

# Towards genomics in Finnish beef cattle - genetic multibreed evaluations

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10.5.2021 | 1

1

## Outline

- Purebred evaluation models
- Data and pedigree
- Fixed effects in multibreed evaluation
- Variance components in multibreed evaluation
- Example of Results
- Conclusions



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2

## Purebred (PB) evaluation models

- Original **purebred** evaluation models were developed for **Angus, Charolais, Hereford, Limousin, and Simmental**
- Separate evaluations for **slaughter, growth, and calving traits**
- Breed specific variance components
- Same model effects in all breeds
- High demand for evaluating crossbred animals!
- Presentation focuses on multibreed evaluation on **slaughter traits**

## Purebred slaughter trait evaluation model

A six trait animal model

Traits:

**Birth, weaning, and yearling weights** from beef recording herds

**Carcass weight, EUROP quality and fat classifications** from slaughterhouses

**Fixed effects:**

Age at measurement, twin indicator, sex, dam's age at calving, calving month, herd-year

**Random effects:**

Permanent DAM environment and genetic animal effect

## Data and pedigree

- Data up to 2007 contains only data for **animals in recording herds**
- Recording herds have mostly **purebred animals**
- Since 2007 almost all slaughtered animals got data from slaughterhouses, **F2 were included into purebred evaluation**
- Pedigree based on EU-bovine register
- Modelling of breed differs between evaluations:
  - Purebreed: breed according to sire breed
  - Multibreed: breed proportion  $p_{bi}$  of each breed  $b$  for animal  $i$  rounded in 25% quantities for 5 main breeds and 'other' breed

## Goals for multibreed (MB) evaluation model

### Development goals for multibreed model

- All animals included
- Logical differences between breeds in breeding values
- High correlation within breed on EBVs between MB and PB evaluations for purebred animals

## Fixed effects in multibreed evaluation model 1/2

We carefully avoided inclusion of BREED means into fixed effects

EXAMPLE: **effect of SEX** defined as "**SEX x BREED**" interaction

Breed proportions  $p_{ib}$  were utilized for fixed effects that required breed interactions

$$\left\{ \begin{array}{l} c_{bull} \quad , \text{ for bulls} \\ \sum_{b=1}^6 p_{ib} c_b \quad , \text{ for cows} \end{array} \right.$$

## Fixed effects in multibreed evaluation model 2/2

- Breed proportion interactions were fitted for the following effects:
  - **Age of dam at calving**
  - **Birth month**
    - In these effects one effect class was defined without breed proportions
- Total heterosis and recombination loss + heterosis coefficients for 10 main breed crosses
- The remaining fixed effects were defined as in purebred models without breed interaction

## Variance components for multibreed model 1/2

For permanent DAM environment the average from covariance matrices of all breeds was used

**Genetic and residual variance** components were defined as **weighted average** of **purebred variance** components  $G_b$  and  $R_b$

$$G_{ib} = \sum_{b=1}^6 p_{ib} G_b, \quad R_{ib} = \sum_{b=1}^6 p_{ib} R_b$$

## Variance components for multibreed model 2/2

- Residual covariance matrices,  $R_{ib}$ , were used as such in the model
- For genetic effects, Cholesky decomposition was used to provide different genetic variances between animals
- In total 126 different breed proportion combinations

## Cholesky decomposition for genetic variance

Multitrait model for animal  $i$  is defined as

$$Y_i = X_i\beta + DAM_i + Z_i u_i + \epsilon_i$$

$$\text{var}(u_i) = I_6, \text{var}(\epsilon_i) = R_{ib}$$

$$G_{ib} = \sum_{b=1}^6 p_{ib} G_b$$

Regression coefficient matrix  $Z_i$  is the lower triangle of Cholesky decomposition of  $G_{ib}$

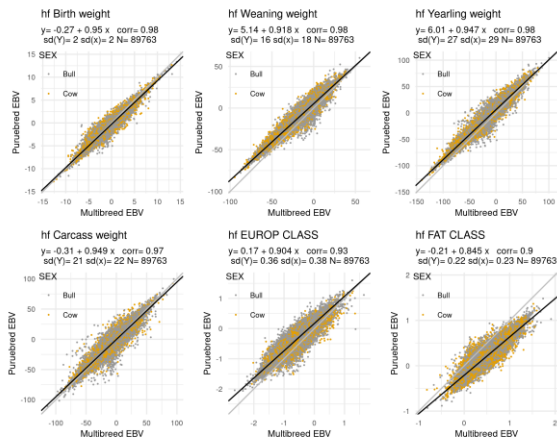
$$R_{ib} = \sum_{b=1}^6 p_{ib} R_b$$

So that:

$$Z_i Z_i' = G_{ib}$$

## Example of model results for pure Hereford animals

## Comparison of results for pure Hereford animals from pure and multibreed models



- No differences between cows and bulls
- Correlations high for all weight traits
- Correlations little bit lower for EUROP and FAT classifications

13

## Conclusions

- Multibreed evaluation improved the pedigree
- More accurate breed definition compared to purebred evaluation
- To model animals with different breed proportions correctly Cholesky decomposition and residual variance classes were fitted
- Correlations between the PB and MB evaluations high and genetic trends did not change
- Next challenge:
  - Growth evaluation fits also maternal genetic effects

14

**Thank you!**

