Chapter 5.7 Next generation: transmission model

The dominance and epistatic effects depend on allele combinations. They are broken in the gamete production and established again in the offspring, but it is unpredictable how. The additive effects, however, are predictable because they do not depend on specific combination of alleles.

To be able to predict the additive genetic effects, we need to develop another model that describes the transmission of the genetic potential from both parents to their offspring. To illustrate that, in figure 3 you see a family of rabbits. The parents each have two different copies of each gene, but they pass only 1 on to their offspring and you don’t know which one. So for each gene there are two alleles per parents, and four different combinations of those alleles possible in the offspring.

![Family of rabbits](image)

**Figure 3. Family of rabbits illustrating that offspring receive half of their genes from each of their parents. Which half is a matter of chance.**

Fact is that each animal receives half of its genes from its father (sire) and half from its mother (dam). But you can see from the figure that with this formula you cannot predict what will be the offspring performance as you will need to know WHICH half of the genes are passed on to the offspring. And that is a chance factor, also called the Mendelian Sampling term. So a part you know: half from sire and half from dam, and the other part is the Mendelian Sampling term (MS).

Remember that in breeding we are only interested in the additive genetic effect \( A \), as half of that is inherited by the offspring. This is also called the true breeding value of an animal.

**Definition**

The *Mendelian Sampling term* indicates the chance factor in distributing half the genetic material from each parent to their offspring.

**Definition**

The *true breeding value (A)* of an animal is its additive genetic component, half of which is inherited by the offspring.

In model terms you can write the breeding value of an offspring as

\[
A_{\text{offspring}} = \frac{1}{2} A_{\text{sire}} + \frac{1}{2} A_{\text{dam}} + MS
\]

If you would estimate variance components of all breeding values in a certain generation, then that is the same as the additive genetic variance. So the variance of \( A \) can be written as

\[
\begin{align*}
\text{Var} (A) &= \text{Var} (\frac{1}{2} A_{\text{sire}}) + \text{Var} (\frac{1}{2} A_{\text{dam}}) + \text{Var} (MS) \\
&= \frac{1}{4} \text{Var} (A_{\text{sire}}) + \frac{1}{4} \text{Var} (A_{\text{dam}}) + \text{Var} (MS) \\
&= \frac{1}{4} \text{Var} (A_{\text{sire}}) + \frac{1}{4} \text{Var} (A_{\text{dam}}) + \text{Var} (MS)
\end{align*}
\]
Under the infinitesimal model we assume that selection has no influence of the size of the genetic variance from one generation to the next. Therefore we assume that \( \text{var}(A_{\text{sire}}) = \text{var}(A_{\text{dam}}) = \text{var}(A) \). This means that \( \text{var}(\text{MS}) \) must be equal to \( \frac{1}{2} \text{var}(A) \). This is quite a large component!

That explains why they say that breeding is genetic gambling... Fortunately there are tools to decrease the chance factor in breeding. More about that in the chapter about ranking the animals.