Towards genomics in Finnish beef cattle

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Abstract

Beef cattle breeding scheme in Finland has been developed for each breed independently without data for F1-animals. The purpose of this work was to combine single breed evaluations into multibreed evaluation combining data for all animals. The multibreed model effects are mainly the same as the single breed model effects, supplemented however with some improvements. For instance, the new model considers heterosis effects and defines breed more accurately than the previous model. Variance components for genetic and residual effects were defined as a weighted average of single breed variance components using animal's breed proportions as weight. There was a high correlation between breeding values of multi-breed and single-breed evaluation models for purebred animals. In all breeds and the traits, the correlations were higher for direct genetic effects and lower for maternal effects.

Key words: Multibreed evaluation, beef, breed crosses, genetic evaluation

Introduction

Beef cattle breeding scheme in Finland has been developed for each breed independently and without data for F1-animals, building mostly on purebred recording herd animals (Kause et al, 2015). Evaluations are divided into three trait groups; slaughter, growth, and calving traits. There has been an increasing demand to include data from F1 animals and publish their estimated breeding values (EBV) also.

The purpose of this work was to combine single-breed evaluation models into a multi-breed evaluation model, including both pure and crossbred animals in the same evaluation. In the future, the developed multi-breed model is used as a basis for genomic evaluations. This paper focuses on the slaughter trait evaluation model.

Materials and Methods

Single-breed evaluation models

Single-breed (SB) evaluations were made for Angus, Charolais, Hereford, Limousine, and Simmental breeds.

Slaughter evaluation includes birth (bw), weaning (ww) and yearling (yw) weights measured in recording herds, and slaughter weight (sw), EUROP quality class (qc) and fat class (fc) measured in slaughterhouses. Since 2007 slaughterhouses have provided slaughter data for all slaughtered animals to be used for genetic evaluations in Finland.

Single-breed evaluation models have the same effect definitions for each breed. Multi-trait model for animal *i,* with dam *d,* and breed *b* can be defined as

$$
\begin{bmatrix} bw_{id} \\ ww_{id} \\ yw_{id} \\ sw_{id} \\ qc_{id} \\ fc_{id} \end{bmatrix} = X_{id}\beta + Z_d^d m_d + Z_i^a u_i + \epsilon_{id} \,,
$$

where the fixed effects, β, include age at measurement, indicator for twin calves, dam's age at calving, calving month, herd-year. Random effects are dam's permanent environment (m_d) for birth, weaning and

yearling weights, and genetic effect (u_i). Matrices Z_d^d and Z_i^a are incidence matrices for maternal, and direct genetic effects, respectively. Variance components and pedigree are breed-specific:

$$var \begin{bmatrix} m \\ u \\ \epsilon \end{bmatrix} = \begin{bmatrix} I \otimes P_b & & \\ & A_b \otimes G_b & \\ & & I \otimes \Sigma_b \end{bmatrix}$$

Multibreed evaluation model

The goals for multi-breed (MB) model were the following: all animals are included in the evaluation, high correlation within breed on EBVs between SB and MB evaluations for purebred animals, and logical differences between breeds in breeding values.

For each animal, breed proportions of 5 main breeds and 'other breed' were approximated in 25% quantities. The animal was considered as a purebred if its main breed share was higher than 87.5%. This definition is more accurate than the one used in the single breed evaluation where an animal's breed was defined according to its sire breed.

Fixed effects for the MB evaluation

We had several prerequisites for the MB models. Fixed effects should not model breed means, i.e. differences between breeds should be directed into breeding values. However, fixed effects should allow the means of cows and bulls differ and allow the difference between cows and bulls to vary between breeds.

Due to this, the effect of a sex in the MB model, for instance, was defined as

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

Thus, all bulls regardless of their breed obtain the same effect, c_{bull}. For a cow i, the effect of the sex is a weighted average of the purebred effects, c_b, weighted by cow's breed proportions, p_{ib}.

Similar breed proportion interactions were applied for the age of the dam at calving and birth month effects. For those effects, the most common effect class was defined without any breed interaction and the rest effect classes were defined as a weighted average of the purebred effects.

To account the crossbreeding effects, total heterosis, a total recombination loss, and heterosis coefficients for the 10 main breed crosses were included as the fixed effects in the model (Lidauer et. al, 2006).

Random effects for the MB evaluation

Model has three random effects; dam's permanent environment, genetic effect, and residual effect.

For dam's permanent environment effect the covariance matrix, **P**, was defined as an average of covariance matrices of purebreds, $P = \sum_{b=1}^{5} P_b / 5$. Thus, it does not depend on the breed of the dam.

For the genetic and residual effects, the covariance matrices for an animal i and breed p having breed proportions p_{ib}, were defined as a weighted average of the purebreed variance components;

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

where G_{ib} and R_{ib} are the covariance matrices for genetic and residual effects, respectively. The covariance matrix for the 'other breed' was defined as an average of the SB covariance matrices.

Multibreed evaluation model

The multi-breed model was defined as

$$y_{id} = \tilde{X}_{id}\tilde{\beta} + \tilde{Z}_d^d \tilde{m}_d + \tilde{Z}_i^a \tilde{u}_i + \tilde{\epsilon}_{id},$$

where $\tilde{\beta}$ is a vector of the fixed effects as defined earlier, $\tilde{m}_d$ a random maternal effect
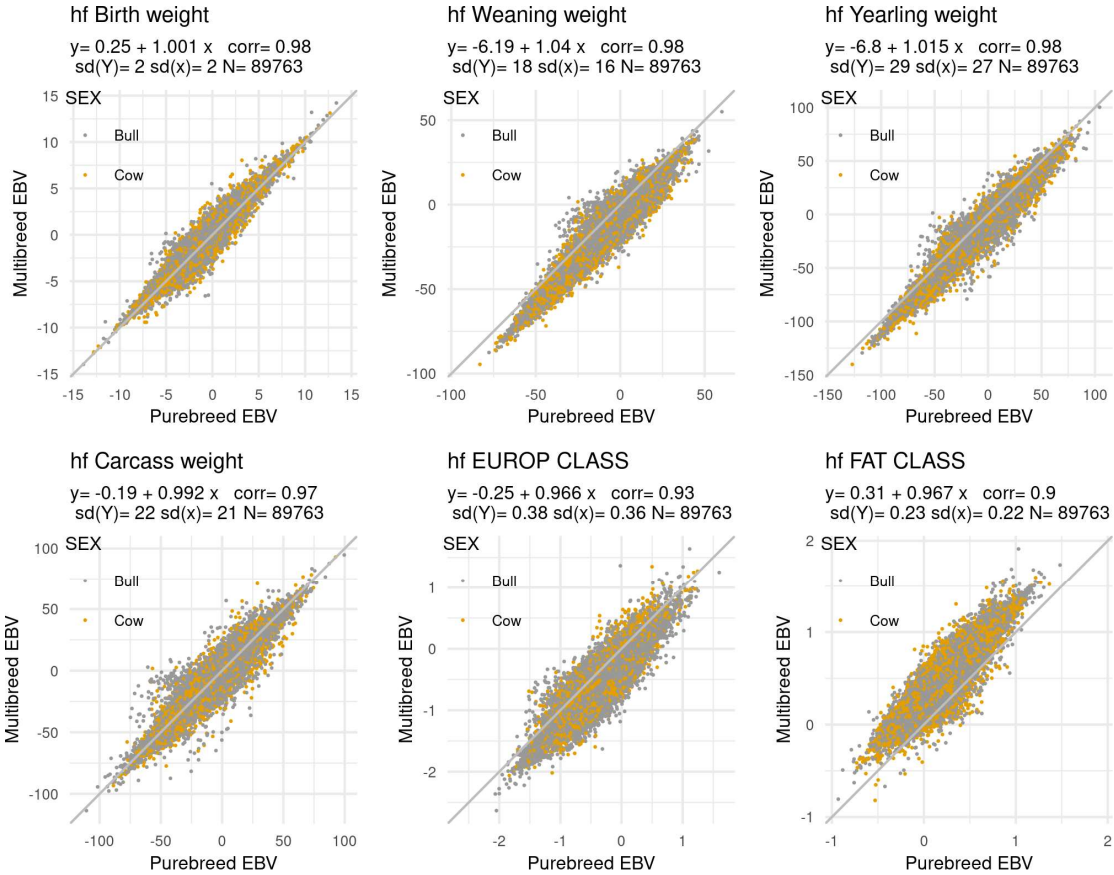
Figure 1. Comparison of breeding values between single-breed and multibreed evaluations for pure Hereford animals from recording herds.

for birth, weaning and yearling weights, and $\widetilde{u}_i$ a random genetic effect, with variance

$$var\begin{bmatrix}\widetilde{m}\\\widetilde{u}\\\widetilde{\epsilon}\end{bmatrix} = \begin{bmatrix}I\otimes P & & \\ & A\otimes I & \\ & & I\otimes\Sigma\end{bmatrix},$$

where Σ is a block diagonal matrix with residual covariance matrices R_{ib} on the diagonal and A is the relationship matrix. $\widetilde{Z}_d^d$ is an incidence matrix for a dam. Due to technical reasons, the breed dependent co-variance matrix for the genetic effect was modelled using Cholesky factorization of the covariance matrix G_{ib} as a covariate for each animal. Thus, $\widetilde{Z}_i^a$ is an upper triangular matrix, such that $var\left(\widetilde{Z}_i^a\widetilde{u}_i\right) = \widetilde{Z}_i^a I\widetilde{Z}_i^{a\prime} = G_{ib}$. Breeding values for an animal i in the multibreed model were defined as $\widetilde{Z}_i^a\widehat{\widetilde{u}}_i$.

All the models were fitted using a MiX99 software suite (MiX99 Development Team, 2021).

Results & Discussion

Breeding values of purebred animals were compared between the original SB models, and the MB model using various plots and statistics. An example of a such plot for Hereford is presented in Figure 1.

Based on the figure the correlations between MB and SB evaluations were high for all traits. Weight traits had the highest correlations, ranging from 0.97 to 0.98. The lowest correlations were 0.93 for EUROP quality, and 0.90 for EUROP fat classifications.

Corresponding results were observed for the other breeds. Genetic trends of the traits were very similar between MB and SB evaluations

within the breed for all purebreed evaluations. Because SB evaluations were independent of each other, the levels of breeding values were not the same between MB and SB evaluations. Larger pedigree, more accurate breed definition, and additional data created some expected differences for the breeding values and for the shape of plotted genetic trend lines. However, under the MB evaluations, the mean levels of estimated breeding values of each breed relative to other breeds were logical (not shown).

Conclusions

The new multibreed evaluation model using breed wise variance components and effect classes based on animal's breed composition was successfully applied. The model allowed simultaneous evaluation of animals from all the breeds and breed crosses. The correlations between multibreed and current single-breed evaluations were high, ensuring no major differences in breeding values (within breed) should occur when the multibreed evaluation is taken into use. The developed multibreed evaluation model will be used as a base for the ssGBLUP evaluation that is under development.

Acknowledgments

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