Dynamic Variation in Disease Susceptibility

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Introduction

Gastrointestinal nematode infections in livestock affect animal health and welfare. Infection may be controlled through grazing management, anthelmintic treatment or through genetic control strategies by selecting more resistant lambs. Selective breeding relies on finding a trait indicative of resistance to infection and selecting animals based on estimated breeding values.

Genetic resistance to disease changes as the adaptive immune system develops. It is important to assess how the heritability of disease resistance changes over time. We aim to quantify seasonal changes in the heritability of resistance to *Teladorsagia* circumcinta infections in lambs.

Variance Components

For a given trait, it is assumed that phenotypic variation between animals is determined by environmental and genetic effects.

$$\begin{matrix}\text{phenotypic}\\ \text{variation}\end{matrix} = \begin{matrix}\text{environmental}\\ \text{effect}\end{matrix} + \begin{matrix}\text{genetic}\\ \text{effect}\end{matrix} + \begin{matrix}\text{residual}\\ \text{variance}\end{matrix}$$

The genetic effect includes several genetic factors, with the most important being the additive effect of the genes received from both parents. The environmental effect refers to permanent between lamb factors and the residual variance refers to any unaccounted for environmental variances.

Estimating the additive genetic variance contributes to a better understanding of the genetic mechanism and is essential for the prediction of breeding values, i.e. the value of an animal as a parent.

Heritability

Given an observation of a trait from an animal, the animal's breeding value depends on:

- How divergent the observed value is from the average value.
- How heritable the trait is.

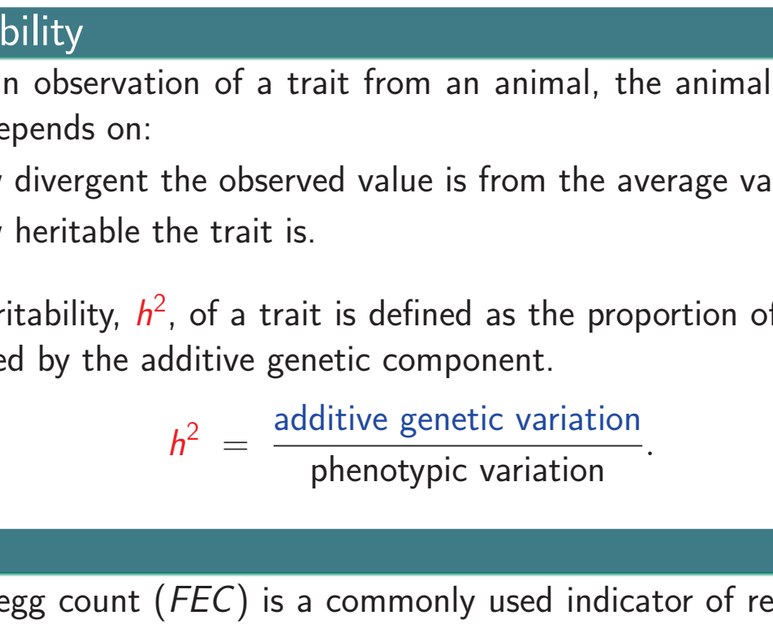
The heritability, h^2, of a trait is defined as the proportion of variability explained by the additive genetic component.

$$h^2 = \frac{\text{additive genetic variation}}{\text{phenotypic variation}}.$$

Data

Faecal egg count (*FEC*) is a commonly used indicator of resistance to nematode infection.

We have egg count data over a seven month period from *Teladorsagia* circumcinta infections of 1000 Scottish Blackface lambs from a commercial farm in South West Strathclyde.



These data are challenging to model statistically because the variance changes over time and the egg count distribution is over-dispersed.

Estimating Variance Components

Random regression models have been widely used to estimate variance components from repeated measurements, such as faecal egg counts, over time.

Fixed effects found to be significant are the *SEX* of the lamb and the *YEAR* of birth. Three random components were fitted as functions of time corresponding to the additive genetic, permanent environmental and maternal effects.

Therefore, for lamb i at time t

$$FEC_{it} = \mu + c_1 SEX_i + c_2 YEAR_i + f_\alpha(\alpha_{it}, t) + f_\gamma(\gamma_{it}, t) + f_\beta(\beta_{it}, t) + \epsilon_{it},$$

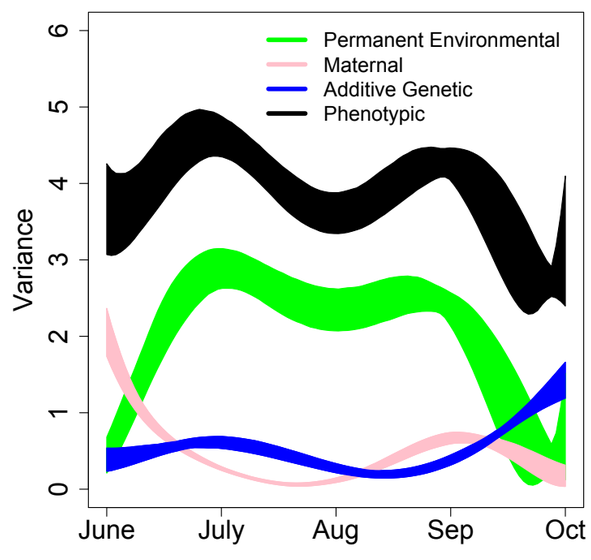
where

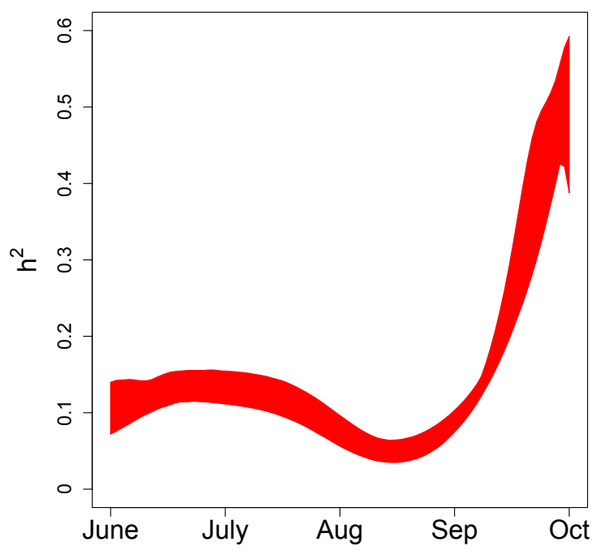
μ is an overall mean.
c_1 and c_2 are coefficients of the *SEX* and *YEAR* effects.
α are coefficients relating to the additive genetic effect.
They are correlated depending on the pedigree of the lambs.
γ are coefficients relating to the permanent environmental effect.
They are independent between lambs.
β are coefficients relating the maternal effect.
They are independent between dams.

The data are unbalanced with as much as $\frac{2}{3}$ of the data missing in May. Post mortem counts were not taken in the last year of the study, with most observed data taken from male lambs. As a result, the first and last time point were removed from analysis.

Results

95% credible regions for each variance component are shown on the left and the heritability shown on the right.





At the beginning of the season, the maternal component explains most of the variation in egg counts whereas by the end of the season, the additive genetic component accounts for most of the variation.

Dam plays an important role in the susceptibility of lambs to nematode infection in their first few months with this effect decreasing throughout their first grazing season.

Once exposed to nematodes, lambs build an increasing immune response to the infection. As the season progresses, this trait becomes more heritable.

All of the estimated variance components show a dip around August. This seems biologically implausible but may be explained by the reduced variability observed in the raw data at this time, which may be due to random sampling.

Summary

Heritability is a commonly measured statistic and it is defined as the amount of variation due to the additive genetic component. Animal breeding programs select animals based on their estimated breeding value of a given trait or multiple traits, which depend on the heritability.

We have shown that heritability can vary substantially over time. It is most effective to select animals based on a trait when it is most heritable.

For *Teladorsagia* circumcinta, selecting sheep at the end of the season is likely to be most effective.