News genomic prediction - NAV routine evaluation
2 July 2013

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 June 14th 2013. Interbull information from April 2013. Nordic phenotypic information used in the genomic prediction was the same as in the 2nd May 2013 routine evaluation.

News in relation to NAV genomic prediction
July 2nd LD (10K) genotypes is included in the routine evaluation. To be able to impute the LD chip a few modifications has been introduced in the editing of SNPs:

- Only SNPs where ≥ 20 % of Animals tested in Denmark, Sweden, and Finland have a result.
- Only SNPs with known position – only one SNP/position allowed (duplicates).

The X-chromosome has until June 2nd been included in the genomic prediction for RDC and Jersey. But imputation from 10K to 54K is complicated for the X-chromosome and requires more research, and the X-chromosome has been removed from the genomic prediction July 2nd. It has earlier been shown that the effect of including SNPs on the X-chromosome was very minor.

The imputation is done by either the Beagle or FImpute software. Beagle has been shown to do best in all imputation studies, but Beagle is very time consuming when the reference panel is large. FImpute is fast and has performed among the best imputations programme next to Beagle. Main difference is that FImpute use pedigree information more than Beagle when doing the imputation. NAV can currently handle Beagle on a routine basis within Jersey and RDC (with some restrictions in the reference panel). For RDC only bull genotypes from Finland, Sweden and Denmark are used in the imputation to be able to apply Beagle. FImpute is used for Holstein. In table 1 results from imputations studies are shown for the three breeds.

Table 1. Genotype error rates (number of animals) – imputation from 10K to 54K. Animals genotyped in 2013

Breed	Imputation software	Only sire genotyped	Sire and dam genotyped
Holstein	FImpute	3.2 (1213)	0.7 (432)
Holstein	Beagle	Cannot be handled on routine basis	
RDC – all genotypes	FImpute	4.3 (1147)	0.7 (234)
RDC – all genotypes	Beagle	1.3 (1147)	1.0 (234)
RDC- all bull genotypes except Geno bulls	Beagle	1.4 (1147)	1.1 (234)**
Jersey	FImpute	1.5 (110)	0.5 (75)
Jersey	Beagle	Not investigated, but Beagle is expected to perform better than FImpute	

The imputation has been applied on:
- 54K genotypes – all missing SNPs are imputed – major effect across Illumina version 1 and version 2
- Imputation from 10K to 54K

In the July 2nd evaluation approx. 700 Eurogenomics bulls have not been included in the reference population due to a minor SNP database problem. The bulls will be included again in the August evaluation.

The changes in editing of SNPs create a little bit bigger changes than we normally have seen when comparing GEBVs from two subsequent evaluations. Furthermore we do see a slightly higher standard deviation and genetic trend for all breeds after introducing the new editing and imputation of 54K genotypes.