News NAV evaluation 6 June 2023

Genetic evaluation of Dairy Cattle

The latest Nordic Cattle Genetic Evaluation (NAV) official genomic prediction took place as scheduled. NAV carried out genomic prediction for Holstein, RDC, Jersey, and dairy crossbreds.

Data used in genomic prediction

Genotypes were extracted from the joint Nordic SNP data base 4 May 2023. INTERBULL information from April 2023 and national information from 2 May 2023 run were included in the genomic prediction.

Publication of GEBVs

GEBVs for bulls and females are published monthly. Nordic phenotypic information is updated 4 times a year (February, May, August and November), and is used in the reference population for genomic prediction. The GEBVs for pure breed animals are expressed on the same cow base as in the February evaluation; cows born from 02.05.2018 to 02.05.2020. The GEBVs for crossbred are expressed on a genetic base of 1-7 year old crossbreds.

News in relation to NAV dairy genomic evaluation

• No changes

Official GEBVs for bulls used for AI in Denmark, Finland or Sweden are published at the <u>NAV Bull</u> <u>Search</u> page.

GEBVs for dairyxdairy crossbreds

Joint Nordic GEBVs for dairyxdairy crossbreed females were published for the first time 7th December 2021. The procedures for calculating GEBVs have not been changed since the introduction, but for a few animals it has been observed that the changes in GEBVs between subsequent evaluations are significantly larger than expected. NAV is investigating what is causing these unexpected large changes.

Publication of NAV EBVs on search pages

Official NAV GEBVs for foreign AI bulls not used for AI in Denmark, Finland and Sweden are published on the <u>NAV homepage</u> in an excel sheet. The excel sheet also includes GEBVs for bulls used for AI in Denmark, Finland and Sweden. The excel sheet includes AI bulls that are from 10 months to 5 years old at the date of publication. The excel sheet is mainly useful for foreign AI-companies.

Interbull EBVs/GEBVs are published at the <u>NAV Interbull Search</u> page. The Nordic total merit index (NTM) is not calculated based on GMACE GEBVs, since Interbull regulations do not require member countries to calculate total Merit Indices based on Interbull GEBVs, and internationally it is not a common practice.

Genetic evaluation of beef bulls used in dairy herds

The latest NAV official evaluation for AI beef bulls based on their crossbred offspring from dairy cows for birth, youngstock survival and carcass traits took place 2 May. Breeding values for AI beef bulls are estimated four times per year, in connection to the NAV routine genetic evaluation for dairy breeds (table 1), and EBVs are published at <u>NAV Beef Search</u>.

Genetic evaluation of pure beef cattle

The latest Nordic Cattle Genetic Evaluation (NAV) official evaluation for calving, growth and carcass traits took place 6 June based on phenotypes from purebred Angus, Charolais, Simmental, Hereford, and Limousine beef cattle.

Table 1. Dates for	r extraction of data	a from the nation	al databases
	oxinuolion or uulu		

Trait	Denmark	Finland	Sweden
Pure beef cattle	15.05.2023	15.05.2023	12.05.2023

News in relation to NAV Beef cattle genetic evaluation

- Upgrade to the common NAV pedigree, including dairy and beef animals.
- Remove of crossbred animals
- Remove incomplete data from Denmark.

Upgrade to the large NAV pedigree, including dairy and beef animals.

The pedigree used up until the May 2023 evaluation was created to participate in Interbeef as DFS, it included only beef animals and there were some problems with double identities and inconsistencies with bull names. In this June 2023 evaluation the common NAV pedigree file with dairy and beef animals which is up to date with changes and corrections have been introduced, which will help in reducing the problems with double identities.

The upgrade to the common NAV pedigree file has increased the pedigree completeness of beef animals and ancestors of dairy and crossbred origin has been added to the traced pedigree. To take into account possible genetic level difference between animals with beef ancestors only versus animals with either dairy or crossbred ancestor's new genetic groups have been created to better estimate the breeding values of those animals that further back in the pedigree have a dairy/crossbred ancestor.

Removal of crossbred animals

The upgrade to the common NAV pedigree opens the possibility to remove, in a systematic way, crossbred animals that have been included in the evaluation up until May 2023. The current NAV purebred beef evaluation doesn't accommodate for the calculation of breeding values for crossbreds and its exclusion in this evaluation is an improvement for the estimation of breeding values for the purebreds.

The new edit removes, from the purebred beef evaluation, animals having a breed proportion less than 87.5% from the main breed. Crossbred animals represented 15% of the calving data and 5% of the carcass data. Table 2 shows the percentage of crossbred animals by country and breed that have been deleted from the evaluation. As shown in table 2 the largest proportion of crossbred animals is from Finland.

	Denmark		Finland		Sweden	
	Crossbred	Purebred	Crossbred	Purebred	Crossbred	Purebred
AAN	1.72	98.28	29.73	70.27	0.38	99.62
CHA	1.48	98.52	26.52	73.48	0.65	99.35
HER	0.90	99.10	18.85	81.15	6.79	93.21
LIM	1.45	98.55	31.16	68.84	0.53	99.47
SIM	1.23	98.77	35.99	64.01	0.40	99.60

Table 2. Percentage of crossbred animals in the phenotype data for Denmark, Finland and Sweden removed from the June 2023 evaluation.

Removal incomplete data from Denmark

Incomplete data from Denmark has been investigated and the results suggested that the large number of Danish animals with missing sire information was causing problems in the estimation of breeding values, especially in the calving evaluation. In this June 2023 evaluation, animals with phenotype and unknown sire and/or maternal-grand sire are removed from the evaluation. Most of the observations removed are from Denmark (10%-70%), for Finland and Sweden only 1-2% of the data is removed.

Results showed that, by removing incomplete recording of Danish animals from the evaluation the power to estimate maternal effects increased and addressed the large standard deviation of breeding values and mean problems observed in earlier evaluations.

The percentage of Danish data removed varies among breeds and traits, below shows the percentage range of data removed by trait and the corresponding breeds. In general LIM and HER showed the lowest and highest percentage of data removed, while the rest of the breeds are in between the two:

- Yearling weight: 10% 23% for CHA and SIM, respectively
- Slaughter data: 50% 70% for LIM and HER, respectively
- Calving ease: 39% 51% for LIM and HER, respectively
- Stillbirth: 47% 62% for LIM and HER, respectively

Effect of the improvements on the EBVs

The three improvements introduced in the June run cause some changes in the estimated EBVs. The largest differences in estimated EBVs, as expected from the changes implemented, are for Danish animals as shown in tables 3 and 4 for both calving and weight/growth index traits. For Finland and Sweden, the implemented changes affected mainly pedigree animals and animals with few observations, for those animals, males and females, with medium-high reliable breeding values the re-ranking is minimal as shown in tables 3 and 4.

Breed	Trait name	Denmark	Finland	Sweden
AAN	Birth index	0.89	0.98	0.98
	Calving index	0.92	0.96	0.97
	Dam index	0.92	0.97	0.98
CHA	Birth index	0.90	0.96	0.99
	Calving index	0.96	0.98	0.99
	Dam index	0.97	0.99	0.99
HER	Birth index	0.96	0.98	0.99
	Calving index	0.92	0.98	0.97
	Dam index	0.95	0.99	0.99
LIM	Birth index	0.85	0.94	0.96
	Calving index	0.94	0.97	0.92
	Dam index	0.94	0.96	0.96
SIM	Birth index	0.95	0.98	0.98
	Calving index	0.94	0.96	0.98
	Dam index	0.95	0.97	0.99

Table 3. Breeding value correlations between May and June 2023 evaluation for animals born between 2010 and 2022 with reliabilities for calving subindex traits of **30%** or higher split by country and breed

Breed	Trait name	Denmark	Finland	Sweden
AAN	Growth index	0.92	0.98	0.99
	Production index	0.92	0.99	0.99
	Slaughter quality index	0.87	0.94	0.97
CHA	Growth index	0.97	0.99	0.99
	Production index	0.94	0.98	0.99
	Slaughter quality index	0.88	0.96	0.98
HER	Growth index	0.93	0.99	1.00
	Production index	0.83	0.98	0.99
	Slaughter quality index	0.82	0.98	0.99
LIM	Growth index	0.97	0.99	0.99
	Production index	0.91	0.94	0.98
	Slaughter quality index	0.89	0.93	0.94
SIM	Growth index	0.96	0.98	0.99
	Production index	0.92	0.97	0.99
	Slaughter quality index	0.88	0.93	0.98

Table 4. Breeding value correlations between May and June 2023 evaluation for animals born between 2010 and 2022 with reliabilities for growth and carcass subindex traits of 50% or higher split by country and breed

There are several sires from all breeds that are used across countries. Changes in the data from Denmark can therefore imply changes in the breeding values of animals from Finland and Sweden. For example, 5% of LIM sires used in Sweden are Danish sires compared to approximately 2% for the other breeds. Considering the large proportion of animals removed from the Danish evaluation to increase the quality of the breeding values estimated, the changes in breeding values for Danish sires used in Sweden can well explain the somewhat lower correlation (0.94) for slaughter quality index shown in table 4 for Sweden.

Genetic base

The genetic base for pure beef animals is based on the same principles for all relative breeding values with a mean of 100 and standard deviation of 10. The selection of animals to form the genetic base includes males and females with birth years 5 to 9 years prior to the publication date and having observations or having at least 5 offspring with observations for one trait in each trait group.

Breeding values for pure beef cattle are estimated four times per year, and EBVs are published at <u>NAV</u> <u>Beef Search</u>.

Interbeef EBVs are published at NAV Interbull Search.

NAV – frequency and timing of official runs

NAV has 4 large dairy evaluations per year, which include updated phenotypic and genomic data, and additional eight small runs including updated genotypes. In Table 5 the NAV and INTERBULL release dates for 2023 are shown. The beef evaluation based on beef x dairy crossbreeds take place along with the large NAV dairy runs 4 times a year. The NAV pure beef evaluation has its own time schedule.

Table 5. NAV and INTERBULL release dates in 2023. EBVs released at NAV dates in bold will be delivered to international genetic evaluation.

	Dairy Cattle			Beef Cattle	
Month	NAV	NAV		NAV	INTERBEEF
Month	Small run ¹⁾	Large runs ²⁾³⁾	INTERBULL	Pure Beef	
January 2023	3				
February 2023		7			
March 2023	7			7	3
April 2023	4		4	18	
May 2023		2			
June 2023	6			6	
July 2023	4				
August 2023		8	8		
September 2023	5				
October 2023	3				20
November 2023		7		7	
December 2023	5		5		

¹⁾ Genotypes updated; ²⁾ Genotypes and phenotypes updated; ³⁾ Beef × dairy evaluation

You can get more information about the joint Nordic evaluation: General about Nordic Cattle Genetic Evaluation: <u>www.nordicebv.info</u> Contact person: Gert Pedersen Aamand, Ph.: +45 21717788 <u>gap@lf.dk</u>

Denmark: www.landbrugsinfo.dk

Contact person: Ulrik Sander Nielsen, Seges Cattle, Ph. +45 29883403, usn@seges.dk

Sweden: <u>www.vxa.se</u> Contact person: Freddy Fikse, Växa, Ph +46 10 4710615. <u>Genetic.Evaluation@vxa.se</u>

Finland: <u>www.faba.fi</u> Contact person: Jukka Pösö, Faba co-op, Ph +358-400614035 jukka.poso@faba.fi