Joint Nordic evaluation for Pure bred Beef

Växa Sverige

Elisenda Rius-Vilarrasa

Freddy Fikse

(Emma Carlén)

SEGES

Lisa Hein

Kevin Byskov

(Anders Fogh)

NAV

Gert Pedersen Aamand

Faba Co-op

Jukka Pösö

Kaisa Sirkko

NAV Pure bred Beef webinar, 19th of January 2021

Aim

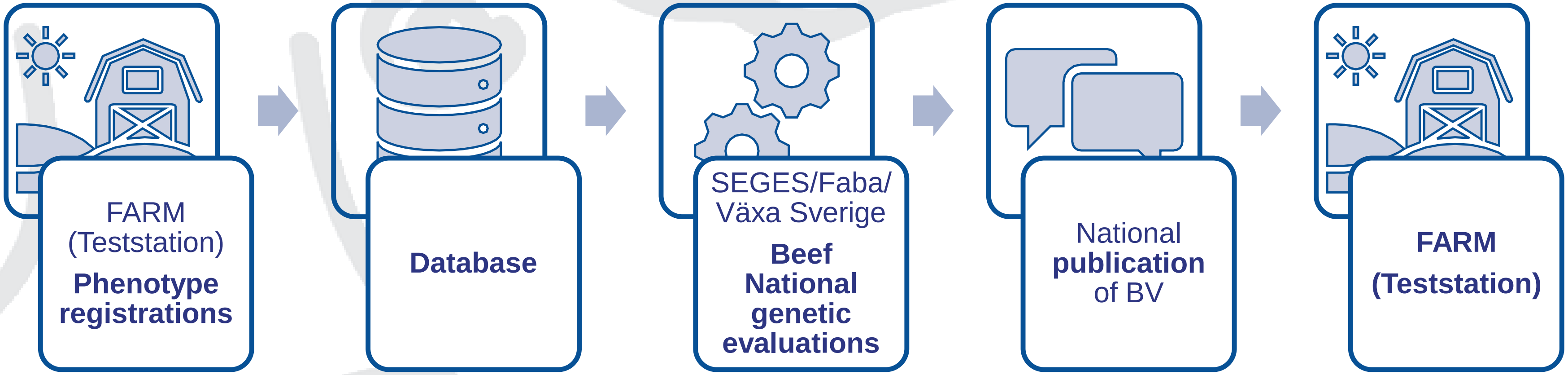
To develop join modern Nordic genetic evaluations for Pure bred Beef

Traits: Calving traits, **growth and carcass traits** (Estimate single breeding values)

Outline

1. Moving from National to Nordic genetic evaluations
2. Differences between NAV vs. National genetic evaluations
   I. Trait definition
   II. Data handling
   III. Genetic model

Current logistics for Pure bred Beef genetic evaluations



FARM (Teststation)

Phenotype registrations

Database

SEGES/Faba/ Växa Sverige

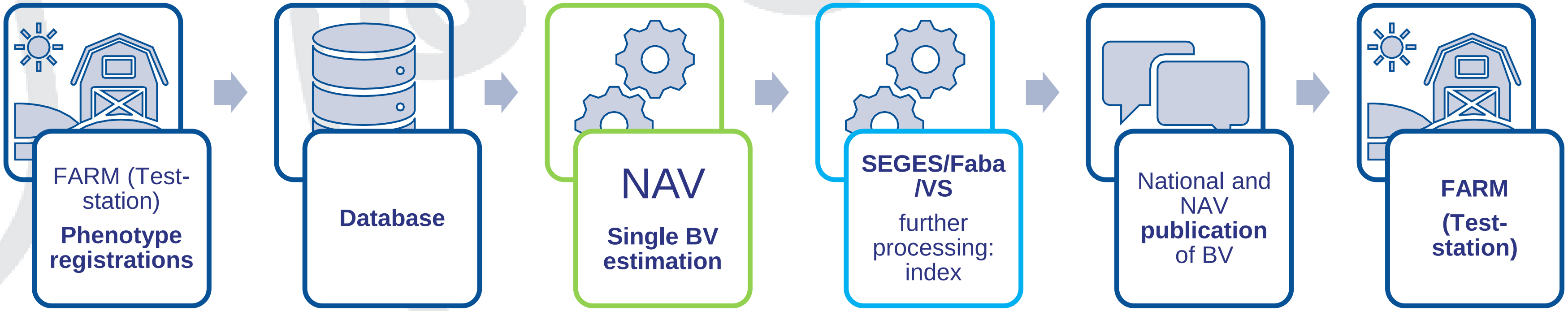
Beef National genetic evaluations

National **publication** of BV

FARM

(Teststation)

Future logistics for Pure bred Beef genetic evaluations



FARM (Test-station)
Phenotype registrations

Database

NAV
Single BV estimation

SEGES/Faba/VS
further processing: index

National and NAV **publication** of BV

FARM (Test-station)

Differences NAV vs. National genetic evaluations

DATA HANDLING

Data – weight and carcass records

- **Data:** Birth, weaning and post-weaning weights and carcass records since the 80's for DNK and SWE and 90's for FIN
- **From:** Farmers, test stations (SWE) and slaughter houses
- **Breeds:** Aberdeen Angus (AAN), Beef Simmental (SIM),Charolais (CHA),Hereford (HER),Limousine (LIM)

Trait definitions

- **Birth weight:** 1 – 5 days
- **Weaning weight:** 50 – 260 kg and 140 – 260 days
- **Yearling weight :** 100 – 850 kg and 290 – 425 days
- **Slaughter weight:** 56 – 1150 kg and 185 – 1200 days
- **Conformation class:** EUROP scale from 1 – 15
- **Fat class:** EUROP scale from 1 – 5

Growth trait definitions

$$\boldsymbol{Weaning\ weigh\ gain} = \frac{Weaning\ weight - birth\ weight}{weaning\ age}$$

$$\boldsymbol{Post - weaning\ weight\ gain} = \frac{Yearling\ weight - weaning\ weight}{Yearling\ age\ - weaning\ age}$$

$$\boldsymbol{Slaughter\ daily\ gain}\ = \frac{Carcass\ weight\ - birth\ weight}{slaughter\ age}$$

Growth trait definitions

$$\boldsymbol{Weaning\ weigh\ gain} = \frac{Weaning\ weight - birth\ weight}{weaning\ age}$$

$$\boldsymbol{Post - weaning\ weight\ gain} = \frac{Yearling\ weight - weaning\ weight}{Yearling\ age\ - weaning\ age}$$

$$\boldsymbol{Slaughter\ daily\ gain}\ = \frac{Carcass\ weight\ - birth\ weight}{slaughter\ age}$$

Note! weaning weights from **DNK** not as complete as from FIN and SWE: **Yearling weight is used** instead of post-weaning weight gain

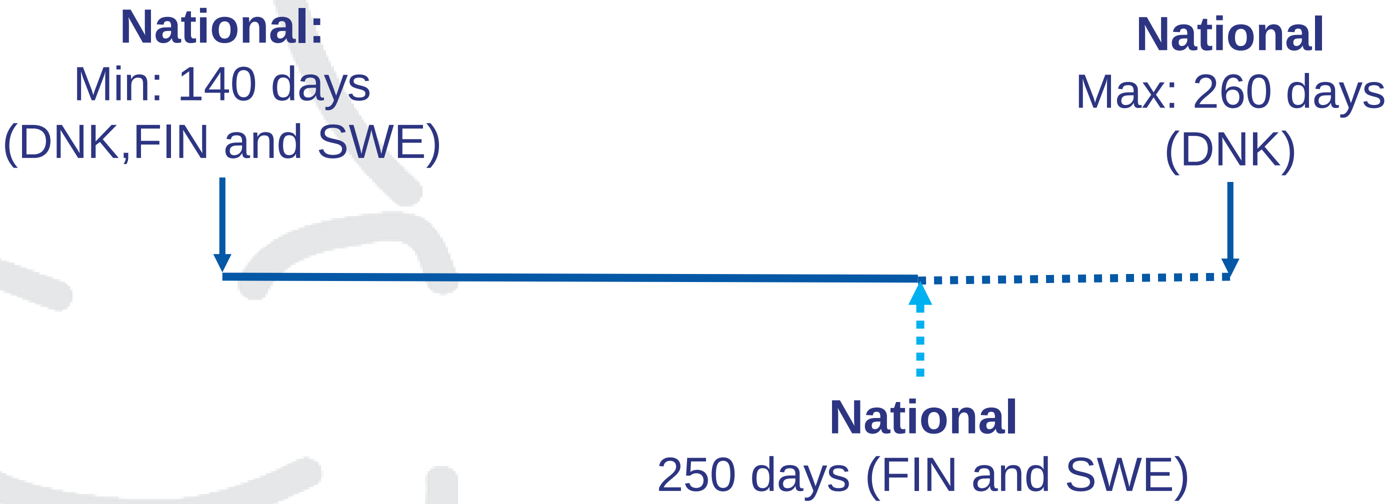
Data

Differences NAV vs. National:

1. Harmonization of traits (common editing rules) over the three Nordic countries
2. Revision of adjustment for heterogeneous variance
3. Revision/harmonization of fixed effects

Harmonization of traits

- Common data edits across countries
- **Example:** same limits on age at weighing



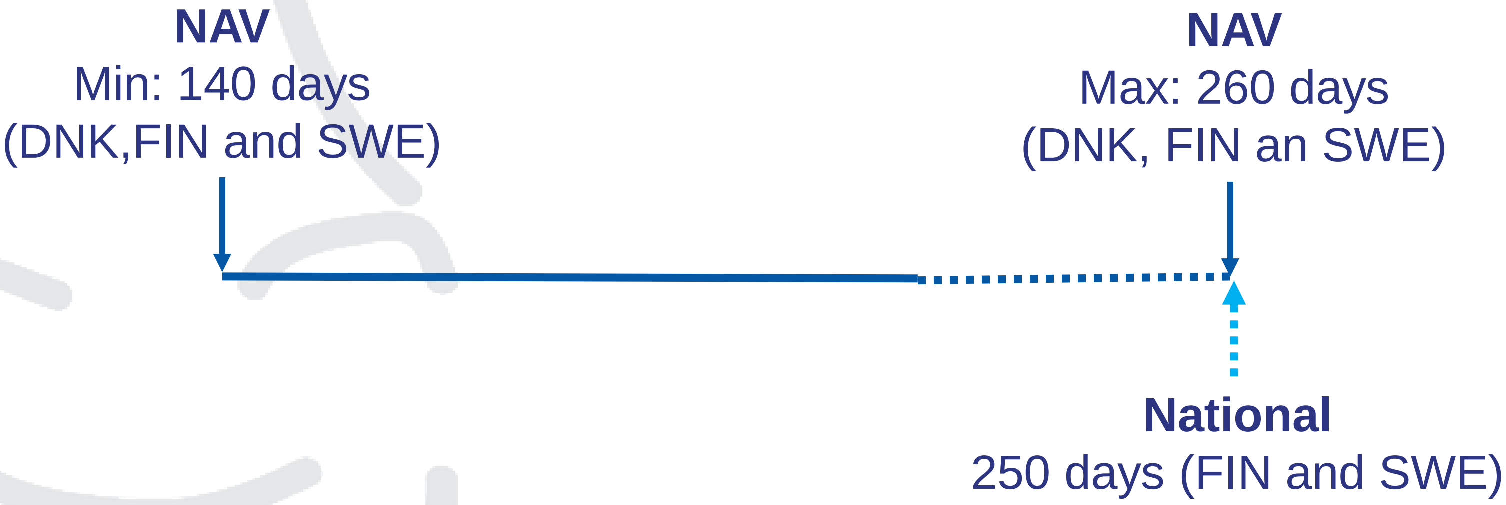
National:
Min: 140 days
(DNK,FIN and SWE)

National
Max: 260 days
(DNK)

National
250 days (FIN and SWE)

Harmonization of traits

- Common data edits across countries
- **Example:** same limits on age at weighing



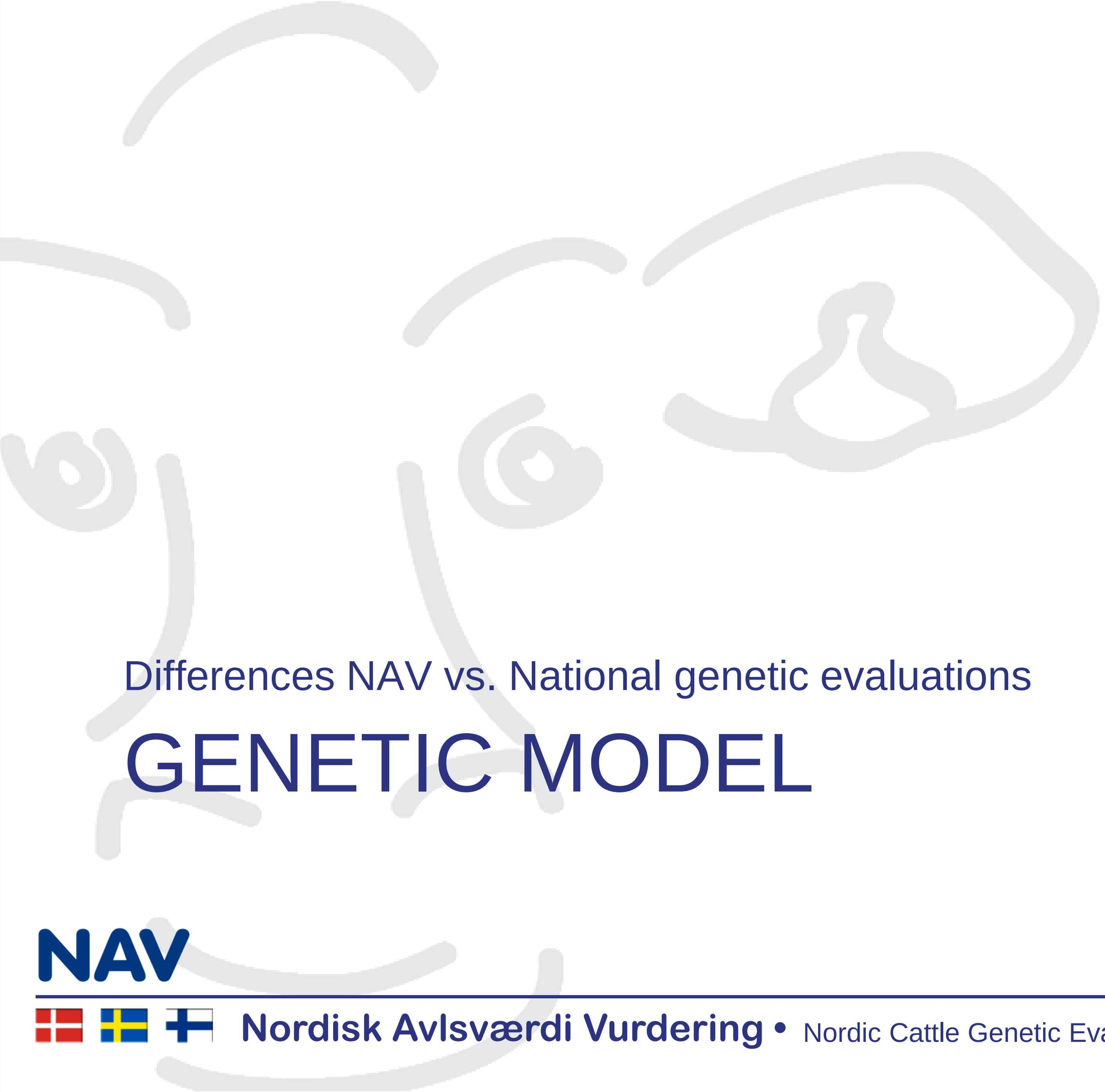
NAV
Min: 140 days
(DNK,FIN and SWE)

NAV
Max: 260 days
(DNK, FIN an SWE)

National
250 days (FIN and SWE)

Revision of the heterogeneous variance adjustment

- Improved method to remove (systematic) differences in the phenotypic variation between birth years, countries and gender which are not due to genetics, Which better..
  - Avoid bias in the estimation of breeding values
  - Improve genetic ranking of animals



Differences NAV vs. National genetic evaluations

GENETIC MODEL

Genetic model

Differences NAV vs. National:

- Genetic groups
- Adjustment for age at weighing for weight, growth and carcass traits
- New genetic parameters

Multi-trait animal model

Fixed

- Country-sex
- Country-twin
- Country-year-month
- Country-dam age-time
- CG: Herd-birth year
- Adjustment for age at weaning

Random

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

Genetic groups (1/2)

- For better estimate breeding values (genetic level) from animals which parents are missing
- With genetic groups we can estimate the genetic level of imported animals more accurately by assigning them to their country of origin and year of birth (capture genetic trend)

Animal	**Sire**	**Dam**	**Breeding value for animal A**
Animal A	Missing	Missing	0
Animal A	*Genetic group*	*Genetic groups*	*Different from 0*

Genetic Groups (2/2)

Formed the groups based on:

- The country of origin and year of birth
    - For 3 breeds: 4 different origins Danish, Finish, Swedish and “rest”
    - For 2 breeds: 6 different origins: Danish, Finish, Swedish, European, American and “rest”
- Year of birth: 10 year groups

Genetic parameters

- Estimated for Charolais and Hereford and applied them within breed group (Continental and British)
- Pattern of genetic correlations among traits was remarkably similar for Charolais and Hereford.
- Genetic correlations show group of traits more strongly correlated than the rest of the traits

Genetic correlations

Groups of traits with stronger genetic correlations than with the rest of the traits

- **Group 1:** Weaning weight gain, yearling weight and slaughter daily gain
  - 0.5 – 0.9
- **Group 2:** Yearling weight, post-weaning weight gain and slaughter daily gain
  - 0.5 – 0.7
- **Slaughter daily gain** with **conformation**:
  - ~ 0.4
- **Conformation** and **fat** class:
  - - 0.1 – 0.1

Heritabilities

	British (HER)		Continental (CHA)	
	h_d^2	h_m^2	h_d^2	h_m^2
Birth weight	0.47	0.11	0.38	0.10
Weaning weight gain	0.15	0.16	0.17	0.13
Yearling weight	0.29	0.10	0.31	0.10
Post-weaning weight gain	0.20		0.20	
Slaughter daily gain	0.46		0.36	
Conformation class	0.28		0.31	
Fat class	0.30		0.34	

National comparisons presentations

EXPECTED CHANGES IN ESTIMATED BREEDING VALUES

NAV