Weaning Weight Contemporary Group

Technical Note

Relates to: Data Quality

Date: October 2022

Summary

- Automatic assignment of a separate mob code for animals recorded as one mob with two or more different recording dates at weaning. This will be applied from weaning for 2022 born lambs onwards.
- This will catch some errors in mob coding- particularly where a mob 1 is used for lambs weaned by ewes and a subsequent mob1 code for lambs weaned by hoggets.
- It is still vitally important that different mob codes are used whenever animals from different mobs are recorded, as this new assignment will not be able to catch all situations (e.g. where different mobs are measured on the same day, the system will still rely on correct mob information being entered).
- Correct weaning mob assignment is fundamental to good data as it forms the foundation for mob assignment for many other traits as well as used to account for pre-culling for later recorded traits – e.g. Meat. Incorrect assignment can lead to significant biases in the evaluation.

Background

Weaning data is an important foundation for the prediction of many traits, such as growth, meat, wool, parasite resistance, resilience and dags, as well survival to weaning. Weaning weight data is also used to account for culling/selection prior to recording of later measurements.

As such it is considered a foundation trait and it is important it is recorded as accurately as practical.

Mob coding is an important aspect of correcting for non-genetic impacts on measured performance and can cause large biases in the BVs if not well recorded. A mob code indicates the animals have experienced the same environmental conditions in the period leading up to measurement and the animals in the mob can be compared directly against each other after accounting for known non-genetic effects such as birthdate, age of dam, birth and rearing rank. If animals have been in different mobs – a between mob correction factor is calculated and used to adjust performance measures within the evaluation. The correction factor is based on the performance of related animals (sire progeny) in the different mobs. For example, after correcting for known genetic effects, the progeny of one sire in mob 1 were on average 2 kg heavier than the progeny of the same sire in mob 2 -infers conditions in mob 1 were more favorable, may have had better feed,

more sheltered, less parasite challenge or combination of multiple factors resulting in an environmental advantage. Accounting for these between non-genetic effect results in more accurate predictions of genetic across all animals in both mobs. Not accounting correctly for mobs can lead to significant biases in the evaluation.

Current Situation

The evaluation uses the mob code to account for differences in recording dates and measured performance between mobs. Any difference in recording date is accounted for by the between mob correction based on the performance of progeny of common sires across the mobs.

Recording weaning weight mobs

Usually after tailing/docking, ewes and lambs are run in larger groups. These larger groups should be recorded as separate mobs at weaning. Where possible be pragmatic about the number of mobs, breaking the weaning data into many small groups is also less desirable as it reduces the number of connected progeny between multiple small groups.

In practise – we would usually expect about 3+ mobs at weaning for medium to larger studs. These could be – early, middle, lates, singles, twins, hill, flats etc, as long as there are sufficient progeny of common sires across the mobs, correction factors can be calculated to remove mob effects from the prediction of breeding values.

Automatic assignment of separate mob code

In nProve, sometimes weaning data has been entered with 1 mob recorded but with different recording dates within the animals in the mob. It is very unlikely these animals were run in the same mob. Sometimes it is a consequence of starting weaning measurements on a new group of animals (e.g. lambs from hoggets) at a later date, and forgetting that the mob number needs to continue from where previous weaning mob codes left off. It is possible with very large mobs, some may have been recorded one day and the remainder the next morning but even then, it is likely gut fill will be different, and this can be up to a 3-5kg per head, so animals would still be best to be assigned a separate mob.

From weaning of 2022-born lambs, the system will assign a unique mob automatically whenever lambs with the same weaning mob code have been measured on different dates.

Care is still needed by the breeder and bureau to assign weaning mob codes, as there are likely to be different weaning mobs recorded on the same day, as the automatic tool would not pick these up.

Hogget weaning and mob coding

Another common error the automatic assigning of a unique mob code will correct is where a mob 1 was used at weaning for a mob of lambs from ewes and later mob 1 is used again when hogget lambs are weaned. This would give one mob1 with 2 different recording dates and very different feed/environmental conditions. This can cause large errors in BV prediction. The automatic tool to assign a unique mob code would then make the later hogget lambs a separate mob, meaning the correct calculation for mob correction would account for the non-genetic (feed/timing etc) effects on performance – assuming a sire was used over both ewes and hoggets as is best practise.

Implementation

The tool was implemented from weaning of 2022-born lambs. Previous data was not back corrected.

Best Practise and Future Proofing

It is important that a recording date as well as a mob is entered for all weaning records.
It is strongly recommended that a recording date is associated with every animal measurement entered into nProve to future proof your data analysis.