II. Genetic effects and variance components

2. Genotypic Effects – one locus model

Phenotype (P) – what we observed and measured that is determined by the genetic make up, environment and genotype-environment interaction

\[ P = G + E + GE \]

Genotype (G) – sum of all genetic effects of genes \( E(G) = \text{Mean genotypic value} \)

Environment (E) – All non-genetic effects \( E(E) = 0 \)

GE - Genotype-Environment interaction \( E(GE) = 0 \)

So with very precise tests and sampled unlimited environments: \( P \cong G \)

Genotypic effects - one locus model

\[
\begin{array}{ccc}
A2A2 & MP & A1A1 \\
-a & 0 & +a \\
\end{array}
\]

\( d = 0 \)  No dominance

\[
\begin{array}{ccc}
A2A2 & MP & A1A2 & A1A1 \\
-a & 0 & d & +a \\
\end{array}
\]

\( d < a \)  Partial dominance

\[
\begin{array}{ccc}
A2A2 & MP & A1A1 \\
-a & 0 & +a \\
\end{array}
\]

\( d = a \)  Complete dominance
**Genetic value**: breeding value + dominance deviation

\[ G = A + D \]

It is the value of a tree’s genes to itself. Genetic value is not transmitted to a progeny because only one of the genes is given to a progeny.

**Average Effect**: Average effect of the gene substitution, i.e., the mean change due to changing A2 genes chosen at random into A1 genes.

**Breeding value (BV)**: A value associated with the genes carried by the individual and transmitted to its offspring. Breeding value is sum of average effects of genes.

Theoretical: For a single locus, the breeding value is \( 2 \times \text{average effect of the gene substitution} \).

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Breeding Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>A1A1</td>
<td>2q \alpha</td>
</tr>
<tr>
<td>A1A2</td>
<td>(q-p) \alpha</td>
</tr>
<tr>
<td>A2A2</td>
<td>2p \alpha</td>
</tr>
</tbody>
</table>

For multiple loci, the breeding value of an individual is the sum of the average effects of the genes it carries.

Practical: An individual’s breeding value is usually measured by the mean value of its progeny because it is impossible to measure the average effects of the genes it
carries. If an individual is mated to a number of individuals taken at random from the population, then its breeding value is twice the mean deviation of the progeny from the population mean. The deviation has to be doubled because the parent provides only half of the genes in the progeny, the other half coming at random from the population.

Breeding value is a property of the individual and the mating population.

BV is due to additive genetic effects of genes, A, a component of the genotypic value, G.

The difference between the genotypic value G and the BV (additive genetic effects) A is the Dominance deviation.

\[ D = G - A \]

Dominance deviation is due to interaction between alleles within locus; the effect of combining genes together that cannot account for by the effects of two single genes. Dominance deviation is also depending on the gene frequencies in the population, i.e., a property of the individual and the mating population. Thus, \[ G = A + D \]

Genotypic value=breeding value + dominance value.
3. Partitioning total genetic variance - One locus model

Genetic variance ($V_G$) is sum of additive ($V_A$) and non-additive genetic variances ($V_D$).

$$V_G = V_A + V_D$$

Values of genotypes in a two-allele system, measured as deviations from the population mean.

Population mean: $M = a(p-q)+2dpq$

Average effect of the gene substitution: $\alpha = a + d(q-p)$

<table>
<thead>
<tr>
<th>Genotypes</th>
<th>A1A1</th>
<th>A1A2</th>
<th>A2A2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Frequencies</td>
<td>$p^2$</td>
<td>$pq$</td>
<td>$q^2$</td>
</tr>
<tr>
<td>Assigned values</td>
<td>$a$</td>
<td>$d$</td>
<td>$-a$</td>
</tr>
</tbody>
</table>

Deviation from population mean

| Genotypic value | $2q(a-pd)$ | $a(q-p)+d(1-2pq)$ | $-2p(a-qd)$ |
| Dominance deviation | $2pq\alpha$ | $(q-p)\alpha+2pqd)$ | $-2p\alpha$ |

$$V_A = 4p^2q^2\alpha^2 + 2pq(q-p)^2\alpha^2 + 4p^2q^2\alpha^2$$

$$= 2pq\alpha^2(2pq+q^2-2pq+p^2 +2pq)$$

$$= 2pq\alpha^2(p^2 +2pq+ q^2)$$

$$= 2pq\alpha^2$$

$$= 2pq[(a-d(q-p))^2$$

$$V_D = d^2(4q^4p^2q^2+8p^3q^3+4p^4q^2)$$

$$= 4d^2p^2q^2(q^2-2pq+p^2)$$

$$= (2pqd)^2$$

$$V_G = V_D + V_D = 2pq[a+d(q-p)^2+[2pqd]^2$$
4. Partitioning total genetic variance - Multiple loci model

\[ G_T = G_1 + G_2 + G_3 + G_{123} \]
\[ G_1 = A_1 + D_1 \]
\[ G_2 = A_2 + D_2 \]
\[ G_3 = A_3 + D_3 \]
\[ I_{123} = A_1A_2 + A_1A_2A_3 + A_1D_1 + A_2D_1 + D_1D_2 + D_1D_2D_3 + \ldots \]

The interaction I is due to interactions of alleles from different loci, defined as epistatic deviation or epistasis genetic effect. Loci may interact in pairs or in three or higher numbers but all treated as single I deviation. Thus genotypic value for multiple loci is:

\[ G = A + D + I \]

Where \( A = A_1 + A_2 + A_3 \)
\[ A = D_1 + D_2 + D_3 \]

Partitioning total genetic variance

\[ V_A = V_{A_1} + V_{A_2} + V_{A_3} + \ldots \]
\[ V_D = V_{D_1} + V_{D_2} + V_{D_3} + \ldots \]

Epistasis effects-interaction between different loci

\[ V_I = V_{AA} + V_{AD} + V_{DD} + \ldots \]

Total genetic variance for multiple loci

\[ V_G = V_A + V_D + V_I \]

Total Phenotypic variance

\[ V_P = V_A + V_D + V_I + V_E + V_{GE} \]