



Genomic prediction of (Swedish) Hereford and Charolais

Freddy Fikse, Växa
Susanne Eriksson, SLU
Anahit Nazari Ghadikolaei, SLU



Svensk Köttrasprövning





Aims of the project

- Start Swedish reference populations for the two most common beef breeds in Sweden: Charolais and Hereford.
- Develop estimation of genomic enhanced breeding values, single-step, using already recorded phenotypic information from Swedish beef recording scheme.
- Literature study: known genes of importance for qualitative traits.

Our study – genotyping

- Eurogenomics bovine MD SNP array, Eurofins DNK.
- SNP-data into NAV-database, available for parentage testing, monogenetic traits and future genomic evaluations.
- Aim ~2000 ind. per breed, easier for CHA than HER.
+ Genotypes from new SNP-pedigree verification (few so far).
- Blood samples collected (since 2008) for station performance tested bulls
 - 706 from "recent" years, 70% CHA, + 17 hair samples sent for genotyping

Going Nordic

- All genotypes stored at NAV (i.e. also Danish and Finnish genotypes)
- NAV Purebred beef evaluation – Mar 2022
 - Carcass traits
- Hereford and Charolais

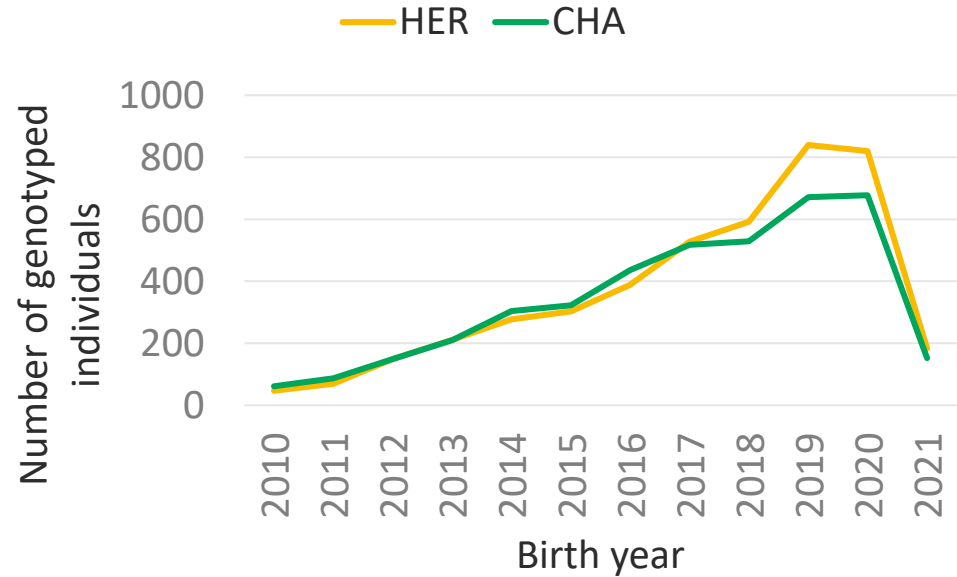
NAV



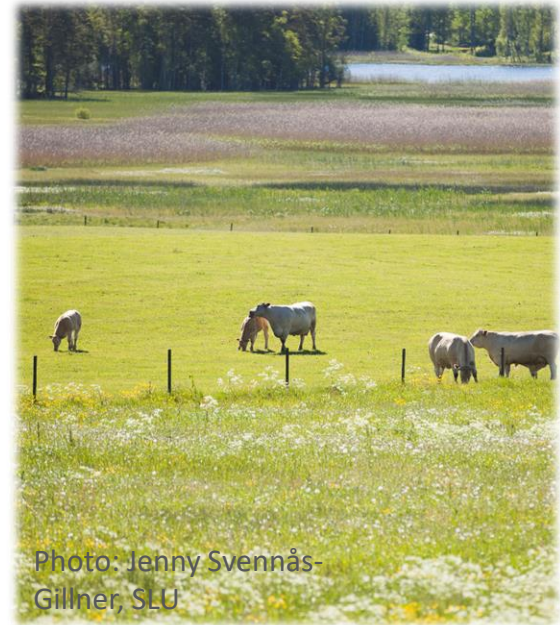
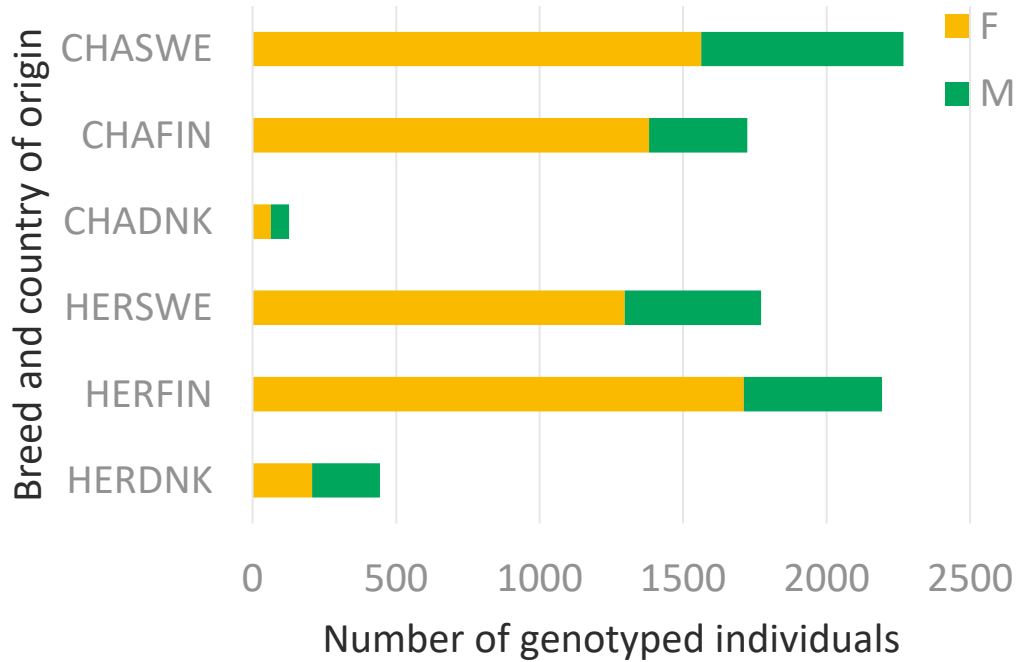
Nordisk Avlsværdis Vurdering •

Genotypes available

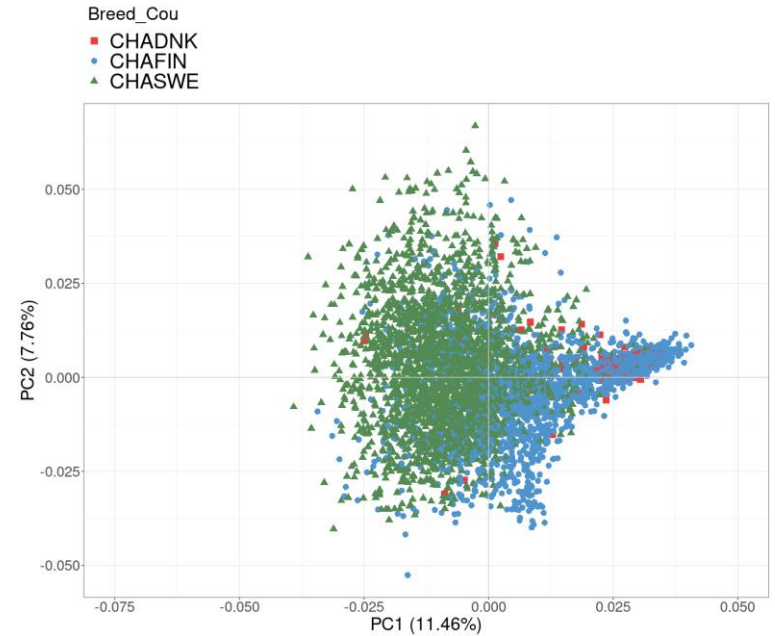
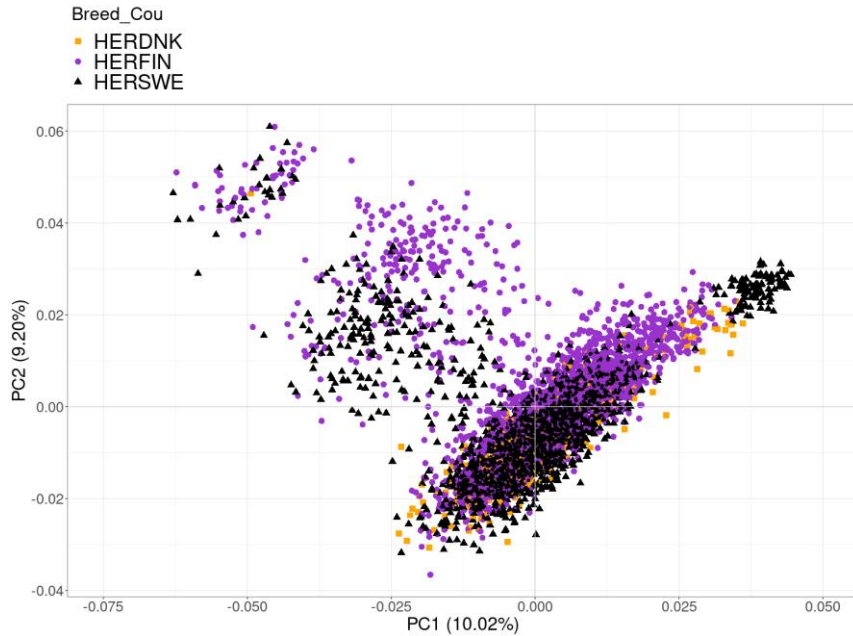
- 9663 animals
- 75699 markers
- Cleaning
- 8527 animals
- ~43000 markers



Genotypes by breed and sex



Nordic populations are well-mixed, genomically

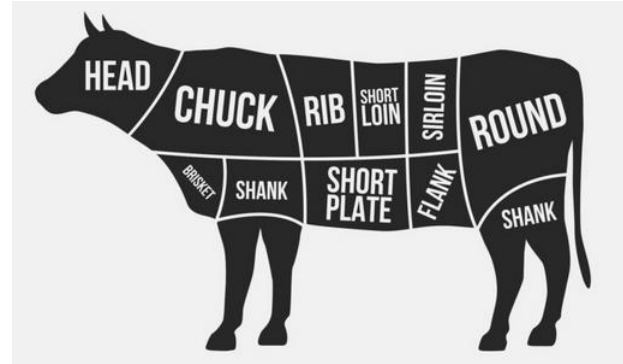


Carcass genetic evaluation

7 traits (10 breeding values)

- Birth weight*
- Weaning weight gain*
- Post-weaning weight gain (FIN&SWE)
- Yearling weight (DNK)*
- Slaughter daily gain
- EUROP conformation class
- EUROP fat class

* *maternal and direct breeding values*



NAV



Nordisk Avlsværdi Vurdering • Nordic Cattle Genetic Evaluation

Analysis

1. Genetic evaluation using phenotypic registrations and **pedigree** (PBLUP / pedigree BLUP)
2. Genetic evaluation using phenotypic registrations and **pedigree** and **genotypes** (ssGBLUP / single-step GBLUP)
 - A. Full: Using all phenotypic registrations
 - B. Reduced: Discarding phenotypic registrations ≥ 2019

What do we look at?

- Genetic trend

We expect:

- Same genetic trend for Pedigree-BLUP and single-step GBLUP
- Same genetic trend in analyses of full and reduced data

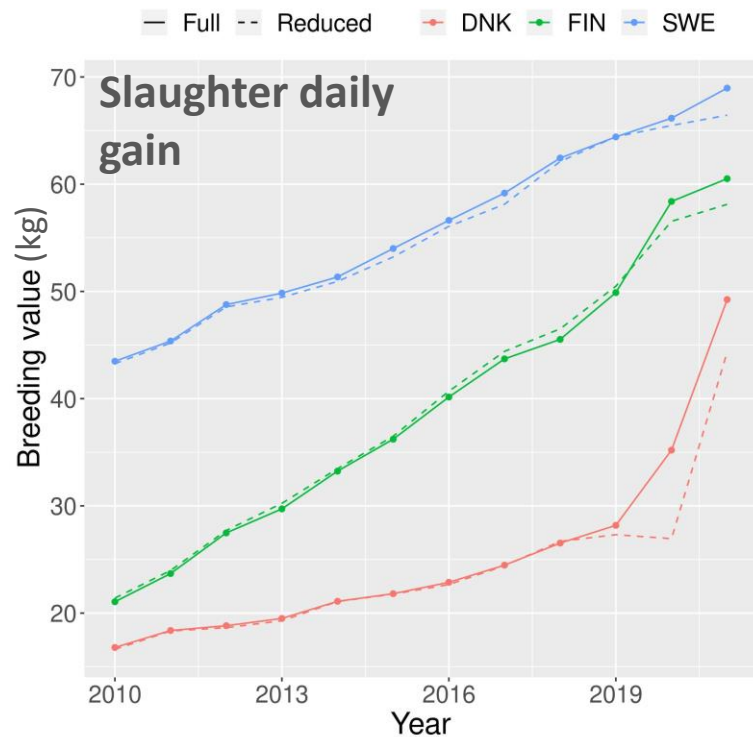
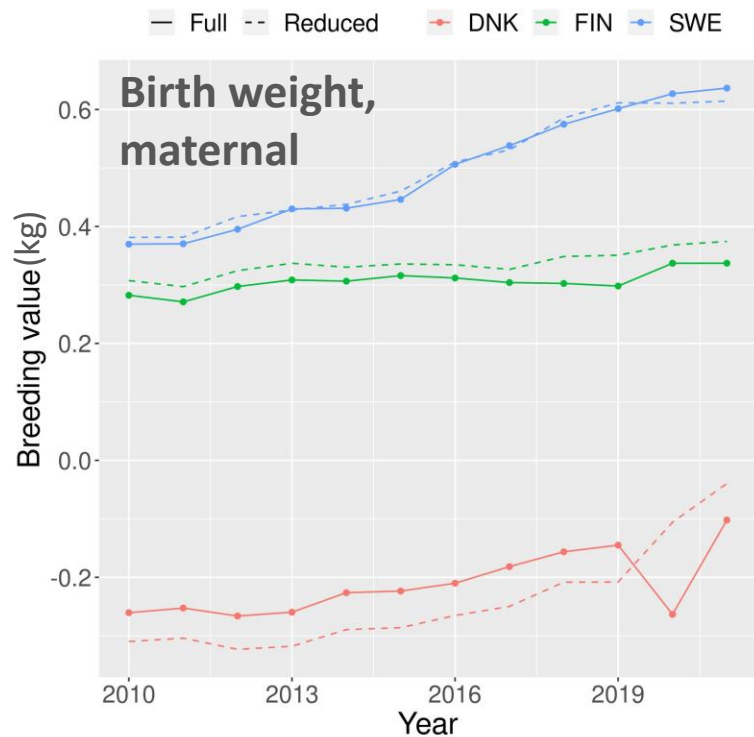
- Reliability

We expect:

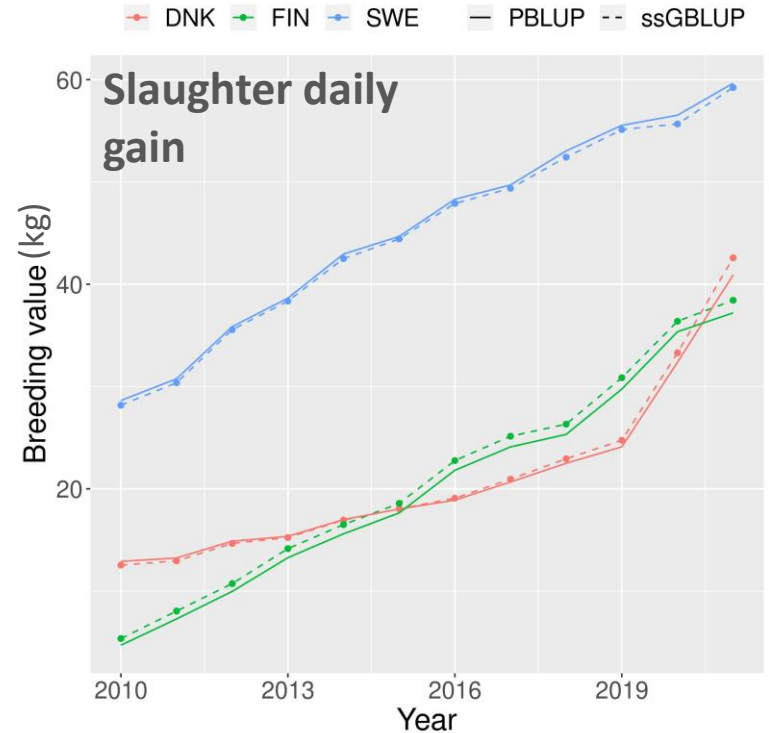
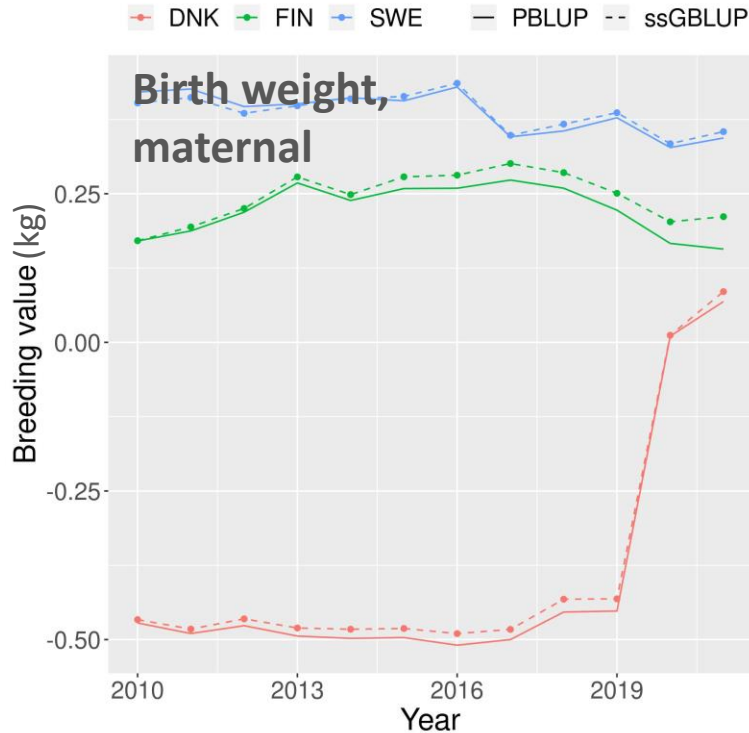
- For ungenotyped animals same reliability with ssGBLUP as with PBLUP
- For genotyped animals higher reliability with ssGBLUP as with PBLUP



Genetic trend with Full and Reduced data Charolais – single-step GBLUP



Genetic trend Pedigree BLUP and single-step GBLUP Hereford



What did we find?

- Genetic trend

We expect:

- Same genetic trend for Pedigree-BLUP and single-step GBLUP

Essentially the same genetic trend

- Same genetic trend in analyses of full and reduced data

Similar genetic trend

- Best for direct traits, somewhat more variation for maternal traits
- Best for Fin and Swe, somewhat more variation for DNK

What did we find?

- Reliability

We expect:

- For ungenotyped animals same reliability with ssGBLUP as with PBLUP

Essentially the same reliability with PBLUP and ssGBLUP for ungenotyped animals

- For genotyped animals higher reliability with ssGBLUP as with PBLUP

Higher reliability (5-71%) with ssGBLUP than with PBLUP

Somewhat larger increase for SWE than for FIN

Relative increase in accuracy PBLUP \Rightarrow ssGBLUP

Hereford ♀	FIN	SWE	Charolais ♀	FIN	SWE
Birth weight, M	31%	38%	Birth weight, M	18%	16%
Birth weight, D	35%	57%	Birth weight, D	20%	22%
Weaning weight, M	24%	40%	Weaning weight, M	19%	34%
Weaning weight, D	64%	51%	Weaning weight, D	26%	42%
Post-weaning gain	33%	71%	Post-weaning gain	11%	26%
Slaughter daily gain	38%	66%	Slaughter daily gain	22%	40%
Carcass conformation	26%	32%	Carcass conformation	05%	16%
Carcass fat	37%	43%	Carcass fat	09%	23%

Genotyping makes finding high index animals easier

Genotyped offspring of a Hereford AI bull

Weaning weight, M (kg)	PBLUP	ssGBLUP
Highest	19.1	21.9
Best 5%	17.3	20.2
Best 10%	16.3	19.0

Genotyped offspring of a Charolais AI bull

Weaning weight, D (kg)	PBLUP	ssGBLUP
Highest	17.0	21.3
Best 5%	15.2	17.1
Best 10%	14.8	16.0

Final Remarks

- Nordic populations well-mixed, genomically
 - Meaningful to have a joint Nordic (genomic) evaluation
- Genetic trends the same with and without the use of genotypes
 - Pedigree BLUP and single-step GBLUP
- Considerable (relative) increase in accuracies
 - The more genotypes (for phenotyped animals), the larger increase in accuracy
- More animals are already genotyped



Picture: Fredrik Saarkoppel, SLU