Towards genomics in Finnish beef cattle - genetic multibreed evaluations

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NAV Nordic Cattle Genetic Evaluation

Outline

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

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 $\boldsymbol{p_{bi}}$ of each breed $\boldsymbol{b}$ for animal $\boldsymbol{i}$ 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

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

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

$$\begin{cases} c_{bull} & , for\ bulls \\ \sum_{b=1}^{6} p_{ib} c_b & , for\ cows \end{cases}$$

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 $\boldsymbol{G_b}$ and $\boldsymbol{R_b}$

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

Variance components for multibreed model 2/2

- Residual covariance matrices, $\boldsymbol{R_{ib}}$, 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 $\boldsymbol{i}$ is defined as

$$\boldsymbol{Y}_i = X_i\beta + DAM_i + \boldsymbol{Z}_i\boldsymbol{u}_i + \boldsymbol{\epsilon}_i$$

$$\mathrm{var}(\boldsymbol{u}_i) = \boldsymbol{I}_6, \quad \mathrm{var}(\boldsymbol{\epsilon}_i) = \boldsymbol{R}_{ib}$$

$$\boldsymbol{G}_{ib} = \sum_{b=1}^{6} p_{ib}\, \boldsymbol{G}_b$$

$$\boldsymbol{R}_{ib} = \sum_{b=1}^{6} p_{ib}\, \boldsymbol{R}_b$$

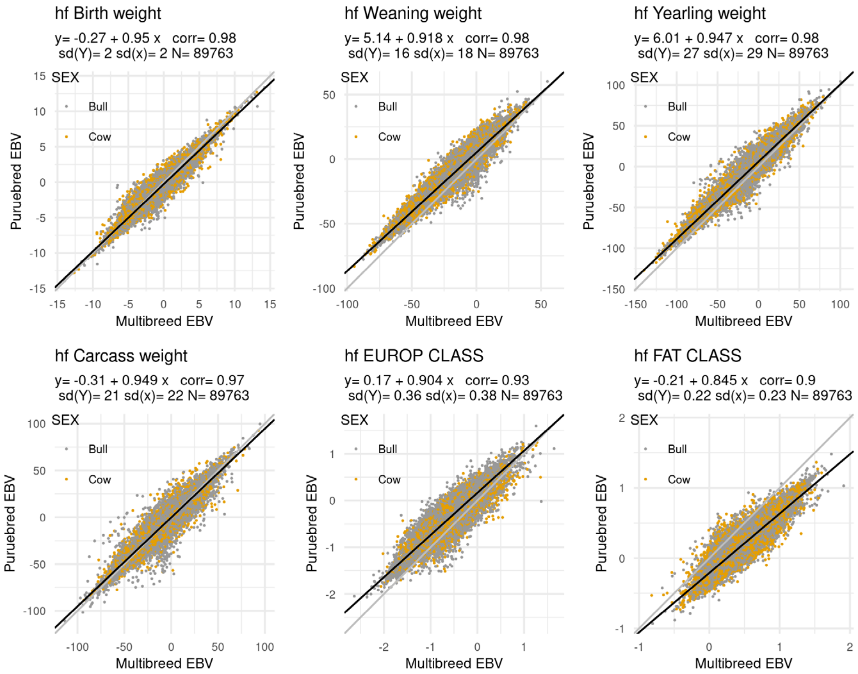
Regression coefficient matrix $\boldsymbol{Z}_i$ is the lower triangle of Cholesky decomposition of $\boldsymbol{G}_{ib}$

So that:

$$\boldsymbol{Z}_i\, \boldsymbol{Z}_i' = \boldsymbol{G}_{ib}$$

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

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

Thank you!

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