Chapter 9.11.1: Special case: indirect selection

Thus far we have assumed that phenotypic information is available for the trait under selection on at least a large part of the population. If selection is on growth then weights at different ages are easily made available, if selection is on milk quality then records are available on relatives. However, in some cases phenotypes are not available, for example in case of an infectious disease, and/or phenotypes for traits that are expensive or invasive to collect. In those cases it is possible that a second trait can be used as indicator of the trait that you want to select for. Important prerequisite is that the indicator trait is correlated with the trait that you want to improve (i.e. the trait in the breeding goal). Obviously, the higher the correlation, the better. In formula the genetic gain in the breeding goal trait, given selection on the indicator trait, can be predicted as:

$$\Delta G = i \cdot r_{IH, \text{indicator trait}} \cdot \sigma_a \text{breeding goal trait} \cdot r_{\text{indicator trait, breeding goal trait}}$$

The selection intensity is the same as with direct selection and depends on the selected proportion. The accuracy of selecting the breeding animals is predicted using the heritability for the indicator trait, as that is what you base your selection on. You are interested in the response to selection in your breeding goal trait, so you want to express the results in units of the breeding goal and thus use the genetic standard deviation of the breeding goal trait. It will depend on the size of the correlation to what extend selection on the indicator trait indeed will result in genetic progress in the breeding goal trait. You, therefore, have to multiply the result with the correlation between indicator and breeding goal trait. The overall accuracy of selection thus both depends on the accuracy of selection on the indicator trait, and the correlation between indicator and breeding goal trait.

Note that it depends on the combination of $r_{IH, \text{indicator trait}}$, determined by the heritability of the indicator trait, and the correlation between breeding goal and indicator trait whether more genetic gain can be achieved with indirect compared to direct selection.

Thus:

An indicator trait provides an indication of the performance for the breeding goal trait, and is useful as replacement of traits that are very difficult or expensive to measure.

Requirements for success are the heritability of the indicator trait and the correlation with the breeding goal trait.

Indirect selection can be a very good solution when traits are difficult or expensive to record.

An example: white line disease in dairy cattle

Results of research on a large number of Dutch dairy cattle herds in 2002-2003 indicated a prevalence of white line disease of 9.6%. The heritability was low, only 0.02% (so the $r_{IH}$ was 0.02 = 0.14). Important reason for the low heritability was that the farms were visited only once, and any cow that was not diseased was considered healthy. However, some cows may have been only just recovered or not been infected. The genetic variance was 0.078, so $a$ was 0.28. These are not very promising figures to achieve large genetic gain with. However, the genetic correlation between white line disease and foot angle is 0.64. Steep angled feet are affected more often than flat feet. Foot angle is an easy to measure trait with heritability of 0.18 (so $r_{IH, \text{foot angle}}$ of 0.42). If we would select on observations related to white line disease, then the genetic gain would be $0.02 \times 0.28 = 0.040$. If we would select on the foot angle to decrease the prevalence of white line disease, then the genetic gain would be $0.18 \times 0.28 \times 0.64 = 0.076$. This is almost a double response if selection is indirectly on foot angle instead of directly on white line disease prevalence!