

News genomic prediction - NAV routine evaluation

2 July 2014

The latest NAV routine genomic prediction took place as scheduled. NAV did the genomic prediction in three breed groups: Holstein, Red Dairy Cattle, and Jersey.

Data used in genomic prediction

Genotypes were extracted from the joint Nordic SNP data base 20th June 2014. Interbull information was from April 2014. Nordic phenotypic information for the reference population used in the genomic prediction was the same as in the 2nd May 2014 routine evaluation.

News in relation to NAV genomic prediction

Significant improvement is introduced in the genomic prediction for RDC and Jersey:

- Females are included in the reference population
- Animal Model pedigree used in genomic prediction
- Revised blending procedure introduced

Inclusion of females gives a considerably higher reliability on genomic breeding values. This means that we more accurately can find the best males for AI, and the best females for ET or to inseminate with sexed semen.

The limited size of the reference group has been the major problem for RDC and especially Jersey since the beginning of calculation of breeding values with genomic information. Holstein has a much larger reference group, because the breed is considerably larger than RDC and Jersey, and because proven bulls from the EuroGenomics cooperation are also included. The possibilities to cooperate with other populations are limited for RDC and Jersey and the only other possibility to increase the reference population is to include females. At the moment Jersey is exchanging genotypes with US Jersey and RDC is exchanging with NRF.

VikingGenetics started in 2012 a cooperation with RDC and Jersey farmers in Denmark, Sweden and Finland genotyping all females of a certain age in the herds. This has increased the number of tested females considerably. Simultaneously with the testing of more females NAV has in close cooperation with MTT and AU developed and tested the genetic models and methods necessary to be able to include genotypes from females in the reference group.

Table 1 give an overview over the changes in the prediction, and table 2 an overview over the used reference populations for the three breeds in the July 2nd evaluation.

Table 1. Overview over changes in the genomic prediction for RDC and Jersey introduced July 2nd 2014

	Old model	New model 2 nd July	Comments
Pedigree in genomic prediction	Sire-Maternal grandsire	Animal Model	
Reference population	Bulls	Bulls + cows	6800 Jersey cows and 10000 RDC Cows included
Blending method	Method developed by MTT in 2010	Revised blending method developed by MTT in 2013/14	Revised method better avoid double counting, which make it possible to include females in ref population

Table 2. Reference population for the different breeds used in routine evaluation July 2nd

	Reference population	
	Bulls	Cows
Holstein	25700 ^{a)}	-
RDC	7800 ^{b)}	10000
Jersey	2400 ^{c)}	6800

a) Including NLD, FRA, DEU, ESP ref bulls; b) including NO ref bulls; c) including US ref bulls

About 10,000 RDC cows are included in the RDC reference population July 2nd and about 6,800 cows in the Jersey reference population. Preliminary studies indicate that adding a bull dam to the reference population has not a significant effect on the offspring's GEBVs. In the coming months we will study in more details the effect of using different groups of females in reference population.

Genotyped females are used in the reference population for the following traits: yield, udder health, conformation, temperament (only RDC) and milking speed. These are the traits where the breeding values of cows today are affected by own performance.

The genomic prediction for RDC and Jersey has been significantly improved, by adding genotyped females and modifying the blending method. The increase in reliabilities for RDC is on average about 5% and for Jersey about 8 % (table 3 and 4).

Table 3 Extra reliabilities for RDC using bulls or bulls+cows in the reference population – female information is included for traits market with **bold**

Reference population	Extra reliabilities next to pedigree information	
	Bulls	Bulls + cows
Trait		
Milk	0.17	0.23
Fat	0.16	0.23
Protein	0.12	0.18
Yield	0.13	0.18
Fertility	0.14	0.14
Birth index	0.18	0.18
Calving index	0.02	0.02
Mastitis	0.17	0.23
Other diseases	0.14	0.14
Body	0.24	0.29
Feet & Legs	0.24	0.33
Mammary	0.23	0.30
Milkability	0.17	0.22
Temperament	0.18	0.21
Longevity	0.07	0.07

Table 4 Extra reliabilities for Jersey using bulls or bulls+cows in the reference population - female information is included for traits market with bold

Reference population	Extra reliabilities next to pedigree information	
	Bulls	Bulls + cows
Trait		
Milk	0.23	0.37
Fat	0.13	0.21
Protein	0.18	0.32
Yield	0.16	0.22
Fertility	0.17	0.17
Birth index	0.00	0.00
Calving index	-0.02	-0.02
Mastitis	0.09	0.16
Other diseases	-0.11	-0.11
Body	0.19	0.30
Feet & Legs	0.05	0.13
Mammary	0.26	0.29
Milkability	0.15	0.34
Temperament	0.00	0.00
Longevity	0.11	0.11

Compared with Holstein the GEBV reliabilities for RDC and Jersey are still lower about 12-15% units lower, but significantly higher than before. In the near future more genotyped RDC and Jersey females will be lactating and be included in the reference population, and the GEBV reliabilities are expected to increase further.

The improvements in the genomic prediction also have the effect that the underestimation of genetic level that has previously been observed in RDC and Jersey is removed. For RDC the genotyped young bulls and heifers increase on average 4 index point for yield index and NTM, and between 0-2 index point for the other traits where cow information contribute to the reference population. For Jersey the corresponding results show an increase of 2 index point for Y-index and NTM, and 0-1 index point for the other traits where cow information contribute to the reference population.

The increase in reliabilities (table 3 and 4) - due to use of significant more information - makes it possible to more accurately identify the genetically best animals. However it also means that some re-ranking occurs among the already tested bulls and females. Results show, that the correlations between GEBVs in June and July will be in the range 0.80-0.90 for traits where cows have been added to the reference population (yield, udder health, conformation, temperament and milking speed). Jersey gain relatively more in reliabilities by adding female to the reference population, since the Jersey bull reference population is quite small, creating the largest re-ranking of animals.

Table 5. Correlations between GEBVs calculated June 2nd and July 2nd 2014

	RDC		Jersey	
	Genotyped young bulls and heifers	Genotyped cows	Genotyped young bulls and heifers	Genotyped cows
Traits without genotyped cows in reference population	0.97-99	0.97-0.99	0.94-0.96	0.94-0.96
Traits with genotyped cows in reference population	0.88-0.93	0.89-0.92	0.77-0.85	0.87-0.90

For yield this means that for about 20% of the heifers and cows the breeding value changes 5 or more index units.

Additional to this effect of reliability we should add the effect of improved mean when looking at changes in GEBV from June to July for genotyped heifers. The mean effect is as mentioned earlier largest for yield and NTM about 4 units for RDC and 2 units for Jersey.

We do see considerable changes in GEBV for RDC and Jersey, but in fact it is a positive story because adding cows to the reference population has increased the reliability of the GEBV for RDC and Jersey significantly, and justified the investment in genotyping females in large scale.

Use of females in reference population for more traits in RDC and Jersey, and inclusion of females in the reference group for Holstein will be investigated in the future.

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