SLU

Single-step GBLUP for growth and carcass traits in Nordic beef cattle

Anahit Nazari-Ghadikolaei, SLU

Susanne Eriksson, SLU

Freddy Fikse, Växa

VÄXA

VIKINGGENETICS

BLUPF90

Stiftelsen Lantbruksforskning

Svensk Köttrasprövning

Introduction

- The importance of specialized beef breeds in Nordic counties:
  - Decrease in number of dairy cattle
  - Usage of beef semen in dairy herds

- Lower accuracy for GEBVs in beef cattle due to :
  - Small reference populations
  - Fewer progeny testing
  - Limited use of artificial insemination (AI)

(Meuwissen *et al.*, 2016)

https://www.nordgen.org/en/native-breed/swedish-mountain-cattle/

- Single-step genomic prediction (ssGBLUP) has been applied successfully, e.g. in Angus breed in the US.

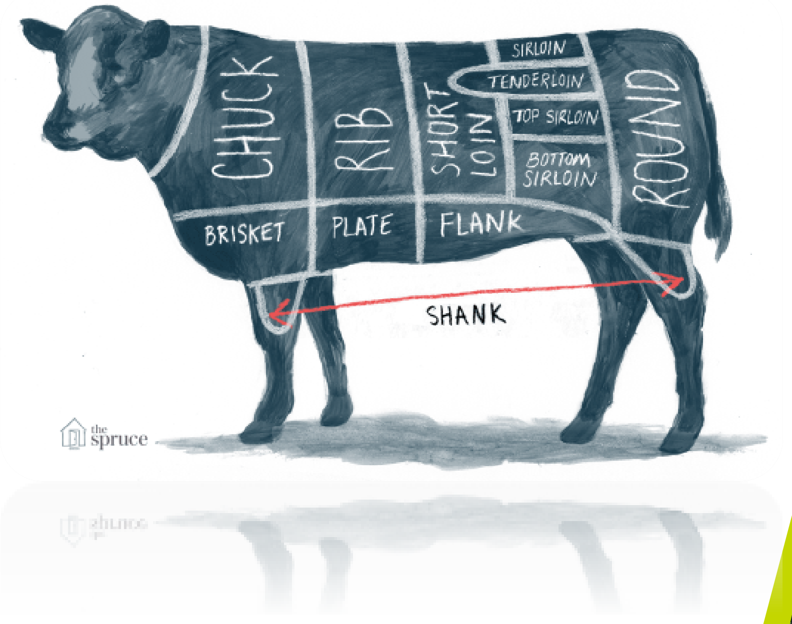
(Lourenco *et al.*, 2015)

Aim of the study

- Building the reference population → **Charolais** and **Hereford** beef breeds in Sweden/Nordic countries
- Enable of introduction of single-step genomic evaluations → **GEBVs**
- Comparing Pedigree BLUP (PBLUP) with ssGBLUP
- Estimating dispersion (b1 value) and relative accuracy improvements using ssGBLUP

https://commons.wikimedia.org/wiki/File:Sweden_(Unsplash_vrT3Z9UKFEg).jpg

Animals and Genotypes



- **7 growth and carcass traits**:
  - Birth weight* (BW)
  - Weaning weight gain* (WWG)
  - Post-weaning weight gain (PWG) → (FIN&SWE)
  - Yearling weight* (YW) → (DNK)
  - Slaughter daily gain (SDG)
  - EUROP conformation class (SCONF)
  - EUROP fat class (SFAT)

** maternal and direct breeding values*

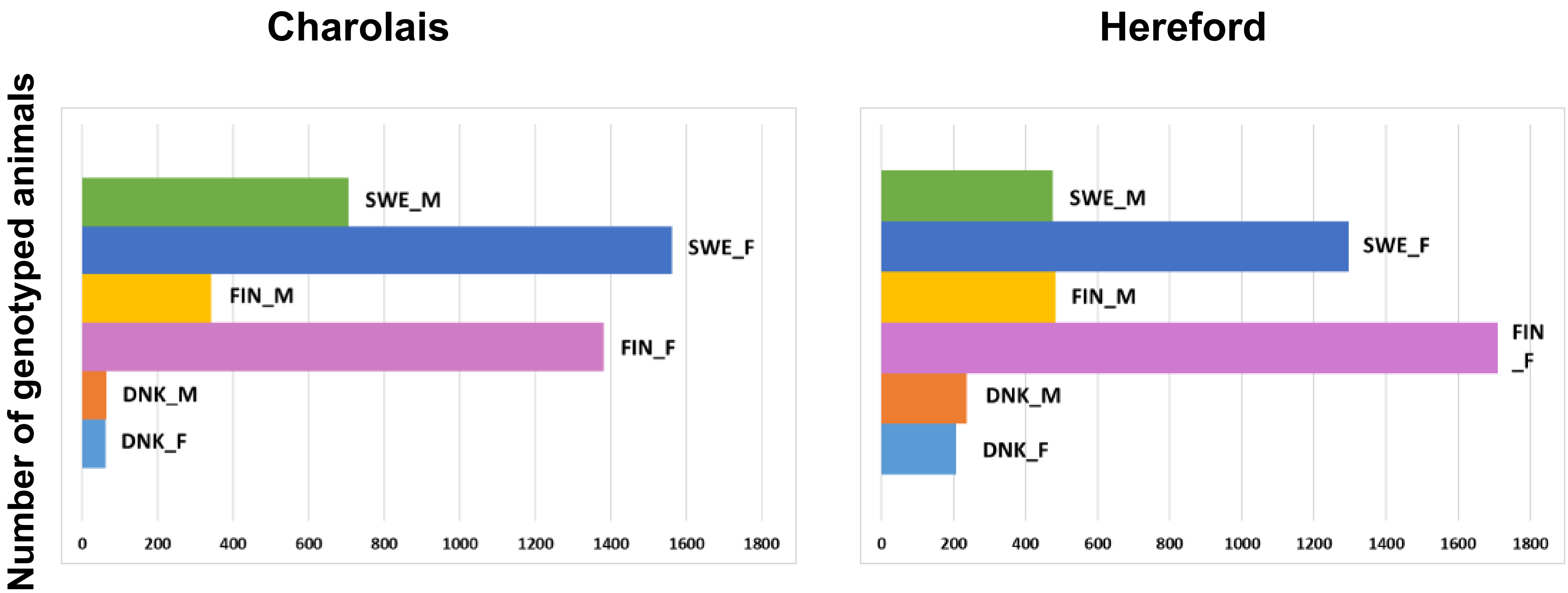
Animals and Genotypes

- **358198** records for **Charolais**
- **406857** records for **Hereford**

- Eurogenomics bovine MD SNP array, Eurofins DNK → **50K**
- **After QC**

- **Charolais:**
  - **4321** Animals, **43141** SNPs
- **Hereford:**
  - **4532** Animals, **40988** SNPs

Number of genotyped animals for each breed, by country and sex



Methods

Breed-wise multi-trait animal model

- **Fixed**

- Country-sex
- Country-twin *(only carcass)*
- Country-year-month
- Country-dam age-time
- CG: Herd-birth year
- Adjustment for age at weighing *(only carcass)*

- **Random**

- Animal genetic
- Maternal genetic
- Dam permanent environmental (maternal)

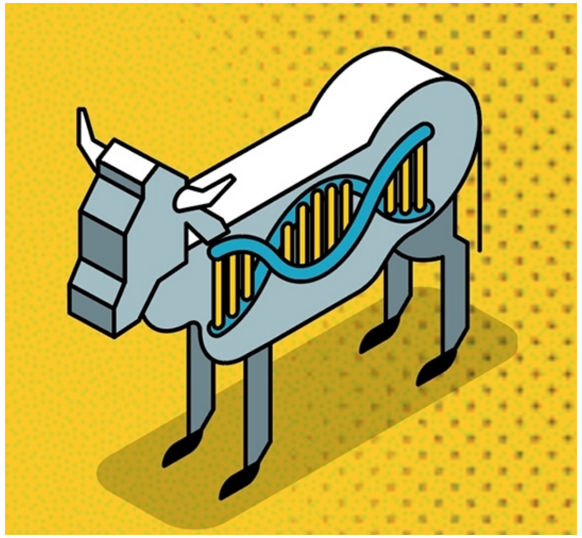
And genetic groups (GG)

Provided by Elisenda Rius-Vilarrasa

NAV

Nordisk Avlsværdi Vurdering •

Methods



- **PCA** → very brief population study
- single-step GBLUP → BLUP90IOD2
- Truncated data set→ removing data **from > 2018**
- Using unknown parent groups (**UPGs)**
- Multi-trait animal model

Methods

- Dispersion (b1 value) and Relative accuracy improvement for female genotyped animals in validation set (2019-2021) → **LR method** by Legarra and Reverter 2018

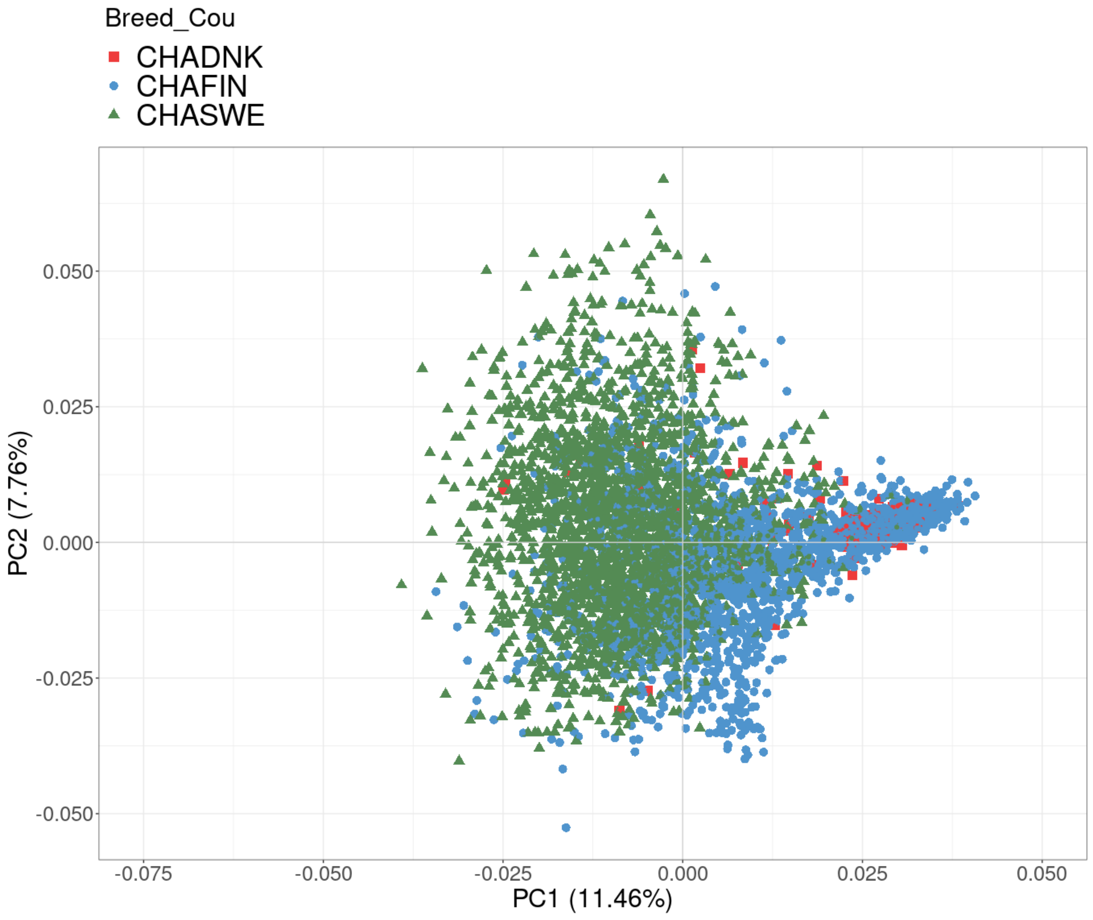
$$b_{w,p} = \frac{cov(u_w, u_p)}{var(u_p)}$$

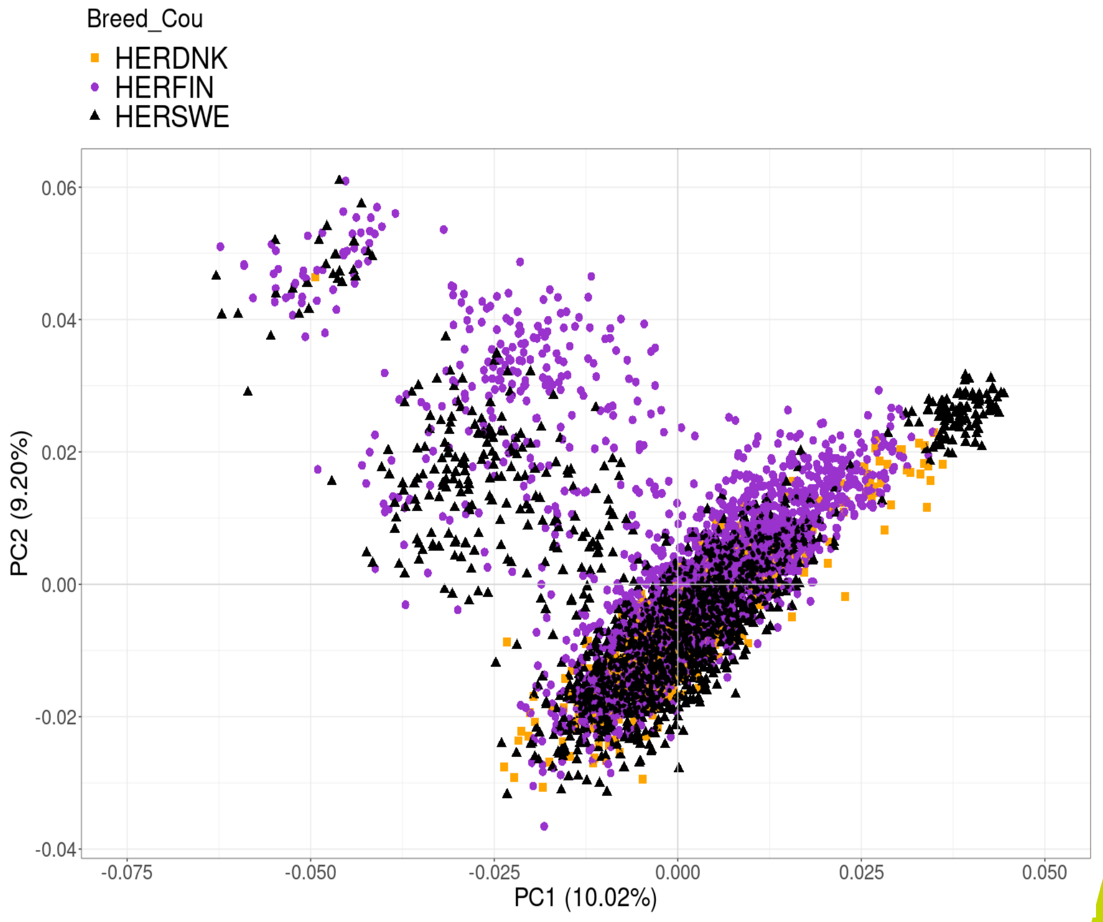
- Estimating **dispersion (b1 values) and relative accuracy improvements** when using different weight for alpha in ssGBLUP for building H inverse matrix → **Alpha=0.95** and **Alpha= 0.70**

$$(G = \boxed{\alpha}G + (1-\alpha)A_{22})$$

Results

Nordic beef populations are genomically well-mixed





Results

Dispersion (b1 value) genotyped females in test set

Charolais ♀	**PBLUP**		**ssGBLUP($\alpha_{0.95}$)**		**ssGBLUP($\alpha_{0.70}$)**	
Traits	FIN	SWE	FIN	SWE	FIN	SWE
BW-D	0.96	0.88	0.99	0.97	1.01	0.99
BW- M	0.93	0.87	0.98	0.98	0.98	0.99
WWG-D	0.92	0.73	0.92	0.87	0.94	0.91
WWG-M	0.88	0.72	0.91	0.90	0.93	0.93
YW-D	0.96	0.66	0.93	0.83	0.96	0.88
YW- M	0.90	0.67	0.98	0.90	0.99	0.93
PWG	1.02	0.70	0.97	0.87	0.98	0.91
SDG	0.94	0.64	0.92	0.80	0.95	0.86
SCONF	1.10	0.90	1.05	0.94	1.05	0.96
SFAT	1.10	0.98	0.97	0.98	0.98	0.99

- **ssGBLUP could result in less dispersion (b1 values closer to 1), especially using alpha value of 0.70.**

Results

Dispersion (b1 value) genotyped females in test set

Hereford ♀	**PBLUP**		**ssGBLUP($\alpha_{0.95}$)**		**ssGBLUP($\alpha_{0.70}$)**	
Traits	FIN	SWE	FIN	SWE	FIN	SWE
BW-D	0.96	0.88	1.02	0.95	1.04	0.99
BW- M	1.00	0.97	1.05	0.88	1.05	0.93
WWG-D	0.71	0.85	0.88	0.90	0.92	0.94
WWG-M	0.89	0.83	0.88	0.88	0.92	0.92
YW-D	0.82	0.86	0.90	0.89	0.94	0.94
YW- M	0.86	0.86	0.90	0.87	0.94	0.92
PWG	0.95	0.77	0.91	0.85	0.94	0.90
SDG	0.79	0.75	0.80	0.84	0.86	0.89
SCONF	1.05	1.03	1.04	1.01	1.04	1.02
SFAT	0.73	0.99	0.92	0.89	0.95	0.94

- **ssGBLUP could result in less dispersion (b1 values closer to 1), especially using alpha value of 0.70.**

Relative increase in accuracy PBLUP ⇨ ssGBLUP in Genotyped Animals

all numbers are shown in%

Genotyped females in test set	**Charolais**				**Hereford**			
	$\alpha_{0.95}$		$\alpha_{0.70}$		$\alpha_{0.95}$		$\alpha_{0.70}$	
Traits	FIN	SWE	FIN	SWE	FIN	SWE	FIN	SWE
BW-D	20	22	14	15	35	57	28	44
BW-M	18	16	10	10	31	38	21	26
WWG-D	26	42	18	30	64	51	48	38
WWG-M	19	34	12	21	24	40	13	22
YW-D	18	4	13	28	52	60	40	46
YW-M	18	38	12	23	25	37	14	20
PWG	11	26	7	18	33	71	23	49
SDG	22	4	16	26	38	66	26	43
SCONF	5	16	3	9	26	32	19	22
SFAT	9	23	6	15	37	43	24	29

Discussion

- Using ssGBLUP could improve the dispersion (b1) values; *(less dispersed and closer to 1).*

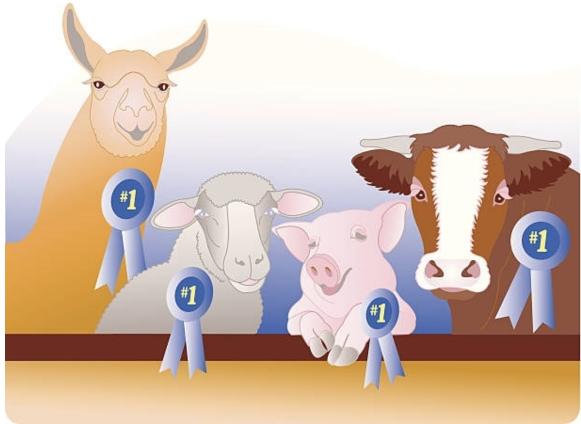
  In line with ➡ Mehrban *et al*., 2019 and Adekale *et al*., 2023 in Hanwoo and German beef breeds.

- Relative accuracy improved using ssGBLUP vs PBLUP.

  In line with ➡ Lourenco *et al*., 2015 and Mehrban *et al*., 2019 in Angus and Hanwoo beef breeds.

Discussion

- Using alpha 0.70 **($G=\alpha G+(1-\alpha)A_{22}$)** could make b1 values less dispersed from 1 (optimum value) in both breeds/countries.
- Using alpha 0.70 reduced relative accuracy improvements in both breeds /countries.
- The results are in agreement with Guarini *et al.*, 2018 and McMillan and Swan (2017) in Holstein cattle and Australian sheep breeds respectively.



https://www.milkgenomics.org/?splash=makes-good-dairy-cow

conclusion

- **PCA**

  -Nordic beef cattle population → **Well Mixed**

  ↓

  Joined evaluation makes sense

- Using **ssGBLUP** in Nordic beef cattle population
  - Less dispersion (deviation from 1)
  - Higher realtive accuracy
- Changing (reducing) alpha value to 0.70, improved the dispersion **(b1 value closer to 1**)

http://honeyrockdawn.com/2013/04/the-story-of-the-gray-baby/

ssGBLUP is beneficial for genomic selection in Nordic beef cattle population

Thank you! ☺

anahit.nazari@slu.se