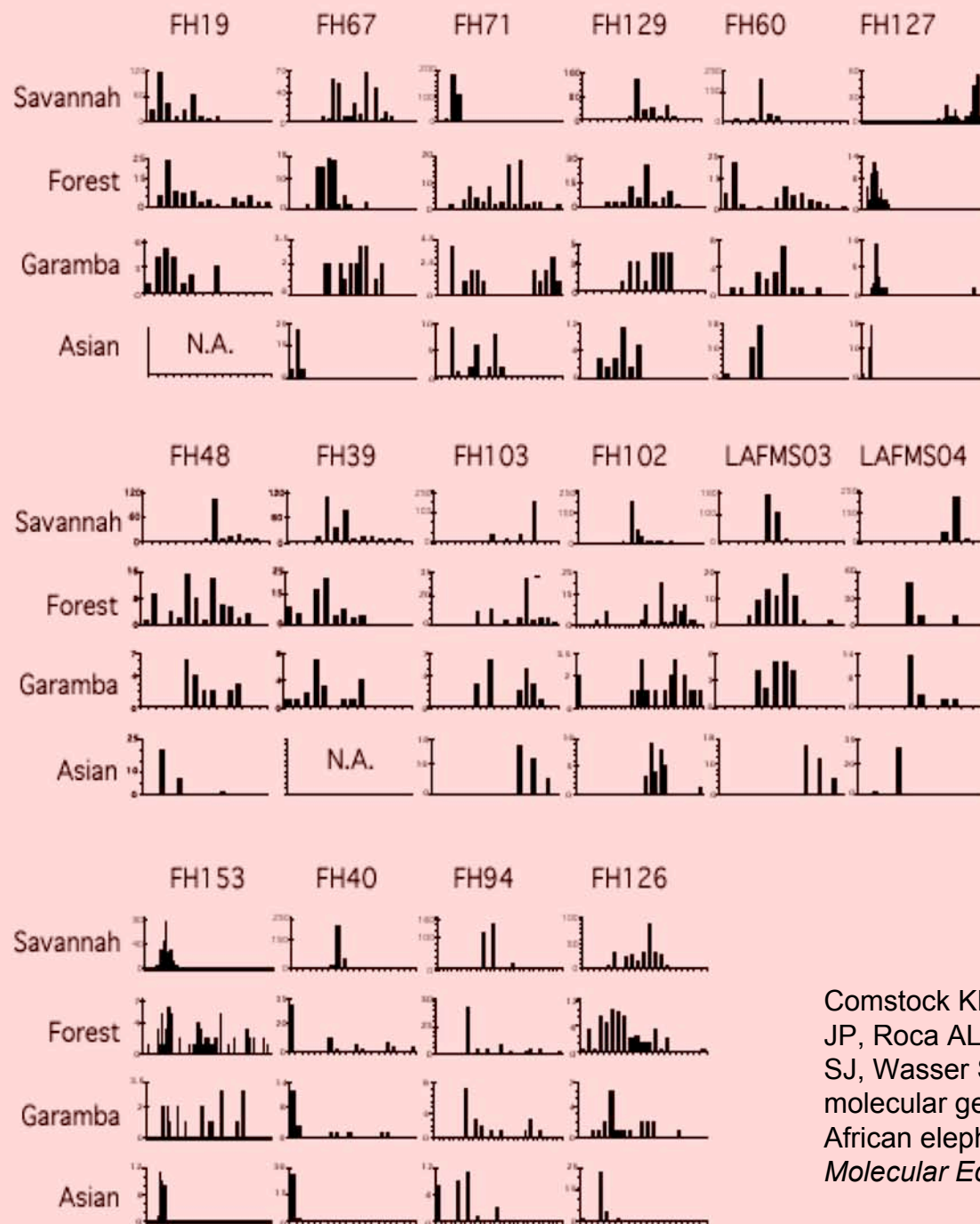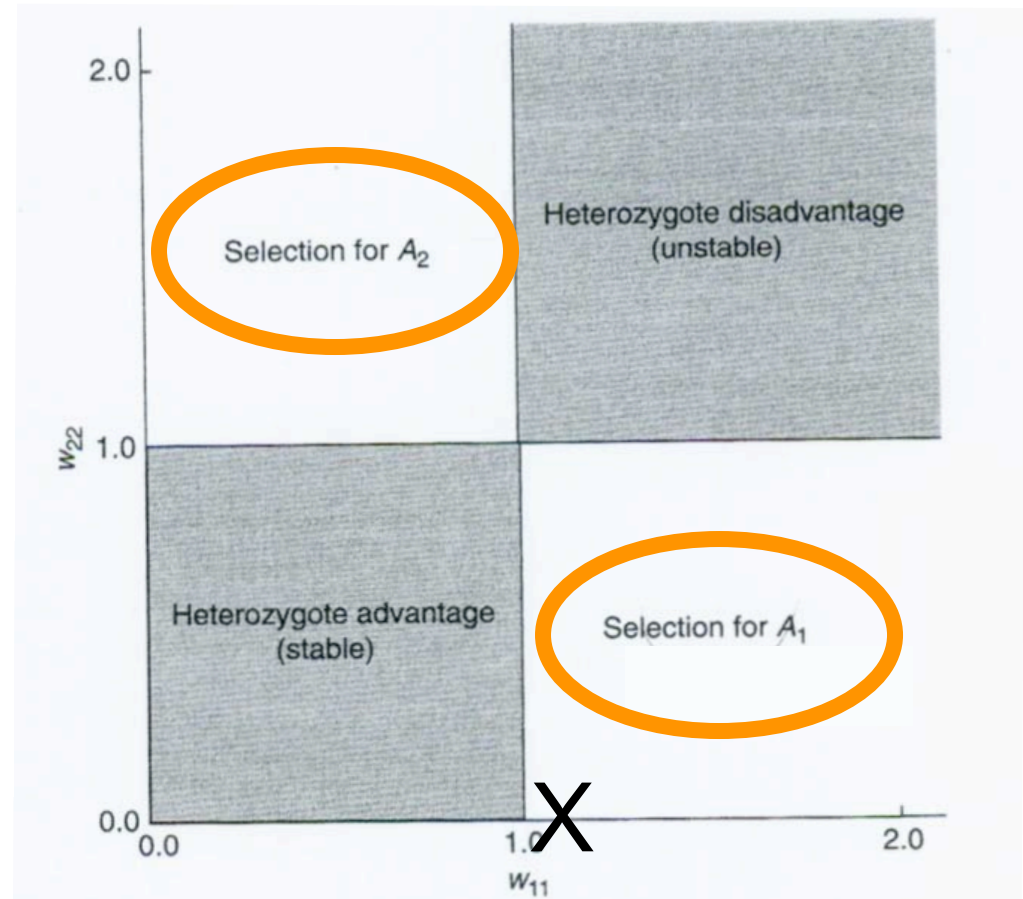$A_1(p)$: $A_1A_1(p^2)$ | $A_1A_2(pq)$

$A_2(q)$: $A_1A_2(pq)$ | $A_2A_2(q^2)$

Comstock KE, Georgiadis N, Slattery JP, Roca AL, Ostrander EA, O'Brien SJ, Wasser SK. (2002) Patterns of molecular genetic variation among African elephant populations. *Molecular Ecology*.

Hedrick example 3.2: selection against a homozygote **lethal** (a phenotype that results in "early death"), *Glued* in *Drosophila melanogaster*.

At high frequencies, lethals decline quickly, but persist at low frequencies (except in this case heterozygotes for *Glued* are also disadvantaged.)
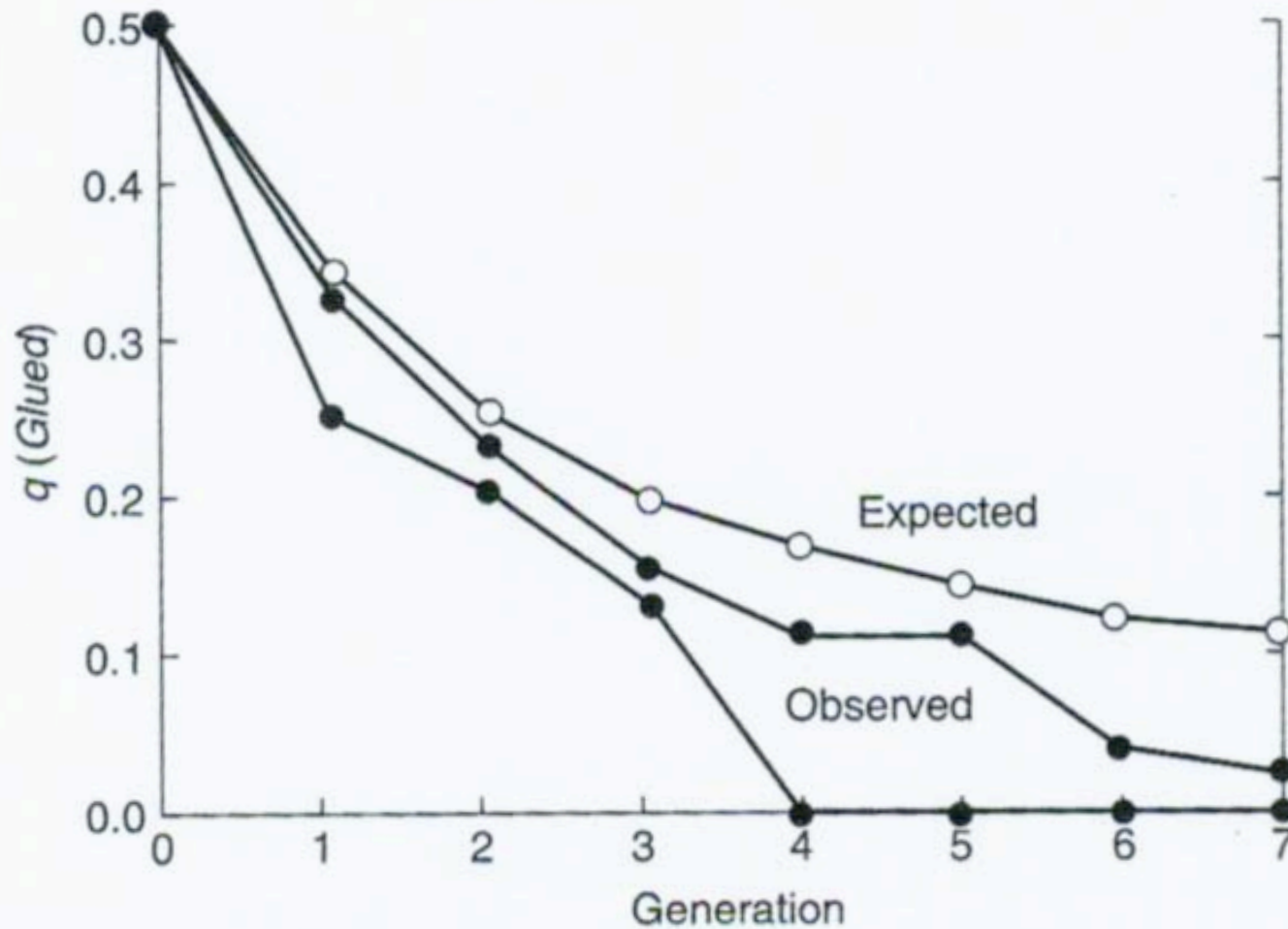
Classic case of Darwinian selection:
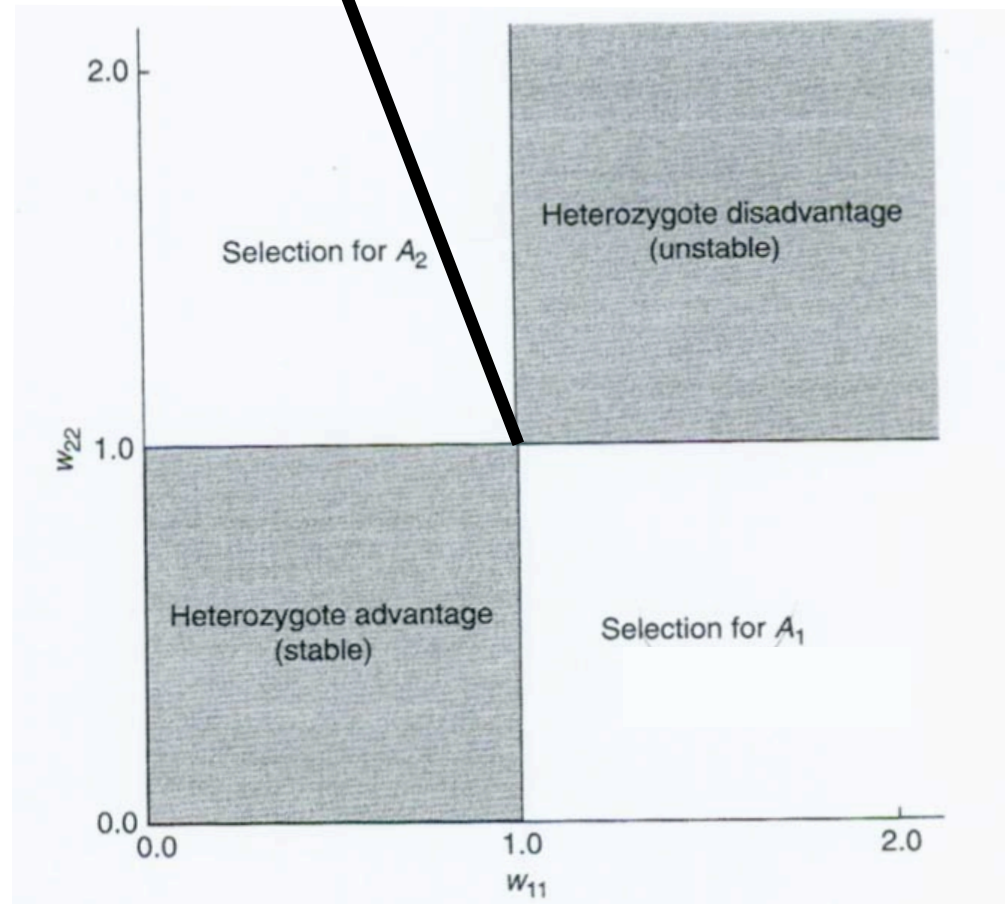
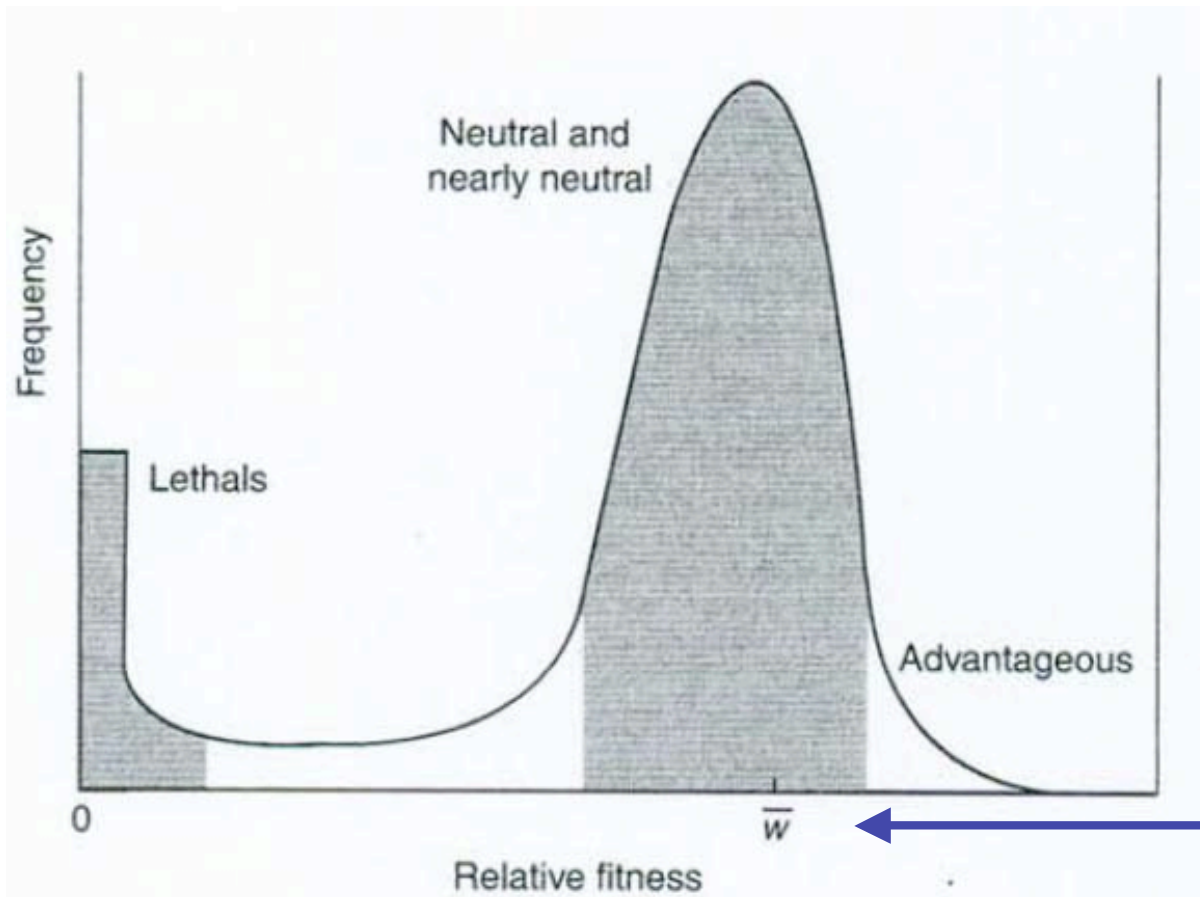## peppered moth, *Biston betularia*

white form

black form

Point at which all genotypes (both homozygotes and the heterozygote) have the same relative fitness.

What is the fitness of new mutations? Hypothetical distribution is bimodal (has two peaks). One peak is lethal mutations; a higher peak is neutral or nearly neutral; a small but important number are advantageous.

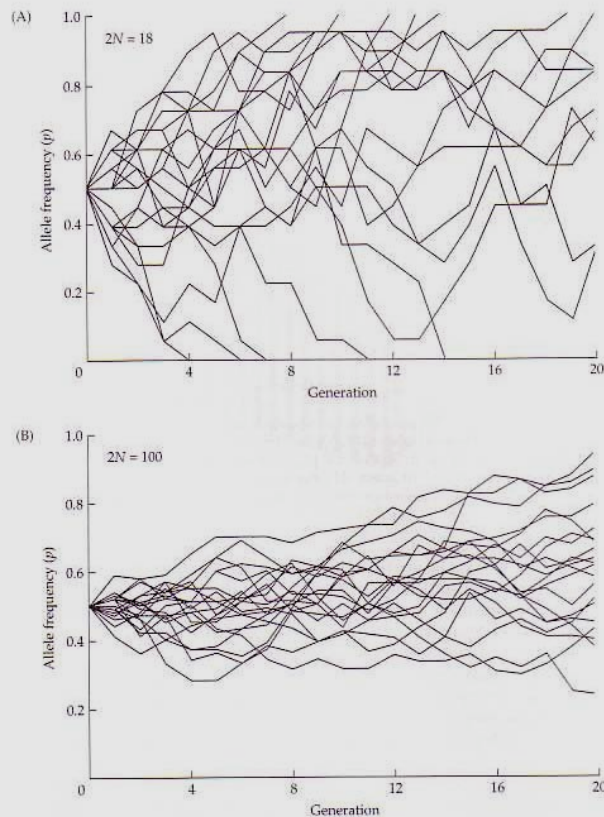
mean population fitness is omega-bar

(A) 2N = 18

Allele frequency (p)

Generation

(B) 2N = 100

Allele frequency (p)

Generation

Figure 7.2 Computer simulations of the Wright-Fisher model of random genetic drift. Each line represents a population of size (A) 2N = 18 or (B) 2N = 100, simulated for 20 generations. Each generation alleles are sampled with replacement as described in the text. An allele frequency of p = 0.5 in A implies that there are nine copies of the A allele, and nine copies of the a allele. In B, an allele frequency of 0.5 implies 50 copies of each allele. Note that the larger population size in B results in smaller oscillations of allele frequency, and a slower rate of fixation.
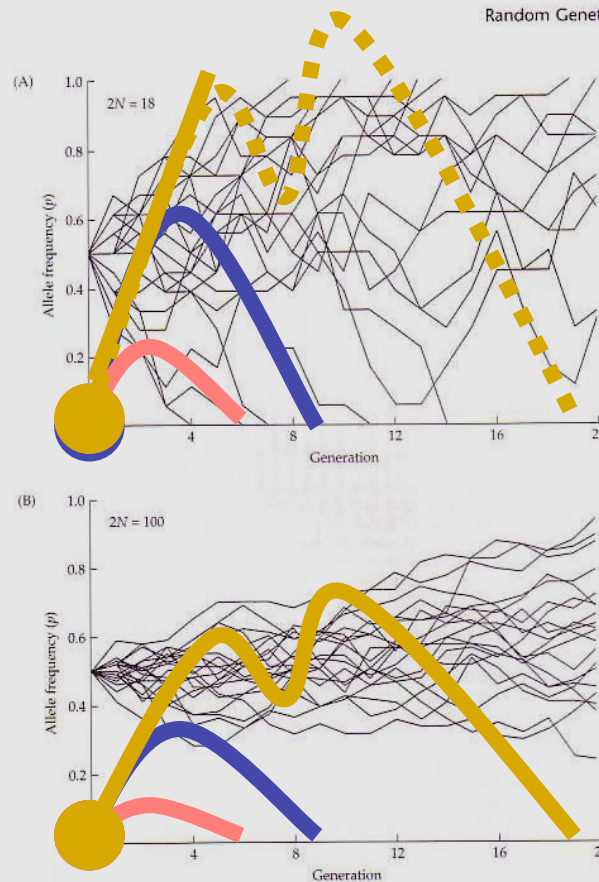
Small populations

genetic drift

Large populations

selection

Detrimental mutations

In highly selfed plants, where f =1, inbreeding would make Ne = N/2

TABLE 6.11 DNA sequence diversity for six loci in *L. crassa* populations with different levels of selfing (Charlesworth, 2003).

Locus	Level of selfing		
	Low	Intermediate	High
Adh1	0.036	0.000	0.000
Adh2	0.008	0.006	0.014
Adh3	0.017	0.007	0.000
Gapc	0.028	0.017	0.014
Nir1	0.023	0.022	0.007
PgiC	0.000	0.013	0.011
Mean	0.019	0.013	0.008

Inbreeding depression: major concern among endangered species.

Florida panther, *Puma concolor coryi*
Culver and colleagues

Mansfield and Land 2002
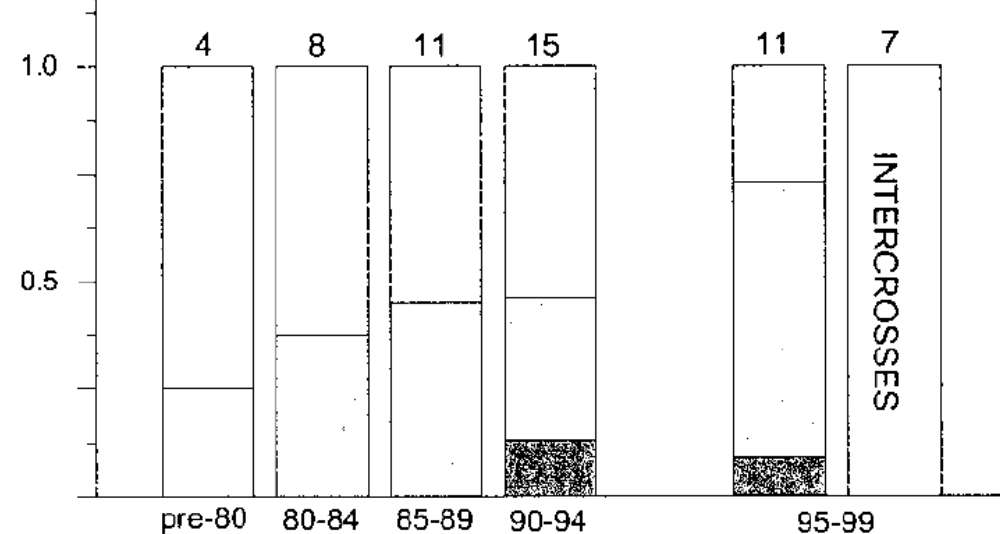
sexual imprinting: European hawk, *Buteo buteo*, leads to positive assortative mating


TABLE 5.17 The observed numbers of newly formed mating pairs of hawks and the expected numbers assuming random mating (Krüger *et al.*, 2001).

| Mating pairs	Observed	Expected	Observed/Expected
Dark × Dark	10	3.6	2.78
Intermediate × Intermediate	136	136.9	0.99
Light × Light	50	37.7	1.33
Dark × Intermediate	52	45.3	1.15
Intermediate × Light	139	144.0	0.97
Dark × Light	4	23.5	0.17

For calculating effective population size, three approaches have been used: inbreeding (loss of heterozygosity), variance and eigenvalue (= loss of allele frequency)

relating the increase in each of these factors to that of an ideal population
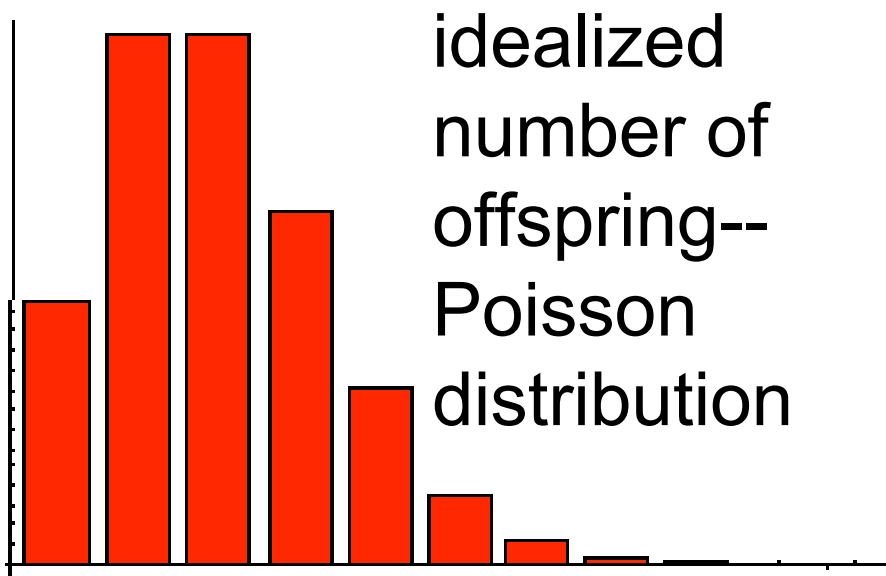
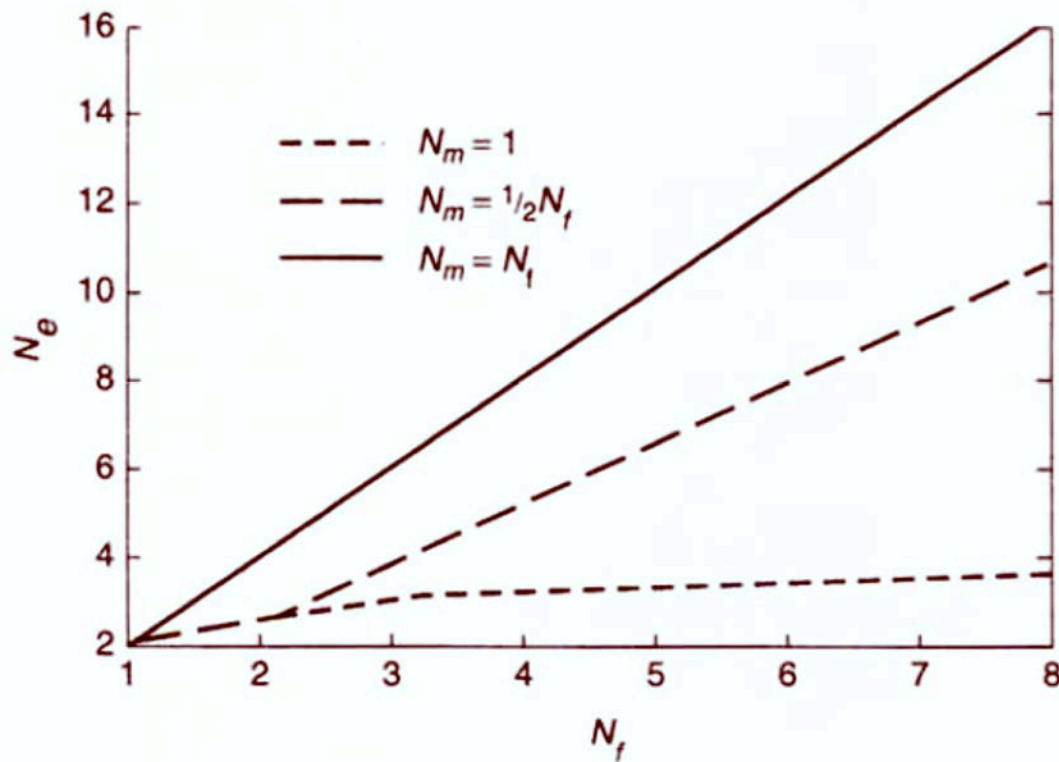idealized number of offspring-- Poisson distribution

Versus maximum variance in reproductive success
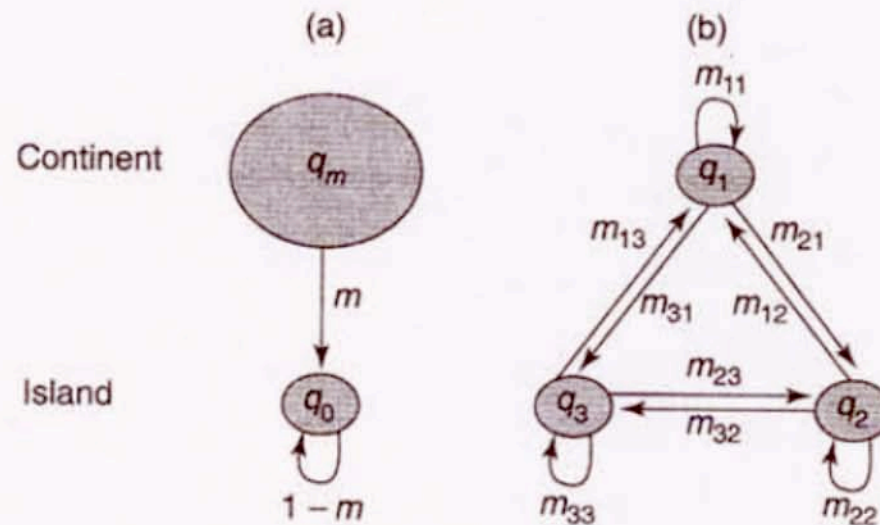
Time
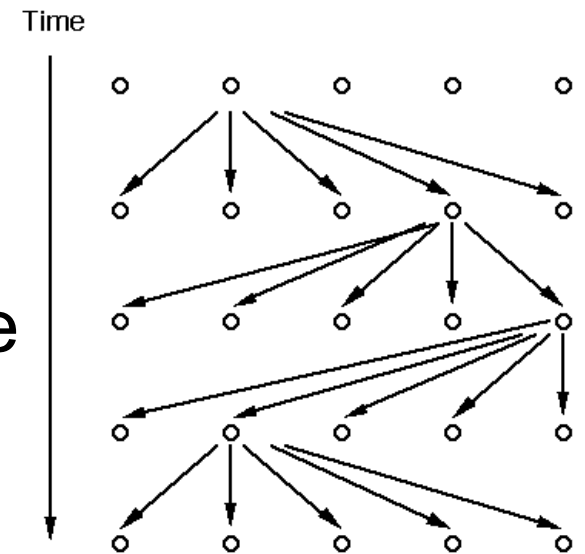
In species where males have harems,

$$N_e = \frac{4N_f}{N_f + 1}$$

so Ne becomes 4

Migration and population structure

Figure 9.1. Illustration of (a) the continent–island model and (b) population structure with three sub-populations.

Continent-island model, example: the red wolf, *Canis rufus*, subject to introgression of alleles from a much larger coyote population.
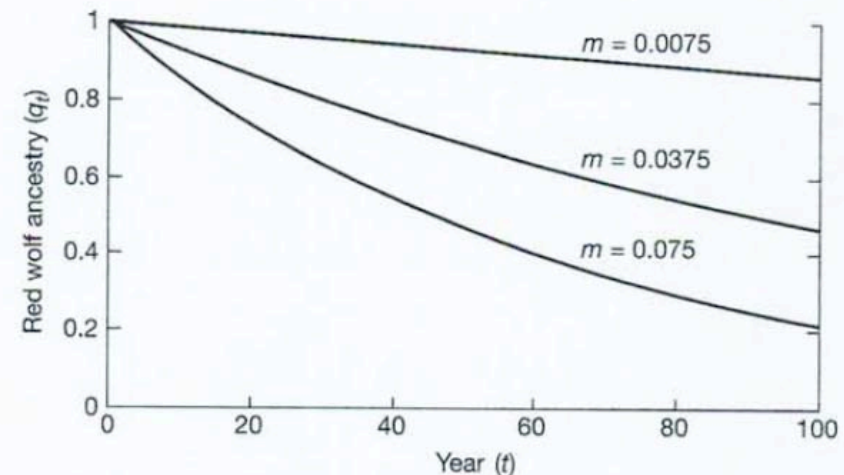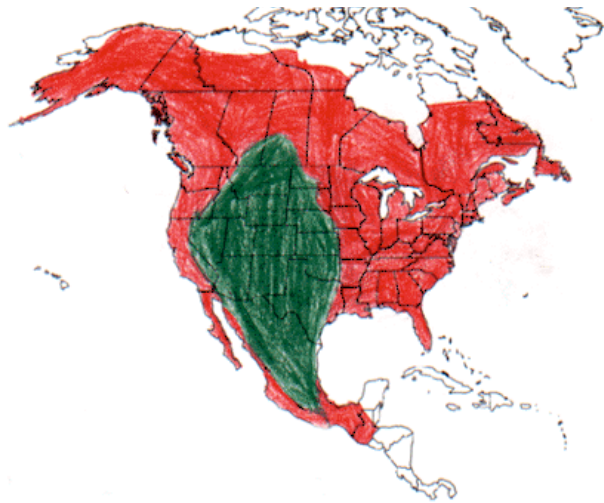

Figure 9.4. The predicted proportion of red wolf ancestry over time when there is gene flow from coyotes as might occur in a continent (coyote)–island (red wolf) model. The proportion of gene flow is assumed to be 0.075 without management intervention and either 0.0375 or 0.0075 if 50% or 90% of the hybrid litters are identified and eliminated.

Measured linkage disequilibrium drops with increasing distance between two loci on a chromosome; eg among 24000 SNPs in human chromosome 21:

Figure 10.3. The decline of linkage disequilibrium as measured by D' between pairs of 24,056 SNPs on human chromosome 21 where the closed circles indicate the observed averages and the line shows the expected decline. (Courtesy of Innan, H., B. Padhukasahasram, and M. Nordborg. 2003. The pattern of polymorphism on human chromosome 21. *Genome Res.* 13:1158–1168.)
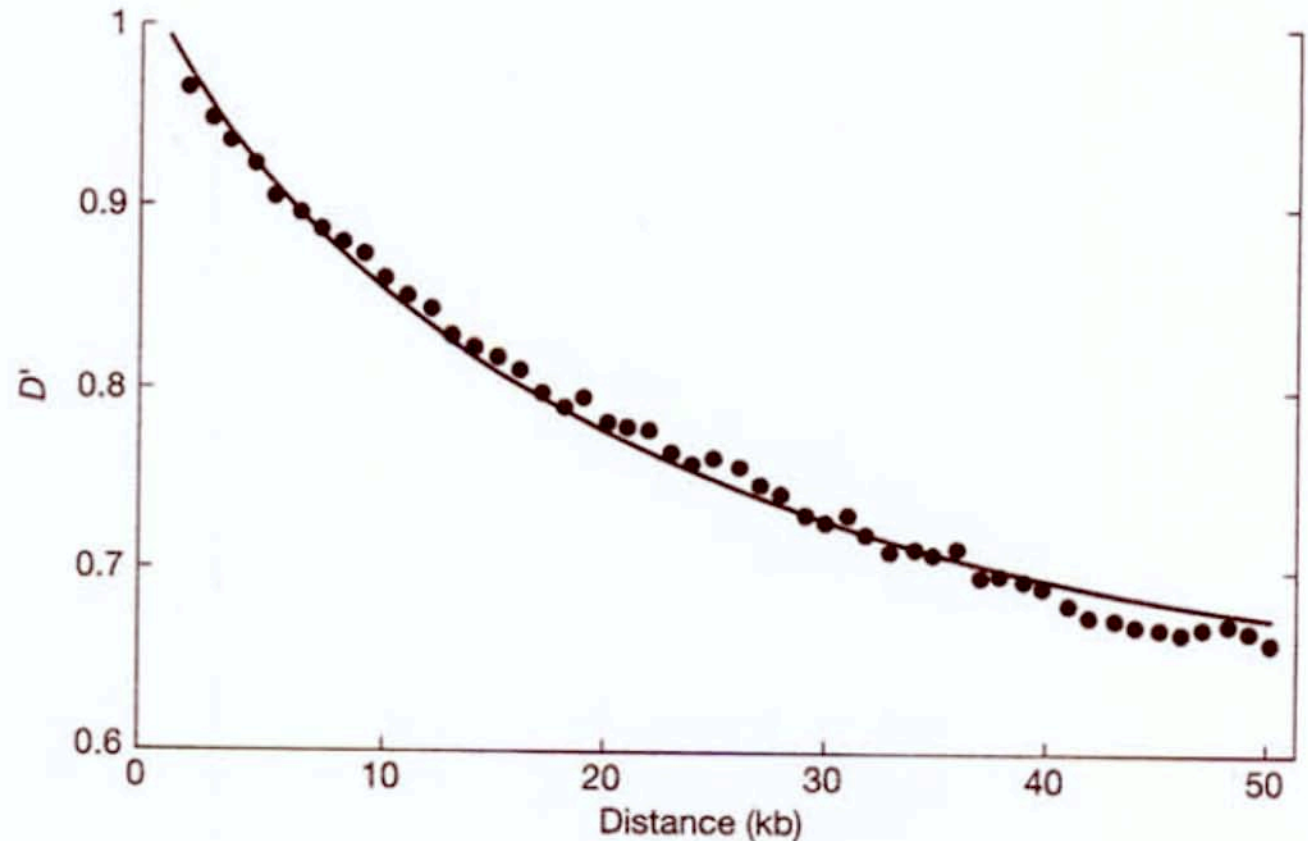
The outgroup:
Primate phylogeny

- The tree of human, chimpanzee and gorilla are rooted with baboon because we know from the fossil record that baboons split from primate lineage before the other 4 species

Figure 19.5 *Genomes 3* (© Garland Science 2007)
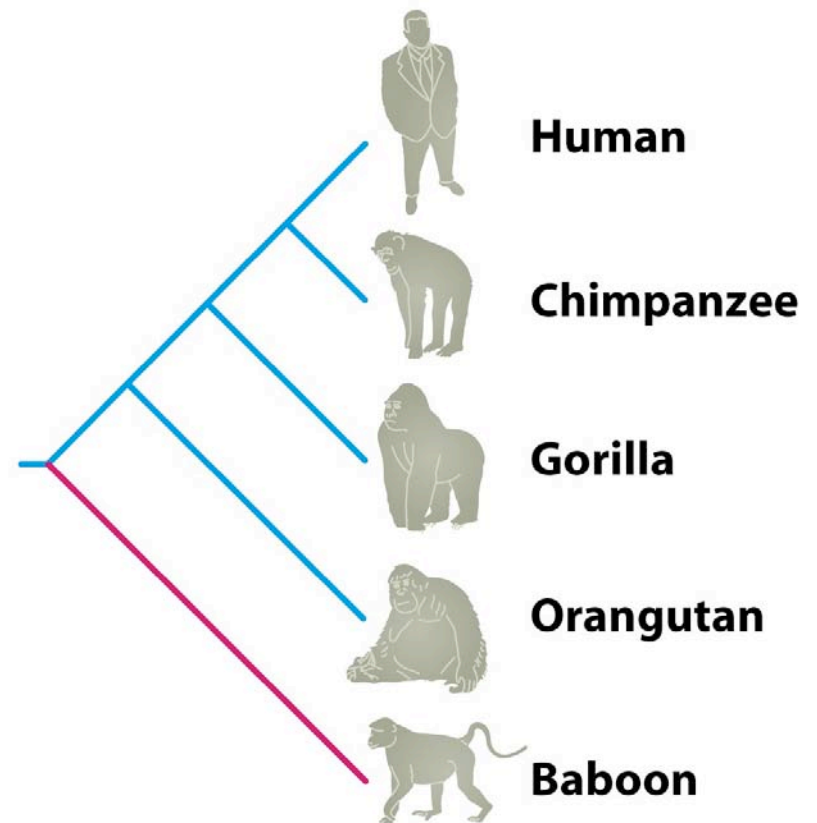
Caspian tiger
Panthera tigris virgata