

Genomic prediction for purebred beef

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In November 2024, NAV published, for the first time, **genomic breeding values**, for **weight, growth, and carcass traits** for the five largest breeds (AAN, CHA, HER, LIM, and SIM). For the rest of the breeds in the weight/growth and carcass evaluation and for all breeds and traits in the calving evaluation a traditional pedigree-based evaluation is still being applied.

NAV Purebred beef genomic prediction

How?

NAV Purebred beef evaluation has published genomic breeding values using the single-step method, where all available information — phenotypic records, pedigree data, and genotypes — is used simultaneously. The used method has the advantage of allowing breeding values for both genotyped and non-genotyped animals to be calculated together in a unified procedure.

This approach ensures that both genomic and pedigree-based relationships are effectively utilized in the calculation of breeding values.

Which animals are included?

Genotyped animals are included if the genotype of the animal and the genotype of the pedigree match. Additionally, the animals have to follow the same editing rules as the animals with phenotypic data 1) their pedigree is complete, i.e. sire and dam are known, and 2) the genotyped animal is classified as purebred (the proportion of the main breed is at least 87.5% or larger).

Why?

The use of genotype information, together with phenotypic records and pedigree data, increases the reliability in which breeding values are calculated. This extra increase in reliability have shown to be around 10% - across all breeds and traits. In practice, an increase in reliability means that more accurate selection decisions can be made, leading to faster genetic progress for the traits of interest.

Breeding value changes when adding genotype information.

In theory

Adding the extra information from genotype data, into the genetic evaluation affects the calculation of the individual breeding values, by increasing breeding values reliability. For animals with only pedigree and phenotype records the changes in breeding values are expected to be insignificant.



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In practice

The comparison between the old NAV purebred beef evaluation with the new NAV purebred beef genomic evaluation showed high alignment in breeding values across breeds. As expected, the biggest differences in the new evaluation were found in animals with genotype and no phenotype registrations. For non-genotyped animals, the re-ranking is minimal.

What is next?

The NAV Purebred beef genomic evaluation continues to develop, and the next step will be to investigate the calculation of genomic reliabilities for the weight/growth and carcass evaluation. Furthermore, it will be explored if minor breeds, i.e. Blonde d'Aquitaine and Highland cattle can be included in the genomic evaluation. By 2025, the plan is that genomic breeding values for calving traits also will be published.