

Handling of inbreeding and semen sire breed in the Nordic Holstein fertility evaluations as part of EuroGenomics Harmonization standard.

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Abstract

Female fertility is a complex trait expected to be highly influenced by inbreeding level. Conception rate (CR), as part of the fertility trait complex, is known to be affected by the mating sire breed. EuroGenomics has decided to establish golden standards for genetic evaluation for all trait groups. Golden standards consider inbreeding in the pedigree relationship (**A**) matrix, and inbreeding depression (effect of the past inbreeding). In fertility golden standard evaluations breed of semen sire should be considered. Implications were tested using Nordic (Denmark, Finland, and Sweden) Holstein (HOL) multi-trait multi-lactation fertility evaluation models. Inclusion of the inbreeding into the **A** matrix had no significant effect on the fertility index but would be beneficial for future single-step implementation. The *inbreeding depression* was found to have limited effect in the HOL Nordic population. Effect of service sire breed was considered important due to the increased use of beef semen in inseminations of dairy cows on second or later parities.

Key words: inbreeding in pedigree relationship matrix, conception rate, inbreeding depression

Introduction

EuroGenomics (EG) cooperation was established by the European Cattle AI industry in 2008 to improve the reliability of genomic evaluations (David et al., 2010). The project to keep participating countries on the same track in terms of data collection, editing, trait definition, and genetic evaluations was named EG Harmonization. It is implying unified standards for all breeding goal traits including fertility.

Nordic (Denmark, Finland, and Sweden) fertility evaluation models were launched in 2005 and updated in 2016 to fulfill genomic evaluations and future EG standards (Muuttoranta et al., 2015; 2019). The evaluation model meets most of the requirements of the so-

called EG “golden standard”, but several alterations, like accounting for inbreeding and breed of service sire were needed.

Pedigree-based inbreeding was decided by EG members as important to account for in the inverse of the relationship matrix (A^{-1}) and in genetic evaluations by regression on inbreeding coefficient. Accounting for inbreeding in A^{-1} would potentially have a limited effect on pedigree-based evaluations, but important to consider when moving towards single-step genomic predictions. Accounting for inbreeding depression might be useful, as inbreeding is causing an unaffordable effect in breeding programs and especially in fertility traits (Kristensen and Sørensen, 2005).

The use of beef semen in terminal matings of dairy cows is constantly growing (Ettema et al., 2017). Because of some difference in male fertility level between breeds it is worth to account for a breed of service sire in the dairy evaluation model. In addition, Morrell et al. (2018) reported differences in quality between dairy and beef bull semen.

In the current study we first present results on the inclusion of inbreeding coefficients to A^{-1} and as regression coefficient in the interval from first to last insemination (IFL) and conception rate (CR) evaluation models. In addition, the results on inclusion of the service sire breed effect into the CR evaluation model are presented. The changes were done for all Nordic fertility traits further to those presented.

Materials and Methods

Pedigree and inbreeding

Pedigree was obtained from the November 2020 Nordic HOL fertility evaluations (Muuttoranta et al., 2019) and included 11,704,880 animals (11,579,196 females and 125,684 males) born 1950 to 2020. Individual inbreeding coefficients (F) were calculated using Meuwissen & Luo (1992) algorithm in Relax2 (Strandén & Vuori, 2006) software.

Data and statistical model

Pre-processed IFL and CR data were extracted from January 2021 Nordic HOL evaluation runs and included records from 9,032,686 and 9,075,954 females for the IFL and CR traits, respectively. The females were also presented by 1,521,070 Finnish Red Dairy cattle cows and heifers which were included to have larger contemporary groups in Finnish herds. The mixed models used in the November 2020 fertility evaluations (hereinafter referred to as default model) were:

IFL

$$y_{ijklmn} = hy_i + ymc_j + agec_k + het_l + a_m + e_{ijklmn},$$

where y_{ijklmn} is a IFL observation; fixed effects: hy_i = herd × birth year for heifers, or herd × first

calving year for cows, ymc_j = first service year × month × country, $agec_k$ = age of heifer at first service × country; het_l is total heterosis modeled as a fixed regression effect across countries; a_m and e_{ijklmn} are random animal and residual effects, respectively.

CR

$$y_{ijklmnopq} = hy_i + ymc_j + agec_k + service_l + stype_m + het_n + pe_o + a_p + e_{ijklmnopq},$$

where $y_{ijklmnopq}$ is a repeated observation for heifers and cows in parities 1 to 3; fixed effects: hy_i = herd × birth year for heifers, or herd × first calving year for cows, ymc_j = insemination year × month × country, $agec_k$ = age of heifer at first service × country, $service_l$ = service number × country, $stypem_m$ = year class × semen type × country; het_n = total heterosis modeled as a fixed regression effect across countries; pe_o , a_p , and $e_{ijklmnopq}$ are permanent environment, additive animal, and residual random effects, respectively.

Inbreeding in A^{-1}

Precomputed F were used by MiX99 software (Strandén & Lidauer, 1999) to construct A^{-1} using standard rules (Henderson 1976; Quaas 1976). Herein after models with the F accounted in the A^{-1} will be denoted as A_F^{-1} .

Regression on inbreeding

To account for negative effect of the F on the fertility traits (IFL and CR), the mixed models were modified by inclusion of a linear regression of cow's phenotype on the continuous variable F , denoted as F_{reg} .

Effect of service sire breed in CR

The fixed effect service sire breed ($Ssbr$) was created as the decade of insemination date × breed of service sire. Four decades were fitted into the period 1984 to 2020. Missing service sire information was observed in 1,961,392 (4.2 %) CR records. In the records with the missing information, the $Ssbr$ effect was created as the decade of insemination date × breed of

inseminated female. The missing breed information was substituted by HOL, Red Dairy cattle (RDC), and Crossbred in 83%, 16%, and 1% of cases, respectively.

The IFL is the summary of multiple inseminations that can be done with different sires from different breeds. Hence, the *Ssbr* effect was not included into the IFL model.

Workflow

In a first step A_F^{-1} was implemented in the IFL and CR models ($IFL A_F^{-1}$ and $CR A_F^{-1}$). In the second step $IFL A_F^{-1}$ and $CR A_F^{-1}$ models were upgraded by inclusion of F_{reg} ($IFL A_F^{-1} \& F_{reg}$ and $CR A_F^{-1} \& F_{reg}$). On the third step $CR A_F^{-1} \& F_{reg}$ model was modified by inclusion of the *Ssbr* effect ($CR A_F^{-1} \& F_{reg} \& Ssbr$).

Results & Discussion

Handling of Inbreeding

A constant growth of the inbreeding level was observed in cows and bulls (Figure 1). Annual gain in the *F* was 0.15% and 0.13% for the AI-bulls and cows, respectively. A sharp increase was observed in the AI-bulls born after 2010 (in the genomic selection era), the *F* level gained by 2% in 6 years.

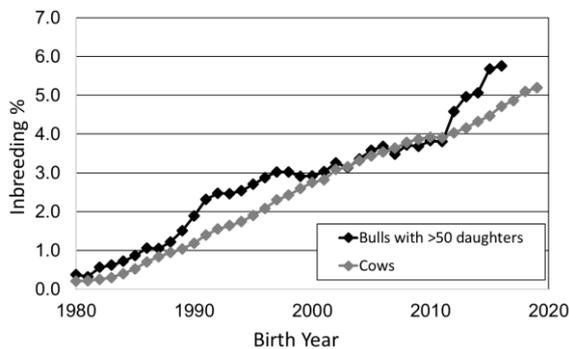


Figure 1. Inbreeding level trend in the Nordic HOL fertility pedigree.

Figures 2 and 3 are presenting the estimated breeding values (EBVs) change caused by the inclusion of the *F* to default fertility evaluation models. The average change in the IFL and CR traits were computed as the difference between EBVs from A_F^{-1} ($A_F^{-1} \& F_{reg}$) and the default

model for bulls and cows. Results from the $CR A_F^{-1}$ model are not presented as they were consistent with the $IFL A_F^{-1}$ results.

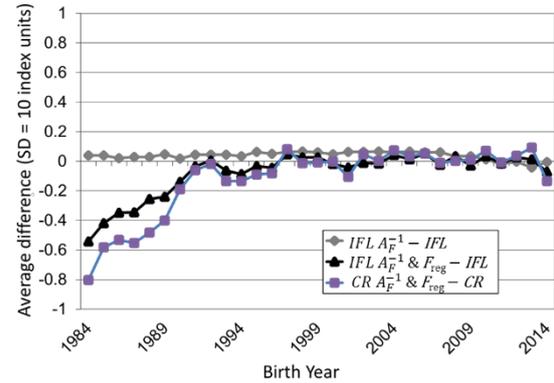


Figure 2. Difference of genetic trends for the IFL and CR traits in HOL bulls obtained from modified and unmodified models. In modified models A_F^{-1} = inbreeding accounted in the A^{-1} and F_{reg} = regression on inbreeding.

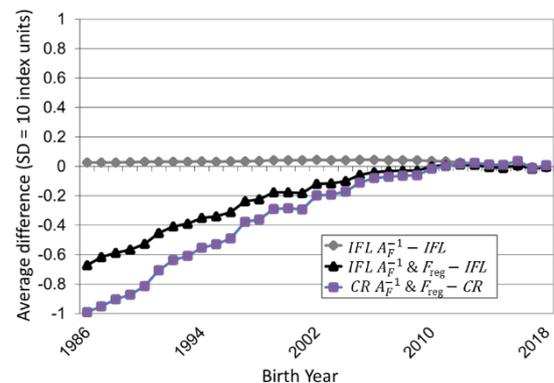


Figure 3. Difference of genetic trends for the IFL and CR traits in the HOL cows obtained from the modified and unmodified models. In the modified models A_F^{-1} = inbreeding accounted in the A^{-1} and F_{reg} = regression on the inbreeding.

A modest change in the EBVs for bulls and cows was observed after accounting for the *F* in the A^{-1} both for the IFL and CR models. The correlation between modified and non-modified EBVs was >0.999, reflecting absence of re-ranking in the cows and bulls. Expectedly, the *F* in the A^{-1} had limited impact on pedigree based evaluation model but would be important when moving towards to the single-step genomic prediction, as the A^{-1} and G^{-1} (genomic relationship) matrices will be used to create the joint matrix H^{-1} . Because G^{-1}

accounts for the F automatically, neglect of F in A^{-1} may lead to biased predictions (Gowane et al., 2018) and convergence problems (Strandén et al., 2017) in the single-step models.

A slight change in average genetic trend for the IFL and CR traits were observed after inclusion of the F_{reg} . The EBVs lowered due to inclusion of an effect of the inbreeding depression. For bulls born after 2000 the change in IFL index fluctuated from -0.10 to 0.05 units, in the CR from -0.13 to 0.1 units. For the cows, nearly no change was observed after 2010, for both the IFL and CR. The EBVs of the bulls born before 2000 and of the cows born before 2010 were penalized by the model which results in difference up to ± 3 index units. Correlation of the EBVs obtained from A_F^{-1} & F_{reg} and current model were same (>0.998) for the IFL and CR traits.

Handling of service sire breed

Analysis of the service sire breeds in the CR data revealed 26 breeds that have been used for insemination of HOL and Finnish RDC heifers and cows. Breeds presented by less than 1000 observations were combined to the same join group. In the final data set, 17 breeds were presented. The ten most frequent breeds in the $Ssbr$ effect are presented in Figure 4. The minimal size of the $Ssbr$ class effect was 400 observations.

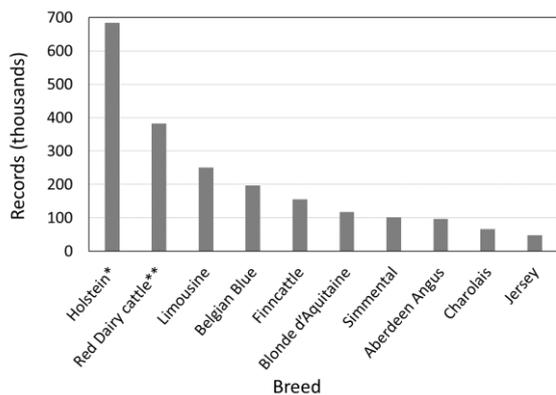


Figure 4. Ten most frequent breeds of service sire in the Nordic HOL CR evaluations.

*number of records was divided by 50;

**number of records was divided by 20.

The impact of the $Ssbr$ effect was illustrated by the difference between the $CR A_F^{-1}$ & F_{reg} & $Ssbr$ and $CR A_F^{-1}$ & F_{reg} models (Figure 5). Slight change was observed for the cows and bulls suggesting a limited effect on the EBVs. The correlation of the EBVs in bulls was >0.999 with no reranking observed.

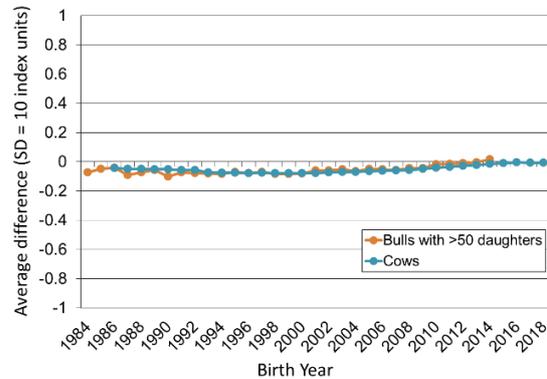


Figure 5. Difference of the CR genetic trends in the HOL bulls and cows obtained as EBVs from $CR A_F^{-1}$ & F_{reg} & $Ssbr$ minus EBVs from $CR A_F^{-1}$ & F_{reg} .

Despite the limited influence, the $Ssbr$ effect is important to consider due to the constantly growing number of dairy x beef crossings. For instance, in the CR data number of crossings with beef breeds (Limousine, Belgian Blue, Blonde d'Aquitaine, Aberdeen Angus, and Charolais) increased from 16,558 in 2000 to 63,737 in 2017.

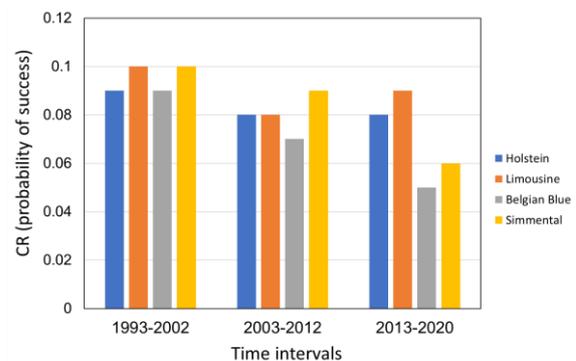


Figure 6. Solutions for the fixed $Ssbr$ effect on the second parity in different breeds.

The difference in solutions for *Ssbr* effect in the HOL and beef breeds was observed across all parties. For instance, for the second lactation solutions for the probability of successful insemination were lower in Belgian Blue and Simmental breeds during recent years (Figure 6).

More improvement of the fertility model could be done by accounting for future inbreeding in addition to the past inbreeding (i.e., expected inbreeding of future progeny). However, the method might be computationally challenging for large populations and solutions are dependent on the subpopulation where bull is used, and the effect in future inbreeding is thus better handled in planning of matings.

Conclusions

Nordic (Denmark, Finland, and Sweden) Holstein fertility evaluations were improved to fulfill EuroGenomics golden standard. Improvements were done by accounting for the inbreeding in the A^{-1} and a regression on the inbreeding coefficient. The relative change of EBVs after model modification was low. Breed of service sire was modeled as a fixed effect in conception rate evaluations. The effect was treated as important due to growing use of beef semen in dairy herds.

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