Genetic parameters for calving and conformation traits in Charolais × Montbéliard and Charolais × Holstein crossbred calves

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ABSTRACT: Charolais sires can be mated to Montbéliard or Holstein dairy cows to produce crossbred calves sold for meat production. Heritabilities and correlations between traits can differ when they are calculated within Charolais × Montbéliard or within Charolais × Holstein population. Moreover, the genetic correlation between the same trait measured on Charolais × Montbéliard and on Charolais × Holstein crossbred calves is not necessarily unity. The first objective of this study was to estimate heritability and genetic correlation between traits within Charolais × Montbéliard and within Charolais × Holstein population. The second objective was to investigate if those traits are genetically identical between crossbred populations. Traits studied were calving difficulty, birth weight, height, bone thinness, and muscular development. Data included 22,852 Charolais × Montbéliard and 16,012 Charolais × Holstein crossbred calves from 391 Charolais sires. Heritabilities estimated separately within each crossbred population were similar. Stronger genetic correlations were observed in Charolais × Holstein population compared with Charolais × Montbéliard between calving difficulty and height (0.67 vs. 0.54), calving difficulty and bone thinness (0.42 vs. 0.27), birth weight and bone thinness (0.52 vs. 0.20), and birth weight and muscular development (0.41 vs. 0.18). Bivariate analysis considering observations on Charolais × Montbéliard and on Charolais × Holstein as different traits showed that genetic variances and heritabilities were similar for all traits except height. Birth weight and muscular development were genetically identical traits in each crossbred populations, with genetic correlations of 0.96 and 0.99. Genetic correlations were 0.91 for calving difficulty, 0.80 for height, and 0.70 for bone thinness and log-likelihood ratio tests indicated that they were significantly different from 1 (P ≤ 0.01). Results show evidence for reranking of Charolais sires for calving difficulty, height, and bone thinness depending on whether they are mated to Montbéliard or Holstein cows.

Key words: calf, crossbred, genetic correlation, maternal environment


INTRODUCTION

To manage the replacement of their dairy cattle herds, farmers can choose to inseminate dairy cows having low milk production potential with semen of beef sires. Calves produced are sold at about 3 wk of age for beef production. Economic value of these crossbred calves is directly linked to their conformation and indirectly linked to calving difficulty (Luo et al., 2002; Hickey et al., 2007). In France, where the data were collected, the 2 main dairy cow breeds mated to Charolais sires are Holstein and Montbéliard.

In various species, prenatal environment provided by the mother was shown to have consequences on progeny (Nicholas, 1996). Allen et al. (2004) used embryo transfer between larger Thoroughbred and smaller Pony mares and determined a difference of 15% for growth at birth. Studies in pigs or poultry have compared genetic parameters of the parental purebred lines to their terminal crossbred lines (Lutaaya et al., 2001). Zumbach et al. (2007) found genetic correlations lower than 1 for same production traits observed in purebred lines and in their reciprocal crosses, which was partly attributed to different environment conditions.

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In bovines, differences in performances and economic impact between crossbred and purebred calves have been reported by few studies (Wolfova et al., 2007; Dal Zotto et al., 2009). Interaction between sire and maternal breed was one explanation, among others, for low to medium correlations (from 0.01 to +0.46) between breeding values of beef sires for growth traits estimated on purebred and on crossbred progeny (Tilsch et al., 1989). However, to our knowledge, no genetic parameters have been estimated within different crossbred populations. In addition, information is lacking on genetic correlations for the same trait between different crossbred populations.

The study will focus on traits measured on Charolais × Montbéliard and Charolais × Holstein crossbred calves including calving difficulty, birth weight, height, bone thinness, and muscular development. Traits observed in Charolais × Holstein and Charolais × Montbéliard populations might be genetically different. Therefore, the first objective is to estimate heritabilities and genetic correlations among traits in each crossbred population separately. Furthermore, the second objective is to estimate genetic correlations between the same trait measured in Charolais × Holstein and Charolais × Montbéliard populations.

**MATERIALS AND METHODS**

Animal Care and Use Committee approval was not obtained for this study because data used is routinely collected as part of the breeding program and collecting these phenotypes does not violate the integrity of the animals.

**Population Structure**

Data were from 38,864 crossbred calves originating from 391 purebred Charolais AI sires mated to dams from Montbéliard or Holstein breeds. Number of males was 20,168 (51.9%) and 18,696 (48.1%) for females. Number of Charolais × Montbéliard calves was 22,852 (58.8%) and 16,012 (41.2%) for females. Number of males was 20,168 (51.9%) and 18,696 (48.1%) for females. Number of males was 20,168 (51.9%) and 18,696 (48.1%) for females. Number of sires with offspring in both crossbred populations was 367. Number of sires with more than 30 calves in each crossbred population was 204. Sires had on average 99 offspring.

**Traits**

Traits included in this study were calving difficulty, birth weight, height, bone thinness, and muscular development. Data were collected through the national progeny testing program on calves born between 1986 and 2012. Herds were located in the midwestern part of France.

Calving difficulty was recorded by farmers and was evaluated on a scale from 1 to 5, in which 1 corresponded to a calving process without difficulty or assistance and 5 corresponded to particular difficult circumstances where the calf died during calving. Birth weight was estimated by farmers immediately after calving and expressed in kilograms. Conformation traits of calves were recorded on average at 22 d of age and included height, bone thinness, and muscular development. These conformation traits were scored by 19 qualified classifiers who followed regular training sessions to score the traits in a consistent way. Classifiers scored both crossbred calves using the same trait definition. Height at withers was scored on a scale from 1 to 5, in which 1 corresponded to shortest calves; bone thinness was also scored on a scale from 1 to 5, in which 1 corresponded to thinnest bone structure. Muscular development was evaluated based on visual inspection of shoulders, back, and rump. Each location was scored on a scale from 1 to 9, in which 1 corresponded to light muscular development. The overall score for muscular development was obtained by averaging the scores for shoulders, back, and rump.

**Statistical Analysis**

Data were analyzed using the following animal model:

\[
Y_{ijklmn} = \mu + S_i + C_j + BYBS_k + \text{Animal}_l + e_{ijkl},
\]

in which \(Y_{ijklmn}\) was the observation, \(\mu\) was the overall mean, \(S_i\) was the fixed effect of sex \(i\) (2 classes), \(C_j\) was the fixed effect of classifier \(j\) (19 classes), \(BYBS_k\) was the fixed effect of the combination between the birth year (from 1986 to 2012) and the birth season defined as 4 classes where 3-mo periods were defined starting in December (104 classes), \(\text{Animal}_l\) was the random additive genetic effect of the \(l\)th calf \(-N(0, A\sigma^2_a)\), in which \(A\) corresponded to additive genetic relationship matrix and \(\sigma^2_a\) corresponded to the additive genetic variance, and \(e_{ijkl}\) was the random residual effect \(-N(0, I\sigma^2_e)\), in which \(I\) corresponded to the identity matrix and \(\sigma^2_e\) corresponded to residual variance.

Only relations on the paternal side were used to construct the additive genetic relationship matrix. Pedigree information on the paternal side was traced back with a minimum of 3 generations. At first, univariate analyses were used to estimate heritabilities and bivariate analyses to estimate genetic correlations between different traits measured within the same crossbred population. Second, bivariate analyses were used to estimate heritabilities and genetic correlations between the same trait measured in the 2 different crossbred populations, as follow:

\[
\begin{bmatrix}
Y_1 \\
Y_2
\end{bmatrix} =
\begin{bmatrix}
X_1 & 0 \\
0 & X_2
\end{bmatrix}
\begin{bmatrix}
b_1 \\
b_2
\end{bmatrix} +
\begin{bmatrix}
Z_1 & 0 \\
0 & Z_2
\end{bmatrix}
\begin{bmatrix}
u_1 \\
u_2
\end{bmatrix} +
\begin{bmatrix}
e_1 \\
e_2
\end{bmatrix},
\]
in which $y_1$ represents traits measured on Montbéliard × Charolais crossbreds and $y_2$ on Holstein × Charolais, $X_1$ and $X_2$ are the incidence matrices for fixed effects $b_1$ and $b_2$, $Z_1$ and $Z_2$ are the incidence matrices for random genetic effects $u_1$ and $u_2$, and $e_1$ and $e_2$ are the error terms. Covariances between $e_1$ and $e_2$ were 0 as traits were measured on different individuals. To test if genetic correlation was significantly different from 1, the log-likelihood ratio test was used. The likelihoods used were of the unconstrained model and of the model where genetic correlation was fixed at 0.998. Constraining genetic correlation at a value of exactly 1 is computationally not possible. Significance levels were obtained from a chi-square distribution with 1 degree of freedom.

Breeding values of the 204 sires with a minimum of 30 calves in each crossbred population were estimated, using a univariate model in Charolais × Montbéliard and in Charolais × Holstein separately.

Genetic parameters were estimated using ASREML (Gilmour et al., 2009).

RESULTS

Descriptive Statistics

Number of observations, means, and standard deviations are given for each crossbred population in Table 1. Charolais × Montbéliard and Charolais × Holstein populations had similar means for calving difficulty and height. Calves from Montbéliard dams had 600 g heavier estimated weights compared with calves from Holstein dams, had 0.17 point higher bone thinness scores, and had 0.35 point higher muscular development scores. Standard deviations were similar in both crossbred populations for all traits.

Heritability and Correlation within Crossbred Population

Heritabilities and phenotypic and genetic correlations among birth and conformation traits for Charolais × Montbéliard population are presented in Table 2 and for Charolais × Holstein population in Table 3. Estimated heritabilities and phenotypic correlations were similar in both crossbred populations. Calving difficulty and birth weight had similar genetic correlation in Charolais × Montbéliard population (0.86) and in Charolais × Holstein population (0.87). Muscular development had in both populations genetic correlations of approximately zero with height and bone thinness (from −0.10 to 0.01). Stronger genetic correlations were observed in Charolais × Holstein population compared with Charolais × Montbéliard between calving difficulty and height (0.67 vs. 0.54), calving difficulty and bone thinness (0.42 vs. 0.27), birth weight and bone thinness (0.52 vs. 0.20), and birth weight and muscular development (0.41 vs. 0.18).

Heritability and Genetic Correlation between Crossbred Populations

Table 4 shows heritabilities and genetic correlations between the same trait measured in Charolais × Montbéliard and in Charolais × Holstein populations. Heritabili-

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### Table 1. Traits description with number of observations, means, and standard deviations for each crossbred population

<table>
<thead>
<tr>
<th>Trait</th>
<th>Scale</th>
<th>Charolais × Montbéliard</th>
<th>Charolais × Holstein</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>n</td>
<td>Mean</td>
<td>SD</td>
</tr>
<tr>
<td>Calving difficulty</td>
<td>1 (easy) to 5 (difficult)</td>
<td>20,806</td>
<td>1.67</td>
</tr>
<tr>
<td>Birth weight</td>
<td>kg</td>
<td>20,064</td>
<td>45.1</td>
</tr>
<tr>
<td>Height</td>
<td>1 (short) to 5 (tall)</td>
<td>18,759</td>
<td>3.15</td>
</tr>
<tr>
<td>Bone thinness</td>
<td>1 (thin) to 5 (thick)</td>
<td>18,772</td>
<td>2.65</td>
</tr>
<tr>
<td>Muscular development</td>
<td>1 (light) to 9 (heavy)</td>
<td>18,882</td>
<td>5.30</td>
</tr>
</tbody>
</table>

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1 Standard errors are between brackets.
ties estimates based on bivariate analysis were similar for Charolais × Montbéliard and Charolais × Holstein for all traits except for height where heritability was lower in Charolais × Montbéliard (0.34) than in Charolais × Holstein (0.55) populations. This difference is mainly due to a lower additive genetic variance in Charolais × Montbéliard (0.23) as compared to Charolais × Holstein (0.44) populations. This difference in heritability and in additive genetic variance was not as pronounced when estimating heritabilities on univariate analysis within population (Tables 2 and 3).

Genetic correlations between crossbred populations for birth weight and for muscular development were not significantly different from 1 ($P = 0.05$ and $P = 0.75$). Genetic correlation between crossbred populations was 0.91 for calving difficulty, 0.80 for height, and 0.70 for bone thinness and all were significantly different from 1 ($P \leq 0.01$).

**Comparison of Breeding Values Estimated within Crossbred Population**

Breeding values of sires estimated on either their Charolais × Montbéliard or their Charolais × Holstein crossbred offspring are shown in Fig. 1. Traits reported in Fig. 1 are bone thinness and muscular development, that is, a situation where the genetic correlation is significantly different from 1 (bone thinness) and a situation where the genetic correlation is not significantly different from 1 (muscular development).

**DISCUSSION**

**Trait Means for Charolais × Montbéliard and Charolais × Holstein Populations**

Calves from crosses between Charolais sires and Montbéliard dams have on average higher birth weight, thicker bones, and higher grades for muscular development. This difference between Charolais × Montbéliard and Charolais × Holstein calves might be due to (maternal) genetic differences between Montbéliard and Holstein dams. However, as Holstein and Montbéliard cows are generally raised in different herds, we cannot exclude specific effects of Montbéliard and Holstein herds such as age at calving or criteria to select females used for terminal cross. In the present study, no information was available on specific farm conditions but Montbéliard and Holstein herds were located in the

**Table 3. Heritability and phenotypic and genetic correlation for preweaning traits measured in Charolais × Holstein calves. Phenotypic correlations are presented above the diagonal (in italics) and genetic correlations are below. Heritabilities on diagonal and genetic variance ($\sigma^2_a$) were estimated on univariate analysis**

<table>
<thead>
<tr>
<th>Trait</th>
<th>Charolais × Holstein</th>
<th>Calving difficulty</th>
<th>Birth weight</th>
<th>Height</th>
<th>Bone thinness</th>
<th>Muscular development</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>$\sigma^2_a$</td>
<td>$\sigma^2_p$</td>
<td>$h^2$</td>
<td>$\sigma^2_a$</td>
<td>$\sigma^2_p$</td>
<td>$h^2$</td>
</tr>
<tr>
<td>Calving difficulty</td>
<td>0.12 (0.02)</td>
<td>0.40 (0.01)</td>
<td>0.23 (0.01)</td>
<td>0.17 (0.01)</td>
<td>0.15 (0.01)</td>
<td></td>
</tr>
<tr>
<td>Birth weight</td>
<td>0.87 (0.04)</td>
<td>0.20 (0.02)</td>
<td>0.51 (0.01)</td>
<td>0.39 (0.01)</td>
<td>0.28 (0.01)</td>
<td></td>
</tr>
<tr>
<td>Height</td>
<td>0.67 (0.06)</td>
<td>0.68 (0.05)</td>
<td>0.36 (0.04)</td>
<td>0.33 (0.01)</td>
<td>0.10 (0.01)</td>
<td></td>
</tr>
<tr>
<td>Bone thinness</td>
<td>0.42 (0.08)</td>
<td>0.52 (0.06)</td>
<td>0.45 (0.07)</td>
<td>0.30 (0.03)</td>
<td>0.13 (0.01)</td>
<td></td>
</tr>
<tr>
<td>Muscular development</td>
<td>0.49 (0.08)</td>
<td>0.41 (0.07)</td>
<td>0.01 (0.08)</td>
<td>0.02 (0.08)</td>
<td>0.30 (0.03)</td>
<td></td>
</tr>
<tr>
<td>$\sigma^2_a$</td>
<td>0.06</td>
<td>11.3</td>
<td>0.26</td>
<td>0.17</td>
<td>0.49</td>
<td></td>
</tr>
</tbody>
</table>

$^1$ Standard errors are between brackets.

**Table 4. Heritabilities and genetic correlations between same traits measured in Charolais × Montbéliard and in Charolais × Holstein populations**

<table>
<thead>
<tr>
<th>Trait</th>
<th>Charolais × Montbéliard</th>
<th>Charolais × Holstein</th>
<th>$r_g^4$</th>
<th>$P$-value$^5$</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>$\sigma^2_a$</td>
<td>$\sigma^2_p$</td>
<td>$h^2$</td>
<td>$\sigma^2_a$</td>
</tr>
<tr>
<td>Calving difficulty</td>
<td>0.08</td>
<td>0.46</td>
<td>0.17 (0.02)$^6$</td>
<td>0.07</td>
</tr>
<tr>
<td>Birth weight</td>
<td>17.8</td>
<td>60.8</td>
<td>0.29 (0.03)</td>
<td>13.1</td>
</tr>
<tr>
<td>Height</td>
<td>0.23</td>
<td>0.67</td>
<td>0.34 (0.03)</td>
<td>0.44</td>
</tr>
<tr>
<td>Bone thinness</td>
<td>0.19</td>
<td>0.59</td>
<td>0.32 (0.03)</td>
<td>0.17</td>
</tr>
<tr>
<td>Muscular development</td>
<td>0.61</td>
<td>1.69</td>
<td>0.36 (0.03)</td>
<td>0.58</td>
</tr>
</tbody>
</table>

$^1\sigma^2_a =$ genetic variance.

$^2\sigma^2_p =$ phenotypic variance.

$^3h^2 =$ heritability.

$^4r_g =$ genetic correlation.

$^5P$-value is based on the log-likelihood ratio test and indicates if genetic correlations differ from unity.

$^6$Standard errors are between brackets.
same region and we are not aware of any systematic differences in management between Montbéliard and Holstein herds. Therefore we expect that (maternal) genetic differences between Montbéliard and Holstein dams are the main reason for differences in mean values between both crossbred populations.

**Heritabilities**

Estimates of heritability obtained for calving difficulty are similar to that reported by Mujibi and Crews (2009) on purebred Charolais who analyzed scores transformed to a continuous scale. Heritability of birth weight is slightly lower than previous studies on purebred Charolais (Phocas and Laloe, 2003; Mujibi and Crews, 2009).

Little information is available on genetic parameters for conformation traits of young calves because most studies considered postweaning traits. Heritability of bone thinness for Piemontese cows was 0.12 (Man-tovani et al., 2010), which is lower than the present results. Heritability of muscularity at weaning for purebred Blonde d’Aquitaine and Limousin animals (Bouquet et al., 2010) was similar than results in the current study. Afolayan et al. (2007) analyzed height and muscularity from weaning to 600 d and estimated heritabilities from 0.42 to 0.60 for height and from 0.19 to 0.44 for muscularity. Heritability estimates for height tend to be higher than results of the current study, which might be due to the objective measurement of this trait in centimeters.

Preweaning traits in beef cattle are affected by maternal effects (Manfredi et al., 1991; Brandt et al., 2010; McHugh et al., 2011). Therefore, most national cattle evaluation programs use statistical models accounting for direct genetic, maternal genetic, and maternal permanent environmental effects (Crews and Wang, 2007). Models used in the present study did not include a maternal (genetic) effect because interest is in genetic parameters for Charolais breed and maternal (genetic) effects would relate to the Holstein or Montbéliard breeds. Present heritabilities are comparable with other studies considering a maternal effect (Phocas and Laloe, 2003; Eriksson et al., 2004). In the current data set herd information was missing for two-thirds of the data and therefore the effect of herd was not included in the model. However, as farmers recorded calving traits, difference in trait values between herds might exist due to the subjective nature of recording. In addition, differences in management between herds might exist, which could affect the traits. Therefore, additional analyses were performed based on observations for which herd information was available. Herd variance explained between 1% (for bone thinness) and 23% (for birth weight) of the phenotypic variance. Herd variance was especially important for traits recorded by the farmer. Adjusting for herd effects led to similar estimates of genetic variance as those from the analysis when not including herd effects. Adjusting for
Genetic parameters in crossbred calves

Influence of Maternal Breed

Genetic differences between traits measured in Charolais × Montbéliard and Charolais × Holstein might originate from several factors, one being differences in maternal environment, that is, environment before (and closely after) birth (e.g., Banos et al., 2007). For example, due to differences in morphology, Montbéliard and Holstein dams might provide different uterine conditions to their offspring, which might result in genotype × (uterine) environment interaction. Studies using embryo transfer and cross-fostering in mice resulted in significant uterine and nursing effects on tail length, body weight, and growth rate (Cowley et al., 1989; Rhees et al., 1999). Studies in human also showed effect of prenatal and postnatal maternal environment on obesity or diabetes phenotypes (Barker, 1998).

Alternatively, epistatic interactions might explain genetic differences between traits measured in Charolais × Montbéliard and Charolais × Holstein. Indeed, the effect of alleles from the Charolais sire might differ depending on the presence of alleles from either Montbéliard or from Holstein breed. In addition, interaction between the maternal genotype and the genotype of the offspring might play a role. This hypothesis is confirmed by observations in mice using embryo transfer, where various responses of the offspring genotypes on body weight were noticed depending on the kind of mother they developed in (Maestripieri and Mateo, 2009).

Implications

Calving difficulty, height, and bone thinness show significant genetic differences when measured in Charolais × Montbéliard or in Charolais × Holstein calves (P-value from 0.01 to < 0.001). Genetic difference for calving difficulty is smaller; however, this trait is of great interest for farmers. Consequently, selection of Charolais sires depends on the dam breed. Separated genetic evaluations for Charolais × Montbéliard and Charolais × Holstein crossbreds should be considered. This would
offer breeding companies the possibility to label their commercial sires depending on their performance with a certain dam breed. Farmers would have the opportunity to make optimal choice when buying sires straws to inseminate their Holstein or Montbéliard females.

**LITERATURE CITED**


