

# News genomic prediction - NAV routine evaluation

## 3 March 2014

STØTTET AF  
mælkeafgiftsfonden

The latest NAV routine genomic prediction took place as scheduled. NAV carried out genomic prediction for Holstein, RDC and Jersey:

### Data used in genomic prediction

Genotypes were extracted from the joint Nordic SNP data base 18<sup>th</sup> February 2014. Interbull information was from December 2013. Genotypes for progeny tested Jersey bulls have been exchanged with US/CDN ultimo December 2013, and 1157 progeny tested US Jersey bulls were added to the Nordic Jersey reference population. Nordic phenotypic information for the reference population used in the genomic prediction was the same as in the 2<sup>nd</sup> February 2014 routine evaluation.

### News in relation to NAV genomic prediction

The US/CDN reference bulls are added to the Jersey reference population in the March 2<sup>nd</sup> routine run. The US jersey bulls contribute with daughter information via Interbull breeding values for traits with an international evaluation. It means that information are added to the reference population for production traits, type traits, longevity, mastitis, and fertility (Interbull traits), but not for birth, calving, milking speed, and other diseases (not Interbull traits)

The added information next to pedigree information, which can be explained by the genotypes, is presented in table 1 for a Nordic and Nordic+US/CDN bull reference population.

Table 1 Extra reliabilities for Jersey using Nordic or Nordic +US/CDN reference bulls

Reference population	Extra reliabilities next to pedigree information	
	Nordic+US/CDN bulls	Nordic bulls
<b>Trait</b>		
Milk	0.23	0.16
Fat	0.13	0.10
Protein	0.18	0.13
Yield	0.16	0.13
Fertility	0.17	0.17
Birth index	0.00	0.00
Calving index	-0.02	-0.02
Mastitis	0.09	0.08
Other diseases	-0.11	-0.11
Body	0.19	0.16
Leg	0.05	0.02
Mammary	0.26	0.11
Milkability	0.14	0.14
Longevity	0.11	0.19

The reliabilities increase for all Interbull traits except longevity by adding US bulls to the reference population. The size of the increase varies by traits, which can be partly explained by the genetic correlation between US/CDN and Nordic countries for the particular trait, and that a relatively low number of bulls are included in the validation data set. For longevity the reliability seems to drop, which is unexpected and has to be studied in details.

The correlations between NTM GEBVs for young bulls from an evaluation with and without US/CDN reference bulls are 92%, indicating that candidate animals as expected are somewhat re-ranked due to the increased reliabilities. The corresponding correlations for the single traits where the US/CDN bulls contribute with information vary from 89% to 97%.

The genetic level of son groups after Danish bull sires are unchanged, but within son groups some re-ranking has taken place due to increase on information. 66 Danish sons of US/CDN bulls have on average increased by 4.4 NTM units, due to more information about Interbull traits from the US/CDN reference bulls.

**General about Nordic Cattle Genetic Evaluation:** [www.nordicebv.info](http://www.nordicebv.info)

Contact person: Gert Pedersen Aamand, Ph.: +45 87405288 [gap@vfl.dk](mailto:gap@vfl.dk),

**Denmark:** <https://www.landbrugsinfo.dk>

Contact person: Ulrik Sander Nielsen, Danish Cattle, Ph. +45 87405289, [usn@vfl.dk](mailto:usn@vfl.dk)

**Sweden:** [www.sweebv.info](http://www.sweebv.info), [www.vxa.se](http://www.vxa.se)

Contact person: Jan-Åke Eriksson, Swedish Dairy Association, Ph. +46 08-790 58 67

[Jan-Ake.Eriksson@vxa.se](mailto:Jan-Ake.Eriksson@vxa.se)

**Finland:** [www.faba.fi](http://www.faba.fi)

Contact person: Jukka Pösö, Faba co-op, Ph +358-(0)207472071 [jukka.poso@faba.fi](mailto:jukka.poso@faba.fi)