Update genomic selection including GMACE

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Status genomic prediction

- **Start 2008**

- **First routine evaluation May 2011**

- **Stepwise improvement from 2011**

Bulls with known EBVs and SNPs create the "DNA-dictionary"

DNA-dictionary

The quality of the dictionary is correlated to the size of the <u>reference population</u>

SNPs ⟷ EBVs

NAV - Routine genomic prediction January 2013

- **Only data from 50K -100 euro per test**
- **Reference population only bulls**
- **GBLUP, 2 step approach**
- **Monthly genomic prediction**
- **Publication age 17 month**

How will the near future look like?

NAV - Routine genomic prediction - identified problems to solve right away

- Some instability in Feet&Legs GEBV for Holstein - bulls with a lots of sons in Eurogenomic countries and lots of daughters genotyped. (We believe the problems relates to the fact that Eurogenomics bulls only have EBVs for 3 out of the 5 traits – has to analyzed further)

- GEBVs for longevity and temperament for Holstein do at the moment not fulfill Interbull validation requirements.

NAV - Routine genomic prediction - short term

- **GEBV for genotyped daughter proven bulls**

- **Official reliability for GEBVs**

- **New exchange of reference bulls – Jersey**

- **Exchange of young bulls RDC (Geno) and Holstein (Eurogenomics) (pilot study)**

- **Service foreign females**

- **Interbull validation**

How to increase genomic reliabilities?

- **Genotyping and sequencing technologies**
- **Statistical models**

How to increase genomic reliabilities?

Genotyping and sequencing technologies

- 7K, **9K**, 50K, (700K), (Sequencing)

Handling 9K and 50K at the same time require routine imputation

- A new routine has to be implemented

- A challenge a long with monthly evaluation

How to increase genomic reliabilities?

Genotyping and sequencing technologies

7K, <u>9K</u>, <u>50K</u>, (700K), (Sequencing)

Lower prices more females tested

- Females in reference population (US has 35,000 Holstein cows in ref. today – Ireland expect to test 25,000 in 2013!)

- More reference animals higher reliabilities

- Largest gain smallest ref. population today

- New traits

How to increase genomic reliabilities?

Future statistical models (<u>GBLUP</u>/SNP-BLUP, Haplotype models, Bayesian, One step)

- **Handle selection (only the best bulls will be daughter proven) (One step)**

- **Use all phenotypes and genotypes simultaneously (One step)**

- **Take as much genetic information as possible out of the SNPs (Haplotype, Bayesian)**

How to look at genomic information

- Give some information about the genetic value of an animal

- Has low to medium reliability 30-60%

- Similar to information from an additional lactation of a cow or new daughters of a bull

- Advantage "expressed" early in an animals life and in both sexes

Bull dam GEBVs?

Bull dam yield records

Some discussion about potential bias in GEBV caused by bull dams own performance

- **Difficult to define which records are biased**

- **Near future with:**

  - **Lots of females tested**

  - **Females in reference population**

  - **One step methods (everything solved simultaneously)**

- **Bull dams are mainly heifers**

Interbull
Validation and plans for international GEBV

April 2012	**Validation fat, protein, milk for HOL, RDC and JER**
September 2012	**Validation selected traits for HOL: SCC, NR56, stature and longevity**
October 2012	**Validation all traits**
September 2012	**Test run for HOL for all Interbull traits**
February 2013	**Validation all traits and 2nd test run**
August 2013	**1st routine run**

Robust GMACE

The method will deliver:

- **GEBV for young genotyped bulls on the same scale as EBVs for the daughter proven bulls (e.g. a German genotyped bull get a GEBV on the NAV scale)**

- **Note direct use of the genotype in the national prediction formulas always give a GEBV with a higher reliability than a "converted" GEBV from GMACE**

NAV has a lot of challenges in 2013