

Accuracy - breeding values and indexes

SIL Technical Note

Relates to: Comparing animals for genetic merit

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Summary

Amount of data and type of data determine the reliability, or accuracy, for measures of genetic merit. SIL can provide guides to characterize the data behind such a measure of merit.

Accuracy is built into estimates of genetic merit. Thus greatest progress in genetic improvement will be achieved through selection on merit while ignoring accuracy.

Sometimes animals must be given the benefit of the doubt because there is no data available from which to estimate genetic merit. The guides SIL has to characterize data can be used to flag such situations (e.g. old homebred sire *versus* young bought-in sire).

Background - statistics

Accuracy of a single measure of genetic merit is a function of how heritable the trait is and how much data has been used to estimate it. Often, accuracy cannot be usefully characterised by a single number. While two measures of genetic merit may be equally accurate, a comparison of the two may not be accurate if the two populations they are from are not linked genetically.

Breeding values, the basic measures of genetic merit, have accuracy “built-in”. Less accurate figures are regressed (pulled back) toward the population average.

- SIL assesses genetic links between groups of animals (e.g. flocks),
- SIL can provide guides to what data is behind a BV.

Accuracies vary for different traits due to differences in heritability, how many relatives have been measured for a trait and when, or if, these measurements have been made. Indexes are made up of many traits which can vary in accuracy. There is no theoretical method commonly accepted for determining the accuracy of an index.

Genetic evaluations

Information from relatives is fundamentally important to the prediction of genetic merit, particularly so when traits are measured late, in one sex or are lowly heritable. As you can see, reproduction (NLB) loses out on all three counts! No other trait suffers in this way.

SIL performs a genetic evaluation that gives estimates of merit information from individuals and their relatives. While all relatives are useful, progeny are particularly valuable. Other relatives “likely” share genes with an animal, to varying degrees, but progeny *must* share half their genes with each parent. Thus most relatives help to *estimate* breeding values but progeny can be used to *prove* a breeding value.

Type and amount of data

How much information is available on relatives and what types of relative both affect breeding value estimates. Tables showing this are appended for a high heritability trait (15%) and a low heritability trait (10%).

Several things are apparent from examining these tables:

- Parents diminish in importance as we get more data for the individual and its siblings.
- Large half-sib families greatly increase accuracy of BVs.
- Progeny prove BVs.
- Only a few progeny give accuracy equal to large numbers of other relatives.

Useful guides to reliability

You can put several useful guidelines on reports to indicate the reliability of BVs and indexes.

Firstly, number of progeny is useful to get a feel for the size of different sire families. This will show up young sires that don't have any progeny yet. Bear in mind that a ram may have progeny but they may have limited, or no, performance measurements collected if he was used recently. SIL recommends that performance measurements are collected for most progeny per sire.

Secondly, we can look at the number of key female relatives with lambing information. This addresses the trait most commonly affected by low reliability – reproduction (number of lambs born). You can look at the number of female relatives that have lambed or the number of lambing events they have had. These are the same if each ewe has lambed only once.

There are a variety of ways this can be calculated for half-sibs and daughters. SIL recommends you use only two of these in where you want to get a feel for reliability.

- Number of events is better than number of animals lambing as it takes account of the more reliable figure coming from ewes with multiple lambings.
- SIL by default does NOT use hogget lambing data to estimate genetic merit for Reproduction. In that case you are best to use the figures that do NOT count hogget lambings as this information would not have been used in deriving estimates of genetic merit.

Table 1. Summary of the variables you can use. SIL recommendations are underlined.

	2-tooth & older		All ewes	
	Number lambing	Number of events	Number lambing	Number of events
Sibs	SL2 ¶	<u>SLR2</u> ¶	SL *	<u>SLR</u> *
Daughters	DL2 ¶	<u>DLR2</u> ¶	DL *	<u>DLR</u> *

¶ when **hogget lambing NOT used** in genetic evaluation
* when **hogget lambing used** in genetic evaluation

Making the best of what we've got

- There is no need to characterize accuracy when it is built into BVs and indexes. **Selecting on index is best.**
- Be aware that animals with few, or no, relatives with performance measurements will have low accuracy BVs. These should be considered separately to those with more reliable BVs and indexes when making selection or culling decisions.
- Number of progeny, and number of female relatives with lambing records can be used to identify animals with different amounts of “background” data for their relatives.

Need more information?

Contact your SIL bureau, SIL adviser or call 0800-745-435 (0800-SIL-HELP).