

## **Agenda for Dairy Cross project meeting November 29<sup>th</sup> -30<sup>th</sup> 2023**

**Location:** Vingsted Centeret, Skovvej 2, 7182 Bredsten <https://www.vingsted.dk/en/>

**Language:** English

### **Wednesday November 29<sup>th</sup> 2023**

**12:00 - 12:45: Lunch**

**12.45 - 13:00: Welcome / Jørn Thomasen, VG**

#### **13:00 - 14:45 AP1 Genetic values**

13:15 – 13:30 Overall project deliverables - learnings and perspectives (Ole Christensen, QGG)

13:50 - 14:20 Experiences from routine evaluations (Huiming Liu, SEGES)

14:20 - 14:50 Results from validations of new BOA model (Emre Karaman, QGG and Huiming Liu, SEGES)

14.50 - 15:00 Plan for implementation of next step for genomic breeding values (Anders Fogh, SEGES)

**14:45 – 15:15 Coffee break**

#### **15:15 - 16:20 AP2 Breeding schemes**

15:15 -15:30 Overall project deliverables - learnings and perspectives (Hanne Marie Nielsen, QGG)

15:30 - 15:50 Heterozygosity (Lisa Hein, QGG)

15:50 - 16:20 Simulation design and breeding strategies (Alban Bouquet and Margot Slagboom, QGG)

**16:20 –16:30 Break**

#### **16.30 - 17:15 AP3 Management**

16:30 - 16:45 Overall project deliverables - learnings and perspectives (Søren Østergaard, ANIVET)

16.45 - 17.15 Sector analysis (Julie Clasen, SimHerd)

**18:00 - 20:00 Dinner**

**20:00 - 21:00 Social activity**

**21:00 - The bar is open**

## **Thursday, November 30th 2023**

### **8.30 - 9:10 AP4 Communication and dissemination**

8.30 - 8:50 Overall project deliverables - learnings and perspectives (Jacob Voergård, SEGES)

8:50 - 9:10 Demonstration of SimHerdCrossbred APP (Developed in AP3) and practical experiences with use of SimherdCrossbred (Julie Clasen, SimHerd)

### **9.10 - 10.00 Did DairyCross fulfil your expectations? How to ensure maximal value creation of results? - 5-10 minutes from each partner**

Søren Borchersen (VikingGenetics), Mogens Lund (QGG, AU), Anders Fogh (SEGES)

Søren Østergård (ANIVET), Søren Østergård (SimHerd), Mads Fjordside (VikingDanmark)

### **10.00- 10.15: Introduction to group work and Coffee**

### **10.15 - 11:15 Group work – Groups within each workpackage**

-Learnings, -Knowledge gaps - collaboration

11:15 - 11:45 Summary of group work

11:45 - 12:00 Concluding remarks

12:00: Lunch

# Plans and implementation of genomic breeding values

Anders Fogh

29. – 30. november 2023

Projekt: DairyCross



CENTER FOR QUANTITATIVE  
GENETICS AND GENOMICS



AARHUS  
UNIVERSITET  
INSTITUT FOR HUSDYRVIDENSKAB



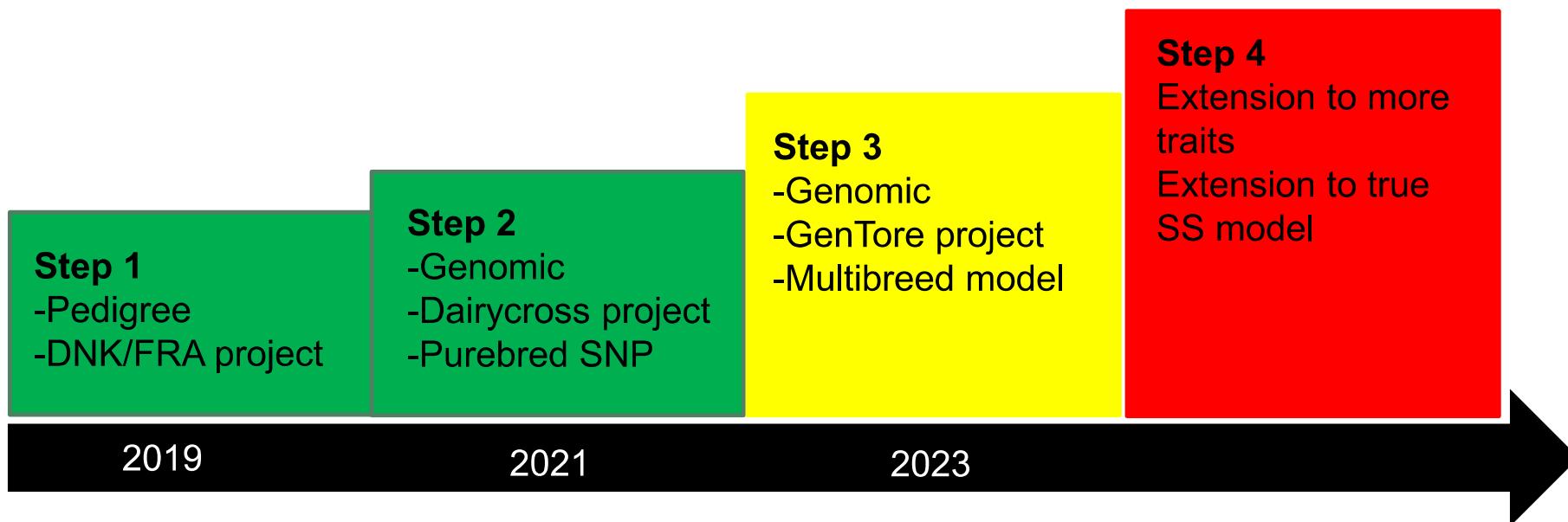
SEGES



Mælkeafgiftsfonden

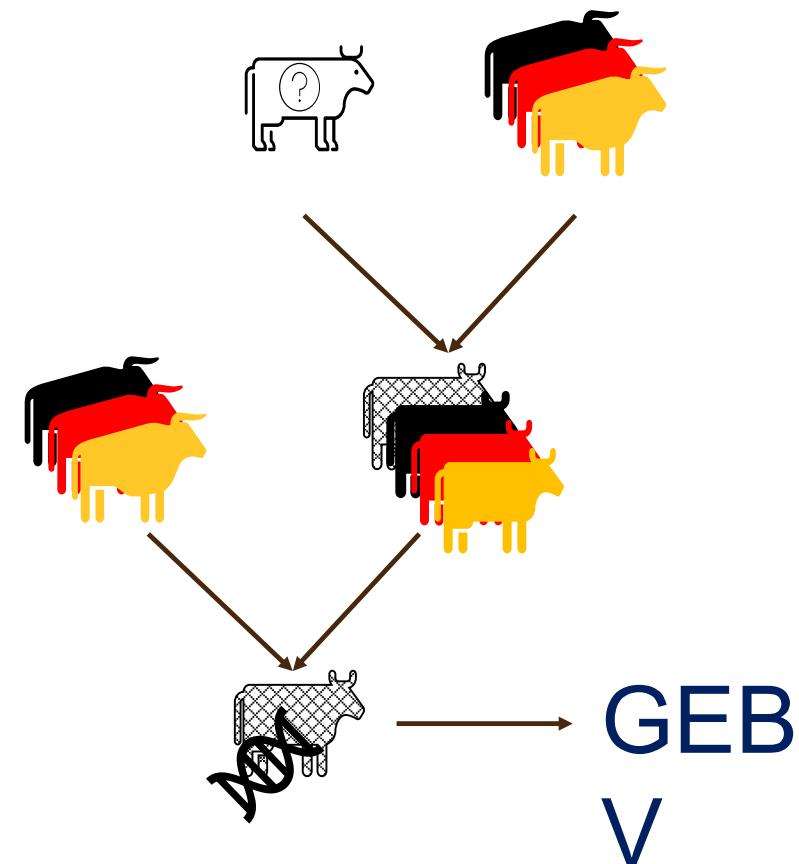


# Steps in crossbred genetic evaluation



## STEP 2: GEBV for Nordic crossbred females

- Genomic tested crossbred females
- Sire and MGS are RDC, HOL or JER
- For each allele we find breed of origin
  - RDC, HOL and JER



# Genomic with a breed origin of allele model

$$GEBV_{BOA,i} = \sum_{b=1}^{N_b} \left( \mu_b \frac{\sum s_{1,i,b} + \sum s_{2,i,b}}{2m} + v'_b (w_{i,1} \circ s_{1,i,b}) + v'_b (w_{i,2} \circ s_{2,i,b}) \right) + \alpha_i$$


Breed difference effect based on genotypes

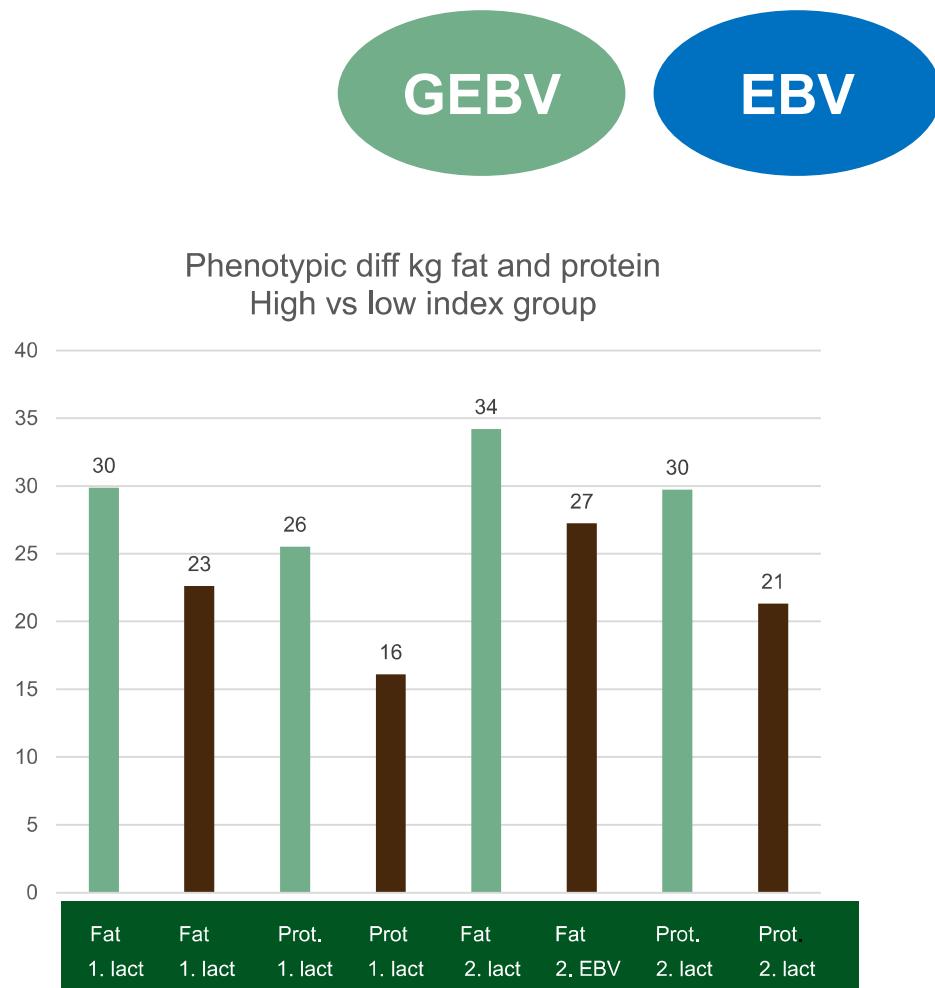
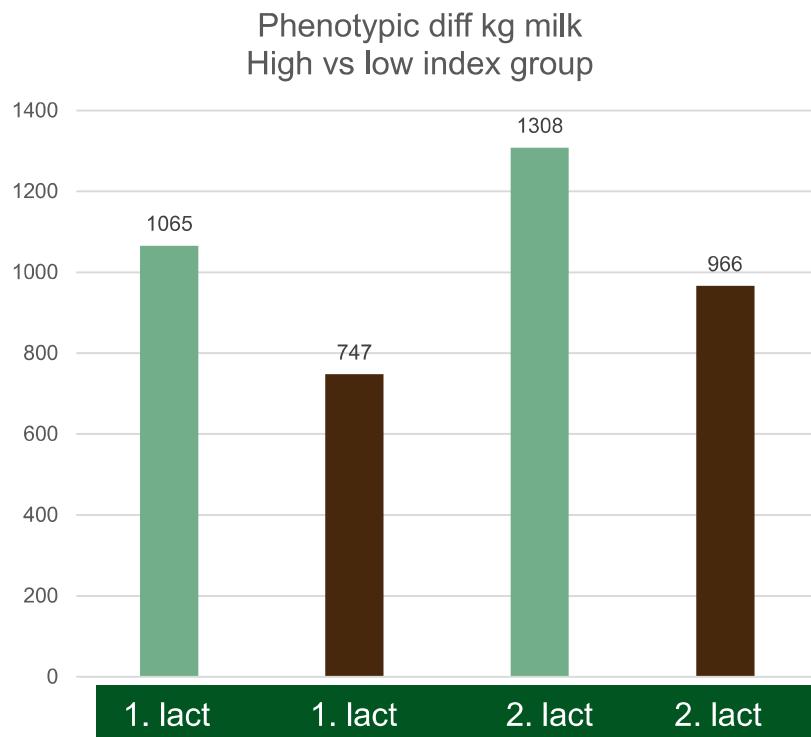
SNP effects based on genotypes

Polygenic

## GEBVs for all traits

- Yield (milk, fat and protein)
- Udder health
- Fertility
- Growth
- Direct and maternal CE,
- Generel health
- Claw health
- Conformation (incl all sub traits)
- Milking speed and temperament
- Longevity
- Saved feed

# High vs low yield index GEBV vs pedigree index



# Future crossbred evaluation

## Step 1. Parent averages

*Used in practice since 2019*

## Step 2. Genomic EBV – purebred SNP solutions (additive effects)

*Used in practice since 2021*



## Step 3. Genomic EBV – GenTore(BOA) model including phenotypes from crossbreds

*Aim to implement in 2023/2024*

## **GenTore crossbred model (Step 3)**

### Plan for implementation

- Only yield traits
- Promising results has been discussed and approved
  - Dairycross group
  - Blending group
- Pipeline will be finished in 2023
- More activities
  - Final approval in Nordic genetic evaluation
  - Expect NAV implementation in 2024

## Next steps

- Extension to:
  - More traits
  - More breeds without reference population
  - New project or?
- Improve genomic models for crossbreed animals
  - Own information
  - Inclusion of heterosis