Estimating Genetic Parameters

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Estimating litter size in Merino sheep

Table 1 gives the mean litter sizes for three genotypes at the FecB gene.

Genotype	Mean Litter Size
A_1A_1	2.66
A_1A_2	2.17
A_2A_2	1.48

Table 1: Mean litter sizes for different genotypes

Question One: *If the frequency of the FecB A2 allele is 0.1, what is the mean litter size of this sheep population?*

If the frequency of the FecB A_2 allele is 0.1, then the frequency of the A_1 allele is 0.9. Let p_1 and p_2 be the frequency for the A_1 and A_2 alleles, respectively. Let V_{ij} be the mean litter size for the genotype with alleles i and j. The formula for the mean litter size (MLS) of the population is then given by:

$$MLS = p_1^2 V_{11} + p_1 p_2 V_{12} + p_2^2 V_{22} \tag{1}$$

Filling in the values for allele frequencies and mean litter size, we get

$$MLS = 0.81(2.66) + 0.18(2.17) + 0.01(1.48) = 2.56 \tag{2}$$

The mean litter size is 2.56.

Question Two: *How does the mean litter size change if the frequency of the FecB A_2 allele is quadrupled in this sheep population?*

If the frequency of the A_2 allele is now 0.4, then the frequency of A_1 is 0.6. This means that the mean litter size is given by

$$MLS = 0.36(2.66) + 0.48(2.17) + 0.16(1.48) = 2.236 \tag{3}$$

The adjusted mean litter size is then 2.236. This gives a change in mean litter size of 0.324.

Question Three: *What is the average effect for the two alleles for the two frequencies?*

In order to calculate average effects, we first need to calculate genetic deviation. Table 2 and 3 show the allele frequency, litter size, and genetic deviation for allele frequencies $p_1 = 0.9$ and $p_1 = 0.6$, respectively.

Genotype	Frequency	Mean Litter Size	Genetic Deviation
A_1A_1	0.81	2.66	0.1
A_1A_2	0.18	2.17	-0.39
A_2A_2	0.01	1.48	-1.08

Table 2: Genotype, frequency, mean litter size, and genetic deviation from the population mean for $p_1 = 0.9$

Genotype	Frequency	Mean Litter Size	Genetic Deviation
A_1A_1	0.36	2.66	0.424
A_1A_2	0.48	2.17	-0.066
A_2A_2	0.16	1.48	-0.756

Table 3: Genotype, frequency, mean litter size, and genetic deviation from the population mean for $p_1 = 0.6$

The average effect α_1 of A_1 is given by

$$\alpha_1 = p_1 Y_{11} + p_2 Y_{12} \tag{4}$$

Similarly, the average effect α_2 of A_2 is given by

$$\alpha_2 = p_1 Y_{12} + p_2 Y_{22} \tag{5}$$

The average effects for each allele with $p = 0.9$ are therfore given by

$$\begin{aligned}
\alpha_1 &= (0.9)(0.1) + (0.1)(-0.39) = 0.051 \\
\alpha_2 &= (0.9)(-0.39) + (0.1)(-1.08) = -0.459
\end{aligned} \tag{6}$$

The average effects for each allele with $p = 0.6$ are given by

$$\begin{aligned}
\alpha_1 &= (0.6)(0.424) + (0.4)(-0.066) = 0.228 \\
\alpha_2 &= (0.6)(-0.066) + (0.4)(-0.756) = -0.1908
\end{aligned} \tag{7}$$