Building blocks of quantitative genetics

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Basis of inheritance

Diploid parents

Meiosis

Haploid gametes (sperm and egg)

Fertilization

Diploid offspring

Basic quantitative genetics
Polygenic model

As the number of genes controlling a trait increases, the distribution of genetic effects becomes more normal.

Quantitative traits are assumed to be controlled by genes at many loci: the polygenic model.

Polygenic effects are the action and interaction of genes at a large number of loci, each with small effect.

Distributions of genetic effects

1 locus, 2 alleles / locus

2 loci, 2 alleles / locus

5 loci, 2 alleles / locus

150 loci, 2 alleles / locus
Phenotypic variation

\[ P = G + E \]

\[ V_P = V_G + V_E \]

Many loci, Genetic value \( G: \)

Environmental deviation \( E: \)

Phenotype, \( P = G + E: \)

\[ \sigma_P = \sigma_G + \sigma_E \]

Basic quantitative genetics

\[ h^2 = 0.1 \]

<table>
<thead>
<tr>
<th></th>
<th>( V_P )</th>
<th>( \sigma_P )</th>
<th>( V_A )</th>
<th>( \sigma_A )</th>
<th>( V_E )</th>
<th>( \sigma_E )</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>0.030</td>
<td>0.173</td>
<td>0.003</td>
<td>0.054</td>
<td>0.027</td>
<td>0.164</td>
</tr>
</tbody>
</table>

Basic quantitative genetics
Breeding value versus genetic value

\[ P = G + E \]
\[ P = A + NA + E \]

Genetic value (G)
- Value of genes to self

Breeding value (A)
- Value of genes to progeny

Difference (G-A)
- Non-additive effects e.g. dominance
Breeding value

Breeding values = the sum of the average effect of alleles ($\alpha$)

Example
- Single locus model;
  - Genotypic values are $G_{A2A2} = -20$, $G_{A1A2} = 0$, $G_{A1A1} = 20$
  - $p=q=0.5$
- An $A1$ gamete will meet an $A1$ or $A2$ gamete at equal frequency
- Progeny are thus $0.5 \times A1A1$ and $0.5 \times A1A2$
- The average value of the progeny is $0.5 \times -20 + 0.5 \times 0 = -10$
- Thus $\alpha_{A1} = -10$ units
- Similarly $\alpha_{A2} = 10$ units

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No dominance, $p=q=0.5$

<table>
<thead>
<tr>
<th>Genotype</th>
<th>$A2A2$</th>
<th>$A1A2$</th>
<th>$A1A1$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Value</td>
<td>280</td>
<td>300</td>
<td>320</td>
</tr>
<tr>
<td>Frequency</td>
<td>0.25</td>
<td>0.50</td>
<td>0.25</td>
</tr>
<tr>
<td>Pop’n mean</td>
<td>300</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Genetic value</td>
<td>-20</td>
<td>0</td>
<td>20</td>
</tr>
<tr>
<td>Breeding value</td>
<td>-20</td>
<td>0</td>
<td>20</td>
</tr>
</tbody>
</table>

$\alpha_{A1} = 10$
$\alpha_{A2} = -10$

- With no dominance the genetic and breeding values are equal.
- With equal allele frequency the average effects of $A1$ and $A2$ are of equal magnitude
Some dominance, p=q=0.5

<table>
<thead>
<tr>
<th>Genotype</th>
<th>$A_2A_2$</th>
<th>$A_1A_2$</th>
<th>$A_1A_1$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Value</td>
<td>280</td>
<td>310</td>
<td>320</td>
</tr>
<tr>
<td>Frequency</td>
<td>0.25</td>
<td>0.50</td>
<td>0.25</td>
</tr>
<tr>
<td>Pop'n mean</td>
<td>305</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Genetic value</td>
<td>-25</td>
<td>5</td>
<td>15</td>
</tr>
<tr>
<td>Breeding value</td>
<td>-20</td>
<td>0</td>
<td>20</td>
</tr>
</tbody>
</table>

$\alpha_{A1} = 10$

$\alpha_{A2} = -10$

- With some dominance the genetic and breeding values differ.
- Dominance deviation is excluded from the breeding value.

Basic quantitative genetics

p=0.1, q=0.9, No dominance

<table>
<thead>
<tr>
<th>Genotype</th>
<th>$A_2A_2$</th>
<th>$A_1A_2$</th>
<th>$A_1A_1$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Value</td>
<td>280</td>
<td>300</td>
<td>320</td>
</tr>
<tr>
<td>Frequency</td>
<td>0.81</td>
<td>0.18</td>
<td>0.01</td>
</tr>
<tr>
<td>Pop'n mean</td>
<td>284</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Genetic value</td>
<td>-4</td>
<td>16</td>
<td>36</td>
</tr>
<tr>
<td>Breeding value</td>
<td>-4</td>
<td>16</td>
<td>36</td>
</tr>
</tbody>
</table>

$\alpha_{A1} = 18$

$\alpha_{A2} = -2$

- With unequal allele frequencies the average effects of $A1$ and $A2$ are of different magnitude.
- The average effect of an allele is greater if the allele is rare.

Basic quantitative genetics
Important points

Breeding values are expressed as a deviation of the population mean (with the population mean dependent on genotypic values and frequencies)

With no dominance \( G=A \), with dominance \( G \neq A \)

Animals with a rare allele will have a larger (either positive or negative) breeding value

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Breeding values and can be used to predict progeny performance

- Using example 1 from before:
  - Genotypic values are \( G_{A1A1} = 20 \), \( G_{A1A2} = 0 \), \( G_{A2A2} = -20 \)
  - \( p=q=0.5 \)

- Genetic value of offspring from an A1A1 sire is

\[
G_o = \frac{A + 0}{2} = \frac{20}{2} = +10
\]

- Check:
  - sire passes on A1, dams have equal frequency of A1 & A2,
  - progeny are equally A1A1 and A1A2, and \((20 \times 0.5 + 0 \times 0.5) = 10\)
Breeding values can be used to predict progeny performance

- Using example 3 from before:
  - Genotypic values are $G_{A1A1} = 36$, $G_{A1A2} = 16$, $G_{A2A2} = -4$
  - $p=0.1$ and $q=0.9$
  - Average effect of $A1 = 18$, of $A2 = -2$

- Genetic value of offspring from an $A1A2$ sire is

$$G_o = \frac{A + 0}{2} = \frac{16}{2} = +8$$

- Check:
  - Sire passes on $A1$ and $A2$ in equal frequency, dams have frequency of $A1 = 0.1$ & $A2 = 0.9$,
  - Progeny are $0.5 (0.1 A1A1 + 0.9 A1A2) + 0.5 (0.1 A2A1 + 0.9 A2A2) = 0.5 (0.1 \times 36 + 0.9 \times 16) + 0.5 (0.1 \times 16 + 0.9 \times -4) = 8$

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Breeding values are halved when used to predict progeny performance

- As breeding value represents the sum of the average effect of two alleles,

- Only one of which is passed on.
Realised vs expected BVs

Realised BVs

- are calculated from progeny performance
- $BV = 2 \times (\text{progeny mean} - \text{population mean})$

Expected BVs

- calculated from knowledge of genotypic values and allele frequencies

These differ because

- Allele frequencies vary from expected, especially for small progeny group sizes
- Effect of environment - expectation of environmental effect is 0, but this is unlikely to be realised for small progeny group sizes.

<table>
<thead>
<tr>
<th>Genotypic Value</th>
<th>$\alpha_{A1}$</th>
<th>$\alpha_{A2}$</th>
<th>$\alpha_{A3}$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Value</td>
<td>200</td>
<td>300</td>
<td>500</td>
</tr>
<tr>
<td>Frequency</td>
<td>0.20</td>
<td>0.47</td>
<td>0.33</td>
</tr>
<tr>
<td>Pop's mean</td>
<td>300</td>
<td>300</td>
<td>300</td>
</tr>
<tr>
<td>Genetic value</td>
<td>-20</td>
<td>0</td>
<td>20</td>
</tr>
<tr>
<td>Breeding value</td>
<td>-25</td>
<td>0</td>
<td>20</td>
</tr>
</tbody>
</table>

$\alpha_{A1} = 10$

$\alpha_{A3} = -10$

Basic quantitative genetics
Predicting effects

At simplest level, own phenotype can be used as the information source

\[ \hat{A} = \frac{V_A}{V_P} P \quad \hat{D} = \frac{V_D}{V_P} P \quad \hat{E} = \frac{V_E}{V_P} P \]

Breeding Value Dominance Environment

Basic quantitative genetics

Heritability

Regression of A on P is equal to heritability

\[ b_{a,p} = \frac{\text{Cov}_{a,p}}{V_P} = \frac{\text{Cov}_{A,A} + \text{Cov}_{A,N} + \text{Cov}_{A,E}}{V_P} = \frac{V_A + 0 + 0}{V_P} = \frac{V_A}{V_P} = h^2 \]

Basic quantitative genetics
Predicting progeny performance

\[ \hat{A} = \frac{V_A}{V_p} \hat{P} = h^2 \hat{P} \quad \hat{G}_o = \frac{\hat{A}_m + \hat{A}_f}{2} \]

Note \( G_o = (A_m + A_f)/2 \) because
- \( G = A + NA + E \)
- NA and E are expected to be 0 on average
- \( A = (A_m + A_f)/2 \).

Example

Ram = 90kg
Ewe = 80 kg
Average of flock = 70 kg
\( h^2 = 0.25 \)

\[ \hat{A}_{\text{ram}} = h^2 \hat{P} = 0.25 \times 20 = 5.0 \text{kg} \]
\[ \hat{A}_{\text{ewe}} = h^2 \hat{P} = 0.25 \times 10 = 2.5 \text{kg} \]
\[ \hat{G}_o = \frac{\hat{A}_{\text{ram}} + \hat{A}_{\text{ewe}}}{2} = \frac{5.0 + 2.5}{2} = 3.75 \text{kg} \]

Note that +3.75 kg is the average we expect for a large group of progeny, individuals will deviate

![Image of sheep with weights]
Why do progeny of the same parents differ?

Genetic variation within families
- each individual received a random one-half of genetic material from each parent
- Mendelian sampling effects
  - e.g. $V_{MS\text{-full sib family}} = 0.5V_A$

Environmental variation
- systematic or random chance

Extending to a QTL model

Genetic variance under a QTL model
- Few genes of large effect
- Many genes of small effect

$$V_P = V_A + V_{QTL} + V_{NA} + V_E$$