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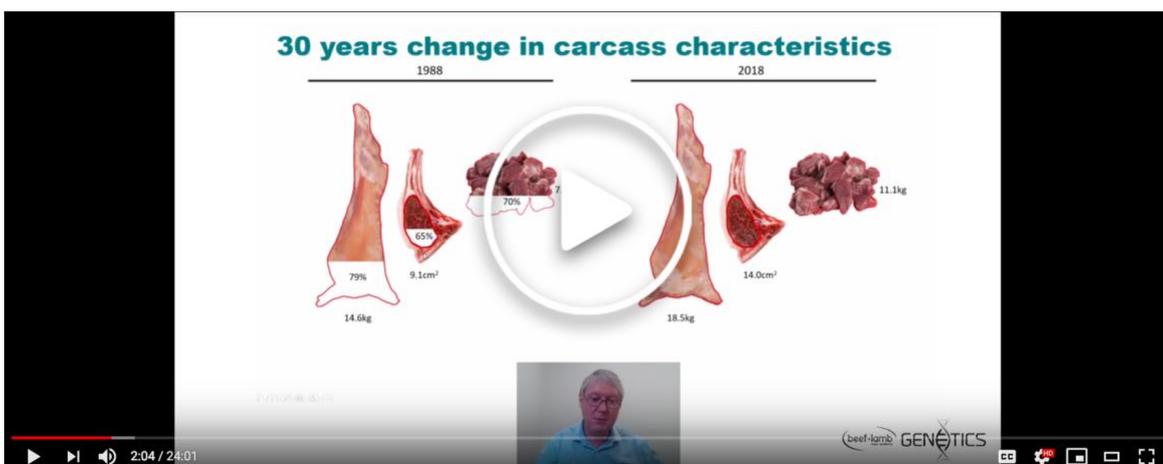
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S.I.L.

**Please note**

NZGE changed from Multi step to Single Step from 1 February

1. Revised Meat Module, including processor information and revised carcass weight reporting, in place
2. Annual year change: Leader Lists sires with progeny born 2016-2018
3. Year change also adjusts the connectedness window



**Revised Meat Module now operating**

The revised Meat Module began informing NZGE on 1 February. To recap, this means:

1. Revised carcass weight reporting
  - a) Carcass Weight breeding value in the Growth sub-index reflects growth information, similar to the previous CW BV.

b) In the Meat sub-index, a new BV – Carcass Weight Yield (CWY) – reflects the change in the carcass weight prediction when live weight and all available meat information are used to predict carcass weight.

2. Meat processor data is included – there are approx. 20,000 carcass weights mostly from progeny test flocks and other processor data now included

#### More information:

1. Video: Dr Neville Jopson (AbacusBio) explains the Meat Module revisions  
[Watch](#) (24 mins)
2. SIL Technical Note: “Inclusion of meat processor information in the Meat module”  
[Download](#)
3. SIL Technical Note: “Revised Meat reporting” [Download](#)



### RamFinder updated

Based on breeder feedback, the changeover of RamFinder to Single Step was delayed till the first NZGE run in February. This allowed breeders selling rams in January to market animals on the same values they were selected on. From now, RamFinder is informed by Single Step NZGE, so incorporates:

- revised Meat Module
- up-to-date genomic information and
- processor information, when available.

### Single Step: Why are there no mBVs?

Because Single Step integrates genotype and phenotype information at the same time, no molecular breeding values (mBVs) are produced under Single Step. mBVs are breeding values predicted when you only have genotype data from an animal. Single Step is set up to use both on-farm (phenotype) measurements and genomic information, seamlessly. It is not set up for genomic-only flocks (i.e. commercial flocks with no pedigree or on-farm measurements).

The main feature of Single Step is to better estimate the genetic contribution an individual receives from relatives. For example, using pedigree only (e.g. NZGE with no genomics), each grandparent is assumed to contribute 25% of their genes to the grand-progeny. In reality, the amount is not 25% and Single Step gives a better estimate of the true amount. So under Single Step, if an individual receives a greater proportion of genes from a grandparent that was of high merit for a trait, the BV is increased. Conversely, if the individual receives a smaller genetic contribution from that grandparent – or more from a grandparent that was poor for the trait – the BV for that trait would be reduced.

Because individuals gather more on-farm measurements as they get older, genomic and phenotype information is continuously adjusted to reflect the best estimate of merit based on available information.

The main advantage of genotyping is earlier prediction of merit on young animals and particularly for traits that are recorded later in life (e.g. number of lambs born), sex-limited, expensive and/or hard to measure and have low heritability.

If there is no genomic information, your BV will be the same as if calculated only using the phenotype measurements. Some of you may not be genotyping, but may have contributed sires to progeny test flocks or have sires used in other flocks that do genotype.



## SIL Reminders

### 1) Recording an adult ewe live weight (LWMATE)

From June 2019, SIL will require flocks to be recording and connected for adult size (DPA), if they are to be connected for NZMW and other Maternal or Dual Purpose standard indexes. As DPA is one of the core sub-indexes in the NZMW and other standard maternal indexes, flocks without adult weights (not connected for DPA) will no longer be shown in RamFinder or on Leader Lists on the SIL website.

[Read more](#)

### 2) Hub site rams

If your ram has been confirmed in the Sheep Progeny Test Hub site, you must advise Nadia McLean ASAP of your Ram ID and have your ram at the AI Centre for semen collection.

[Contact Nadia](#) | [Ram supply agreement form](#)

### 3) Ram sharing

A table of rams being assessed in the Hub site can be found on the SIL website. To be connected to the Hub site, you can contact a breeder on this list to check if additional straws are available. Best practice for achieving connectedness to the Hub site is to use the same ram, in the same year and measure the same traits.

[View table of rams](#)

### 4) Weaning data onto SIL

February is a new calendar year on SIL. It is important all breeders have loaded their 2018-born weaning weights onto SIL to ensure connectedness. See Chapter 5 of the Best Practice Guide for more information about recording and measuring weaning weights.

[Best Practice Guide](#)

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SHEEP



## Sheep Forum takes a break

As previously communicated, we are taking a year off from the mid-year forum and instead extending the scale of the Roadshow in spring 2019. The 2020 Sheep Breeder Forum is scheduled for mid next year in Napier.

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## Sheep Progeny Test updates

### Taratahi liquidation: Impact on Hub site

Despite the news of Taratahi Agricultural Training Centre's liquidation, the 2019 Sheep Progeny Test Hub flock mating will proceed – just not at Taratahi's Mangarata farm – so please continue with the collection of semen as planned. We are investigating an alternative site for the North Island flock.

### Low Input site 2019

The Sheep Progeny Test Low Input site is going ahead in time for the 2019 mating, after B+LNZ Genetics' successful application to the Sustainable Farming Fund yielded \$600,000 over three years. The test will be hosted by [Orari Gorge Station](#), using its commercial flock. If you are one of the breeders confirmed in the Low Input group, please select rams for semen collection. (Expect 60 straws per ram, with a preference for two-tooth rams.)

This site will accept foundation ewes given on loan and returned at the end of the trial. Purebred female progeny from a breeder's own sire and own ewes will be returned at the end of the trial. Halfbred female progeny will be available for auction at the end of the trial. All male progeny will be castrated and processed as part of the trial.

[Low Input Protocol](#) (pdf)

For any questions about this new site, please contact [Annie O'Connell](#)

### FE Progeny Test: 2019 mating

The B+LNZ Genetics Sheep Progeny Test site focused on Facial Eczema tolerance has chosen to take a one-year break from the programme, which means there will be no 2019 mating. Alongside FE ram breeders, B+LNZ Genetics will use the break to review if a progeny test is the best option for achieving FE breeders' long-term goals or if another approach may be more effective. In the meantime, link sire positions for FE rams in the Sheep Progeny Test Hub programme will continue to be available.



## Dairy Beef Progeny Test Cohort 1/2 interim sire report

An analysis of sire performance in the Dairy Beef Progeny test is available on B+LNZ Genetics website.

[Download report](#)

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## Beef Progeny Test: AI underway

Close to 3100 beef and dairy cows have been inseminated across five properties, kicking off Cohort 5 for the Beef Progeny Test. The next job is pregnancy testing beginning at Whangara Farms in February.

Meanwhile, spring processing of progeny is complete and the last of Cohort 2 will be processed in autumn, wrapping up terminal data collecting for that cohort.

*Pictured: Cohort 4 Simmental-sired calves at Rangitaiki Station, Taupo.*

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## A snapshot: Irish beef genetics

B+LNZ Genetics National Beef Genetics Manager Max Tweedie was in the UK last month. He spoke at the British Cattle Breeders Club Conference and at several other on farm workshops for the UK Agriculture & Horticulture Development Board. He shares observations from his time in Ireland.

- The Irish Cattle Breeders Federation is responsible for the genetic infrastructure in Ireland. Kiwi Brian Wickham helped set it up and it's doing an outstanding job of providing value for its breeders.
- Many commercial cattle have Indexes and EBVs. These are often supplied at the sale yards and used to market cattle.
- Data generated by studs is only a fraction of the total data collection: from commercial genotypes and birth records, all the way to maternal performance from AI technicians and data from processing plants. Records from all cattle slaughtered in Ireland are used for genetic use.
- The level and quality of recording – although incentivised – is impressively high.
- The next phase is to get the entire commercial herd genotyped.
- Research in Ireland has shown a direct relationship between increasing Self Replacement Index and a reduction of Greenhouse Gas Emissions (GHG).

*Pictured: Feed efficiency and GHG units are used to assess individual animals by measuring the GHG content of their breath.*



The team (from left): General Manager Graham Alder, IT Programme Manager David Campbell, Lead Scientist Dr Michael Lee, Genetic Evaluation Technical Manager Sharon McIntyre, Sheep Genetics Manager Dr Annie O'Connell, Beef Genetics Manager Max Tweedie, Genetic Systems Analyst Jacqui Edwards and Office Administrator Pam Schofield.

[More information about team](#)

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