Genetic correlations among longevity, fertility, udder health and type traits including or not genomic information

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Abstract

The aim of the study was to estimate genetic correlations among functional longevity, conception rate of heifers and of lactating cows, somatic cell score, clinical mastitis, udder depth and udder balance in Montbéliarde breed. Bivariate random regression sire models including a pedigree or a genomic relationship matrix were used to compute (co)variance components. Genetic correlations obtained including genomic information were consistent with those estimated using the pedigree relationship matrix. Conception rate, somatic cell score, clinical mastitis and udder depth showed moderate to high genetic correlations with functional longevity, suggesting that they can be good indirect predictors of length of productive life when included in a combined genomic evaluation. In addition, the large genetic correlations among the two udder health traits and udder depth indicate that they can improve the prediction of the other traits in a multi-trait single-step model.

Introduction

Functional longevity (**FL**) is defined as the ability of a cow to avoid being culled for other reasons than low milk production (e.g. illness or infertility; Ducrocq et al., 1988). Dairy cow's longevity can be expressed as the length of productive life, that is the time between the date of the first calving and the culling or death date. Similarly to other functional traits, FL is increasingly considered in breeding programs because of growing concerns about animal welfare. As reported in Rostellato et al. (2020), it is affected by factors that are known to reflect resilience, such as fertility problems and diseases, suggesting that FL can be used as an indicator of long-term resilience.

In French dairy cattle, FL is analysed using a Weibull proportional hazard model. The heritability estimated for the trait using such model is small and accuracy of EBVs of young bulls is low given that the majority of their daughters are censored (Ducrocq and Sölkner, 1998). To overcome those drawbacks and to include EBVs for FL in total merit index, a combined polygenic evaluation was developed (Ducrocq et al., 2001). This methodology consists in an approximate multi-trait animal model, where several genetically correlated traits are included and used as predictors of the other traits. In addition to FL, the functional traits considered are female fertility, udder health and type traits (GenEval, 2021).

Variance and covariance components used in the current combined polygenic evaluation have been estimated ignoring genomic information. The development of a single-step combined evaluation is of great interest given that it allows to take into account genomic preselection (Jibrila et al., 2020).

Hence, the objective of the present study was to estimate genetic correlations (r_g) among FL, reproductive, udder health and udder type traits including or not genomic information.

Materials & Methods

Data. The data were extracted from the French bovine national database. The dataset included 1,308,066 cows, born between 2000 and 2019, from sires with a minimum of 30 daughters (N

= 2,345). The investigated traits were FL, conception rate of heifers (CR_h) and of lactating dairy cows (CR_c), somatic cell score (SCS), clinical mastitis (CM), udder depth (UDE), and udder balance (UDB).

Sires of cows (N = 2,345) were genotyped using the BovineSNP50 BeadChip (Illumina Inc., San Diego, CA). Markers exhibiting call rate < 0.9 or minor allele frequency < 5% and monomorphic SNPs were discarded. After quality control, 37,133 SNPs remained.

The sire's pedigree was traced back for 3 generations and it included the identification of cow's sire, cow's paternal grand-sire and sire's maternal grandsire for 5,946 animals.

Estimation of genetic correlations. The investigated traits are described by very different statistical models (e.g. FL is analysed using a survival model). It makes the use of a multiple trait animal model not feasible to compute r_g among traits. Hence, pre-adjusted performances (i.e. phenotypes corrected for all non-genetic effects) adjusted for the dam's EBV and their associated weight were computed for each cow and each of the investigated traits by means of an accurate model as described in GenEVAL, (2021). Then, these corrected records were used as pseudo-phenotypes in a simple and unique model for all traits, whatever the complexity of the original univariate model of analysis, as proposed by Ducrocq et al. (2001).

Variance and covariance components were estimated using bivariate random regression sire models. To take into account heterogeneous residual variance for each pre-adjusted performance due to the different amounts of information (weight), the statistical model was as follows:

$$y_{i,m}^{\#} = v_{i,m}y_{i,m}^{*} = v_{i,m} * \mu_i + v_{i,m} * a_{i,m} + \varepsilon_{i,m} \tag{1}$$

where $v_{i,m}$ is the square root of weight, $y_{i,m}^{*}$ is the pre-adjusted performance corrected for the dam's EBV of trait i and animal m, μ_i is the overall mean of trait i, $a_{i,m}$ is the additive genetic value of animal m for trait i and $\varepsilon_{i,m}$ is a residual.

Two distinct analyses were carried out in order to estimate (co)variance components using a pedigree (**A**) relationship matrix or a genomic (**G**) relationship matrix, respectively.

Variance and covariance components were estimated using the average information REML algorithm implemented in AIREMLF90 program (Mistzal et al., 2014).

Results

Genetic correlations among the investigated traits including or not genomic information are presented in Table 1.

Comparison of estimates including or not genomic information. Genetic correlations estimated using the **A** matrix were consistent to those estimated with **G** matrix. The inclusion of genomic information gave higher r_g among FL, SCC and CM, as well as between the two fertility traits.

Only r_g estimated using **G** matrix are presented and discussed hereinafter.

Genetic correlations between FL and the other investigated traits. Genetic correlations between FL and the two fertility traits were favourable. Conception rate of heifers exhibited a lower r_g compared to CR_c.

High and favourable (i.e, lower culling risk when lower SCS or CM) r_g were found between FL and the two udder health traits. Udder depth and UDB exhibited a moderate and favourable r_g with FL (lower culling risk when shallow and/or balanced udder).

Genetic correlations among fertility, udder health and udder type traits. Genetic correlation between CR_h and CR_c was moderately positive. Conception rate of heifers did not show significant genetic relationships with udder health and udder type traits. In contrast, conception rate of lactating cows exhibited moderate and favourable r_g with SCS, CM and UDE (higher conception rate when low SCS or CM or UDE).

A very high and positive r_g was found between the two udder health traits. Moreover, SCS and CM were positively correlated with UDE.

A negative and moderate r_g was estimated between the two udder type traits.

Table 1. Genetic correlations among the investigated traits using pedigree relationship matrix (above diagonal) and genomic relationship matrix (below diagonal) [1,2].

	FL	CR_h	CR_c	SCS	CM	UDE	UDB
FL	-	-0.21 (0.03)	-0.42 (0.03)	0.45 (0.02)	0.47 (0.03)	0.44 (0.02)	-0.29 (0.03)
CR_h	-0.20 (0.04)	-	0.34 (0.04)	-0.08 (0.03)	-0.02 (0.05)	-0.02 (0.03)	-0.1 (0.03)
CR_c	-0.43 (0.03)	0.44 (0.04)	-	-0.23 (0.03)	-0.23 (0.04)	-0.24 (0.03)	0.04 (0.03)
SCS	0.50 (0.02)	-0.08 (0.04)	-0.28 (0.03)	-	0.71 (0.02)	0.33 (0.02)	-0.11 (0.02)
CM	0.53 (0.04)	-0.04 (0.05)	-0.26 (0.05)	0.82 (0.02)	-	0.41 (0.03)	-0.08 (0.02)
UDE	0.42 (0.03)	0.08 (0.04)	-0.26 (0.03)	0.33 (0.02)	0.46 (0.04)	-	-0.39 (0.02)
UDB	-0.29 (0.03)	0.06 (0.04)	-0.05 (0.04)	-0.11 (0.03)	-0.09 (0.04)	-0.36 (0.02)	-

[1] FL : functional longevity (low risk to be culled → high risk to be culled), CR_h : conception rate of heifers (poor conception rate → good conception rate), CR_c : conception rate of lactating dairy cows (poor conception rate → good conception rate), SCS : somatic cell score (low somatic cell score → high somatic cell score), CM : clinical mastitis (few clinical mastitis events → several clinical mastitis events), UDE : udder depth (shallow udder → deep udder), UDB : udder balance (unbalanced udder → balanced udder)
[2] Sample standard deviation within parentheses

Discussion

Comparison of estimates including or not genomic information. The increase of the magnitude of r_g for FL, fertility and udder health traits when genomic information was taken into account was related to higher genetic covariances with respect the estimates obtained using a pedigree relationship matrix (data not shown). Similar results were also found by Gordo et al. (2016).

Genetic correlations between FL and the other investigated traits. In our study, we found that FL is genetically correlated with fertility, udder health, and udder type traits, suggesting that they are good indirect predictors of length of productive life.

The favourable genetic relationships between FL and conception rate indicates that selection for a better fertility can prolong the length of productive life of dairy cows. In addition, it confirms the major importance of reproductive problems in culling-decision making (Rostellato et al., 2020).

Functional longevity exhibited a quite large relationship with SCC and CM. It suggests that the risk of being culled increased when the cow is more prone to develop sub-clinical or clinical mastitis. Hence, selective breeding to improve udder health improve on length of productive life and animal welfare.

The r_g between FL and UDE indicates that a deep udder is associated with poor longevity, as reported in Larroque and Ducrocq (2001).

Genetic correlations among the fertility, udder health and udder type traits. Conception rate of heifers did not show a significant r_g with the investigated traits, except with CR_c. However, its inclusion in a multi-trait genomic evaluation can improve the prediction of conception rate in multiparous cows.

A strong positive genetic relationship between the two udder health traits is reported in many other studies (e.g. Rupp and Boichard, 1999; Govignon-Gion et al., 2016), confirming that SCS can be uses as an indicator of CM. In addition, the positive r_g with UDE indicates that deep udders are associated with an increase of the number mastitis events and that this type trait can be used as a predictor of mastitis resistance.

Conclusion. Genetic correlations among functional longevity, conception rate, udder health and udder type traits estimated including genomic information were consistent with those obtained using a pedigree relationship matrix. The analysis presented in this study will be extended to other breeds and the results will be used in the development of a combined single-step evaluation in French dairy cattle.

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