

NAV Purebred beef genomic prediction for weight/growth and carcass traits for 5 main breeds

Elisenda Rius-Vilarrasa, Växa.

In November 2024, NAV published, for the first time, **genomic breeding values**, using a single step approach, for **weight, growth, and carcass traits** for the five largest breeds (AAN, CHA, HER, LIM, and SIM). Table 1, show the list of breeds and number of genotypes available for the November 2024 evaluation.

Table 1. List of breeds with number of genotypes by country included in the November 2024 genomic evaluation.

Breed name	DNK	FIN	SWE	Other	Total
Aberdeen Angus	1608	4504	2241	154	8507
Charolais	408	3912	5289	188	9797
Hereford	1518	4807	5723	86	12134
Limousin	2538	2474	1584	162	6758
Simmental	1546	3029	2386	102	7063

NAV Purebred beef single step genomic prediction

– how?

For the first time, the NAV Purebred beef evaluation has published genomic breeding values using the so called single-step approach, where all available information — phenotypic records, pedigree data, and genotypes — is used simultaneously. This method has the advantage of allowing breeding values for both genotyped and non-genotyped animals to be calculated together in a unified procedure and is the method of choice for most commercial livestock genomic evaluations today.

While genomic information can accurately estimate family relationships, particularly when many animals are genotyped, also using pedigree information it often increases the reliability of breeding values. Therefore, the NAV Purebred beef genomic evaluation incorporates both pedigree and genotype data. Pedigree data provides deep insights into family relationships, accumulated over multiple generations of record keeping. Drawing from in-house investigations and prior knowledge, the NAV Purebred beef genomic evaluation optimizes the integration of genotype and pedigree data, assigning 70% weight to genotype data and 30% to pedigree data. This approach ensures that both genomic and pedigree-based relationships are effectively utilized in the calculation of breeding values.

– Are all genotyped animals included?

To maintain the quality of the evaluation, genotyped animals are included if the pedigree and genotype data match. Additionally, following the same editing rules as for the phenotypic data, genotyped animals are included if, 1) their pedigree is complete, i.e. sire and dam are known, and 2) if the genotyped animal is classified as purebred (the proportion of the main breed is at least 87.5% or larger). Since genotype information is a valuable source of information, genotyped animals that have passed the pedigree filters but don't have phenotypic records are kept in the evaluation.

– 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 breeding values reliability have shown to be of about 10% - across all breeds and traits – compared to using only phenotypes and pedigree in a traditional pedigree model.

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. The higher reliability of breeding values enables breeders to identify superior animals with greater confidence, reducing the risk of selecting animals with less favourable genetics. However, it is important to mentioned that this 10% relates to animals with at least one phenotypic record in the evaluation, for genotyped animals without phenotypic records the reliability increase might be larger in unit increase but the overall level of reliability might be still lower compared to the genotype animals with phenotype records.

Breeding value changes when adding genotype information.

– in theory

By adding an extra source of information, such as genotype data, into the genetic evaluation affects the calculation of individual breeding values, especially for genotyped animals by increasing breeding values reliability. For animals with only pedigree and phenotype records the changes in breeding values are expected to be insignificant or in line with an increased relationship links coming from the genotype data.

– in practice

The comparison between the old NAV purebred beef evaluation (pedigree-based model) with the new NAV purebred beef genomic evaluation (genotype and pedigree-based model) showed high agreement in breeding values across breeds and traits and for all three countries (Table 2). As expected, the biggest differences were found in animals where their genotype was used in the new evaluation, compared to just using pedigree information in the old evaluation.

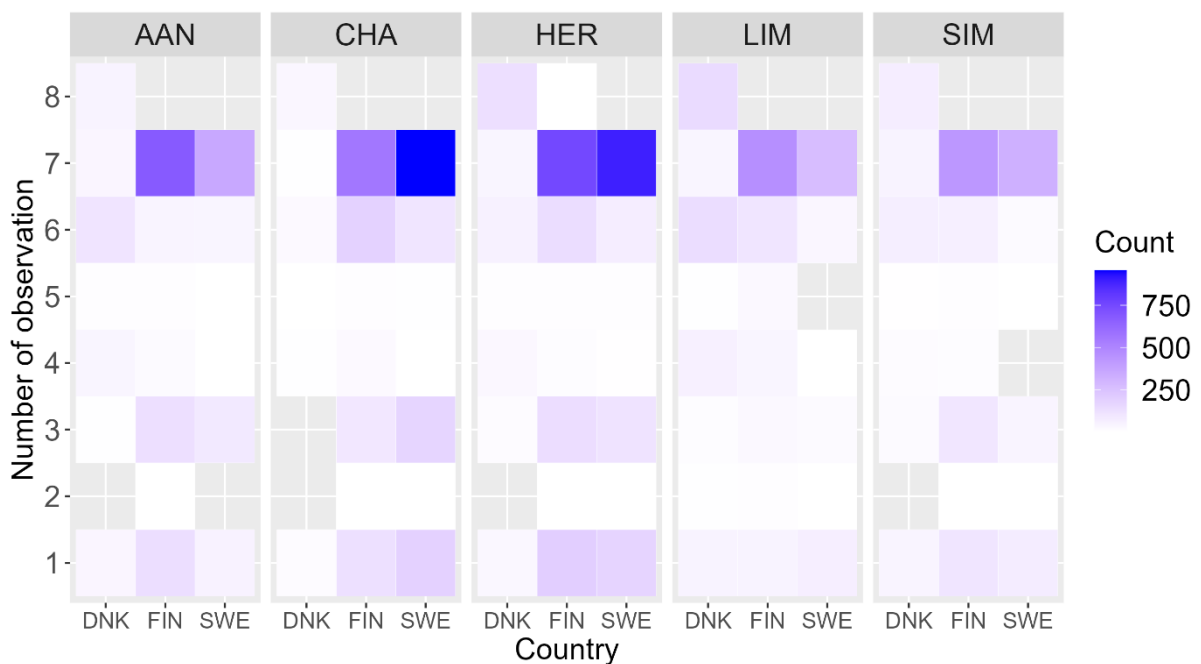
Table 2. Correlation of combined breeding values for growth, production, and slaughter quality from the old NAV purebred beef evaluation (pedigree-based model) with the new NAV purebred beef single step genomic evaluation (genotype and pedigree-based model), split between non-genotyped and genotyped animals within country and breed (phenotypic and pedigree data from the June 2024 evaluation from males and females born after 2012 with at least one phenotypic record)

	DNK		FIN		SWE	
	Non-genotyped	Genotyped	Non-genotyped	Genotyped	Non-genotyped	Genotyped
Aberdeen Angus						
Growth index	0.97	0.87	0.99	0.94	0.98	0.94
Production index	0.97	0.86	0.99	0.94	0.97	0.93
Slaughter quality index	0.97	0.88	0.99	0.93	0.93	0.79
Charolais						
Growth index	0.97	0.90	0.99	0.96	0.98	0.93
Production index	0.98	0.91	0.99	0.96	0.98	0.93
Slaughter quality index	0.99	0.95	0.99	0.97	0.98	0.94

Hereford						
Growth index	0.97	0.85	0.99	0.92	0.98	0.89
Production index	0.97	0.86	0.99	0.92	0.98	0.88
Slaughter quality index	0.98	0.88	0.99	0.93	0.97	0.87
Limousin						
Growth index	0.99	0.92	0.99	0.95	0.98	0.94
Production index	0.99	0.92	0.99	0.95	0.98	0.93
Slaughter quality index	0.99	0.93	0.99	0.95	0.99	0.93
Simmental						
Growth index	0.99	0.93	0.99	0.96	0.98	0.94
Production index	0.99	0.93	0.99	0.96	0.98	0.93
Slaughter quality index	0.99	0.96	0.99	0.96	0.99	0.94

For non-genotyped animals, the re-ranking is minimal, particularly in Finland. A possible explanation for this is that only about 4-5% of the total slaughtered animals have genotype information, which limits its influence on the overall correlations shown in Table 2. Furthermore, Table 2 highlights that the use of genotype data affects re-ranking of animals differently across countries, as indicated by the varying correlation levels. This variation may reflect differences in pedigree completeness and phenotype recording among genotype animals across countries. Figure 1 further illustrates this, with Finland, displaying stronger colour intensity for number of observations followed by Sweden and then Denmark, representing a higher number of phenotype registrations for genotyped animals in these countries.

Figure 1. Observation pattern by country and breed for genotyped animals. Number of observations 1 shows the number of genotype animals with only one phenotype record in the weight/growth and carcass evaluation whereas number of observations 8 shows the number of genotype animals that have 8 phenotype records in the evaluation.



Publication of breeding values

– genomic breeding values (GEBVs) and pedigree-based breeding values (EBVs)

The November 2024 NAV PbB evaluation has run a NAV genomic evaluation for weight/growth and carcass traits for the main 5 breeds and a traditional NAV pedigree-based evaluation for the rest of the breeds in the weight/growth and carcass evaluation and for all breeds and traits in the calving evaluation.

Breeding values for calving and weight/growth and carcass traits are expressed as the difference between an individual estimated breeding value and the genetic base to which the animal is compared. Both GEBVs and EBVs are compared to the same group of reference animals (standardization of breeding values). A summary of the publication of breeding values for all breeds and traits for the November 2024 evaluation are shown in Table 3.

Table 3. Type of breeding value, genomic (GEBV) or pedigree-base (EBV) calculated in the November 2024, for all breeds, traits, and indexes.

Breed name	Weight/growth and carcass traits	Calving traits	Growth, carcass quality and production index	Dam index	Calving index	Birth index
Aberdeen Angus	GEBV	EBV	GEBV	GEBV+EBV	EBV	EBV
Charolais	GEBV	EBV	GEBV	GEBV+EBV	EBV	EBV
Hereford	GEBV	EBV	GEBV	GEBV+EBV	EBV	EBV
Limousin	GEBV	EBV	GEBV	GEBV+EBV	EBV	EBV
Simmental	GEBV	EBV	GEBV	GEBV+EBV	EBV	EBV
Blonde D'Aquitaine	EBV	EBV	EBV	EBV	EBV	EBV
Highland Cattle	EBV	EBV	EBV	EBV	EBV	EBV
Other	EBV	EBV	EBV	EBV	EBV	EBV

Validation of the NAV Purebred beef genomic evaluation

The new NAV Purebred Beef genomic evaluation has been carefully examined for bias, i.e. it doesn't consistently overestimate or underestimate the value of certain animals or traits. To check for bias, different methods have been used. First, the new genomic evaluation has been compared with old pedigree-based evaluation by looking at genetic trends and breeding value variation for all traits and breeds from both evaluations. Additionally, the two evaluations were assessed in their ability to predict the breeding value of animals without phenotypic information. Results showed that the new genomic-based evaluation is less biased and more reliable in the prediction of breeding values for those animals compared to the pedigree-based evaluation.

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 from the NAV Purebred beef genomic evaluation will also be published.