

## Breeding values from NZGE

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### SIL TECHNICAL NOTE

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Relates to: NZGE molecular breeding values, estimated breeding values

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#### Background

SIL has been operating two evaluations, the New Zealand Genetic Evaluation (NZGE) which uses recorded or DNA pedigree and performance measurements and the National Genomic Evaluation (NGE) that also includes genotype information.

For animals that are genotyped this information is used to predict a molecular BV (mBV). Performance and pedigree measurements are used to produce an eBV. In the NGE these are combined, based on their relative accuracy, to calculate a genomic breeding value (gBV). For individuals in these flocks without genotype information, the gBV is based only on the performance measurements, so it is the same as the eBV value.

For genotyped individuals  $gBV = mBV + eBV$ , combined on basis of accuracy

For non- genotyped individuals  $gBV = eBV$

The NGE evaluation included about 100 flocks with differing amounts of genotype testing, from a few to a lot of animals. Because this evaluation had different flocks and goal trait groups in the analysis it resulted in different breeding values, making it hard to compare them with other flocks that use the NZGE evaluation.

#### New Development

The ability to combine different sources of information to produce the best estimate of genetic merit has been now been automated in the NZGE, so BVs for all animals can use all available information to produce the best estimate of genetic merit.

The gBV combines all available sources of information for each animal and produces the best estimate of genetic merit based on the information available. This may include:

- DNA parentage or standard pedigree recording
- Genotype information for a number of traits (varies by breed) if available
- On farm performance measurements (phenotype information)
- Specialist information - CT, RamGuard™ etc

SIL recommends gBVs be used on all reports whether flocks are genotyping or not. gBVs are automatically used in indexes when available from an analysis, whether a flock is genotyping or not. Where breeding values are listed on reports, eBVs should be updated to gBVs for completeness, especially for genotyped flocks. Then breeders are assured of the most informative breeding values whether they are genotyping or not as some outside sires may have genotype information.

The current system only uses the genotype information in the individual’s own breeding value, it does not carry through to progeny or other relatives. The new ‘single step’ system under development uses pedigree, phenotype and genotype information for all animals, including relatives.

**How to tell if the gBV includes genotype information**

For an animal that has been genotyped, flags on the gBVs indicate whether the molecular BV (mBV) information contributes in the gBV calculation.

gBV flags on SIL reports include † and §:

† indicates that eBV and mBV information are used in gBV calculation.

§ indicates that only mBV information used in gBV calculation (where eBV accuracy is low or the trait is not measured).

**Example of a report with flagged gBVs**

<u>WWT<sub>e</sub>BV</u>	<u>WWTM<sub>e</sub>BV</u>	<u>LW8<sub>e</sub>BV</u>	<u>LW12<sub>e</sub>BV</u>	<u>FW12<sub>e</sub>BV</u>	<u>NLB<sub>e</sub>BV</u>	<u>SUR<sub>e</sub>BV</u>	<u>LDAG<sub>e</sub>BV</u>	<u>FEC2<sub>e</sub>BV</u>
4.3	2.014	6.69	6.09	0.44	0.323	0.0479	-0.085	-13.52
3.1	†1.396	5.70	6.41	0.59	†0.319	0.0617	§0.574	§-23.52
3.2	1.503	6.63	5.14	0.54	0.235	0.0577	0.238	-14.44
3.7	†2.589	6.35	†1.27	†0.01	†0.256	0.0502	§-0.120	§-27.40
4.0	†2.074	6.75	†2.46	†0.10	§0.247	0.0502	§0.598	§-29.00
5.1	2.340	8.33	7.15	0.77	0.188	0.0404	0.280	-8.74

In the example above there are several animals that have both weaning weight measurements and genotype information in the weaning weight maternal gBV as indicated by the † flag. Two individuals have only genotype information informing the gBV for lamb dag score (LDAGgBV) and WormFEC (FEC2gBV) as indicated by the § flag.

**SIL recommends using all available information to ensure the best estimate of genetic merit by using gBV on all reports in place of eBV.**

