Does Selection for Production Affect Type Traits Genetic Evaluation in Italian Holstein?

Filippo Biscarini, Stefano Biffani and Fabiola Canavesi

A.N.A.F.I. Italian Holstein Breeders Association Via Bergamo, 292 – Cremona ITALY

Abstract

In the process of revising the procedures of genetic evaluation for conformation in Italian Holsteins, the effect of continued selection for production on type traits breeding values estimation has been investigated, together with the comparison of multiple-trait and single-trait estimates. The use of a multiple-trait model leads to the greatest changes: mean reliability for final score increases from 0.80 to 0.86, and rank correlation is 0,95.On the contrary, the effect of production is quite mild: mean reliabilities for final score is 0,85 instead of 0,86 and rank correlation is 0,99. The adoption of a multiple-trait model will considerably increase the accuracy and quality of Italian genetic evaluation for conformation.

Keywords: Holstein, type traits, correlation with milk yield.

Introduction

Current genetic evaluation for Italian Holstein type traits is based on a single-trait animal model analysis for 17 linear traits plus final score. These procedures are now undergoing a revision, aiming to improve the accuracy and quality of the evaluation. Different options were considered:

- 1. the inclusion of some new traits (udder symmetry, rear teat placement and conformation)
- 2. the adoption of a multiple-trait animal model for the simultaneous evaluation of all type traits
- 3. accounting for the effect of milk production as correlated trait in the multiple-trait evaluation.

The adoption of a multivariate analysis of conformation is now possible due to the increased capacity and power of our computers.

The first of this revision step was the multivariate estimation of heritabilities and genetic correlations for the 18 official type traits plus the 3 new ones carried out last

December (Biscarini, 2003). This is of course a fundamental passage prior calculation of breeding values.

The second step, object of this work, has been the assessment of the impact of selection for production on type traits genetic evaluation and the comparison of multiple-trait estimates of breeding values to the current situation.

Material and Methods

This study is based on the database situation of the Italian Holstein-Friesian population in November 2003, consisting of 58,502 bulls and 3,008,610 cows for a total of 3,067,112 animals.

In order to have a "deeper" dataset and to make more efficient use of the relationships among animals the analysis has been limited to 16 type-traits, final score already included, letting off the 5 most recently introduced traits, as reported in table 1; this was also required by the canonical transformation that can't cope with missing data.

For the estimation of both (co)variance components and BVs two distinct pathways have been undertaken and followed in this study: one that takes into account dairy production including milk yield in the model and one that does not; these are going to be referred to as "TYPE" and "TYPEM" from now on, respectively.

Milk yield was 305-d mature equivalent yield of first lactation.

Initially, genetic parameters for conformation have been re-estimated including milk yield in the analysis.

For the estimation of genetic parameters random samples of approximately 10,000 - 15,000 animals have been taken from the population, while breeding values have been calculated on the complete database.

Genetic groups have been used to deal with animals with unknown parents.

The same fixed effects used in the official italian genetic evaluation have been considered: herd-year-season and the interaction of age and lactation stage. Thus, the linear mixed model used both for the estimation of genetic parameters and for the calculation of EBVs was:

$\mathbf{y} = \mathbf{h}\mathbf{y}\mathbf{s} + \mathbf{a}\mathbf{s}\mathbf{l} + \mathbf{a} + \mathbf{e},$

where:

у	=	trait score
hys	=	fixed effect of herd, year and round
asl	=	of evaluation fixed effect of age and stage of lactation
a	=	random animal effect

e = residual effect.

For both the estimation of (co)variance components and of BVs a multiple-trait animal model was used.

The publicly available computer program MTC (Misztal et al., 1994) has been used to (co)variance estimate components. This program was chosen because it makes use of the canonical transformation to deal with the number large of traits under study. Heritabilities and genetic correlations have thus been estimated on 6 samples, either including or omitting milk yield. A nonparametric paired-data sign test has been used to assess the significance of the influence of production on the estimation (Table 1).

These data were passed on to the program MTJAAM (Gengler *et al.*, 1999), that also makes use of the canonical transformation, for the estimation of breeding values: the mean genetic parameters of 6 samples have been used for the "TYPEM" estimates while those of only 1 sample for the "TYPE" estimates.

Breeding values have been estimated for 3,067,112 animals and 21 genetic groups; genetic groups have been defined according to year of birth intervals; there were 146,793 herd-year-season effects and 228 age-stage of lactation effects.

In order to analyze the effect of production on type traits evaluation, genetic trends of EBVs for the 5 traits with the highest correlation with milk yield, therefore more likely to detect an influence of production if this exists, have been drawn for all bulls and cows separately and for proven bulls with at least 10 daughters in 5 herds; such trends have later been compared to the current single-trait ones.

This allowed comparisons between multivariate type-traits-only EBVs, type-traits EBVs after accounting for production and current single-trait EBVs for conformation.

Finally, in order to quantify the observed differences and make further comparisons, reliabilities, regression coefficients and Spearman rank correlation coefficients have been calculated for TYPE, TYPEM and current single-trait results; SAS[®] statistical procedures have been used for the purpose.

Results

Table 1 shows heritabilities from TYPE and TYPEM estimations, the significance of the differences between them and the correlations of the 16 type traits with milk production; the 5 traits most correlated with milk kilograms, highlighted in the table, are: final score, angularity, rear udder height, rear udder width and udder depth; this is consistent with other studies as for angularity and udder traits but not as for final score, which results to have here a higher correlation than that found by Short *et al.* (1992) and by Sanjabi *et al.* (2003). A more general consistency was found with the results of Misztal *et al.* (1991).

The genetic trends shown in figures 1 to 4 point out the existence of some differences among the estimates, especially when comparing to the current single-trait genetic evaluation for type.

To quantify these differences, regression coefficients have been compared: differences greater than 2 standard deviations have been considered to be significant, having a 0.95 probability of being actually different. Table 2 shows that only some traits are actually different when accounting for milk yield or using a multiple-trait analysis, and that rear udder height and udder depth show no significance in any of the comparisons. The latter, in particular, hasn't got a clear trend, indicating perhaps that udder where growing deeper when selection was for production only and began getting less and less deep when considering udder depth and somatic cells in the breeding objective and criterion; this is confirmed by analyzing trends and regression coefficients for udder depth until 1989 and from 1990: trends are clearer and have much higher coefficients of determination (r^2) and differences among TYPE, TYPEM and single trait estimates are more significant. Genetic trends for TYPE and TYPEM EBVs quite overlap, while those for single-trait EBVs are quite different in absolute values though not in slope and direction, as shown by the similarity of regression coefficients.

Spearman rank correlation coefficients (table 3) are quite high for all paired rankings, but a bit lower when comparing single- to multiple-trait estimates; this could mean that the impact of adoption of a multiple-trait model is greater than that of simply including milk yield.

Mean reliabilities, reported in table 4, remarkably increase switching from a singleto a multiple-trait model, but almost show no changes if accounting or not for milk yield; they even look to be a little lower when production is considered, but the difference is too small to have any significance.

Conclusions

Emphasized selection for production through years has not only altered some physical and physiological characteristics of dairy cows as underlined by Hansen (2000); it also has an influence, though mild, on the correctness of genetic evaluation for conformation.

This study, in fact, shows that genetic trends for at least some type traits tend to be higher when milk yield is taken into account, indicating that current BVs for conformation are slightly under-estimated, even though the effect is very light and focused only on 3 of the traits analysed: final score, angularity and udder depth.

The impact of a multi-variate analysis is much stronger, leading to major changes in genetic trends, breeding values estimates and ranking of animals, more or less for all the traits.

Therefore, while adopting a multiple-trait model is great change, accounting for the effect of production is perhaps just refinement: nevertheless it would probably lead to more accurate estimates, which are particularly desirable for those traits somehow related to longevity, whose importance has been stressed by several studies, for instance by Short *et al.* (1992) and by Hansen (2000).

With the aim of verifying a possible bias due to the different number of samples of genetic parameters used in BVs estimation, a control analysis is being carried out

References

- Biscarini, F. 2003. Advancements in Italian Holstein type traits evaluation. International Cattle Breeders Round Table, Edimburgh, 2003: *personal communication*.
- Hansen, L.B. 2000. Consequences of selection for milk yield from a geneticist's viewpoint. *J. Dairy Sci.* 83, 1145-1150.
- Misztal, I., Lawlor, T.J., Short, T.H. & van Raden, P.M. 1991. Genetics and breeding. J. Dairy Sci. 75, 544-551.
- Sanjabi, M.R., Govindaiah, M.G. & Moeini, M.M. 2003. Relationships among udder type traits and milk yield of Iranian Holstein-

Friesian cattle. *Proceedings of the British* Society of Animal Science, 2003.

and herd life in Holsteins. J. Dairy Sci. 75, 1987-1998.

Short, T.H. & Lawlor, T.J. 1992. Genetic parameters of conformation traits, milk yield

SAS® 1982. User's Guide: Statistics. Version 5.18. SAS Inst., Inc., Cary, NC.

Table 1. Type traits milk and non milk heritabilities, significance of the difference and correlations with milk yield (these data refer to one single sample while mean genetic parameters of a number of samples have been used in subsequent calculations).

	TYPEM h ²	TYPE h ²	sign	r with milk
Final score	0,215	0,215		0,288
Stature	0,418	0,417	+	0,105
Chest width	0,268	0,265	+	-0,028
Body depth	0,296	0,295	+	0,055
<u>Angularity</u>	0,230	0,228	+	0,425
Rump angle	0,258	0,257	+	0,063
Rump width	0,230	0,228	+	0,133
Rear legs rear view	0,158	0,158		0,158
Foot angle	0,104	0,103	+	0,020
Fore udder	0,220	0,218	+	-0,038
Rear udder height	0,229	0,230	-	0,335
Rear udder width	0,145	0,145		0,515
Udder support	0,176	0,175	+	0,130
Udder depth	0,335	0,335		-0,278
Teat placement	0,184	0,183	+	0,078
Teat length	0,219	0,218	+	0,105
<u>Milk kg</u>	0,292			
	х		11	
	n	l	12	
	p)	0,003	significant
	p)*	0,05	Significant

Table 2. Significance of differences among regression coefficients (FS: Final score; Ang: angularity; RUH: Rear udder height; RUW: Rear udder width; UD: Udder depth). *all bulls; **all cows; ***high reliability bulls only.

	TYPEM-TYPE*	TYPEM-TYPE**	TYPEM-TYPEM***	TYPE-sing	TYPEM-sing
FS	2,857	2,750	1,143	0,769	0,462
Ang	2,250	3,556	1,000	1,857	0,857
RUH	0,800	0,750	0,154	1,200	1,040
RUW	5,778	6,857	1,619	0,381	1,300
UD	1,200	1,375	0,143	0,615	0,769
UD up to 1989			0,800	3,580	2,558
UD from 1990			0,110	1,225	1,116

	Final score	Angularity	Rear udder height	Rear udder width	Udder depth
TYPEM - TYPE (bulls)	0,992	0,987	0,989	0,981	0,958
TYPEM - TYPE (cows)	0,985	0,970	0,974	0,961	0,950
<u> TYPEM - TYPE (high</u>					
<u>r2 bulls)</u>	0,986	0,959	0,987	0,963	0,990
single trait - TYPE	0,954	0,909	0,947	0,910	0,956
single trait - TYPEM	0,968	0,957	0,965	0,944	0,966

Table 3. Spearman rank correlation coefficient.

Table 4. BVs reliabilities.

	r^2	n
TYPE (all animals)	0,42	3067112
TYPEM (all animals)	0,39	3067112
single-trait (high reliability bulls only)	0,80	4264
TYPE (high reliability bulls only)	0,86	4175
TYPEM (high reliability bulls only)	0,85	4175

Picture 1-4. Genetic trends for high reliability bulls.





