# Software expectations from the industry: genetic evaluations for the future

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NAV

# Nordic Cattle Genetic Evaluations

- Responsible for joint genetic evaluation for dairy cattle across Sweden, Finland and Denmark
- Populations sizes
  - 360,000 RDC cows
  - 800,000 Holstein cows
  - 70,000 Jersey cows

# NAV routine genetic evaluation

- Traditional genetic evaluation (4 times a year)
  - Phenotypes
- Genomic prediction (12 times a year)
  - Genotypes+Phenotypes (DRP)
    - Two steps

# Traits in genetic evaluation

- Yield traits
- Beef traits
- Fertility traits
- Calving traits
- Udder health
- Claw health
- Other disease
- Longevity
- Type traits
- Young stock survival

**On average 25 years of data**

# Traditional genetic evaluation

## How are traits measured?

- Continuous
- Classes (0/1 or 0-4)

## Statistical models

- We apply linear Multi Trait and Multi Lactation models
- We assume normality - not 100% perfect

# Genetic evaluation

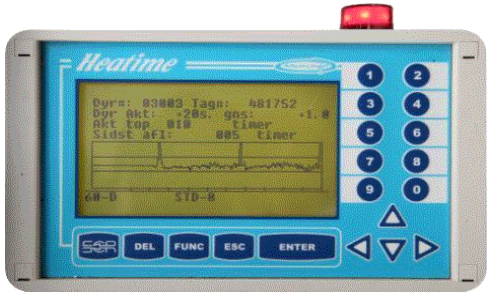
- Traditional genetic evaluation (4 times a year)
  - Phenotypes all traits

**New phenotypes**

**AMS systems**


**Yield per quarter, milking time, weight, activity, rumination ect.**

**Stand-alone systems**




**Activity and rumination**

**Milk recording - New lab tests**

**Pregnancy tests and BHB (beta-hydroxybutyrate)**

# Last 5 years

- **Tissue sampling**
- **>20.000 in 2014 – increasing!**

**SNP's**

# Routine genomic prediction

Phenotype eg milk yield
(DRP derived from EBV)

SNP's

GEBV

# Traditional evaluation and genomic prediction for Holstein - yield information

| | | |
|---|---|---|
| 100 mio testdays | 22 mio testdays | 60 mio testdays |
| 12.000 GT cows | 5.000 GT cows | 3.000 GT cows |

26.000 Nordic and foreign bulls

NAV

390 mio MME solved to calculate GEBV

# Next 5 years

- **Tissue sampling**
- **all animals at birth in 2018 (?) – increasing number of genotypes!**

**SNP's**

# Genetic evaluation

- Traditional genetic evaluation (4 times a year)
  - Phenotypes (+ more daily measurements)
- Genomic prediction (weekly)
  - More genotypes+phenotypes
  - Two steps (simultaneously use of genotypes and phenotypes–one step)
  - Include knowledge about QTLs or SNPs carrying substantial amount of information

# MIX99 use in NAV

- MIX99 used since the first joint Nordic routine run in 2005
  - Current use
    - Estimation of breeding values – mastitis, milk yield incl. HV correction
    - DRP calculations in relation genomic prediction
    - Reliabilities

# Software - key point for routine evaluation in practice

- A reliable software program with backup from program developer
- Flexible models
- Optimal use of computer capacity
- Efficient solving algorithm – has always been critical within dairy cattle breeding and will also in the near future be a challenge

**MIX99 has so far done an excellent job for NAV**