## Genetic parameters for type and functional traits in the French Holstein breed

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#### Abstract

In France, EBVs are routinely estimated for lactation somatic cell counts, female fertility, and functional longevity. These functional traits have rather low heritabilities, leading to limited reliabilities for young sires. To include these traits in a total merit index, it is desirable to improve their genetic evaluations taking advantage of indirect information. Type traits are potential early predictors of functional traits, because they are early scored and because their heritability is moderate to high. To combine the direct information on functional traits with the indirect information on type traits, it is necessary to know the genetic correlations between all traits. But it is difficult to estimate the genetic relationship between all these traits directly from the data. This is especially true when one of the traits is functional longevity evaluated by survival analysis. Here we present an approximate estimation of these genetic correlations. These estimates are compared to correlations between proofs and, for some traits, to REML estimates obtained from smaller data samples. According to these estimates, prediction of functional longevity could be improved by udder depth and temperament, somatic cell counts by milking speed and udder depth, and (to a smaller extend) female fertility by temperament and rump angle.

#### **1. Introduction**

In many countries, genetic evaluations of functional traits such as longevity, female fertility, and udder health are now common in dairy cattle. Farmers are these interested in traits for the improvement of their herd profitability. To efficiently include these traits in breeding programs, it is necessary to combine estimated breeding values (EBVs) in a total merit index. Economic studies such as by Colleau et al. (1999a), lead to the choice of the most important traits and provide the economic weight for each of them. If EBVs for the selected traits are evaluated using a multiple trait BLUP, then the weight of each trait in the total merit index is its economic weight. Unfortunately, EBVs are often evaluated separately, and it is necessary to

approximate a multiple trait BLUP evaluation to combine functional traits information (Colleau *et al.*, 1999b). The multiple trait BLUP (true or approximate) requires the knowledge of the dispersion parameters.

France, EBVs for functional In longevity (FL, with a survival analysis), lactation somatic cell scores (LSCS), and female fertility (FER) are routinely estimated. Because of the low heritability of these traits, a long delay is required to get genetic evaluations with a reasonable reliability. This delay is often not compatible with the timing of selection decisions of young bulls after progeny test. In this context, the MT-BLUP is a judicious way to elaborate an improved EBV for each functional trait combining direct information with indirect information brought by early predictors.

Type traits, because they are early scored and have moderate to high heritabilities, are good candidate predictors.

combine direct То and indirect information, it is essential to know the genetic correlations between type and functional traits, and to select in the long list of type traits those that are most correlated with functional traits. In the French Holstein breed, REML estimates of genetic correlations are available only between LSCS (and clinical mastitis) and udder traits (Rupp and Boichard, 1999). For functional longevity and type traits, Larroque and Ducrocq (1999) estimated genetic correlations by an indirect approach using the MACE methodology. The same method was applied in this study to estimate all the genetic correlations between type and functional traits.

## 2. Methods

The Multiple trait Across Country Evaluation (MACE) procedure was developed in order to evaluate dairy bulls used in several countries. Schaeffer (1994) proposed a multiple trait sire model which considers milk yield in different countries as different traits. To avoid the use of individual records, the right hand side of the multiple trait BLUP mixed model equations is built using the information brought by within-country sire EBVs. This information should be made independent from the reliability of evaluations and from the relationships between sires. This is done using the technique referred to deregression (Banos, 1990; Sigurdsson and Banos, 1995). Genetic correlations between countries are calculated applying REML to these "deregressed" EBVs (Sigurdsson et al., 1996).

In both deregression and REML estimation of genetic correlations, the model is the following:

$$\mathbf{y}_{\mathbf{i}} = \boldsymbol{\mu}_{\mathbf{i}} \mathbf{1} + \mathbf{Z}_{\mathbf{i}} \mathbf{Q} \mathbf{g}_{\mathbf{i}} + \mathbf{Z}_{\mathbf{i}} \mathbf{s}_{\mathbf{i}} + \mathbf{e}_{\mathbf{i}}$$
(1)

where:  $\mathbf{y}_i$  is the vector of deregressed breeding values for trait i;  $\mu_i$  is the mean of trait i; **Q** is the matrix relating sires to groups of unknown parents;  $Z_i$  is the incidence matrix relating deregressed proofs to sires;  $\mathbf{g}_{\mathbf{i}}$  is the vector of effects of unknown parents groups for trait i;  $s_i$  is the vector of transmitting abilities for trait i as deviations from  $\mu_i \mathbf{1} + \mathbf{Q} \mathbf{g}_i$ ;  $\mathbf{e}_i$  is the vector of random residuals. The assumptions about the variance-covariance structure  $var(e_i) = R_i \sigma_{e_i}^2, \quad cov(e_i, e_j') = 0,$ are:  $\operatorname{var}(\mathbf{s}) = \mathbf{A} \otimes \mathbf{G}$  with  $\mathbf{G} = \{g_{ij}\}, \text{ where }$  $g_{ii}$  is the sire (co)variance between traits i and j, A is the relationship matrix between all males (sires and maternal grand-sires),  $\sigma_{ei}^2$  is the residual variance for trait i and  $\mathbf{R}_{i}$  is a diagonal matrix the diagonal elements of which are equal to the inverse of the number of daughters included in the calculation of the deregressed proofs.

This method can be extended to estimate genetic correlations not only between countries but also between traits. However, this usage of MACE out of its original context must be tempered:

First, the main feature of MACE is that residuals correlations are assumed to be zero. In the international evaluations. EBVs of a sire in different countries are estimated using distinct samples daughters. So the performances of daughters are not influenced by the same unidentified environmental effects. This is obviously no longer the case when MACE is applied to the evaluation of traits within country. Batches of daughters recorded on different traits are not distinct. Larroque and Ducrocq (1999) studied the influence of this assumption on the estimation of correlations between functional longevity and type traits. This was done by comparing MACE estimates of genetic correlations when data sets for different traits were forced to be the same or distinct. They did not find important

differences between these situations. This that suggests if nonzero residual correlations exist between functional longevity and type traits, they are probably rather small. In the present study, we made assumption zero the of residual correlations between functional traits and type traits. For a number of combinations of traits, REML estimates were obtained from raw data and were compared to MACE estimates, indicating how strong was the assumption of zero residual correlation.

Second, some authors reported some problems for low heritability traits either in the deregression (Rogers et al., 1996; Druet et al., 1999) or in the estimation of genetic correlations (Larroque and Ducrocq, 1999). They concluded that for the deregression as well as for the estimation of genetic correlations it is necessary to restrict the analysis to bulls with a minimum number of daughters. For traits recently recorded, this may lead to keep mostly proven bulls, with many second crop daughters. Because they represent a selected sample, the correlation estimates may be biased (Larroque and Ducrocq, 1999).

## 3. Material

## 3.1. Data

EBVs used in this study were the French national evaluations available in January 1999 for Holstein bulls. Twenty one traits were considered: lactation SCS (LSCS), post-partum fertility (PFER), functional longevity (FL), and eighteen type traits (including milking speed and temperament).

• LSCS is based on data recorded after 01/09/1989. Test day somatic cell scores are defined as SCS= $log_2$  (SCC/100000)+3. LSCS, defined as a weighted average of monthly cell scores over the whole lactation, is analysed with a BLUP animal model (Rupp and Boichard, 1997).

• For PFER, the trait considered is the result (success/failure) of A.I. that have been made in milk recorded herds since 1993. This trait is evaluated with a BLUP procedure with sire and maternal grand sire effects (Boichard *et al.*, 1999).

• FL considers length of productive life for cows with first lactation started after 01/12/1984. A Weibull model with sire and maternal grand sire model is used (Ducrocq and Sölkner, 1998).

• Genetic evaluation for type traits was based on data since 1987. Rear udder attachment and heel depth, however, were added in 1993, as well as temperament and fore udder attachment in 1996. EBVs for the eighteen type traits are estimated using a multiple trait animal model (Ducrocq, 1993).

Description of traits and heritabilities used in the genetic evaluations are given in Table 1. Because of differences in the starting date of data recording according to the traits, EBVs of French bulls born since 1988 were included in this analysis.

## 3.2. Data selection for deregression

Breeding values were selected only if the number of daughters used in the EBV computation was higher than or equal to 10 for lactation SCS and type traits, 10 uncensored daughters for functional longevity and 35 daughters for postpartum fertility (because of its very low heritability). The final data set included:

- 4468 bulls with EBVs for LSCS, and 824 additional ancestors;
- 2811 with PFER (and 0 ancestor, because EBVs for PFER were obtained without relationship matrix);
- 3038 bulls with FL and 498 ancestors;
- 3886 bulls with type traits and 449 ancestors, except for rear udder attachment and heel depth (3820 evaluated sires and 443 ancestors) and for temperament and fore udder attachment (2117 evaluated sires and 316 ancestors).

Each trait was deregressed separately. For all traits but PFER, 20 groups of unknown parents were defined according to status (sire, grand sire and grand dam), country of birth and year of birth.

### 3.3. Data selection for genetic correlations

At most 10 traits were analysed simultaneously. This constraint led to the definition of eight batches of traits (A to H) for estimation of genetic correlations. In all batches, "deregressed" breeding values were kept if the number of daughters were higher than or equal to 50 for each trait. For batch H, however, ie between FL and temperament and fore udder attachment, only 30 daughters were required. 12 groups of unknown parents were defined after some deregression phantom groups were merged. Table 2 shows the number of evaluated sires and the number of additional ancestors for each batch of traits.

Table 1. Traits description and heritabilities

Trait	EBVs definition	Heritability
Lactation SCS	High $\rightarrow$ low	0.15
Post-partum fertility	Low success rate $\rightarrow$ high	0.02
Functional longevity	Short $\rightarrow$ long	0.22
Milking speed (MS)	Slow $\rightarrow$ fast	0.32
Udder cleft (UC)	Absent →deep	0.26
Udder depth (UD)	Low $\rightarrow$ high	0.35
Udder balance (UB)	Low rear $\rightarrow$ high rear	0.34
Distance between teats (DT)	Apart → close	0.25
Teat placement front (TPF)	Apart → close	0.30
Teat direction rear (TDR)	External $\rightarrow$ internal	0.23
Teat length (TL)	Short $\rightarrow$ long	0.30
Rear udder attachment (RUA)	Low $\rightarrow$ high	0.20
Fore udder attachment (FUA)	Short $\rightarrow$ long	0.20
Height at sacrum (HS)	Short $\rightarrow$ tall	0.47
Chest depth (CD)	Shallow $\rightarrow$ deep	0.36
Rump length (RL)	Short $\rightarrow$ long	0.29
Rump width (RW)	Narrow $\rightarrow$ wide	0.32
Rump angle (RA)	High pins $\rightarrow$ low pins	0.34
Rear leg set (RLS)	Straight $\rightarrow$ sickled	0.07
Heel depth (HD)	Shallow $\rightarrow$ deep	0.10
Temperament (TE)	Nervous→ quiet	0.10

Table 2.	Number	of	evaluated	sires	and	additional	ancestors	for	the	estimation	of	genetic
correlati	ons											

Batch of traits considered simultaneously	Evaluated sires	Additional ancestors
А	2561	362
В	2378	351
С	2045	321
D	2002	320
E	569	243
F	812	227
G	805	274
Н	264	173

#### 4. Results

Table 3 presents MACE estimates of genetic correlations between functional traits (LSCS, PFER, LF) and type traits.

4.1. Genetic correlations between LSCS and type traits

MACE estimates of genetic correlations between LSCS and capacity traits or feet and legs traits were closed to 0. A genetic antagonism (-0.37) was found between LSCS and milking speed. Fast milking cows were found to have high LSCS. Favourable genetic correlations were obtained with udder traits. These correlations ranged from 0.01 (for teat length) to 0.37 (for udder depth). The strongest relationships were found with traits related to udder support: udder depth (0.37), udder balance (0.20), and rear udder attachment (0.17). Higher udder was associated with lower LSCS. Udder cleft had a low correlation (0.11) with LSCS.

Only one trait related to teat placement, distance between teats (side view) had a moderate genetic correlation (0.23) with LSCS. Closer teat distance was associated with lower LSCS. These results were quite consistent with the REML estimates of Rupp and Boichard (1999) based on individual data, except for fore udder attachment. They found a moderate genetic correlation (0.32) between this trait and LSCS, but based on few records. In their study, they found very low environmental correlations between LSCS and udder traits. This indicates that the assumption of zero residual correlation in the MACE procedure is fulfilled for these traits. This may also explain the close agreement between MACE estimates and REML estimates (Table 6).

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Type traits	LSCS	PFER	LF
MS	-0.37 (A)	-0.07 (C)	0.19 (G)
UC	0.11 (A)	0.00 (C)	0.21 (G)
UD	0.37 (A)	0.20 (C)	0.49 (G)
UB	0.20 (A)	0.01 (C)	0.28 (G)
DT	0.23 (A)	0.19 (C)	0.20 (G)
TPF	0.09 (B)	0.01 (C)	0.15 (G)
TDR	0.04 (B)	0.01 (D)	0.09 (G)
TL	0.01 (B)	0.00 (D)	-0.21 (G)
RUA	0.17 (B)	0.03 (D)	0.27 (G)
FUA	0.14 (F)	0.08 (F)	0.17 (H)
HS	-0.07 (B)	-0.03 (E)	0.08 (E)
CD	-0.04 (B)	-0.18 (E)	-0.06 (E)
RL	-0.03 (B)	0.04 (E)	0.02 (E)
RW	-0.01 (B)	-0.05 (E)	0.04 (E)
RA	-0.02 (B)	0.16 (E)	0.09 (E)
RLS	-0.07 (B)	0.00 (E)	-0.07 (E)
HD	0.08 (B)	0.03 (E)	0.11 (E)
TE	-0.01 (F)	-0.26 (F)	0.23 (H)

<sup>1</sup> Type trait definition: as in table 1.A same letter in parenthesis indicates traits analysed simultaneously.

4.2. Genetic correlations between PFER and type traits

Estimates of genetic correlations between PFER and type traits were low, ranging from -0.26 to +0.20. The highest correlation (-0.26) was found with temperament, indicating surprisingly that nervous cows had somewhat better success to A.I. Two capacity traits were also related to PFER. First, rump angle showed a positive correlation (+0.16) and cows with low pins had a higher success to A.I. Second, chest depth presented a negative correlation (-0.18), indicating that shallow cows had a higher success to A.I. Two udder traits, udder depth and distance between teats (side view), had slightly positive correlations with PFER: (0.20 and 0.19, respectively). The biological basis of these latter correlations, if any, is still unclear

4.3. Genetic correlations between FL and type traits

MACE estimates of genetic correlations between FL and capacity traits or feet and legs traits were closed to 0. As found in a similar study (Larroque and Ducrocq, 1999), feet and legs traits did not contribute to longevity in the French Holstein breed. This was not the case in many other countries (see Vollema, 1997, for a review). The absence of genetic correlation may be related to inconsistencies in the way these feet and legs traits are scored, and to an inadequate choice of feet and legs traits.

The strongest favourable correlations found with udder traits were and especially with traits related to udder support: udder depth (0.49), udder balance (0.28), rear udder attachment (0.27) and fore udder attachment (0.17). Cows with a well attached udder had a lower risk to be culled. These results were consistent with the previous study (Larroque and Ducrocq, 1999). Low correlations were also found with some traits related to teat

placement: 0.20 for distance between teats (side view) and 0.15 for teat placement front. These latter results may reflect the correlations between udder traits and LSCS. Indeed, after correction for milk production, udder disorders are an important health-related culling reason (Beaudeau et al., 1999). It is interesting to note that udder cleft had a higher correlation with functional longevity (0.21) than with LSCS (0.11). In the same way, no genetic correlation was found between teat length and LSCS, but an unfavourable low correlation (-0.21) was found with FL, indicating that cows with long teats had a higher risk to be culled. Whereas milking speed was negatively associated with LSCS (-0.37), it was favourably correlated with FL. A breeder prefers to voluntarily cull a cow with a slow milking, even though LSCS is generally lower.

Temperament had a low genetic correlation (0.23) with FL, indicating that a nervous cow had a higher risk to be culled.

# 5. List of type traits predictors for functional traits

## 5.1. A first list

These estimates of genetic correlations are the base for the choice of early type traits predictors for each functional trait.

For LSCS, the most important traits were: milking speed, udder depth, udder balance and distance between teats (side view), with genetic correlations (in absolute value) ranging from 0.37 to 0.20. For PFER, genetic correlations with type traits were lower and needed to be confirmed. Rump angle and temperament were probably the only logical candidates but the correlation was quite low for the first one and its sign was surprising for the second one. For functional longevity, the most important type traits were: udder udder balance, udder depth. rear

attachment, temperament, udder cleft, distance between teats (side view) and teat length, with genetic correlations ranging in absolute value from 0.49 to 0.20.

So nine type traits were considered as possible predictors for the three functional traits.

5.2. Genetic correlations between type traits

Some of these type traits (in particular udder traits) are moderately to highly correlated to each other. Table 4 presents REML estimates of genetic correlations between these type traits (except for temperament) obtained in the French Holstein breed in a previous study (Larroque, 1998). Clearly udder cleft, udder depth, udder balance are genetically correlated. Distance between teats is only moderately correlated to udder depth and udder balance. Teat length has a moderate correlation with the other udder traits except with distance between teats. Rump angle is not related to any other trait. One may wonder whether some of these traits do not influence functional traits per se but appear important only because of these correlations.

## 5.3. Stepwise regression

Table 5 provides the best combinations with 1 to 9 predictors, with their corresponding maximum accuracy, derived from the genetic correlations between traits and, therefore, assuming a complete accuracy of the evaluation for type predictors.

Clearly, the three functional traits were not accurately predicted by indirect information on type traits.

• Functional longevity was the one better explained by information on type traits. The  $R^2$  reached to 0.33 with information on: udder depth, temperament and distance between teats. Udder balance, udder cleft and rear udder attachment were not retained in this model, probably

because of their high correlations with udder depth. Functional longevity is the functional trait for which reliabilities on EBVs request the longest delay. It seems that some type traits are able to give an early information on this trait.

• LSCS, was the second functional trait better explained by type traits. The stepwise regression led to keep two out the four type traits given in the section 5.1 "A first list". Udder balance, with a high genetic correlation with udder depth (0.54), was excluded. LSCS, however, is already the functional trait with the highest (although limited) reliability of evaluations based on direct information. Therefore, the marginal gain due to indirect predictors is more limited.

• PFER was difficult to explain with type traits. Only temperament and rump angle appeared to significantly increased the  $R^2$  up to 0.11.

The results would suggest to retain as type traits predictors of functional traits: udder depth, milking speed, distance between teats, teat length, rump angle and temperament.

# 6. Genetic correlations between selected type traits and functional traits

After selection of early predictors among the list of type traits, genetic correlations between all predictors and all functional traits are needed for the multitrait BLUP evaluations (Colleau *et al.*, 1999). Results obtained using different methods were compared.

REML estimates of genetic correlations were available between type traits (Larroque, 1998) and between udder traits and LSCS (Rupp and Boichard, 1999). These estimates were also available between udder traits and clinical mastitis (CM), and between LSCS and CM.

	UC	UD	UB	DT	TL	RUA	RA
MS	0.21	0.26	0.23	0.02	-0.25	0.25	0.03
UC		0.47	0.44	0.02	-0.20	0.53	-0.03
UD			0.54	0.25	-0.28	0.58	0.02
UB				-0.20	-0.15	0.55	-0.02
DT					-0.03	0.12	0.08
TL						-0.23	0.03
RUA							-0.02

Table 4. **REML estimates of genetic correlation between type traits**<sup>i</sup>

<sup>i</sup>Type trait definition: as in Table 1

Functional trait	Type traits	$R^2$
LSCS	MS	0.137
	MS+UD	0.217
	MS+UD+TL	0.248
	MS+UD+TL+DT	0.271
	MS+UD+TL+DT+UC	0.276
	MS+UD+TL+DT+UC+RA	0.280
	MS+UD+TL+DT+UC+RA+UB	0.282
	MS+UD+TL+DT+UC+RA+UB+RUA	0.282
	MS+UD+TL+DT+UC+RA+UB+RUA+TE	0.282
PFER	TE	0.068
	TE+RA	0.107
	TE+RA+UD	0.135
	TE+RA+UD+DT	0.149
	TE+RA+UD+DT+UC	0.160
	TE+RA+UD+DT+UC+MS	0.168
	TE+RA+ UD+DT+UC+MS+TL	0.170
	TE+RA+ UD+DT+UC+MS+TL+UB	0.171
	TE+RA+ UD+DT+UC+MS+TL+UB+RUA	0.171
FL	UD	0.240
	UD+TE	0.319
	UD+TE+DT	0.327
	UD+TE+DT+TL	0.336
	UD+TE+DT+TL+UB	0.339
	UD+TE+DT+TL+UB+RA	0.340
	UD+TE+DT+TL+UB+RA+MS	0.341
	UD+TE+DT+TL+UB+RA+MS+UC	0.341
	UD+TE+DT+TL+UB+RA+MS+UC+RUA	0.341

## Table 5. Stepwise regression of functional traits on type traits<sup>i</sup>

<sup>i</sup> Type trait definition: as in Table 1

	PFER	FL	MS	UD	DT	TL	RA	TE	СМ
LSCS	0.23 (J) 0.12	0.37 (J) 0.31	-0.44 (R) -0.37 (A) -0.36	0.40 (R) 0.37 (A) 0.33	0.26 (R) 0.23 (A) 0.06	0.08 (R) 0.01 (B) 0.18	-0.02 (B) 0.00	-0.01 (F) -0.10	0.72 (R)
		0.39 (J) 0.11	-0.07 (C) 0.02	0.20 (C) 0.17	0.19 (C) 0.16	0.00 (D) 0.09	0.16 (E) 0.15	-0.26 (F) -0.20	
FL			0.19 (G) 0.04	0.49 (G) 0.36	0.20 (G) 0.01	-0.21 (G)	0.09 (E) 0.14	0.23 (H) 0.11	
MS			0.04	0.26 (R) 0.30 (G)	0.02 (R) 0.04 (G)	-0.25 (R) -0.34 (G)	0.03 (R)	0.06 (F)	0.06 (R)
UD				0.24	0.14 0.25 (R) 0.38 (G)	-0.17 -0.28 (R) -0.24 (G)	0.05 0.02 (R)	-0.03 -0.10 (F)	0.46 (R)
DT					0.27	-0.04 -0.03 (R) -0.05 (G)	0.03 0.08 (R)	-0.16	0.20 (R)
TL						-0.06	-0.03 0.03 (R)	-0.10 0.07 (I)	0.12 (R)
RA							0.09	-0.17	
TE								0.07	

 Table 6. REML (first row), MACE (second row) estimates of genetic correlations between traits, and correlations between EBVs (third row)

CM= clinical mastitis (more  $\rightarrow$  less matitis)

- MACE estimates were calculated between type traits and functional traits, but also between functional traits. The same procedure as described in sections 2 and 3 was applied to these traits. Two other batches of traits were also defined: I with 865 evaluated sires and 231 additional ancestors, J with 607 evaluated sires and 246 additional ancestors.
- Finally, as a comparison, raw correlations between EBVs for all traits were calculated. For this analysis, bulls were required to have at least 35 daughters for type traits, 50 daughters for LSCS, 100 daughters for PFER, 35 daughters for FL.

Table 6 presents these different estimates.Clearly, correlations between EBVs were not very consistent with the genetic correlations estimated by REML or MACE. This was specially true for the traits with low heritability such as PFER, FL or temperament. Therefore, this simple approach could be used only when the reliability of proofs is high. On the opposite, REML and MACE estimates were rather close. This is especially true between LSCS and udder traits. In this case, residual correlations were very low (Rupp and Boichard, 1999) and explain these consistent results. REML and MACE estimates of genetic correlation, however, were also very consistent between milking speed, udder depth, and residual udder balance, although correlations were positive (ranging from

0.03 to 0.20 in absolute value). Estimates of genetic correlations were rather high between functional longevity and LSCS or PFER. These results were expected, because reproductive and udder disorders are the two main reasons of culling (Beaudeau *et al.*, 1999). However, the genetic correlation between LSCS and PFER (0.23) was quite surprising and may reflect some indirect relationship with production.

## 7. Conclusion

REML estimation in the MACE framework is an interesting approach when it is not possible to directly compute the genetic correlations from the raw data. The assumption of zero residual correlations between traits is sometimes a strong one. In some situations, however, the hypothesis of zero residual correlations may be perfectly valid. This is the case when REML estimates are available and are actually very small, or when it is possible to estimate MACE genetic from in different correlations data environments. In this study, such comparisons with true REML estimates for LSCS with type traits, indicated that if non zero residual correlations exist, they have a low impact on MACE estimates for these traits. Our estimates of genetic correlations between type traits and functional traits clearly show the key importance of udder traits and especially of udder depth. This may be related to the udder health: cows with a deep udder have more SCS and a higher risk of mastitis and also a higher risk to be culled. Milking speed is also an important trait with an opposite relation with LSCS and with FL. As in previous studies (Larroque and Ducrocq, 1999), but in contrast with other authors, no genetic relation was found between feet and legs traits and functional longevity. The importance of temperament on PFER is quite surprising and genetic correlations between PFER and udder

traits are unexpected. This study is a primary approach to identify important type traits and must be enlarged. For a proper choice of type traits. the improvement of reliabilities of each functional trait by indirect information must be evaluated (Druet et al., 1999). Furthermore, it is also important to quantify the standard error of MACE estimates, Druet et al. (1999) gave an with observed example standard deviations over four samples. It is also important to assess the sensitivity of optimal EBVs from MT-BLUP to changes in dispersion parameters. Finally, this study stresses that, whenever possible, estimates of dispersion parameters obtained from actual data should be derived from preferred to values approximate methods.

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