Nordic genomic prediction for crossbred dairy females

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ICAR/Interbull Annual Conference

Montréal, May 30- June 3, 2022

NAV

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Why?

- **Possibility at herd level to select more accurately across crossbred females in Nordic countries**
  - **Female sexed semen, Beef semen or culling**

- **Until now phenotypic evaluation in Denmark for yield and pedigree index corrected for breed level for fertility and mastitis**

- **GEBVs calculated for 15 composite traits and NTM**
  - **Additionally sub traits for yield and conformation**

Which animals get XXX-GEBV

- XXX females with genomic test and approved pedigree

- Sire and MGS either RDC, HOL, JER

- Genotypes imputed and phased
  - Fimpute (Sargolzaei et al., 2014)

- Assigned Breed of Origin >0.9
  - AllOr (Eiriksson, 2021)

GEBV
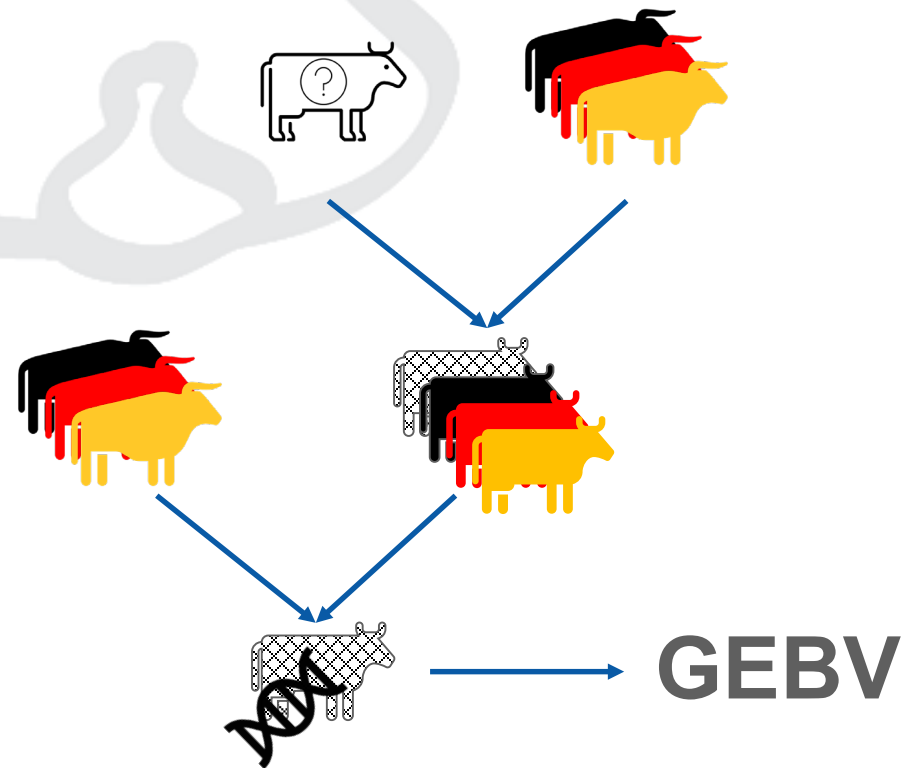
Choice of method

- **In the DairyCross project a Breed Origin Model (BOM) and a Breed Proportion Model (BPM) were compared for protein yield and fertility trait IFL.**

- **BOM where more accurate and experienced less breed level bias than BPM.**

Eiríksson et al., 2022, J Dairy Sci, Volume 105

BOM model

Intercept · Snp solutions · polygenic

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

- μ_b is the intercept, accounting for difference in breed averages for breed b (phenotype average- average DGV)

- $s_{j,i,b}$ is a vector of breed of origin indication for allele j of animal i to breed b, with 1 for alleles assigned to breed b and 0 for alleles assigned to other breeds and proportional values for alleles that could not be assigned

- m is the number of markers

- v_b is a vector of marker effects for breed b

- where $w_{i,j}$ contains haplotype j coded as 0 and 1 for the alternative alleles

- $\circ$ is element vise multiplication

- a_i is a residual polygenic effect

BOM model

Intercept · Snp solutions · polygenic

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

- μ_b is the intercept, accounting for difference in breed averages for breed b (phenotype mean - average DGV)

- $s_{j,i,b}$ is a vector of breed of origin indication for allele j of animal i to breed b, with 1 for alleles assigned to breed b and 0 for alleles assigned to other breeds and proportional values for alleles that could not be assigned

	HOL	JER	RDC
1	1.00000000	0.00000000	0.00000000
2	0.00000000	1.00000000	0.00000000
3	0.500000000	0.500000000	0.00000000
4	0.00000000	0.00000000	1.00000000
5	0.500000000	0.00000000	0.500000000
6	0.00000000	0.500000000	0.500000000
7	0.333333343	0.333333343	0.333333343

$s_{1,i,HOL} = 0$
$s_{1,i,JER} = 1$
$s_{1,i,RDC} = 0$

- m is the number of markers

- vb is a vector of marker effects for breed b

- $w_{i,j}$ contains haplotype j coded as 0 and 1 for the alternative alleles

- ∘ is element vise multiplication

- ai is a residual polygenic effect

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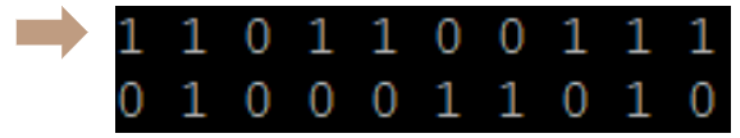
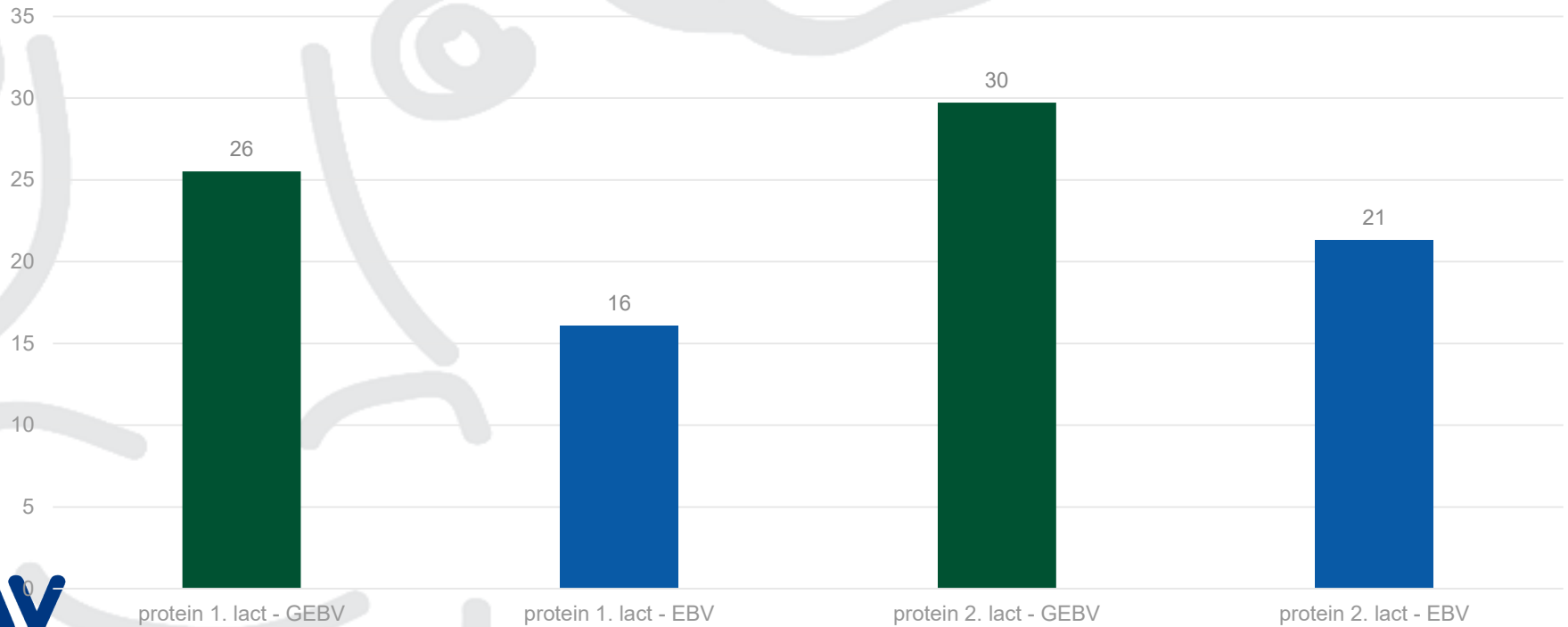# Theory is rather straight forward…

- **But need to overcome some practical challenges**
  - **Marker effects and polygenic effects on index scale.**
    - **Differences in phenotypic effect of an index unit among breeds**
  - **Some traits were composite traits**
    - **Summarize breed level differences over more sub-traits**

Conclusions

- **A Breed of Origin Model for GEBV calculation of XXX Nordic females have been implemented.**

- **Utilize marker effects from the official genomic predictions of HOL, RDC and JER**

- **Within herd phenotypic differences indicate higher accuracy than pedigree index from current non-genomic evaluation**

Next step

- **Utilize models developed in GenTORE project with summary statistics**

  - **Include breeds without Nordic pure breed genomic evaluation – especially MON**

  - **Include phenotypic performance from crossbred cows in the evaluation**

Karaman et al., 2021, GSE, Volume 53

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