Single Step Genetic Evaluation

Single Step key messages

- Applies to the common Maternal breeds (Romney, Perendale, Coopworth and Composites) in the first instance.
- Seamless integration of genomic information with pedigree and performance records resulting in more accurate breeding values particularly in young animals.
- Better comparisons between genotyped and non-genotyped animals and between flocks with appropriate connectedness
- Most changes will be seen in young animals with very little phenotype information allowing better selection at younger ages. Whereas sires with lots of measured progeny will see less change
- With single step some of the benefits of genomics are passed onto close relatives
- No more changes due to annual recalibration as these are no longer necessary
- Single step is becoming the new standard internationally for national genetic evaluations and represents the most cost effective solution for industry.
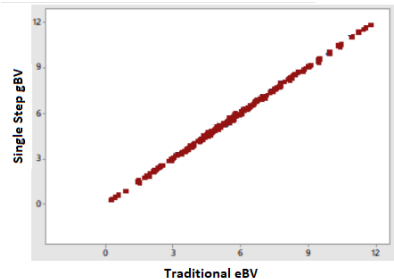
Genomics key messages

- Genomic information is able to show how closely an animal is truly related to its parents, grandparents and other near relatives increasing the breeding value accuracy.
- Genomic selection gives the most advantage for hard to measure, sex limited and traits that are measured late in life.
- Genomic information does not replace the need to collect accurate performance records but can help expand the value of collected phenotypes to a wider related population.
- Cumulative small changes in breeding values can build into large changes in index.

Single Step Results

The Single Step evaluation will result in some changes in breeding values and indexes for common Maternal breeds with genomic or connected to flocks with genomic information including progeny test flocks. We have tested the method to ensure that the genomic information improves the accuracy of the breeding values above what you would get using just pedigree, particularly for animals with little or no records e.g. young animals. A lot of validation, including tracking of changes, has been done and we are confident Single Step results in better breeding value estimates and allows for better or more robust comparison between individuals with or without genomic information.

Below are examples of differences observed between Single Step and Multi Step (Traditional eBV) and common reasons for the result.
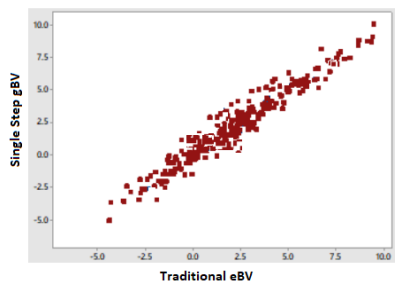
Example A: little or no difference between the Traditional eBV and Single Step.

Common reasons:
- Proven animals with high accuracies eBVs
- No or few genotyped animals
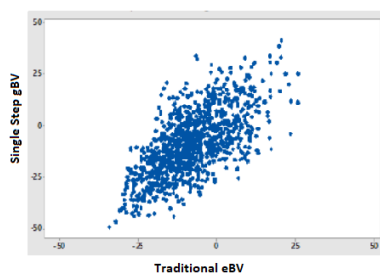- No or limited relatives in the genomic reference population

Example B: moderate change with genomic information in Single Step

Common reasons
- Single step is adding extra information to genotyped animals
- Flock has relatives in the genomic reference population
- Young animals with low accuracy eBV's are gaining extra information which is improving their accuracy
- Extra information is provided on traits that are expressed/recorded later in life

Example C large change with genomic information in Single Step

Common reasons:
- Traits with lower accuracy eBV's
- Traits that are not recorded or not fully recorded in the flock
- Recorded performance remains important for getting the best value from genomics

Multiple small changes in individual breeding values can combine to make larger changes in indexes and result in re-ranking for some individuals. The seamless integration of all data could be thought of as a final calibration and from this point forward values will only change with addition of new data, both phenotypic and genomic.

Single step has also used an improved 'best match' approach for assigning parentage based on genomic information where that has been provided. This will result in some changes for some animals where previous pedigree errors have now been corrected to this 'best match' pedigree.

Proven Sires versus Young Sires

On sire summaries there are a range of sires, from older sires with lots of progeny measurements to young sires which may only have growth measurements on progeny. For older sires that are well proven through progeny performance, we would expect little change BVs with Single Step.

For younger sires, with progeny records for early traits such as growth and meat but no records yet for later traits such as number of lambs born, genomic information will add more value to the estimation of the later traits.

As a breeder, what is in it for me?

For those not using genomic information the values provided in Single Step will be very similar to values provided in the current Multi Step. There may be small changes where relatives in progeny test flocks or other connected flocks have genomic and performance information.

Those using genomic information will see the most benefit as Single Step provides better values for genomically tested animals and their close relatives. The integration of genomic and performance information means selection and culling decisions can be made earlier and decisions on which animals to invest more expensive testing on (eg Facial Eczema testing) can be made with more confidence. There are also better comparisons between animals with and without genomic information. Using genomic information wisely will accelerate your genetic gain.

Genomic information can improve the BV predictions for animals with unknown parentage (i.e. screened in animals) but does not fully compensate for lack of pedigree and performance information together with genomics.

How to get started with genomics

For flocks or breed groups that have lots of historical genomic and performance information (eg Maternal breeds such as Romney, Perendale, Coopworth Composites) the use of genomics is well established. For Terminal and other breed groups a genomic plan to build an understanding of the relationship between genomics and performance phenotype is needed first. As a rule of thumb this begins with 100 sires with high density genomic tests each with 10 progeny with genomic and performance records. B+LNZ Genetics will work with groups to design and advise on genomic development programs.

Revised Meat module – what changes?

<u>Meat module key messages</u>

- The revised Meat module reflects genetic relationships describing the current carcass weights (18.6kg), composition and breed diversity.
- The primary change is carcass weight BV (CWBV) which is now calculated in the Meat module using live weight and meat measurements, whereas previously it only used live weights.
- The secondary change is in meat yield BVs (LNLY, HQLY, SHLY, FATY) which are adjusted for carcass weight.
- DP Growth (DPG) and TS Growth (TSG) sub-indexes use revised CWBV, so these change.
- DP Meat (DPM) and TS Meat (TSM) sub-indexes use revised meat yield BVs, so these change.
- Maternal Sires will see changes NZ Maternal Worth (NZMW) based on changes in DPG and changes in Maternal Worth + Meat (MW+M) based on changes in DPG and DPM.
- Terminal Sires will see changes in NZTW based on changes in both TSG and TSM.
- Because some of the variation that was in Meat is now included in Growth through CWBV, consider both Growth and Meat together.

The original meat module was based on Romney lambs with 14.6kg carcass weight from the late 1980's. Carcass weights were scaled over time to account for heavier animals and included additional measurements such as VIAscan and CT-Scan as they became available.

The revised Meat module better reflects current carcass weights (18.6kg), composition and breeds. It also includes an increased number of carcass measurements for both terminal and maternal breeds from progeny tests flocks. The genetic parameters, heritabilities and the relationships between carcass trait, have also been updated. The revised Meat module results in accurate predictions of carcass merit.

30 years change in carcass characteristics

What changes will breeders see?

The primary change is an improved carcass weight breeding value (CWBV).

- The old CWBV was calculated in the Growth module using only live weight information
- The new CWBV is calculated in the Meat module using live weights and all available carcass information

The secondary change is an improved calculation of the lean and fat yield breeding values (LNLY, HQLY, SHLY, FATY BVs).

Terminal Sire – what changes in the NZTW?

NZTW consists of Growth, Meat and Survival sub-indexes.

Both the TSG and TSM will change as both sub-indexes have BVs (in bold below) calculated differently in the revised meat module.

$$NZTW = \widehat{TSG} + \widehat{TSM} + TSS$$

$$TSG = WWT + \mathbf{CW}$$

$$TSM = \mathbf{LNLY} + \mathbf{HQLY} + \mathbf{SHLY} - \mathbf{FATY}$$

The new values change some individuals upwards and some downwards as indicated by the width of the blue dots on the graph below. Overall the better animals are still the better and the poorer animals are still poorer, though some individuals may change significantly.
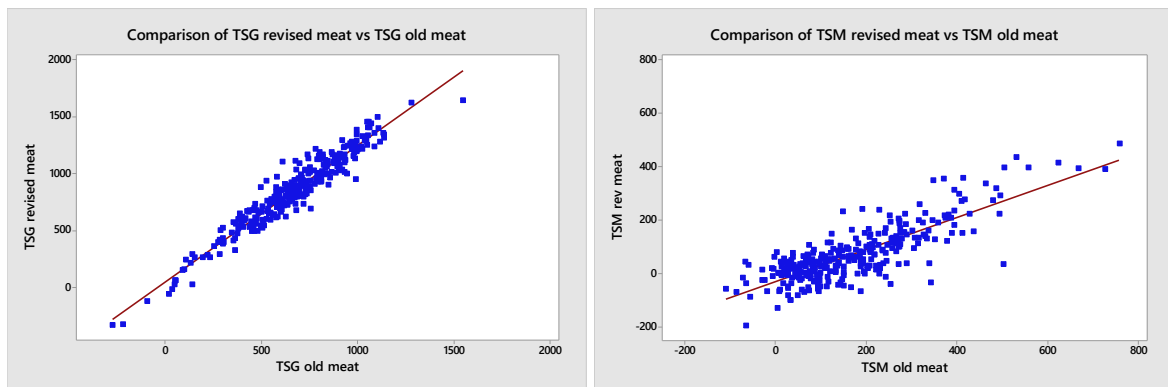
Graph 1: Terminal Sire Across-flock sire summary comparing NZTW with revised and old meat module values with progeny born in 2015-2017.

In the revised Meat module, both TSG and TSM change. Some of the variation that had been in TSM has now shifted to the TSG where CWBV is reported reducing the amount of variation in the carcass lean and fat yield BVs. The graphs below show TSG values are generally higher and TSM values are lower in the revised Meat module.
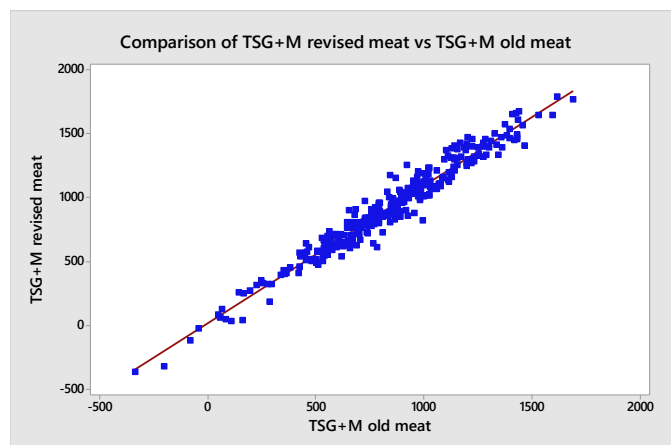
As weaning weight breeding values are not changed, the change in TSG values is only due to the improved CWBV. TSM values are generally lower and show reduced variation relative to current TSM as now some of the variation is accounted for in the improved CWBV.

Graphs 2 and 3: Change in TSG and TSM revised values compared to old meat values (Across-flock sire summary)

On its own the change in TSM appears to be surprisingly large. However, when we combine TSG and TSM together to account for all the changes in Meat, as in the graph below, the revised and old Meat values are more similar.

Graph 4: Comparison of combined TSG and TSM from revised Meat and old Meat module.

Maternal Flocks – what change will there be in NZMW and MW+M?
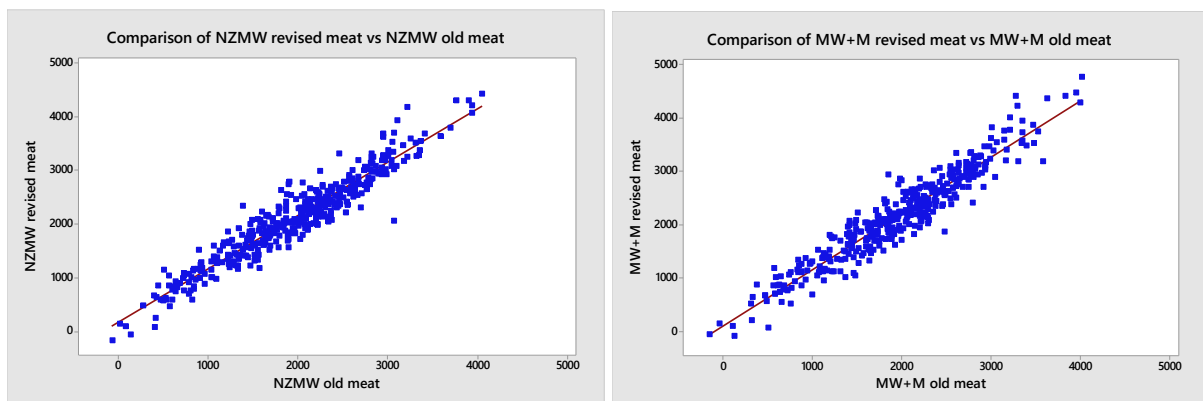
NZMW consists of Reproduction, Survival, Growth, Adult size and Wool sub-indexes and MW+M includes the addition of the Meat sub-index. Both the DPG and DPM will change as both sub-indexes have BVs (in bold below) calculated differently in the revised Meat module.

NZMW = DPCR + DPS + DPG + DPA + DPW   MW+M = DPCR + DPS + DPG + DPA + DPM + DPW

DPG = WWT + WWTM + *CW*   DPG = WWT + WWTM + *CW*

DPM = *LNLY + HQLY + SHLY*

As CWBV is reported in the DPG sub-index and now includes all available carcass data the DPG will change and so will the NZMW.   The MW+M contains both the changes in DPG and the DPM.

The new values move some individuals upwards and some downwards as indicated by the width of the blue dots in graphs 5 and 6. Overall the better animals are still the better and the poorer animals are still poorer, though some individuals may change significantly.
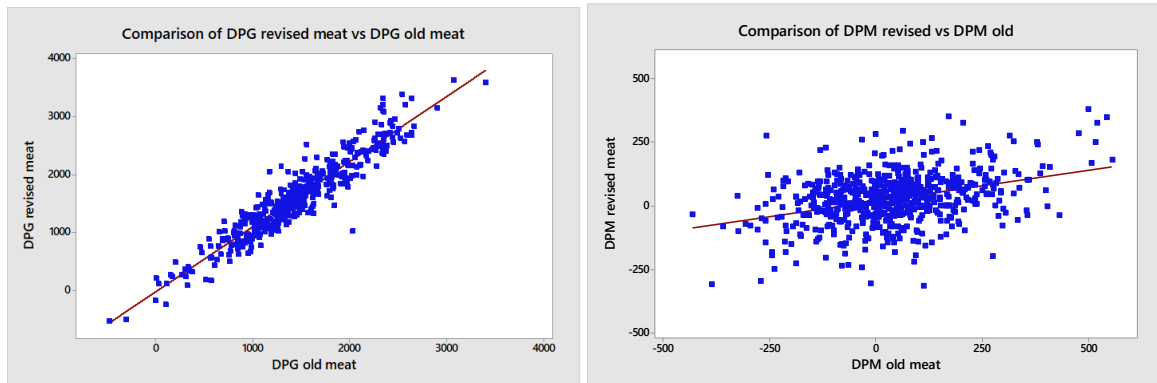
Graph 5 and 6: Maternal Across-flock sire summary comparing NZMW and MW+M with revised and old meat module values with progeny born in 2015-2017.

The change in the NZMW values is due only to the improved CWBV in the DPG. The change in the MW+M values is due to both the changes in DPG and DPM.
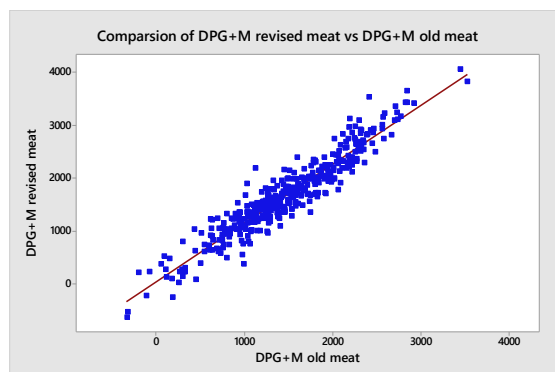
In the revised Meat module, both DPG and DPM change. Some of the variation that had been in DPM has now shifted to the DPG where CWBV is reported reducing the amount of variation in the lean yield BVs (LNLY, HQLY, SHLY). Note fat yield is not included in DPM. The graphs 7 and 8 show DPG values are generally higher and DPM values are lower and less variable in the revised Meat module.

Graph 7 and 8: Change in DPG and DPM revised values compared to old meat values (Across-flock sire summary)

On its own the change in DPM appears to be surprisingly large. However, when we combine DPG and DPM together to account for all the changes in Meat, as in the graph 9, the revised and old Meat values are more similar.

Graph 9: Comparison of combined DPG and DPM from revised old Meat module.

In Summary

The inclusion of additional measures of carcass merit combined with updated genetic parameters results in improved estimates of merit for Terminal and Maternal animals. The primary change is in the CWBV with secondary changes in lean and fat yield BVs.

Terminal Sires will see changes in NZTW based on changes in both TSG and TSM.

Maternal Sires will see changes NZMW based on changes in DPG and changes in MW+M based on changes in DPG and DPM.

The Growth and Meat sub-index in combination more accurately describe an animals merit for meat than using the Meat sub-index alone.