

Inbreeding & Relationship

Inbreeding

mating of related individuals

mating of individuals more closely related than the average of the breed

animal is inbred if, and only if, its parents are related

Genetic results from inbreeding

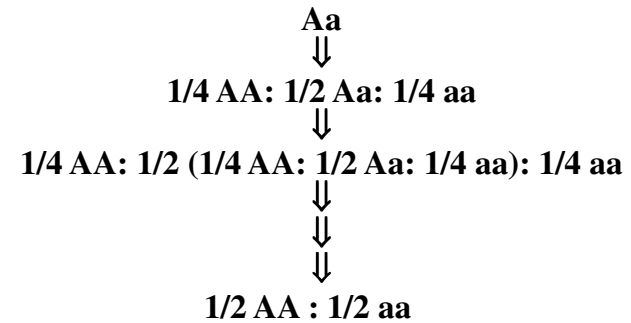


TABLE 10.1 Example Showing How Inbreeding Increases the Number of Pairs of Homozygous Genes

Generation Number	Genotype	Percent Homozygous Gene Pairs	Frequency of <i>d</i> Gene	Frequency of <i>dd</i> Genotype
0	1600 <i>Dd</i>	0	0.50	0
1	400 <i>DD</i> ← 800 <i>Dd</i> → 400 <i>dd</i>	50	0.50	0.25
2	400 <i>DD</i> + 200 <i>DD</i> ← 400 <i>Dd</i> → 200 <i>dd</i> + 400 <i>dd</i>	75	0.50	0.375
3	600 <i>DD</i> + 100 <i>DD</i> ← 200 <i>Dd</i> → 100 <i>dd</i> + 600 <i>dd</i>	87.5	0.50	0.437
4	700 <i>DD</i> + 50 <i>DD</i> ← 100 <i>Dd</i> → 50 <i>dd</i> + 700 <i>dd</i>	93.8	0.50	0.468
5	750 <i>DD</i> + 25 <i>DD</i> ← 50 <i>Dd</i> → 25 <i>dd</i> + 750 <i>dd</i>	96.9	0.50	0.484

Source: Adapted from *General Genetics* by A. M. Srb and R. D. Owen (San Francisco: W. H. Freeman and Company, 1952).

Note: This example assumes self-fertilization with no selection practiced against the recessive gene. Inbreeding in animals where self-fertilization cannot be practiced would progress in the same way, except that homozygosity would be increased more slowly.

Genetic result of inbreeding

increased homozygosity

if there is dominance:

aa may be inferior

inbreeding will cause decrease in performance .

TABLE 10.2 Hypothetical Example Showing the Influence of Inbreeding or Increased Homozygosity on Different Types of Gene Action (Self-Fertilization)

Number of Generation	Genotypes	Population Average in Units						
		Dominance*	Overdominance†	Additives‡				
0	1600Dd	180	180	180				
1	400DD ← 800Dd → 400dd	170	160	180				
2	400DD + 200DD ← 400Dd → 200dd + 400dd	165	150	180				
3	600DD + 100DD ← 200Dd → 100dd + 600dd	163	145	180				
4	700DD + 50DD ← 100Dd → 50dd + 700dd	161	180	5	750DD + 25DD ← 50Dd → 25dd + 750dd	161	141	180
5	750DD + 25DD ← 50Dd → 25dd + 750dd	161	141	180				

Source: Adapted from *General Genetics* by A. M. Srb and R. D. Owen (San Francisco: W. H. Freeman and Company, 1952).
 *Assume that *dd* gives 140 units and *DD* and *Dd* 180 units.
 †Assume that *dd* and *DD* give 140 units and *Dd* 180 units.
 ‡Assume that *dd* gives 160 units, *Dd* 180 units, and *DD* 200 units or that each, plus gene *D*, adds 20 units to the residual genotype (*dd*) of 160 units.

TABLE 10.3 Hypothetical Example Showing the Influence of Inbreeding or Increased Homozygosity on Epistatic Gene Action

Number of Generation	Genotypes	Average of Population in Units
0	1600 <i>AaBb</i>	200
1	100 <i>AABB</i> (200)	178
	200 <i>AABb</i> (200)	
	100 <i>AAbb</i> (150)	
	200 <i>AaBB</i> (200)	
	400 <i>AaBb</i> (200)	
2	100 <i>aabb</i> (150)	172
	200 <i>aabb</i> (150)	
	100 <i>aaBB</i> (150)	
	100 <i>AaBB</i> (200)	
	200 <i>AaBb</i> (200)	
	50 <i>Aabb</i> (150)	
	200 <i>aaBB</i> (150)	
200 <i>aaBb</i> (150)		
	300 <i>aabb</i> (150)	

Note: The following assumptions were made in this example: that each new generation was propagated by self-fertilization; that combinations of *A-B-* resulted in 200 units and all other combinations in 150 units.

Phenotypic result of inbreeding

inbreeding depression

decline in performance from mating related individuals

result of inbreeding when there is non-additive gene action (dominance)

Phenotypic result of inbreeding

inbreeding depression

more pronounced for lowly heritable traits

reproduction	high
growth	moderate
carcass	low

Measurement of inbreeding

inbreeding coefficient (F)

degree of homozygosity

**% increase in homozygosity above
the average of the breed**

**if F = .25 the animal is 25% more
homozygous than
the average of the
breed**

Inbreeding coefficient (F)

minimum value = 0

maximum value = 1

for livestock

rare for F > .6

lab animals

F can approach .9

plants with self-fertilization

F can approach 1.0

Calculation of Inbreeding coefficient (F)

$$F_X = \sum \left[\left(\frac{1}{2} \right)^{n+1} (1 + F_A) \right]$$

F_X = inbreeding coefficient of individual X

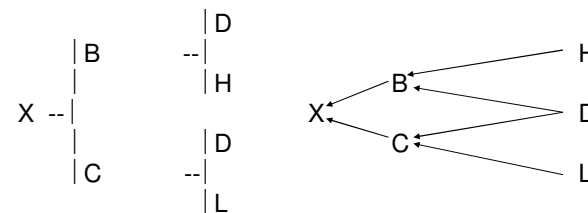
Σ = summation sign

n = number of segregations (arrows) between
the sire and dam in each separate path

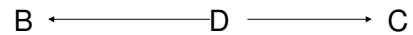
F_A = inbreeding coefficient of the common
ancestor in each path

common ancestor - appears in both sire
and dam portions of the pedigree .

Step 1: Generate an arrow pedigree



Step 2: List all paths that connect the sire and the dam.



Step 3: Identify the common ancestor in each path



Step 4: Calculate the inbreeding coefficient of the common ancestors.

$$F_D = 0$$

Step 5: Count the number of arrows in each path to determine "n".

Only one path and it has two arrows.
Therefore, n=2.

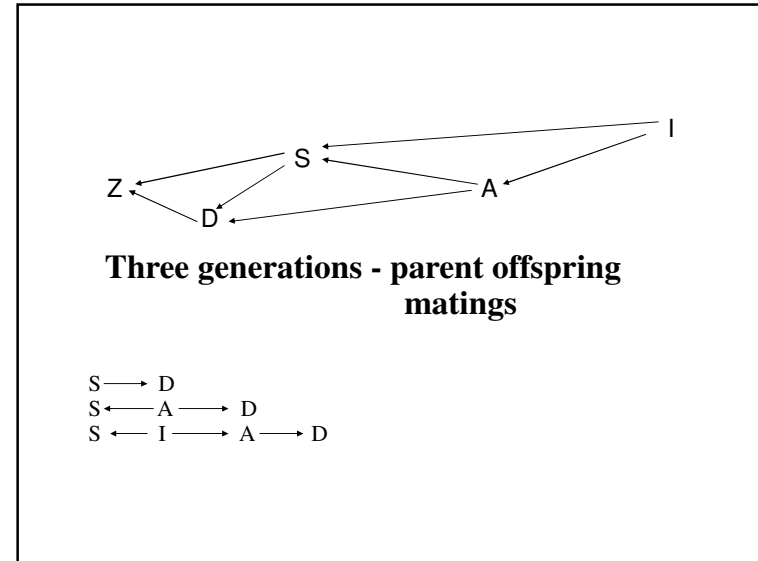
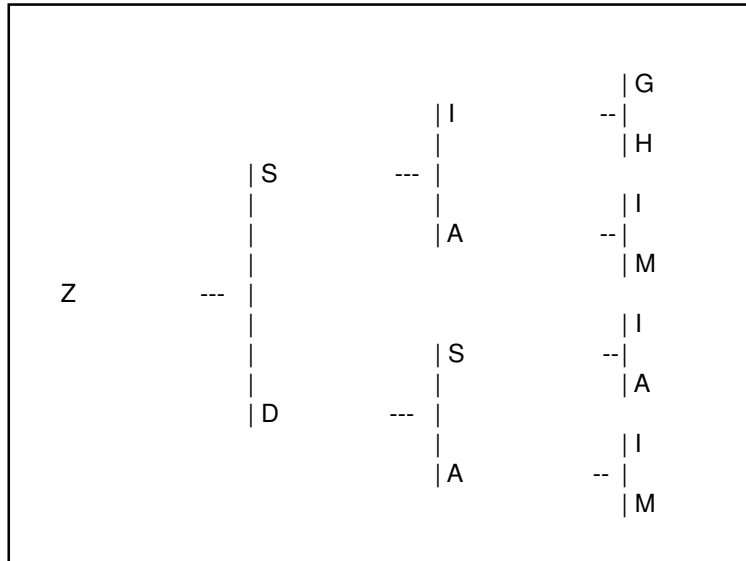
Step 6: Calculate the value of each path connecting the sire and dam

$$\begin{aligned} \text{value of path} &= \frac{1}{2}^{n+1} (1 + F_A) \\ &= \frac{1}{2}^{n+1} (1 + 0) \\ &= \frac{1}{2}^3 = .125 \end{aligned}$$

Step 7: Add together the value for each path connecting the sire and dam

$$F_X = \sum \left[\frac{1}{2}^{n+1} (1 + F_A) \right]$$

$$F = .125$$



$\textcircled{S} \rightarrow D$	$F_S = .25^*$	1	$\frac{1}{2}^{1+1} (1+.25)$	= .3125
$S \leftarrow \textcircled{A} \rightarrow D$	$F_A = 0$	2	$\frac{1}{2}^{2+1} (1+0)$	= .125
$S \leftarrow \textcircled{I} \rightarrow A \rightarrow D$	$F_I = 0$	3	$\frac{1}{2}^{3+1} (1+0)$	= <u>.0625</u>
			$\Sigma =$	<u>.500</u>

$F = .50$

* Inbreeding of S
 path $\textcircled{I} \rightarrow A$
 value = $\frac{1}{2}^{1+1} (1+0) = .25$

Measurement of relationship

relationship coefficient (R_{XY})

proportion of genes in common between relatives

if $R_{XY} = .25$

the two individuals have 25% more genes in common than two random members of the breed

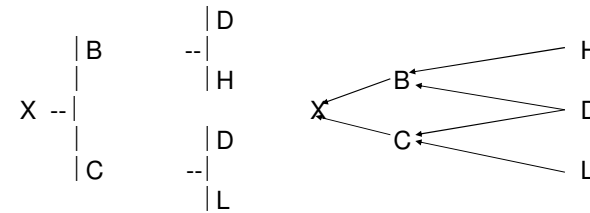
Measurement of relationship

relationship coefficient (R_{XY})

$$R_{XY} = \frac{\sum \left[\frac{1}{2}^n (1 + F_A) \right]}{\sqrt{(1 + F_X)(1 + F_Y)}}$$

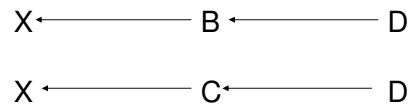
- R = relationship between individuals X and Y
- Σ = sum together all the values of the paths
- n = number of arrows connecting X and Y
- F_A = inbreeding coefficient of the common ancestor
- F_X & F_Y = inbreeding coefficients of animals X and Y

Step 1: Generate an arrow pedigree

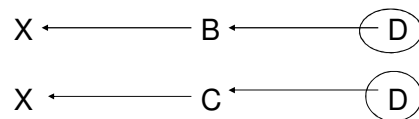


Calculate relationship between X and D

Step 2: List all paths that connect the X with D.



Step 3: Identify the common ancestor in each path



Step 4: Calculate the inbreeding coefficient of the common ancestors

$$F_D = 0$$

Step 5: Count the number of arrows in each path to determine "n"

Two paths, each has two arrows
Therefore, $n=2$ (for each path).

Step 6: Calculate the value of each path connecting the sire and dam

value of paths $\frac{1}{2}^n (1+F_A)$

1st path $\frac{1}{2}^2 (1+0) = .25$

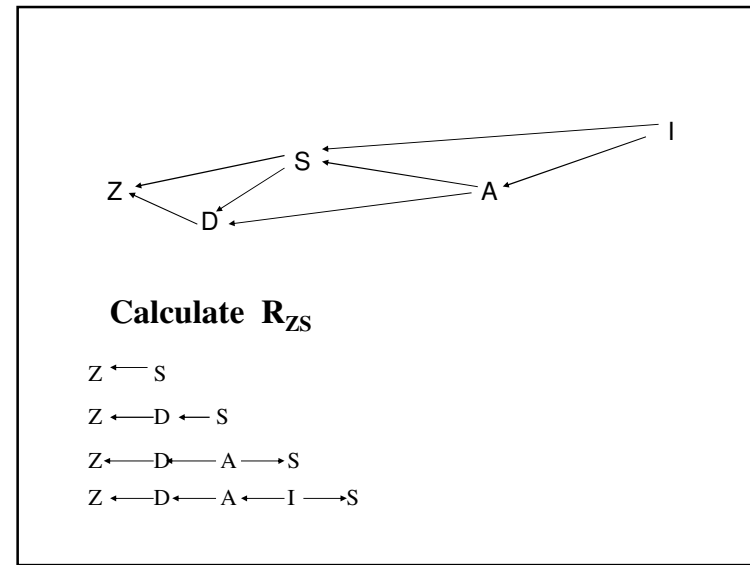
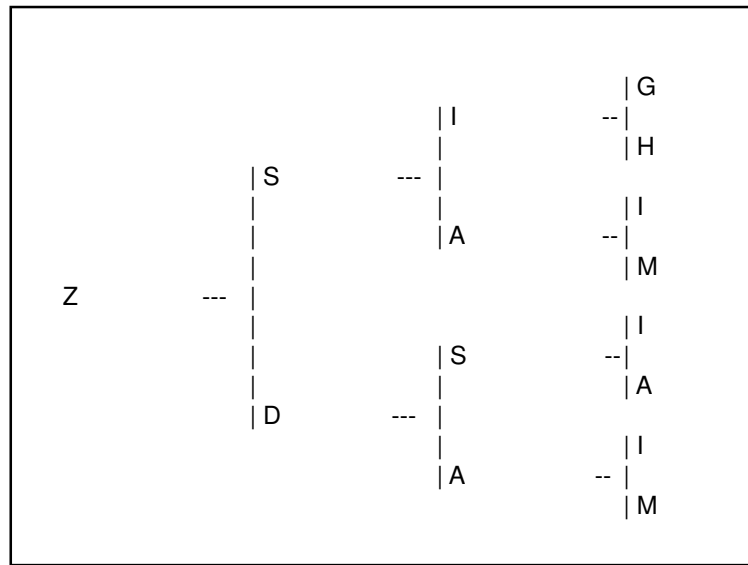
2nd path $\frac{1}{2}^2 (1+0) = .25$

Step 7: Add together the value for each path connecting the sire and dam

$$R_{XY} = \frac{\sum \left[\frac{1}{2}^n (1+F_A) \right]}{\sqrt{(1+F_X)(1+F_Y)}} \quad \text{sum} = .50$$

Step 8: divide by value in denominator

$$R_{XD} = \frac{.50}{\sqrt{(1+.125)(1+0)}} = .4714$$



$Z \leftarrow \textcircled{S}$	$F_S = .25$	1	$\frac{1}{2}^1 (1+.25) = .625$
$Z \leftarrow D \leftarrow \textcircled{S}$	$F_S = .25$	2	$\frac{1}{2}^2 (1+.25) = .3125$
$Z \leftarrow D \leftarrow \textcircled{A} \rightarrow S$	$F_A = 0$	3	$\frac{1}{2}^3 (1+0) = .125$
$Z \leftarrow D \leftarrow A \leftarrow \textcircled{I} \rightarrow S$	$F_I = 0$	4	$\frac{1}{2}^4 (1+0) = .0625$
$\Sigma =$			1.125

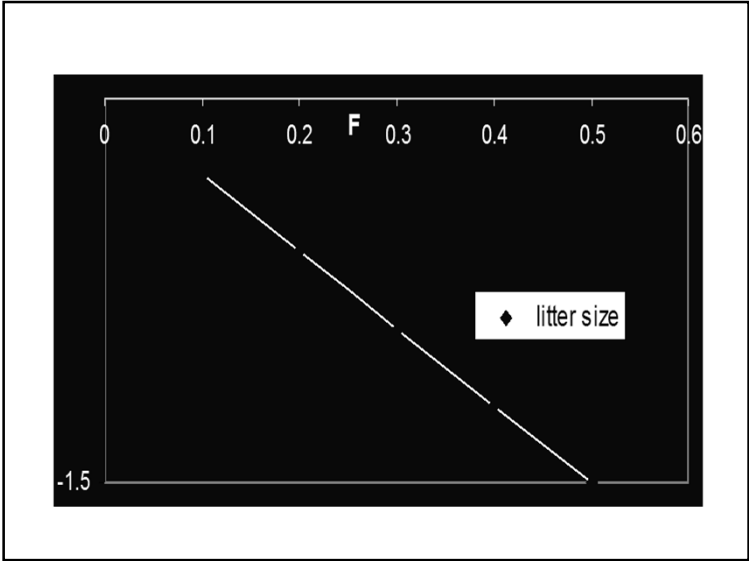
$$R_{ZS} = \frac{1.125}{\sqrt{(1+.5)(1+.25)}} = .8216$$

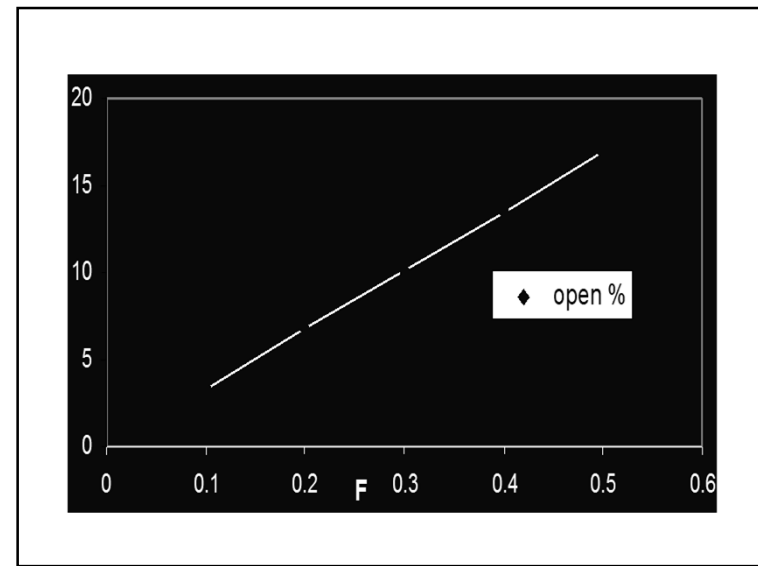
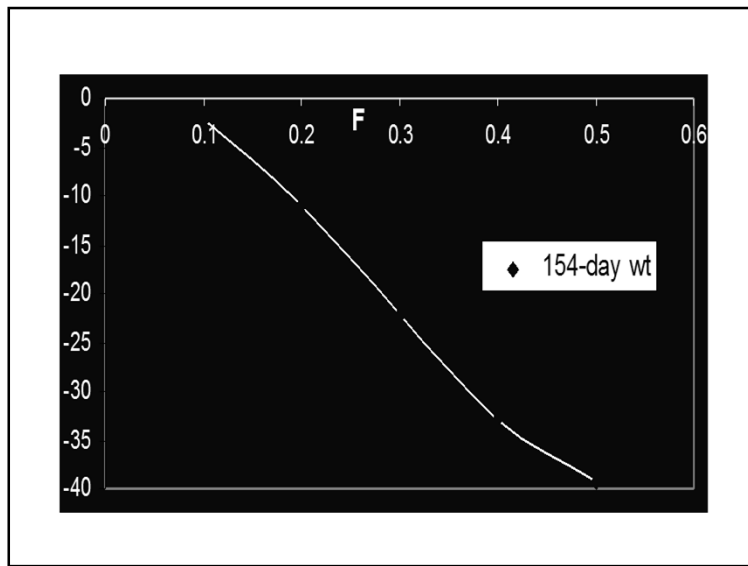
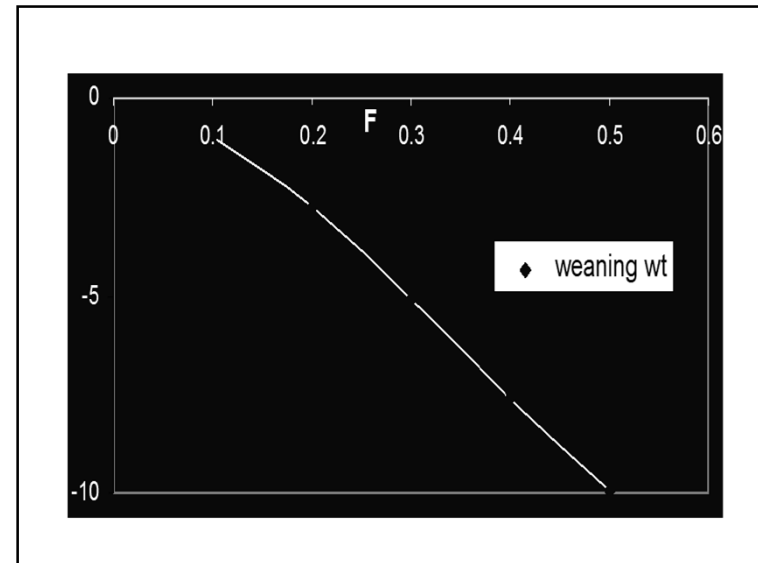
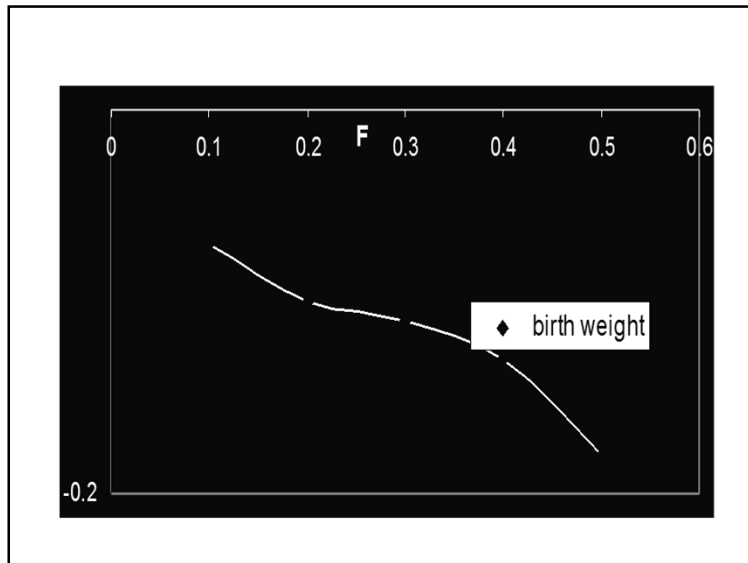
Phenotypic effects of inbreeding

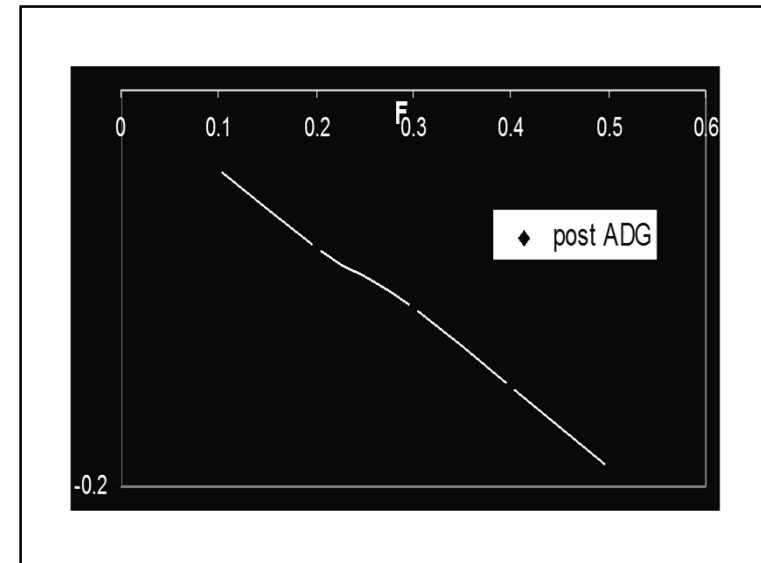
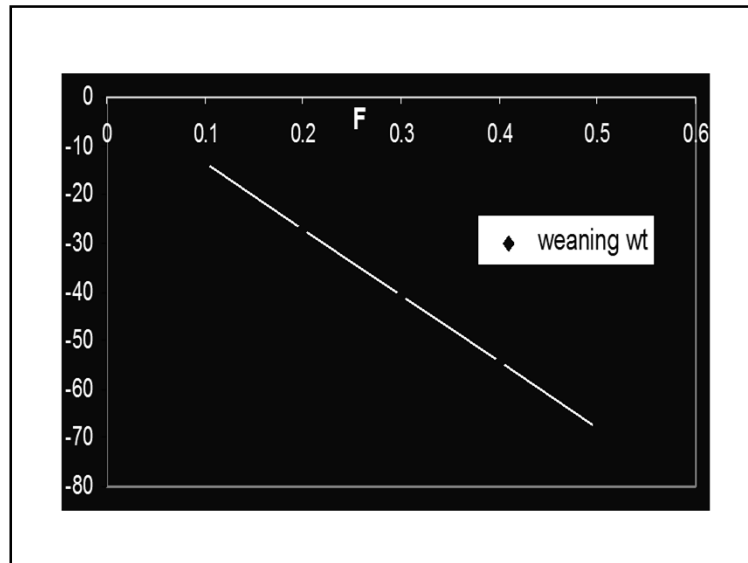
- increased homozygosity
- leads to more homozygotes
- recessive homozygotes tend to be inferior
- large loss in reproduction and livability
- some loss in growth and efficiency
- little loss in carcass merit

Phenotypic effects of inbreeding

- ↓ litter size
- ↓ libido
- ↓ sperm count
- ↓ conception rate
- ↓ survival rate
- ↓ ovulation rate
- ↑ rebreeding interval
- ↓ growth





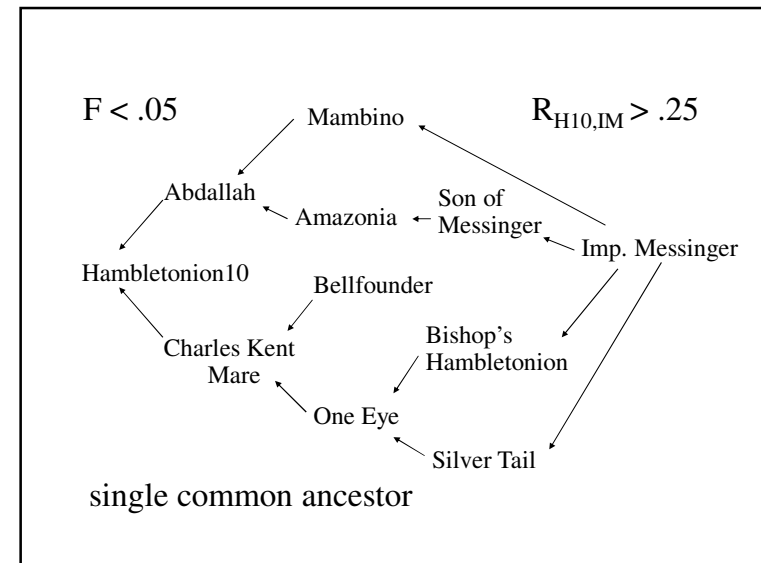


Linebreeding

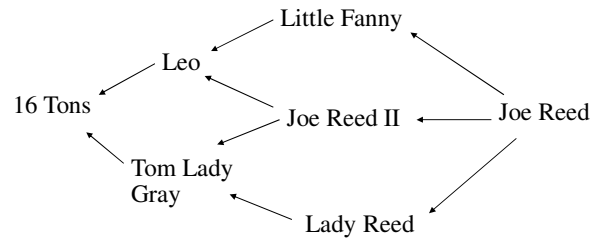
pedigrees constructed so that

F < .1
R > .25 to a single common ancestor

single common ancestor appears several times > 3 generations back



F too high more than one common ancestor



Linebreeding

dangers of linebreeding

inbreeding will build up

may linebreed to inferior son of
outstanding ancestor

ideals may change

Linebreeding

who should linebreed?

Outstanding purebred herd
hard to find breeding stock to
improve the herd

Clearly identified outstanding ancestor

Good knowledge of pedigrees and
inbreeding

Avoidance of inbreeding

need to keep inbreeding at low level

$F > .1$ time to think about it

$F > .2$ time to worry about it

producers should not actively pursue
inbreeding

Avoidance of inbreeding

avoid mating close relatives
nothing closer than cousins

keep ratio of males / females high

keep replacements from several families

avoid bottlenecks (period of reduced
census number) .