

# Variance and Inbreeding

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# Assumption

- ▶ Variance of breeding value  $u_i$ :  $\text{var}(u_i) = (A)_{ii}\sigma_u^2$
- ▶ Diagonal elements of numerator relationship matrix  $A$

$$(A)_{ii} = (1 + F_i)$$

where

$F_i$     inbreeding coefficient of animal  $i$   
 $\sigma_u^2$     genetic additive variance

- ▶ The higher  $F_i$ , the higher the similarity, the higher the variance

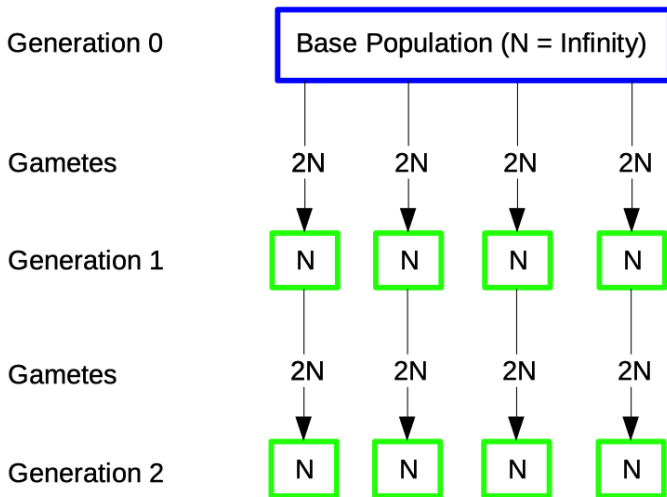
→ Contradiction?

# Variance and Inbreeding

- ▶ Relationship between variance and inbreeding
- ▶ How does inbreeding affect the genetic variance?
- ▶ How do we get inbreeding in a population?

→ Population separates into different lines

# Population with Inbreeding



# Assumptions

- ▶  $N$  individuals
- ▶ self-fertilizing, shedding constant rate of eggs and sperm
- ▶ at a given locus: alleles in base population are non-identical by descent
- ▶  $N$  individuals produce  $2N$  gametes (eggs and sperm) at constant rate
- ▶ probability that a pair of gametes taken at random carry identical alleles:  $1/2N$
- ▶ probability corresponds to the **inbreeding coefficient** ( $F$ )

# Inbreeding Coefficient

- ▶ In generation 1:

$$F_1 = \frac{1}{2N}$$

- ▶ second generation
  - ▶ either de-novo match of alleles or
  - ▶ the same alleles from generation 1

$$F_2 = \frac{1}{2N} + \left(1 - \frac{1}{2N}\right) * F_1$$

- ▶ new variable  $\Delta F = \frac{1}{2N}$ , then

$$F_2 = \Delta F + (1 - \Delta F) * F_1$$

## Inbreeding Coefficient II

- ▶ Generation  $t$ :  $F_t = \Delta F + (1 - \Delta F) * F_{t-1}$
- ▶ Solving for  $\Delta F$

$$\Delta F = \frac{F_t - F_{t-1}}{1 - F_{t-1}}$$

- ▶ Panmictic Index  $P = 1 - F$

$$\frac{P_t}{P_{t-1}} = 1 - \Delta F$$

$$P_t = (1 - \Delta F)^t * P_0 \text{ with } P_0 = 1$$

$$F_t = 1 - (1 - \Delta F)^t$$

# Variance of Gene Frequency

- ▶ Allele frequencies ( $p$  and  $q$ ) no longer constant in lines  $\rightarrow$  variation
- ▶ Variance of change of  $q$  (same for  $p$ )

$$\sigma_{\Delta q}^2 = \frac{p_0 q_0}{2N} = p_0 q_0 \Delta F$$

- ▶ Variance of  $q$  (same for  $p$ )

$$\sigma_q^2 = p_0 q_0 F$$



# Genotype Frequencies

- ▶ Average genotype frequency of homozygotes across all lines:  $\bar{q}^2$
- ▶ Definition of variance

$$\sigma_q^2 = \bar{q}^2 - \bar{q}^2$$

where  $\bar{q}$  is the mean allele frequency across all lines and hence is the same as  $q_0$  in the base population

- ▶ Therefore

$$\bar{q}^2 = q_0^2 + \sigma_q^2 = q_0^2 + p_0 q_0 F$$

## Genotype Frequencies II

Table 1: Genotype Frequencies for a bi-allelic locus, expressed in terms of inbreeding coefficient  $F$

Genotype	Original Frequencies	Changes due to inbreeding
$A_1A_1$	$p_0^2$	$+p_0q_0F$
$A_1A_2$	$2p_0q_0$	$-2p_0q_0F$
$A_2A_2$	$q_0^2$	$+p_0q_0F$

## Changes of Mean Value

Table 2: Derivation of Inbreeding Depression

Genotype	Frequency	Value	Product
$A_1A_1$	$\bar{p}^2 + \bar{p}\bar{q}F$	$a$	$(\bar{p}^2 + \bar{p}\bar{q}F)a$
$A_1A_2$	$2\bar{p}\bar{q} - 2\bar{p}\bar{q}F$	$d$	$(2\bar{p}\bar{q} - 2\bar{p}\bar{q}F)d$
$A_2A_2$	$\bar{q}^2 + \bar{p}\bar{q}F$	$-a$	$-(\bar{q}^2 + \bar{p}\bar{q}F)a$

## Inbreeding Depression

$$\begin{aligned}M_F &= (\bar{p}^2 + \bar{p}\bar{q}F)a + (2\bar{p}\bar{q} - 2\bar{p}\bar{q}F)d - (\bar{q}^2 + \bar{p}\bar{q}F)a \\&= a(\bar{p} - \bar{q}) + 2d\bar{p}\bar{q} - 2d\bar{p}\bar{q}F \\&= a(\bar{p} - \bar{q}) + 2d\bar{p}\bar{q}(1 - F) \\&= M_0 - 2d\bar{p}\bar{q}F\end{aligned}$$

# Changes of Variance

- ▶ Only additive locus
- ▶ Within line: as before

$$\begin{aligned}V_{\bar{G}} &= 2(\bar{p}\bar{q})a^2 \\&= 2p_0q_0(1 - F) \\&= V_G(1 - F)\end{aligned}$$

- ▶ New variance component: between line

$$\text{var}(M) = \sigma_M^2 = 4a^2\sigma_q^2 = 4a^2p_0q_0F = 2FV_G$$

# Summary

Table 3: Partitioning of the variance in a population with inbreeding coefficient  $F$

Source	Variance
Between lines	$2FV_G$
Within lines	$(1 - F)V_G$
Total	$(1 + F)V_G$