Genetic correlations between juvenile mortality traits and traits in selection on French dairy cattle breeds

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Abstract

Reducing juvenile mortality is a pressing challenge for the dairy cattle industry due to its economic, environmental, and animal welfare impacts. While juvenile mortality has multiple causes, genetics plays a substantial role. The implementation of a routine genomic evaluation could therefore contribute to achieving this goal. In France, a genomic evaluation for mortality within the first 48 hours of life is already available for dairy cattle breeds. As part of the SEVITAL project, new juvenile mortality traits covering the first year of life are being studied for inclusion, in the breeding programs of nine dairy breeds (Abondance, Brown Swiss, Holstein, Jersey, Montbéliarde, Normande, Simmental, Tarentaise and Vosgienne). Life history information, i.e. date of birth, date and cause of death (natural death or slaughter) were extracted from the French national cattle database for females born from 2010 to 2024. Three traits have been defined based on the age at which the animal died: 3-30 days, when the leading cause of calf mortality is diarrhea; 31-365 days, when calf mortality is mainly due to respiratory diseases; 3-365 days, to cover the whole period. These traits were defined as binary traits: 0 was assigned to animals still alive during the considered period, and a value of 100 was assigned to animals that died. For each trait, single-step genomic evaluations were carried out with HSSGBLUP (Tribout *et al.*, 2020) using a univariate animal model that included *herd x year-of-birth* and *region x month-of-birth x year-of-birth* as fixed effects. Estimated breeding values (EBVs) of bulls were calculated using the performances of a total number of 4,750 to 2,236,362 animals depending on the breed, among which 2,683 to 608,585 were genotyped. Correlations between juvenile mortality traits and traits routinely evaluated (milk production traits, udder health, fertility, mortality within the first 48 hours) were estimated using Calo's method (Calo et al., 1973). The correlations between EBVs adjusted for their reliability estimated with this method provided an approximation of the genetic correlations. By offering a better understanding of the genetic relationships between traits, these results will help breeding companies determine how to incorporate juvenile mortality traits in their overall breeding objectives.

Key words: Dairy cattle, juvenile mortality, genetic correlations

Introduction

Juvenile mortality is an important challenge for the cattle sector as it represents a major animal welfare issue and is associated with important economic losses and impacts on selection opportunities.

In addition to management practices, genetic selection can be a useful tool to improve calf survival. Several countries have developed genomic evaluations to (i) reduce calf mortality such as the Netherlands (van Pelt et al., 2012), the Nordic countries (Nordic Cattle Genetic Evaluation, 2025) or the United Stats (Neupane

et al., 2021) or (ii) improve resistance to its main underlying causes, i.e. digestive and respiratory diseases such as Canada (Lynch et al., 2024) or the United States (Neupane et al., 2025).

In France, a routine genomic evaluation exists only for perinatal mortality for dairy cattle breeds (GenEval, 2026). To go further, a genomic evaluation for juvenile mortality traits covering the first year of life is being developed. As part of this work, relationships between juvenile mortality traits and traits currently selected for were investigated.

Materials and Methods

Juvenile mortality traits

Datasets

Life-history information including date of birth and date and cause of death (slaughter or natural death) were extracted from the French national bovine database for nine dairy breeds (Abondance, Brown Swiss, Holstein, Jersey, Montbéliarde, Normande, Simmental, Tarentaise and Vosgienne).

The first year of life was divided into two periods to reflect the principal underlying cause of mortality: 3–30 days, during which digestive diseases are the most frequent cause of death, and 31–365 days, during which mortality is mainly due to respiratory diseases. The overall period of 3–365 days was also studied. Perinatal mortality, which includes stillbirth and death within the first 48 hours of life, is already evaluated. Therefore, the first two days of life were excluded from the analyses.

Juvenile mortality was analyzed as a binary trait. For a given period, animals were considered alive if they were alive at the end of the period or slaughtered during that period, and dead if they died of natural causes during the period.

Data of singletons females born in France between 2010 and 2025 were considered (Table 1). Females that did not stayed in the farm where they were born farm during the considered period and males were not taken into account in this study. Indeed, these animals can face health challenges during transport and variable conditions from one farm to another. At least 5 females were included for each herd x birth year and region x birth month x birth year combination. At least 10 paternal half-sisters born in a minimum of 5 herds were retained.

Table 1: Number of calf records available for each period in the nine French dairy cattle breeds

Breed	**n phenotypes**		
	3-30 days	**31-365 days**	**3-365 days**
Abondance	60 508	49 785	53 695
Brown Swiss	58 969	49 183	54 003
Holstein	2 784 101	2 118 154	2 236 354
Jersey	42 509	31 335	36 745
Montbéliarde	1 725 075	1 477 134	1 583 405
Normande	945 345	839 798	894 760
Simmental	64 062	55 219	58 660
Tarentaise	23 221	18 512	20 503
Vosgienne	5 423	4 498	4 750

Model

Estimated breeding values (EBVs) were estimated for each period with a hybrid single step model (Fernando et al., 2016) using HSSGBLUP program (Tribout et al., 2020):

$$\begin{bmatrix} y_n \\ y_g \end{bmatrix} = X\beta + \begin{bmatrix} Z_n & 0 \\ 0 & Z_g M_g \end{bmatrix} \begin{bmatrix} u_n \\ \alpha \end{bmatrix} + e$$

where y is the vector with phenotypes; n refers to non-genotyped animals and g to genotyped animals; β is the vector of fixed effects of herd x birth year and of region x birth month x birth year; M_g are centered SNP genotypes of genotyped animals; $u_n \sim N(0, A_{nn}\sigma_g^2)$ corresponds to EBVs of non-genotyped animals; $\alpha \sim N(0, I\sigma_\alpha^2)$ is the vector of markers effects with $\sigma_\alpha^2 = \frac{\sigma_g^2}{\sum_{1st\ SNP}^{n^{th}\ SNP} 2p_k(1-p_k)}$; $e \sim N(0, I\sigma_e^2)$ is the vector of residual effects; X and Z are incidence matrices for fixed and random animal effects, respectively, and I is the identity matrix.

EBVs were then inverted so that a positive EBV indicates better survival.

Genetic correlations

Genetic correlations between juvenile mortality traits and traits in selection including milk yield (MY), fat yield (FY), protein yield (PY), fat content (FC), protein content (PC), somatic cell score (SCS), survival at birth (SURVIVAL_B), survival at calving (SURVIVAL_C), cows and heifers fertility (FERT_COW, FERT_HEIFER), interval between calving and first artificial insemination (CALV_AI1), non-return rate for cows and heifers (NR_COW, NR_HEIFER) were approximated using Calo's method (Calo et al., 1973):

$$r_g = \frac{\sqrt{\sum_{i=1}^{n} \rho_{i,EBV1} \times \sum_{i=1}^{n} \rho_{i,EBV2}}}{\sum_{i=1}^{n} \rho_{i,EBV1} \times \rho_{i,EBV2} \times r_{EBV1,EBV2}}$$

where $\rho_{i,EBV1}$ is the reliability of the EBV for trait 1 for the bull i, $\rho_{i,EBV2}$ is the reliability of the EBV for trait 2, and $r_{EBV1,EBV2}$ is the Pearson correlation between the EBV for trait 1 and EBV for trait 2. EBVs with a reliability lower than 0.4 were not included.

Results & Discussion

Low to moderate estimates were obtained for the genetic correlations between juvenile mortality traits and traits currently selected for (Table 2). Higher estimates were obtained for the longest periods (31-365days and 3-365 days) in comparison with the estimates obtained for 3-30days. The positive values of estimated correlations indicate favourable relationships between traits as EBVs were inverted for juvenile mortality traits.

In the literature, genetic correlations between calf survival or resistance to diarrhea and respiratory diseases are generally low to moderate (Axford et al., 2024; Jamrozik et al., 2025; Gonzales-Peña et al., 2019, 2020; Neupane et al., 2021, 2025). Our estimated correlations between juvenile mortality traits and milk production traits (between 0.038 and 0.272) were in accordance with the values obtained by Neupane et al. (2021) who found

Table 2: Estimated genetic correlations between juvenile mortality traits and traits in selection in Holstein and Montbéliarde breeds.

	Holstein			Montbéliarde		
Trait	**3-30 days**	**31-365 days**	**3-365 days**	**3-30 days**	**31-365 days**	**3-365 days**
Milk yield	0.122	0.141	0.149	0.494	0.480	0.542
Fat yield	0.145	0.272	0.248	0.484	0.476	0.535
Protein yield	0.190	0.267	0.263	0.599	0.577	0.645
Fat content	0.038	0.155	0.123	0.023	0.026	0.011
Protein content	0.099	0.186	0.169	0.257	0.211	0.241
SCS	0.121	0.231	0.228	0.363	0.299	0.344
Survival at birth	0.329	0.294	0.309	0.514	0.542	0.562
Survival at calving	0.391	0.420	0.473	0.327	0.358	0.297
Cow fertility	0.261	0.424	0.355	0.542	0.577	0.601
Heifer fertility	0.179	0.339	0.260	0.317	0.288	0.343
Interval between calving and 1rst AI	-0.046	0.032	-0.002	0.009	-0.011	-0.058
Cow non return rate	0.356	0.436	0.409	0.278	0.289	0.370
Heifer non return rate	0.168	0.213	0.175	0.071	-0.018	0.114

EBVs for juvenile mortality traits were inverted so that positive EBVs are associated with better survival.

correlations ranging from 0.18 and 0.22 between heifer liveability and milk yields in Holstein. Although, our estimates for correlations with fertility traits (between -0.002 and 0.436) were mostly higher than those of Neupane et al. (2021)

Same trends could be observed in Holstein and Montbéliarde breeds. However, it can be noted that the correlations were substantially higher in Montbéliarde for milk production traits.

For local breeds, reasonable estimation of genetic correlations could not be achieved. This is probably due to the low reliabilities associated with EBVs for juvenile mortality traits as a result of low heritabilities and limited number of performances

Conclusions

Low to moderate favourable correlations were estimated between juvenile mortality traits and traits currently selected for. These results suggest that juvenile mortality can be reduced without impairing selection for other economically important traits.

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