# Mean and Variance of a Quantitative Trait in Outbred and Inbred Populations

# General Expression for Quantitative Traits for Multi-allelic Locus

- For an arbitrary number of alleles at a locus, the genetic value for genotype $A_i A_j$ can be written as

$$G_{ij} = \mu_G + \alpha_i + \alpha_j + \delta_{ij}$$

and values assigned to the coefficients are:

$$\mu_G = \sum_i \sum_j p_i p_j G_{ij} = G_{..}$$

$$\alpha_i = \sum_j p_j G_{ij} - \mu_G = G_{i.} - G_{..}$$

$$\delta_{ij} = G_{ij} - \mu_G - \alpha_i - \alpha_j = G_{ij} - G_{i.} - G_{j.} + G_{..}$$

- Show that $\sum_i p_i \alpha_i = 0$ and $\sum_i p_i \delta_{ij} = 0$

# Mean Trait Value in Inbred Populations

- We previously derived expression for the mean and the variance of a quantitative trait in outbred populations for a single causal genetic locus. We will now focus on deriving these expressions in populations that are inbred.
- Finding the first two moments (the means and variances) for quantitative trait values in inbred populations proceeds by tracing the relevant genes back to genes in a reference (or founder) population.
- For a single-locus trait this requires the inbreeding coefficient that we introduced and discussed in the previous lecture.
- For a random member of a population inbred to an extent $F$ relative to the reference population, the genotype frequencies at a multi-allelic locus are

$$P_{ii} = p_i^2 + Fp_i(1 - p_i)$$

$$P_{ij} = 2p_i p_j(1 - F)$$

- What is the expected trait value for this population.

# Mean Trait Value in Inbred Populations

- The expected trait value for an individual with inbreeding coefficient $F$ is

$$
\begin{aligned}
\mu_{G_F} &= \sum_i \sum_j P_{ij}(\mu_G + \alpha_i + \alpha_j + \delta_{ij}) \\
&= \sum_i [p_i^2 + Fp_i(1 - p_i)](\mu_G + 2\alpha_i + \delta_{ii}) \\
&+ \sum_{i \neq j} [p_i p_j (1 - F)](\mu_G + \alpha_i + \alpha_j + \delta_{ij}) \\
&= \sum_i [p_i^2(1 - F) + Fp_i](\mu_G + 2\alpha_i + \delta_{ii}) \\
&+ \sum_{i \neq j} [p_i p_j (1 - F)](\mu_G + \alpha_i + \alpha_j + \delta_{ij})
\end{aligned}
$$

# Mean Trait Value in Inbred Populations

$$= F\sum_i p_i(\mu_G + 2\alpha_i + \delta_{ii})$$

$$+(1-F)\sum_i\sum_j p_i p_j(\mu_G + \alpha_i + \alpha_j + \delta_{ij})$$

$$= F(\mu_G + \sum_i p_i\delta_{ii}) + (1-F)(\mu_G)$$

$$= \mu_G + FH$$

where $H = \sum_i p_i\delta_{ii}$ and the $\delta_{ij}$ terms are the same as in the non-inbreeding case.

- So the mean trait value in an inbred population is $\mu_{G_F} = \mu_G + FH$
- $\mu_{G_F}$ changes with the degree of inbreeding in the population and the degree of dominance for the trait.

# Inbreeding Depression

- Remember that for the two-allelic case we have the following dominance effects:
  - $\delta_{11} = -2q^2 d$
  - $\delta_{12} = 2pqd$
  - $\delta_{22} = -2p^2 d$
- Assume that there is some dominance for the trait, e.g., $d > 0$. What effect would we expect this have on the mean trait values in inbred populations relative to outbred populations?
- What about if there is no dominance e.g., $d = 0$?
- The decline in the mean phenotype with increasing homozygosity within populations is known as **inbreeding depression**
- Inbred individuals are almost always less fit than progeny of nonrelatives

# Trait Value Moments in Inbred Populations

- We derived an expression for the first moment (the mean) for the trait value distribution in an inbreed population.
- To obtain the trait variance, we need to obtain the second moment, which is the expected value of the square of the linear model for the trait values.
- Using a similar approach used to obtain the first moment, we will now obtain the second moment.

# Genetic Variance of Trait Values in Inbred Populations

- For a random member of a population inbred to an extent $F$ relative to the reference population, the genotype frequencies are

$$P_{ii} = p_i^2 + Fp_i(1-p_i)$$

$$P_{ij} = 2p_ip_j(1-F)$$

- So we have that

$$E(G_F^2) = \sum_i \sum_j P_{ij}(\mu_G + \alpha_i + \alpha_j + \delta_{ij})^2$$

$$= \sum_i [p_i^2 + Fp_i(1-p_i)](\mu_G + 2\alpha_i + \delta_{ii})^2$$

$$+ \sum_{i \neq j} [p_ip_j(1-F)](\mu_G + \alpha_i + \alpha_j + \delta_{ij})^2$$

# Genetic Variance of Trait Values in Inbred Populations

$$= \sum_i [p_i^2(1-F) + Fp_i](\mu_G^2 + 4\alpha_i^2 + \delta_{ii}^2 + 4\mu_G\alpha_i + 2\mu_G\delta_{ii} + 4\alpha_i\delta_{ii})$$

$$+ \sum_{i \neq j} [p_i p_j (1-F)](\mu_G^2 + \alpha_i^2 + \alpha_j^2 + \delta_{ij}^2 + 2\mu_G\alpha_i + 2\mu_G\alpha_j$$

$$+ 2\mu_G\delta_{ij} + 2\alpha_i\alpha_j + 2\alpha_i\delta_{ij} + 2\alpha_j\delta_{ij})$$

$$= \sum_i Fp_i(\mu_G^2 + 4\alpha_i^2 + \delta_{ii}^2 + 4\mu_G\alpha_i + 2\mu_G\delta_{ii} + 4\alpha_i\delta_{ii})$$

$$+ \sum_i \sum_j [p_i p_j (1-F)](\mu_G^2 + \alpha_i^2 + \alpha_j^2 + \delta_{ij}^2 + 2\mu_G\alpha_i + 2\mu_G\alpha_j$$

$$+ 2\mu_G\delta_{ij} + 2\alpha_i\alpha_j + 2\alpha_i\delta_{ij} + 2\alpha_j\delta_{ij})$$

# Genetic Variance of Trait Values in Inbred Populations

- Let's focus on the first summand involving $F$
- Recall that we previously showed that $\sum_i p_i \alpha_i = 0$ and $\sum_i p_i \delta_{ij} = 0$. So

$$F\left(\mu_G^2 + 4\sum_i p_i \alpha_i^2 + \sum_i p_i \delta_{ii}^2 + 4\mu_G \sum_i p_i \alpha_i \right.$$

$$\left. + 2\mu_G \sum_i p_i \delta_{ii} + 4\sum_i p_i \alpha_i \delta_{ii} \right)$$

$$= F\left(\mu_G^2 + 4\sum_i p_i \alpha_i^2 + \sum_i p_i \delta_{ii}^2 + 2\mu_G \sum_i p_i \delta_{ii} + 4\sum_i p_i \alpha_i \delta_{ii}\right)$$

# Genetic Variance of Trait Values in Inbred Populations

- Now focus on the second summand involving $1 - F$

$$\sum_i \sum_j [p_i p_j (1-F)](\mu_G^2 + \alpha_i^2 + \alpha_j^2 + \delta_{ij}^2 + 2\mu_G \alpha_i + 2\mu_G \alpha_j$$

$$+2\mu_G \delta_{ij} + 2\alpha_i \alpha_j + 2\alpha_i \delta_{ij} + 2\alpha_j \delta_{ij})$$

- Simplify this term using $\sum_i p_i \alpha_i = 0$ and $\sum_i p_i \delta_{ij} = 0$.

# Genetic Variance of Trait Values in Inbred Populations

$$= (1-F)\Bigg(\mu_G^2 + \sum_i\sum_j p_i p_j \alpha_i^2 + \sum_i\sum_j p_i p_j \alpha_j^2$$

$$+ \sum_i\sum_j p_i p_j \delta_{ij}^2 + 2\mu_G \sum_i\sum_j p_i p_j \alpha_i + 2\mu_G \sum_i\sum_j p_i p_j \alpha_j$$

$$+ 2\mu_G \sum_i\sum_j p_i p_j \delta_{ij} + 2\sum_i\sum_j p_i p_j \alpha_i \alpha_j + 2\sum_i\sum_j p_i p_j \alpha_i \delta_{ij}$$

$$+ 2\sum_i\sum_j p_i p_j \alpha_j \delta_{ij}\Bigg)$$

# Genetic Variance of Trait Values in Inbred Populations

$$= (1-F)\left(\mu_G^2 + \sum_j p_j \sum_i p_i \alpha_i^2 + \sum_i p_i \sum_j p_j \alpha_j^2\right.$$

$$+ \sum_i \sum_j p_i p_j \delta_{ij}^2 + 2\mu_G \sum_j p_j \sum_i p_i \alpha_i + 2\mu_G \sum_i p_i \sum_j p_j \alpha_j$$

$$+ 2\mu_G \sum_i p_i \sum_j p_j \delta_{ij} + 2\sum_i p_i \alpha_i \sum_j p_j \alpha_j + 2\sum_i p_i \alpha_i \sum_j p_j \delta_{ij}$$

$$\left. + 2\sum_j p_j \alpha_j \sum_i p_i \delta_{ij}\right)$$

$$= (1-F)\left(\mu_G^2 + 2\sum_i p_i \alpha_i^2 + \sum_i \sum_j p_i p_j \delta_{ij}^2\right)$$

# Genetic Variance of Trait Values in Inbred Populations

- Combining the simplified two terms together we have that

$$
\begin{aligned}
E(G_F^2) = F\Bigg(\mu_G^2 + 4\sum_i p_i\alpha_i^2 + \sum_i p_i\delta_{ii}^2 + \\
2\mu_G\sum_i p_i\delta_{ii} + 4\sum_i p_i\alpha_i\delta_{ii}\Bigg) \\
+(1-F)\left(\mu_G^2 + 2\sum_i p_i\alpha_i^2 + \sum_i\sum_j p_i p_j\delta_{ij}^2\right) \\
= \mu_G^2 + 2(1+F)\sum_i p_i\alpha_i^2 + (1-F)\sum_i\sum_j p_i p_j\delta_{ij}^2 \\
+F\sum_i p_i\delta_{ii}^2 + 4F\sum_i p_i\alpha_i\delta_{ii} + 2F\mu_G\sum_i p_i\delta_{ii}
\end{aligned}
$$

# Genetic Variance of Trait Values in Inbred Populations

- So
$$E(G_F^2) = \mu_G^2 + 2(1+F)\sum_i p_i\alpha_i^2 + (1-F)\sum_i\sum_j p_i p_j \delta_{ij}^2$$
$$+F\sum_i p_i\delta_{ii}^2 + 4F\sum_i p_i\alpha_i\delta_{ii} + 2F\mu_G\sum_i p_i\delta_{ii}$$
- Now calculate the variance of $G_F$ noting that $E(G_F) = \mu_G + FH$ where $H = \sum_i p_i\delta_{ii}$

# Genetic Variance of Trait Values in Inbred Populations

- We have that

$$Var(G_F) = E(G_F^2) - [E(G_F)]^2 =$$

$$(1+F)2\sum_i p_i\alpha_i^2 + (1-F)\sum_i\sum_j p_i p_j \delta_{ij}^2$$

$$+F\sum_i p_i\delta_{ii}^2 + 4F\sum_i p_i\alpha_i\delta_{ii} - F^2H^2$$

$$= (1+F)\sigma_A^2 + (1-F)\sigma_D^2 + 4FD_1 + FD_2 + F(1-F)H^2$$

  where $H = \sum_i p_i\delta_{ii}$, $D_1 = \sum_i p_i\alpha_i\delta_{ii}$, and $D_2 = \sum_i p_i\delta_{ii}^2 - H^2$. Note that $D_2$ is the variance of the $\delta_{ii}$'s

- So the genetic variance for an inbreed populations can be written in terms of five components
- For a non-inbreed population, $F = 0$ and the genetic variance is $\sigma_A^2 + \sigma_D^2$, as we previously showed.

# Terminology and Expressions for Genetic Trait Variance

- The following terms are commonly used for expressing the variances and covariances of trait values

| Components | Multi-allelic | Bi-allelic |
|---|---|---|
| Additive Variance | $\sigma_A^2 = 2\sum_i p_i \alpha_i^2$ | $\sigma_A^2 = 2pq\alpha^2$ |
| Dominance Variance | $\sigma_D^2 = \sum_i \sum_j p_i p_j \delta_{ij}^2$ | $\sigma_D^2 = (2pqd)^2$ |
| Inbreeding depression | $H = \sum_i p_i \delta_{ii}$ | H=-2qpd |
| Covariance of $\alpha_i$'s and $\delta_{ii}$'s | $D_1 = \sum_i p_i \alpha_i \delta_{ii}$ | $D_1 = 2pqd\alpha(p-q)$ |
| Variance of $\delta_{ii}$'s | $D_2 = \sum_i p_i \delta_{ii}^2 - H^2$ | $D_2 = 4pq(1-4pq)d^2$ |

  where $\alpha = \alpha_1 - \alpha_2$ for the bi-allelic case.
- For the bi-allelic case, if the frequency of the two alleles are the same, what is $D_1$ and $D_2$?
- For the bi-allelic case, if the trait is additive, what is $H$, $D_1$, and $D_2$?