

LectureHandout 13:

Hypothetical pedigree
with complicated history
of inbreeding

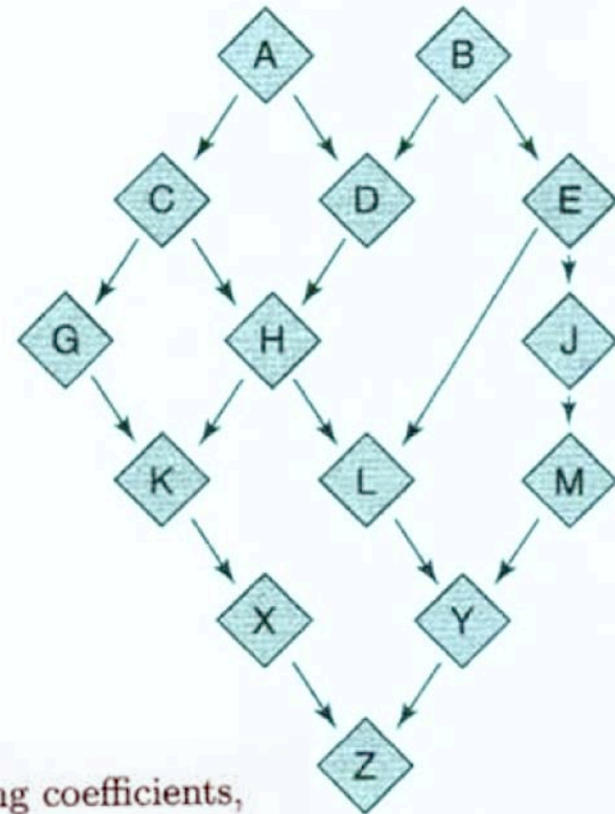


TABLE 5.11 The common ancestors and their chains, inbreeding coefficients, and contribution to the inbreeding coefficient of Z in Figure 5.14.

Common ancestor	Chain	N_i	$f_{CA(i)}$	Contribution to f
A	X-K-G-C-A-D-H-L-Y	9	0.0	$(\frac{1}{2})^9 = 0.0020$
B	X-K-H-D-B-E-J-M-Y	9	0.0	$(\frac{1}{2})^9 = 0.0020$
B	X-K-H-D-B-E-L-Y	8	0.0	$(\frac{1}{2})^8 = 0.0039$
C	X-K-G-C-H-L-Y	7	0.0	$(\frac{1}{2})^7 = 0.0078$
H	X-K-H-L-Y	5	0.125	$(\frac{1}{2})^5(1.125) = 0.0352$
				$f = 0.0509$

Philopatry: tendency of progeny to remain near their natal (or parental) territory. Also called matrilocality.

Kin selection: selection acts through effects on close relatives of individuals. Individual actions may increase the fitness of kin who share their alleles. Kin selection may allow development of **altruistic behavior**. The altruistic individual sacrifices some fitness to increase the fitness of other individuals.

The frequency of an altruistic allele increases when $r > c/b$

r , coefficient of relatedness (0.5 for full sibs)

c , cost in fitness to the altruist

b , benefit in fitness to the recipient

Inclusive fitness: fitness of an individual plus his/her effect on the relatives of the individual weighted by their coefficient of relationship.

Effects of inbreeding on fitness:

- Can affect mean fitness of population
- Can affect rate of allele frequency change
- Can affect conditions for stable polymorphism.

Inbreeding depression: decline in fitness due to inbreeding. Very common.

Inbreeding depression: mice siblings

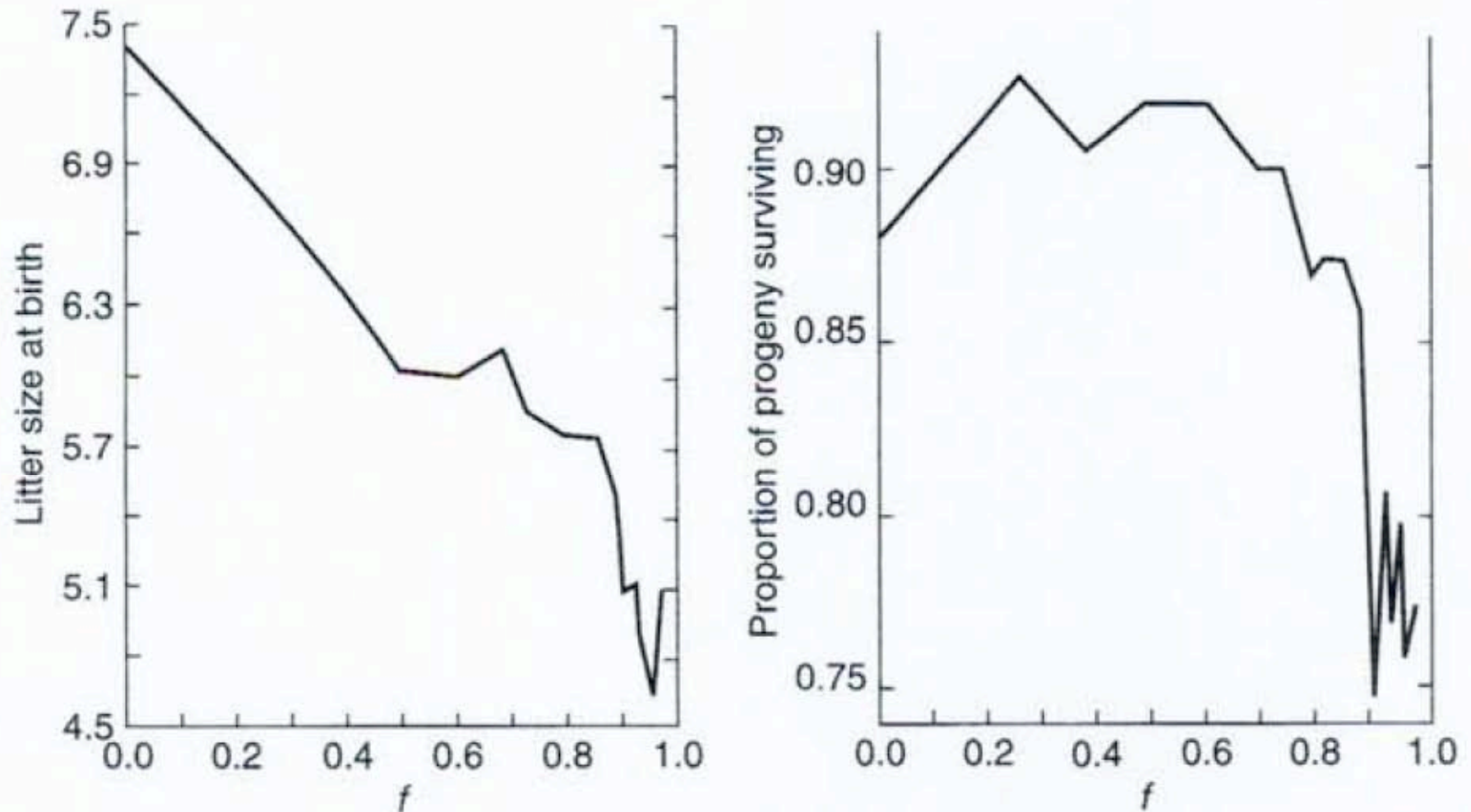


Figure 5.18. The litter size and progeny survival for lines of mice inbred for 20 generations (after Connor and Bellucci, 1979).

Inbreeding depression: can be defined as the difference in fitness between an outbred and an inbred population:

$$\bar{w} - \bar{w}_f = -fpq(w_{11} + w_{22} - 2w_{12})$$

In a model that assumes survival (viability) is the only trait affecting fitness. Fitness of individuals with inbreeding f approximates:

$$w_f = w_0 e^{-Bf}$$

where w_0 and w_f are fitness before and after inbreeding to the level f . B is regression coefficient that measures how fast fitness decreases with inbreeding

Number of lethal equivalents: in a zygote, the group of genes that, when made homozygous, would on average cause $2B$ deaths, eg if one lethal allele is present a heterozygote, there would be one lethal equivalent.

May also be defined as: the number of deleterious genes per haploid genome whose cumulative effect is the equivalent of one lethal gene.

Inbreeding depression may lead to reduced resistance to disease.



TABLE 5.16 The number of outbred and inbred ($f = 0.25$) winter-run Chinook salmon exposed and resistant to the parasite that causes whirling disease in five families (Arkush *et al.*, 2002).

Family	Outbred			Inbred		
	Exposed	Resistance	Proportion	Exposed	Resistance	Proportion
1	60	58	0.97	55	46	0.84
2	58	53	0.91	51	30	0.59
3	58	41	0.71	54	17	0.71
4	58	47	0.81	60	37	0.62
5	30	18	0.60	31	19	0.61
Total	264	217	0.822	251	149	0.594

Inbreeding depression: major concern among endangered species.



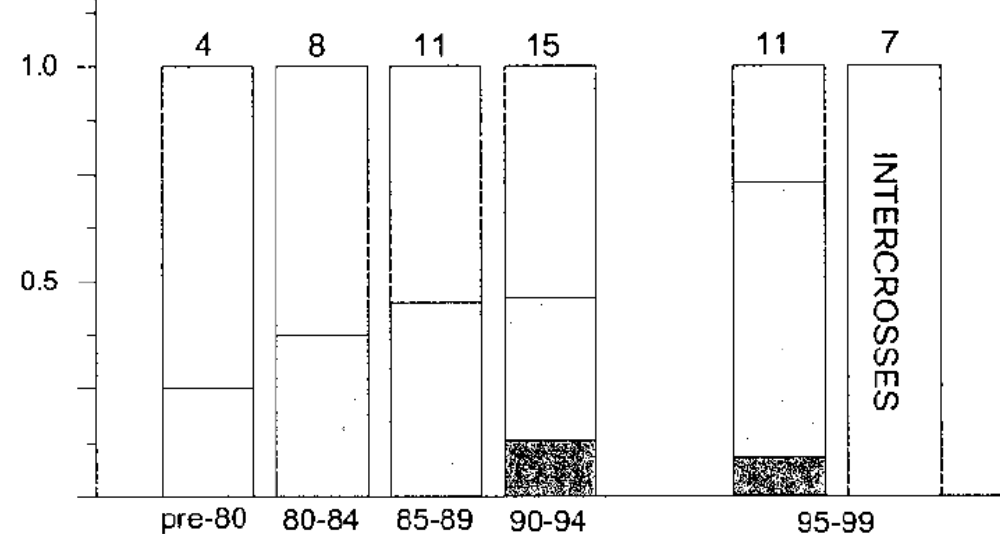
Florida panther, *Puma concolor coryi*
Culver and colleagues



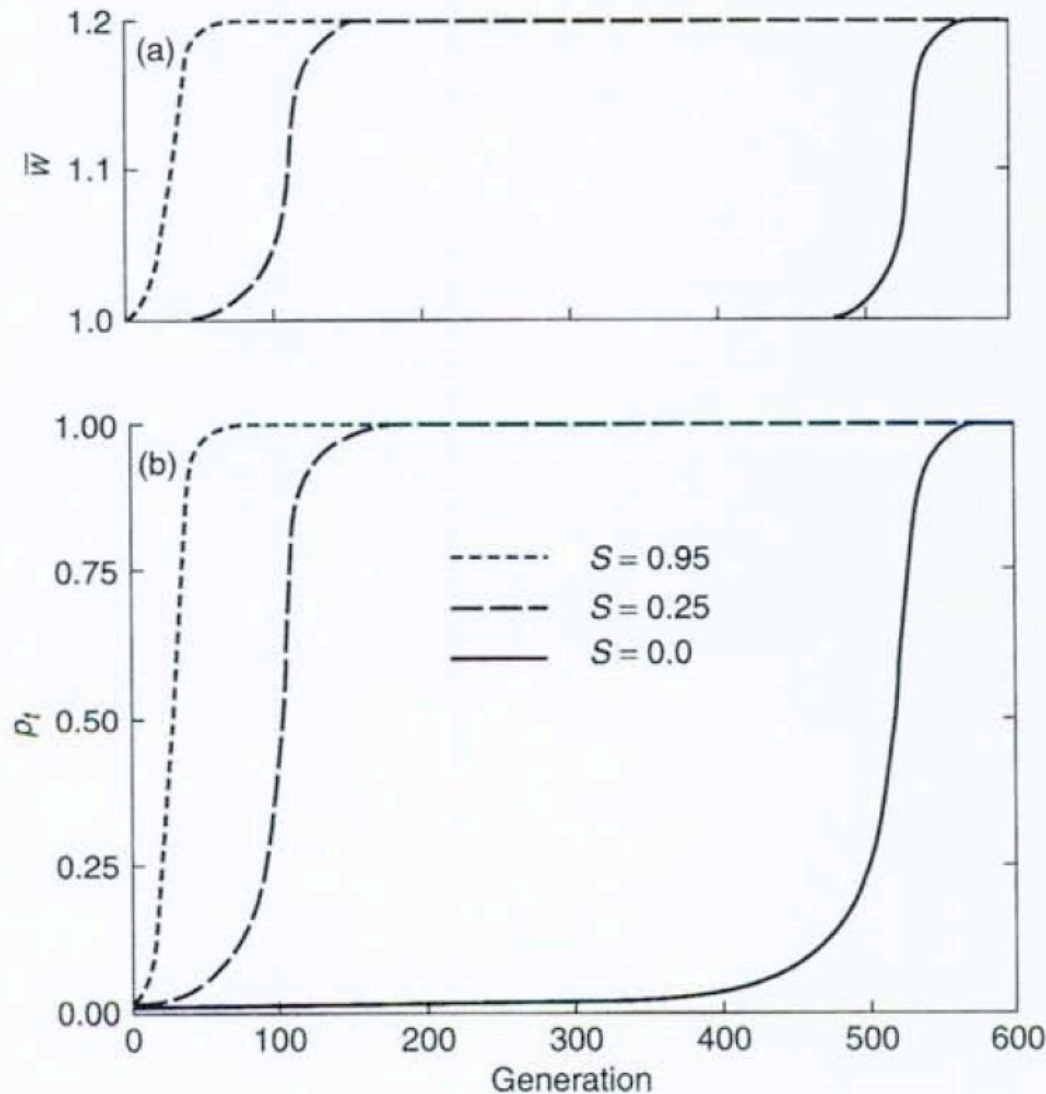
RELATIVE FREQUENCY

Mansfield and Land 2002

Number of
Descended
Testicles



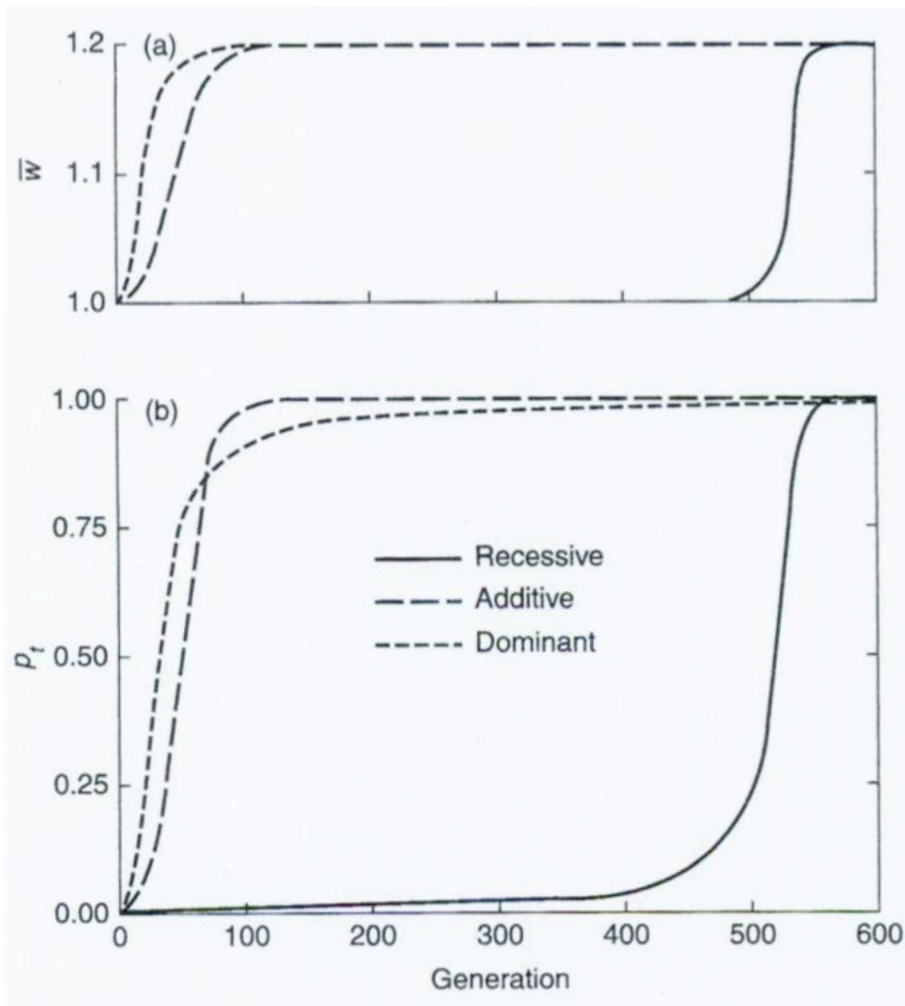
Inbreeding depression affects directional (adaptive Darwinian) selection, generally increasing changes in allele frequencies.



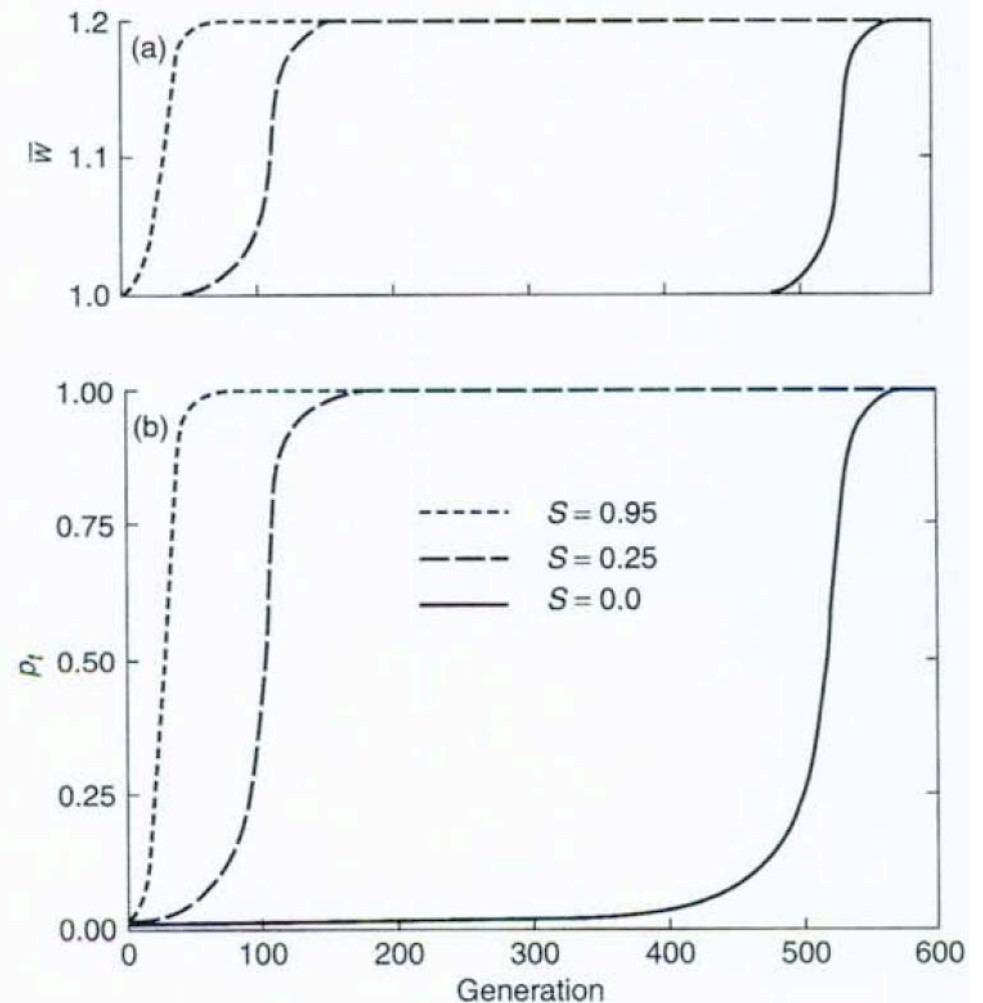
Effect of partial selfing **S** of 0, 0.25, or 0.95 (upper case S) on change in allele frequency for a beneficial recessive allele with selection coefficient of **s** = 0.2 (lower case s)

Note similarity of dominance and selfing effects on the change in allele frequencies due to directional selection

dominant vs recessive



inbred vs outbred



Purging of deleterious alleles: selection more effective at purging when inbreeding is present; eg, selfing an outcrossed population of water hyacinth led eventually to reduced inbreeding depression (yet surveys of literature on the purging of deleterious alleles have been inconclusive).

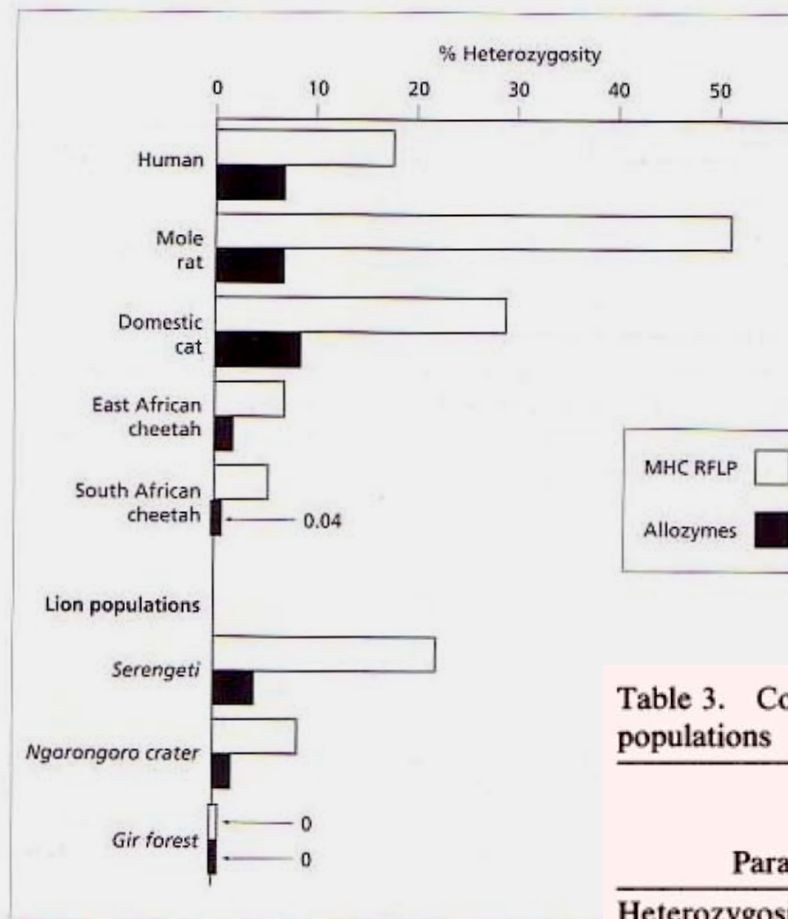


Fig. 4.9 Heterozygosity in different animal populations showing variation in cheetahs and lions. The Serengeti lion population numbers about 1000 live in the Ngorongoro crater (also in Tanzania) followed by 1962. The Gir Forest (India) population today numbers about 250 and suffered a severe bottleneck at the turn of the century. Data from O'Brien et al. (1990).



Asiatic lion,
Panthera leo persica

Gir Forest in Gujarat



Table 3. Correlation of genetic variation and reproductive parameters in three lion populations

Parameter	Serengeti, Tanzania	Ngorongoro Crater, Tanzania	Gir Forest, India
Heterozygosity, %			
Allozyme	3.1	1.5	0.0
MHC RFLP	21.8	8.0	0.0
DNA fingerprint	48.1	43.5	2.8
Reproductive measure			
Sperm count ($\times 10^{-6}$)	34.4 ± 12.8	25.8 ± 11.01	3.3 ± 2.8
% sperm abnormality	24.8 ± 4.0	50.5 ± 6.8	66.2 ± 3.6
No. motile sperm ($\times 10^{-6}$) per ejaculate	228.5 ± 65.5	236.0 ± 93.0	45.3 ± 9.9
Testosterone, ng/ml	1.3–1.7	0.5–0.6	0.1–0.3

Refs. 27, 47–49, and 51 are sources. When indicated, data are the mean \pm SEM.

S. J. O'Brien and colleagues

Since proportions of heterozygous genotypes are reduced: when there is **heterozygote advantage**, inbreeding can drastically reduce the rate of change in allele frequency; and can reduce the region of stability for a stable equilibrium.

assortative mating: mated pairs in a population are composed of the same phenotype more often or less often than expected by chance.

sexual imprinting: in birds, individuals with a phenotype similar to the maternal phenotype are preferred. Usually (but not always) leads to positive assortative mating.

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).

<i>Mating pairs</i>	<i>Observed</i>	<i>Expected</i>	<i>Observed/Expected</i>
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

Complete positive assortative mating at a dominant gene. (Note: no change in allele frequency).

TABLE 5.18 The mating types and frequencies of progeny when there is complete positive-assortative mating at a dominant gene.

<i>Mating type</i>	<i>Frequency</i>	<i>Progeny</i>		
		A_1A_1	A_1A_2	A_2A_2
$A_1A_1 \times A_1A_1$	$P^2/(1 - Q)$	$P^2/(1 - Q)$	—	—
$A_1A_1 \times A_1A_2$	$2PH/(1 - Q)$	$PH/(1 - Q)$	$PH/(1 - Q)$	—
$A_1A_2 \times A_1A_2$	$H^2/(1 - Q)$	$H^2/[4(1 - Q)]$	$H^2/[2(1 - Q)]$	$H^2/[4(1 - Q)]$
$A_2A_2 \times A_2A_2$	Q	—	—	Q
	1	$\frac{p^2}{1 - Q}$	$\frac{pH}{1 - Q}$	$\frac{q^2 + Q(p - q)}{1 - Q}$

R is proportion of positive-assortative mating and T is proportion of random mating, where $R+T = 1$. Heterozygosity continuously declines over time with complete positive assortative mating ($R=1$)



$$H_t = \frac{2pH_0}{2p + tH_0}$$

