New Zealand Genetic Evaluation (NZGE) for Terminal Breeds

Technical Note

Subject:	**NZGE Terminal Evaluation**
Relates to:	NZGE genomic breeding values, NZGE genotype inclusion
Date:	November 2023

Summary

- NZGE evaluations incorporating genotypes from Terminal type breeds (Texel, SufTex, Suffolk, South Suffolk, White Suffolk, South Dorset, Poll Dorset, Dorset Horn, Dorset Down, Ranger, Primera or Lamb Supreme) are available in SIL and nProve as "*Research NZGE Term…*" evaluations (Research NZGE Terminal evaluations).
- Research NZGE Terminal evaluations are run each week, in addition to the NZGE Maternal evaluation, with data extracts for both beginning on Friday evenings.
- Research NZGE Terminal evaluations include genotypes from animals that meet the Terminal inclusion criteria (details below).
- Values from the Research NZGE Terminal evaluations are slightly lower on average than NZGE Maternal evaluations. Percentile band tables allow relative comparison of NZGE results.

Background

The New Zealand Genetic Evaluation (NZGE) has included genotype information from maternal-type sheep breeds (i.e., Romney, Coopworth, Perendale & their composites; NZGE Maternal) since 2017. Over this time, the genotyping of other breeds has increased (particularly in terminal or meat breeds) in conjunction with phenotyping for meat quality traits. This work was started as a research project via FARMIQ and funded, in part, by the Ministry of Primary industries (New Zealand). Subsequently, it was further developed via the South Island Genomic Calibration (SIGC) group. The impetus for this was due largely to the desire for improved terminal sire genetics that included traits for meat quality.

Our research shows that a separate evaluation, including terminal breed genotypes, provides more accurate breeding values than a combined evaluation of terminal and maternal breed genotypes together. Consequently, a second evaluation, the NZGE Terminal evaluation, has been developed to give breeders and purchasers of terminal breeds the option to include genomics into estimation of breeding values. The NZGE Terminal evaluation is currently still in a research phase and some adjustments to BV calculations may be made before it is finalised.

The Research NZGE Terminal evaluation runs weekly – like NZGE Maternal. Both evaluations use the same pedigree and performance data, with the NZGE Maternal continuing to use genotypes from maternal breed animals (as described in NZGEv4 Technical Note) and the Research NZGE Terminal using genotypes from terminal breed animals (described below).

Results from both evaluations are available to all NZGE flocks for reporting separately from SIL/nProve. BVs from the two evaluations are similar unless they are genomically enhanced by the Maternal breed genotypes in the Maternal NZGE, or Terminal breed genotypes in the Terminal NZGE.

Animals whose evaluations are impacted by genomic enhancement include:
- Animals with genotypes included in the evaluation, particularly those with genotyped, phenotyped relatives.
- Non-genotyped animals with close relatives with genotypes included in the evaluation, particularly if those relatives also have relevant phenotype information.

Genomically enhanced BVs are indicated by the dagger (†) in SIL reports and the GenEnh column in nProve.

Research NZGE Terminal genotype inclusion criteria

An animal must meet all the following genotype, breed, and pedigree criteria for its genotype to be included in the Research NZGE Terminal evaluation.

Genotype

- The animal has a genotype loaded into SIL/nProve by a B+LNZ Genetics approved lab and,
- The genotype meets the genotype QC criteria.

Breed

- The animal has a SIL breed of ≥ 75% Texel, SufTex, Suffolk, South Suffolk, White Suffolk, South Dorset, Poll Dorset, Dorset Horn, Dorset Down, Ranger, Primera or Lamb Supreme, or,
- The animal has a combined SIL breed of ≥37.5% Texel, SufTex, Suffolk, South Suffolk, White Suffolk, South Dorset, Poll Dorset, Dorset Horn, Dorset Down, Ranger, Primera or Lamb Supreme

Pedigree Status

- The animal has at least one recorded or DNA assigned parent.

Goal Trait Group records

Genotype inclusion criteria are examined separately for each Goal Trait Group (GTG). Genotypes are only included in the Terminal evaluation for GTGs listed in Table 1. Only pedigree is used for all other GTGs.

An animal’s genotype will be included in the Terminal evaluation if the above Genotype, Breed and Pedigree Status criteria are met, the GTG is listed in Table 1 and:

- The animal is a sire and is less than 10 years old or,
- The animal is a dam and is 6 or less years old or,

- The animal has a SIL status of Alive/transferred and is a young animal (less than 2 years old, where a birth month of August is assumed i.e., in October of 2023 animals born in 2022 and 2023 will be included).

Table 1. Goal Trait Groups evaluated with Terminal genotypes.

Goal Trait Group (GTG)	Associated Breeding Values
Dag	ADAG, LDAG
Growth early	WWT, LW8, LW12
Meat Yield	CW, CWY, EMAc, HQLY, LNLY, SHLY, LEANY
Meat Quality IMF	IMF
Meat Quality	CPH, SHF, COLA24
WormFEC	FEC1, FEC2, AFEC

Additional Genotype Inclusions

For animals that are not a sire, dam or young animal, some additional genotypes are included if they have informative phenotypes, as detailed in Table 2. below.

Table 2. Additional Goal Trait Group genotype inclusion criteria

Goal Trait Group (GTG)	Additional Inclusion Criteria
Dag	Both DAG3 and DAG8 recorded, or ADAG recorded
Growth early	WWT, LW8 and LW12 recorded
Meat Yield	At least 3 of the following traits recorded: FDM, EMD, EMW, CTLEG, CTSHLD, CTLOIN, CTFAT, CWTC, CBUTT or any VIASCAN
Meat Quality IMF	At least one IMF trait recorded using: Marble Score or IMF via CT scan, Near Infra-red (NIR), Wet Chemistry or hyperspectral imaging (HYP)
Meat Quality	CPHSHF or COLA24 recorded
WormFEC	At least 2 of the following traits recorded: FEC1, NEM1, FEC2, NEM2 or AFEC

Which Evaluation should I use?

The Research NZGE Terminal evaluation, using genotypes from terminal breeds, has been validated as providing more accurate breeding values for terminal breeds. When selecting terminal sires, it is recommended that Research NZGE Terminal analysis is used. Similarly, when selecting from maternal breeds it is recommended that the NZGE Maternal evaluation is used.

Terminal breeders may choose to sell on Research NZGE Terminal results or, as the selling season has already begun, may wish to continue using NZGE Maternal results, especially if the terminal breed flock is not genotyping and not related to genotyping flocks.

The Genotyping Decision Tree provides more detail on which NZGE to report from and is available from the SIL website.