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Increasing accuracy of Single-Step evaluations of functional longevity including information from correlated traits

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Abstract

Breeding values for low heritable traits are difficult to estimate. Often, if traits are correlated to each other they should be analysed together in a multivariate genetic evaluation to improve accuracy. However, the correlated traits may not be described by the same model. To overcome the resulting complexity, a “combined” genetic evaluation consisting of two successive evaluations has been implemented in France, resulting in more accurate breeding values. The aim of this study was to verify that a combined Single-Step evaluation is more accurate than a univariate Single-Step evaluation. To that end, genomic breeding values obtained with univariate and combined Single-Step evaluation were compared for functional longevity and five other correlated traits in 2016 and 2021. The average and the correlation between breeding values in 2021 and 2016 suggested that the combined Single-Step evaluation is more accurate than univariate Single-Step evaluations.

Introduction

Longevity is a complex trait with a low heritability. Genetic evaluation for this trait requires a complex survival model to account for highly nonlinear data and for the existence of censored records, corresponding to cows that are still alive (i.e., only a lower bound of their actual longevity is known). Another level of complexity is added by the fact that we are mostly interested in the functional longevity (FL), i.e. the ability to avoid involuntary culling regardless to the milk production level of a cow. Because of these intricacies, the genetic evaluation of French dairy cows on FL is based on a Weibull sire model (Ducrocq, 2005). Moreover, FL is correlated to other traits such as udder health, fertility and type traits that can be used as predictors. Unfortunately, all these traits are described by very different models, making difficult the development of a multiple trait evaluation of FL and of its predictors using raw performances. This is why a “combined” genetic evaluation was developed (Ducrocq *et al.*, 2001) including FL and correlated traits. It relies on a two-step approach: first, univariate evaluations (or multivariate evaluations by group of traits described by a same model) are performed. For all traits, records are corrected for all fixed effects (and possibly for the heterogeneity of residual variances). As a result, each recorded animal gets one “pseudo-record” for each observed trait and an associated weight is calculated. Then a multivariate genetic evaluation is carried out on these weighted pseudo-records, based on a very simple model with only one fixed effect, a year of birth effect, in order to account for selection on correlated traits not accounted for in the first step, and the individual genetic value of each animal (Govignon-Gion *et al.*, 2016). Such combined evaluations have major advantages: as a result, all animals have an estimated breeding value (EBV) on all traits and the construction of a total merit index is straightforward.

In the context of single step evaluations, the combination of Genomic Estimated Breeding Values (GEBVs) from separate genomic evaluations is not optimal. In order to illustrate the benefits of a combined Single-Step (CSS) approach and to evaluate low heritability traits such as FL and its predictors in comparison with several univariate SS (USS) evaluations,

performances of six correlated traits were used in the Montbéliarde breed: FL, somatic cell score (SCS), conception rate in heifers (CRH) and lactating cows (CRC), clinical mastitis (CM) and udder depth (UD).

Materials & Methods

Data. The number of records available in Montbéliarde since 2002 and included in the analyses is listed in Table 1. Records were obtained from the French bovine national database.

Table 1: Number of records for the investigated traits¹

	FL	SCS	CRH	CRC	CM	UD
From 2002 to 2021	1,781,415	4,095,686	2,123,962	5,566,297	2,028,701	1,142,654
From 2016 to 2021	553,930	1,342,868	505,578	1,775,346	689,419	351,915
% of erased performances ²	31.1%	32.8%	23.8%	31.9%	34%	30.8%

¹: FL: functional longevity, SCS: milk somatic cell score, CRH: conception rate of heifers, CRC: conception rate of lactating cows, CM: clinical mastitis, UD: udder depth; ² i.e., ignored in the 2016 analyses.

Method. The FL pseudo-records were derived from the Weibull sire model mentioned above (Ducrocq, 2005). For the other traits, pseudo-records were derived from the SS evaluation results, applying the same univariate models as in the corresponding current official evaluations. Two SS evaluations were run: one considering all available performances (recorded from 2002 to mid-2021) and one considering truncated data after deletion of the performances recorded from 2016 to 2021 to mimic a SS evaluation performed on data available in 2016.

The objective was to verify whether the GEBVs obtained for young animals (2016 SS evaluations) predicted more accurately the CSS GEBVs of 2021 (supposedly the most accurate GEBVs), using a CSS instead of a USS. For this purpose, the GEBVs of the 10% best cows estimated using a CSS evaluation and all data available in 2021 were compared to the GEBVs calculated with a USS or a CSS, and using only data available five years before. This group of best cows included 1,972 cows born and genotyped in 2014, having their first performances in 2016 or later.

Model and software. The general Single-Step model equation for the first step of the CSS evaluation can be summarised as:

$$\mathbf{y}_{kj} = \sum_{i=0}^n \mathbf{b}_k + \mathbf{a}_j + \mathbf{e}_{kj} \quad (1)$$

with \mathbf{y}_{kj} the vector of performances of animal j , \mathbf{b}_k the corresponding vector of fixed effects k . For each trait, performances were modelled using the effects used in the current routine evaluation run by GenEval (<https://www.geneval.fr/indexations-mutualisees>), these models being adapted to each group of traits. \mathbf{a}_j is the vector of additive genetic effects of animal j with $\mathbf{a} = \{\mathbf{a}_j\} \sim N(0, \mathbf{H} \otimes \mathbf{G})$, \mathbf{G} is the genetic (co)variance matrix between traits (in the case of multivariate evaluation), \mathbf{H} is the genetic/genomic relationship matrix between animals, and \mathbf{e}_{kj} is the vector of residuals for animal j with $\mathbf{e} = \{\mathbf{e}_j\} \sim N(0, \mathbf{I} \otimes \mathbf{R})$, \mathbf{R} being the residual (co)variance matrix between traits (in the case of multivariate evaluation). For UD and CM, phenotypic heterogeneous variances were accounted for using Meuwissen's approach (Meuwissen *et al.*, 1996).

GEBVs for USS_2016 and pseudo-records for each trait are estimated using model (1). These pseudo-records are used in the second step of the CSS evaluation of which the equation is:

$$\mathbf{y}_{kj} = \mu_{year} + \mathbf{a}_j + \mathbf{e}_{kj}, \quad (2)$$

where \mathbf{y}_{kj} are the pseudo-records of animal j for trait k , μ_{year} is the birth year of the animal. The objective of μ_{year} is to adjust the additive genetic effects for potential selection on correlated traits not accounted for in the (univariate) first step. \mathbf{a}_j and \mathbf{e}_{kj} are the same as in (1) but in a multivariate context.

Unknown parent groups were used in the SS evaluations. They were defined according to the birth year of the animals with unknown parent.

Both Single Step evaluations were performed using the HSSGBLUP software (Tribout *et al.*, 2020).

Results and discussion

Average of GEBVs. In Figure 1, the average GEBVs of the top 10% cows increased between 2016 (CSS or USS) and 2021. This was expected, since the increase in accuracy due to additional information leads to a greater variability of GEBVs in 2021 and thus to higher GEBV means of the best females. Moreover, for CM, CRH and CRC in 2016 the average GEBV for USS is lower than for CSS, which could be explained again by higher accuracies obtained with the CSS. For the other traits, the difference is small. It could be explained for UD and SCS by the fact that the accuracy is not much improved using a combined evaluation, since the heritability of these traits is high enough (SCS: 15%; UD: 38%). For FL, the difference between average GEBVs in USS_2016 and CSS_2016 are about 0.02 while is it about 0 for SCS and UD. The theoretical heritability of FL is about 14.5% but is lower in practice because of censored animals (i.e. still alive) at the time of evaluation (GenEval, 2021).

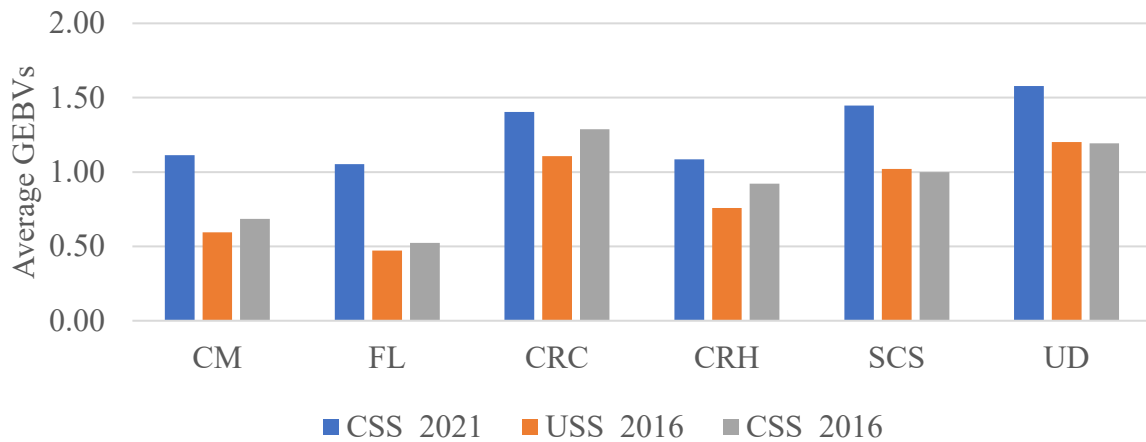


Figure 1. Average GEBVs obtained with the different evaluations for the top 10% cows and for the investigated traits. FL: functional longevity, SCS: milk somatic cell score, CRH: conception rate of heifers, CRC: conception rate of lactating cows, CM: clinical mastitis, UD: udder depth, CSS 2021: combined Single-Step evaluation of 2021, CSS 2016: combined Single-Step evaluation of 2016, USS 2016: univariate Single-Step evaluation of 2016. All results expressed in genetic standard deviation units.

Correlation between GEBVs. Correlations between GEBVs (Figure 2) are higher with the CSS than with the USS evaluation for all traits. It indicates that in 2016, CSS is more efficient than USS to predict CSS in 2021. These differences are small for the most heritable traits (SCS and UD) but are quite clear for the low heritable traits (CM, FL, CRC and CRH).

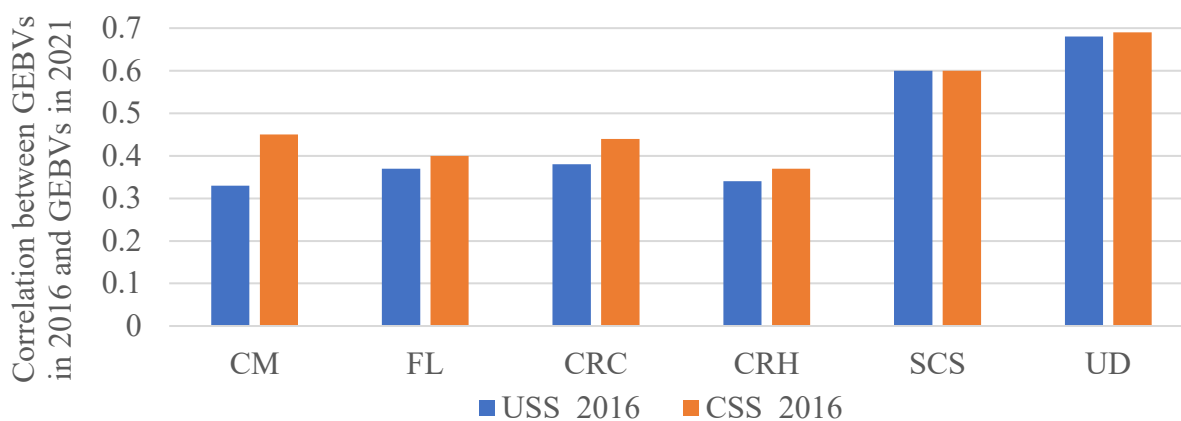


Figure 2. Correlations between GEBVs obtained in 2021 with those obtained in 2016 (USS or CSS) for the top 10% cows and for the investigated traits. FL: functional longevity, SCS: milk somatic cell score, CRH: conception rate of heifers, CRC: conception rate of lactating cows, CM: clinical mastitis, UD: udder depth, CSS 2021: combined Single-Step evaluation of 2021, CSS 2016: combined Single-Step evaluation of 2016, USS 2016: univariate Single-Step evaluation of 2016.

Conclusion. A combined (multivariate) SS evaluation leads to a gain in accuracy for GEBVs for low heritable traits. Even though differences between GEBVs in USS 2016 and CSS 2016 were expected to be higher, the results of this preliminary study are encouraging.

The genetic parameters (particularly genetic correlations) used in our study were estimated a few years ago and did not consider the genomic information on bulls. This could explain why relatively minor differences were found. Therefore, we plan to use updated genetic parameters and to complete the analyses with a study of the GEBV reliability of bulls and cows.

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