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Genetic analysis of calf vitality, survival and disease resistance in Charolais beef cattle

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Summary

The objective of the present study was to investigate calf health and survival. Data of 2740 Charolais calves, born in 16 French farms and observed from birth until 30 d of age wereanalyzed. Both direct and maternal genetic parameters were estimated for vitality of the calf at birth (NV), survival at 30d (Surv), umbilical infections and diarrhea for 2 age slots: 0-5d and 6-20d (respectively, Umb1, Diar1, Umb2, Diar2). Direct and maternal heritabilities ranged respectively from 0 to 0.081 and from 0 to 0.096. Maternal genetic effects were clearly more important to explain health performance than direct genetic effects for Surv, Diar1 and Umb2. Genetic correlations were estimated with large standard errors and varied markedly between traits varied strongly (from 0 to 1 in absolute values) depending on traits, age slot for a given trait and the nature of the genetic effects considered, direct or maternal. Therefore, the question of the priority arises for the breeding objective because all health traits will be difficult to improve simultaneously in Charolais cattle.

Keywords: diarrhea, health, mortality, navel illness, umbilical infection, vigor

Introduction

Calfhood diseases have a substantial economic impact on beef and dairy farms, and most cases occurred in calves less than 1 month old. Literature on genetics of calf health is scarce, especially on beef calf health. Because French breeders were interested in improving viability of Charolais beef calves, 16 selected herds from a collaborative network of 75 herds were engaged in recording of various calf health performance from birth to one month of age during two successive birth years: from August 2013 to July 2015. The aim of the study was to estimate genetic parameters for calf health traits in order to answer two key questions: Is it feasible to directly select calf health traits? Can we make an indirect selection of calf health through more general performance such as survival or vitality of the calf at birth?

Material and methods

The analysed data came from 16 Charolais herds, including the two INRA experimental Charolais farms located at Bourges in Berry and at Pin-aux-Haras in Normandy, that were dedicated to the on-farm DEGERAM project managed by the French Charolais breeding

society to develop genomic selection on new traits. Selected herds had a minimum of 3 health events per herd-yearand were genetically connected to each other by the use of at least one artificial insemination sire with progenies in a minimum of three herds. 2740 calves bred by 2044 dams and 252 bulls from 16 connected herds were included in the final data set. Performance recording included vitality of the calf at birth (NV) and all health events from birth to one month of age and was directly recorded by the breeders. NV was scored from 1 (very vigorous calf reaching the udder within the first hour after birth) to 4 (assisted calf who needs help to stand and reach the udder) with intermediate scores of 2 (vigorous calf reaching the udder between 1 and 3 h after the birth) and 3 (weak calf needing more than 4 hours to reach the udder). For each health event, the breeder was requested to record the date of occurrence and the suspected disease. Health events occurring at different time slots were defined as binary disease traits (0=no disease event; 1=at least one disease event during the considered time slot) based on whether or not the calf had at least one health event recorded within the considered period. From this database, genetic analyses were conducted on the two most frequent diseases: umbilical infections and diarrhea occurring either between 0 and 5 d of age (Umb1, Diar1) or between 6 and 20 d of age (Umb2, Diar2). The time slots were defined because they were the ones that allow to detect the most significant genetic variations and because of prior knowledge about the different causes of infections for diarrhea depending on the calf age (Cho & Yoon, 2014; Gruenberg, 2016). Survival (Surv) was defined as a binary trait (0=dead; 1=alive), based on whether or not the calf was still alive at 30 d of age. This information was extracted from the French Charolais national database used for the on-farm genetic evaluation for all newborn calves, after excluding calves from twin birth. A pedigree file composed of 6530 individuals and 3 generations of ancestors for the 2740 calves with performance was considered in the genetic analysis.

Mixed linear single and multitrait BLUP animal models wereused to estimate direct and maternal genetic (co)variances, common maternal and residual environmental (co)variances of each trait using ASREML software (Gilmour *et al.,* 1995). Covariance between direct and maternal genetic effects was neither considered within trait nor between traits. The fixed effects identified for each trait were a combination of age and parity of the dam and the calf contemporary group, defined as a combination of herd, birth year and birth season. In addition, a sex effect was significant for NV, Umb1, Umb2 and Surv and calf born as twin was only a significant effect for NV.

Results and discussion

Table 1 gives the phenotypic means and the raw standard deviations for the 6 traits considered in the study. Calf survival at 30 days (96%) was above the national average (93%) for Charolais breed (Leclerc *et al.*, 2016). Concerning NV, 62.28% of calves were very vigorous, 32.19% vigorous, 4.04% weak and 1.49% assisted at birth. No health event was recorded for 1947 calves of the 2740 calves of the dataset while 1052 health events were recorded for the remaining 793 calves. The total incidence risks (number of calves treated for the first time during the considered slot divided by the number of calves eligible to be treated) of umbilical infections and diarrhea during the first month of life were about 6% and 17% respectively.

Estimates of genetic parameters and common maternal environmental (co)variances are presented in Tables 2 and 3. Large standard errors were calculated for all parameters, and in particular for all estimates of genetic correlations. Although we found similar value for direct heritability of NV (8% *vs* 9%) as in Riley *et al*. (2004), these authors estimated a maternal heritability of 10% not in accordance with our current nul estimate. In our study, a

large proportion (nearly 17%) of phenotypic variance for NV was explained by maternal common environmental variance (Table 3). Concerning survival, we estimated a low direct heritability (2.6%) in the range of most values found in the literature (Fuerst-Waltl & Sorensen, 2010; Leclerc *et al*., 2016) and a maternal genetic heritability (9.6%) almost 4 times larger than the direct heritability (Table 2). Genetic effects involved in resistance to diarrhea seemed to depend on calf age: only maternal genetic effects were detected for early diarrhea (Diar1) whereas the two types of genetic effects, direct and maternal, were observed in later diarrhea (Diar2). In Holstein, Mahmoud *et al*. (2017) have estimated only direct genetic heritability for calf diarrhea with estimate of 6%. Significant larger proportion of phenotypic variance of Diar2 was explained by maternal common environment effects (8.7%, Table 3) rather than by any genetic effects (h^2d=1.6% and h^2m=2.4%, Table 2). As regards to umbilical infections (Table 2), the genetic effects involved in Umb1 are mainly direct genetic effects (h^2d=8.1%) whereas genetic effects involved in later infections Umb2 are exclusively maternal genetic effects (h^2m=7.9%). Such a result is unusual because in general maternal effects had more impact on performance at younger ages. No maternal common environmental variance was detected for navel illness at any stage. Our results are not fully in agreement with the only other estimate of direct heritability for umbilical infections of 14% in Holstein heifers from birth to 3 months of age (Henderson *et al*., 2011).

In terms of direct genetic correlations between Surv and NV, our results showed that the more vigourous at birth the calf is, the higher is the probability to survive at one month of age (Table 2). In consequence, a reduction of death loss may be envisioned by genetic improvement of NV, which has a significantly higher heritability than Surv. Direct genetic effects for Surv and NV were also strongly favourably correlated to direct genetic resistance to Diar2 (Table 2). In addition, correlations between maternal genetic effects for Surv and any maternal genetic disease trait were positive (correlation estimates ranging from 0.34 to 0.59, Table 2). Therefore selecting for any maternal genetic disease resistance trait may be not recommended to improve calf survival. However due to the limited data for estimation of genetic correlations, caution should be taken in interpreting all these results. Most maternal genetic correlations between disease resistance traits were highly unfavourable (Table 2) suggesting that selection to improve maternal genetic resistance to one kind of calf infection may severely affect the resistance to other infections. In view of these last counterintuitive results and the associated high standard errors, further analysis on large-scale datasets should confirm or infirm these results.

Conclusion

Our study revealed some significant genetic variability in beef calf health traits, in particular neonatal vitality, survival and umbilical infections. In addition, maternal genetic effects were clearly more important to explain health performance than direct genetic effects for survival at 30 days, early diarrhea and umbilical infections between 6 and 20 days of age. These first results for beef calf health genetics will have to be strengthened by large scale studies with several tens of thousands of phenotyped calves. In the current genomics era, the extent of genetic variation presents in calf health traits makes it possible to propose direct genomic selection on calfhood disease resistance if an adequate reference population is constituted and managed over time. This also implies that breeding goals should considered health traits not only directly through the use of health phenotypes, but also indirectly through the use of correlated traits such as calf survival or neonatal vitality.

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Table 1. Number of records, mean value (incidence in case of disease traits) and raw standard deviations for calf health traits.

	Surv[a]	NV[b]	Umb1[c]	Umb2[d]	Diar1[e]	Diar2[f]
Number of records	2356	2423	2740	2740	2740	2740

Mean value / incidence	96.31 %	1.447 pt	2.92 %	3.47 %	5.26 %	11.68 %
Raw standard deviation	18.86 %	0.646 pt	16.84 %	18.30 %	22.32 %	32.12 %

[a] Surv = survival at 30 d ; [b] NV = neonatal vitality scored from 1 (very vigorous – calf standing, walking and reaching for an udder within the first hour after birth) to 4 (assisted calf who requires help to stand and reach an udder); [c]Umb1 = umbilical infections occurring between 0 and 5 d of age; [d]Umb2 = umbilical infections occurring between 6 and 20 d of age; [e]Diar1 = diarrhea occurring between 0 and 5 d of age; [f]Diar2 = diarrhea occurring between 6 and 20 d of age.

Table 2. Direct and maternal heritabilities respectively on the first and second lines of the diagonal, direct genetic correlations on the upper triangle and maternal genetic correlations on the lower triangle (standard errors are in brackets).

	Surv[a]	NV[b]	Umb1[c]	Umb2[d]	Diar1[e]	Diar2[f]
Surv	0.026 (0.03) 0.096 (0.04)	-0.53 (0.56)	-0.32 (0.52)	-	-	-0.71 (1.01)
NV	-	0.078 (0.04) 0 (ne)	0.27 (0.33)	-	-	0.999 (ne)
Umb1	0.52 (0.50)	-	0.081 (0.04) 0.019 (0.02)	-	-	-0.07 (0.61)
Umb2	0.34 (0.27)	-	-0.68 (0.87)	0 (ne) 0.079 (0.02)	-	-
Diar1	0.48 (0.39)	-	0.49 (0.78)	-0.68 (0.32)	0 (ne) 0.048 (0.03)	-
Diar2	0.59 (0.53)	-	-0.999 (ne)	-0.85 (0.49)	0.33 (0.52)	0.016 (0.02) 0.024 (0.02)

ne: not estimable

[a] Surv = survival at 30 d ; [b] NV = neonatal vitality scored from 1 (very vigorous – calf standing, walking and reaching for an udder within the first hour after birth) to 4 (assisted calf who requires help to stand and reach an udder); [c]Umb1 = umbilical infections occurring between 0 and 5 d of age; [d]Umb2 = umbilical infections occurring between 6 and 20 d of age; [e]Diar1 = diarrhea occurring between 0 and 5 d of age; [f]Diar2 = diarrhea occurring between 6 and 20 d of age.

Table 3. Proportion of phenotypic variance due to maternal common environmental effect (on the diagonal) and correlations between maternal environmental effects (above the diagonal).

	Surv[a]	NV[b]	Diar1[c]	Diar2[d]
Surv	0.065 (0.06)	0.05 (0.33)	-0.85 (0.86)	0.03 (0.50)
NV		0.166 (0.04)	0.69 (0.53)	0.05 (0.22)
Diar1			0.044 (0.04)	0.999 (ne)
Diar2				0.087 (0.04)

ne: not estimable

[a] Surv = survival at 30 d ; [b] NV = neonatal vitality scored from 1 (very vigorous – calf standing, walking and reaching for an udder within the first hour after birth) to 4 (assisted calf who requires help to stand and reach an udder); [c]Diar1 = diarrhea occurring between 0 and 5 d of age; [d]Diar2 = diarrhea occurring between 6 and 20 d of age.