

Genetic Analysis of Type Traits for the Italian Jersey Breed

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Abstract

Anafi (Associazione Nazionale Allevatori Frisone Italiana) is also in charge of the Italian Jersey cattle genetic evaluations. Since interest about this dairy breed is steadily mounting, (co)variance components for 16 type traits of Italian Jersey cows were estimated, in order to start thinking of how to develop a new and more comprehensive selection index. The canonical transformation, in the frame of a multiple-trait animal model, has been used to cope with the high number of traits contemporarily evaluated. These estimates were necessary to calculate heritabilities and correlations and, through these, the EBVs of bulls and cows by two different models, a single- and a multiple-trait animal model. The results of the two models have eventually been compared, mainly as for differences in reliability: mean reliability increased from 0.20 to 0.24 (20%) using a multiple-trait model; these values are higher if calculations are limited to bulls with at least 20 daughters.

Keywords: Jersey, type traits, heritability.

Introduction

Italian Jersey type evaluation began in 1995 when the first Jersey cows have been scored. Since then, interest about this dairy breed constantly increased through years and now there currently are around 4,300 cows routinely assessed for type traits by the classifiers of ANAFI; the Italian Holstein Breeders Association is, in fact, also in charge of Jersey cattle genetic evaluations and of maintaining its national herd book.

Although Jerseys are definitely fine cows, superb in dairy character, it sounds reasonable to start selecting for conformation even in this breed in which in Italy, until now, improvement relied only on production merit; this is especially sensible if we regard the current emphasis placed upon longevity and functionality in farm animals. In fact, profitability will be higher, in general, if cows produce large quantities of milk in routinely initiated lactations while also remaining sound (Misztal *et al.*, 1999). That is why the need of evaluating genetic parameters for type traits arose.

The aim of the present study is to estimate genetic parameters for 16 type traits in the Italian Jersey population and to compute single- and multiple-trait BVs estimates, in order to compare the accuracy of the evaluations.

Material and Methods

The Jersey population the estimates are based on, consists of a total of 7,714 animals (789 bulls and 6,925 cows), referring to primiparous cows that have been scored for conformation (3,012) and their relatives back to three generations.

In order to identify the effects to include in the model, preliminary analyses with the Proc GLM of SAS[®] were performed, and the significant effects were selected.

Thus, the linear mixed model used was:

$$y = hyc + mpd + a + e,$$

where:

- y = trait score
- hyc = fixed effect of herd, year of evaluation and classifier
- mpd = fixed effect of month of calving and distance between calving and evaluation
- a = random animal effect
- e = residual effect.

For the estimation of (co)variance components a multiple-trait animal model was used, whereas for the estimation of breeding values both single- and multiple-trait animal models were used.

The model included, after editing, 3,012 records of primiparous cows, 240 “herd-year-classifier” effects and 131 “month of calving-distance between calving and evaluation” effects.

The 16 traits taken into account are shown in table 1, each with its mean and standard deviation.

The publicly available computer programs MTC (Misztal *et al.*, 1994) and MTJAAM (Gengler *et al.*, 1999) were used; the former for the estimation of (co)variance components, the latter for the estimation of BVs and related reliabilities. These programs were chosen because they both make use of the canonical transformation to deal with the large number of traits under study; the use of the canonical transformation has been possible because the model was the same for all the traits and this is a requirement of the MTC and MTJAAM programs.

Results

Obtained heritabilities (diagonal) and genetic and phenotypic correlations (respectively above and below the diagonal) are reported in table 1. Heritabilities ranged from 0.09 to 0.41; the largest value was for udder depth, the smallest for foot angle. The largest positive correlations were between body depth and chest width (0.90), rump width and chest width (0.87), udder depth and foot angle (0.82); the largest negative correlations were between teat

length and rear legs side view (-0.52) and between teat length and udder support (-0.50).

The heritability estimates found were smaller than those from other studies; this is probably due to the small size of the Italian Jersey population and to the incompleteness of the pedigree file in which many informations are still lacking. For instance, Gengler *et al.* (1997), in a Jersey population about ten times larger than Italy's, reported a mean heritability for type traits of 0.26, 16% higher compared to the mean heritability estimated in this study (0.23). Nonetheless the usage of an animal model instead of a sire model has been helpful in keeping the (co)variance components estimates consistent, as indicated by Misztal *et al.* (1991); in fact, as a result of the much greater selection intensity, male genetic variance is smaller than that of females and a sire model would underestimate genetic variability in the population leading to poor estimates of genetic parameters and loss of accuracy. This would be particularly dramatic in small sized populations, as the one under study.

Correlations between BVs estimates for each type trait obtained with single- and multiple-trait animal models, are shown in table 2. Table 3 reports the same results limited to bulls with at least 20 daughters; the correlations, in this case, are generally higher.

Mean reliabilities are reported in table 4, in a comparison between single- and multiple-trait animal model. To compare the two models mean reliability for final score only has been used as a reference measure of total reliability.

The use of a multiple-trait model noticeably increases the reliability of estimates, compared to a simpler single-trait model; mean reliability increases from 0.20 to 0.24 for all animals (a 20% rise) and from 0.63 to 0.67 for bulls with at least 20 daughters (a 6% rise).

Conclusions

As shown in table 4, reliability of BV estimates increases noticeably using a multiple-trait instead of a single-trait animal model. This is especially feasible and

advisable in small populations such as the Italian Jersey: on the one hand, multi-trait analyses make efficient use of the available data, where each measurement on each trait provides some information on the breeding values of correlated traits, being extremely useful when analysing small data sets; on the other hand, a small data set is not heavily demanding as for computational capacity. Moreover, it can be seen that limiting calculations to animals with a substantial number of offspring (at least 20 in our work) increases both the reliability of BV estimates and the correlations between the estimates calculated with the two different models.

Further studies are needed to check whether the use of random instead of fixed contemporary group effects, as suggested by L.Schaeffer *et al.* (2000), can increase reliabilities of estimates, considered that the Italian Jersey population is small and some records are lost because of the lack of contemporaries.

The results obtained will be used to complete the current selection index of the Italian Jersey, the IQJ (*“Indice Qualità Jersey”*, in italian), at present based

exclusively on production traits (Biffani *et al.*, 2003); after estimating heritabilities and correlations for 16 type traits, the best way of incorporating this information in the oncoming new selection index for the Italian Jersey population will be investigated.

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Table 1. Type traits general statistics.

Variable	Mean	Std. Dev.	Minimum	Maximum
<i>Final Score (FS)</i>	80,38	2,39	70	87
<i>Stature (ST)</i>	16,97	8,35	1	50
<i>Chest Width (CW)</i>	24,12	5,51	3	48
<i>Rump Angle (RA)</i>	24,35	6,44	3	45
<i>Angularity (ANG)</i>	27,63	5,46	3	45
<i>Rump Width (RW)</i>	23,89	6,00	4	40
<i>Rear Udder Width (RUW)</i>	28,09	6,20	5	48
<i>Rear Udder Height (RUH)</i>	24,38	6,00	5	46
<i>Rear Legs Side View (RLSW)</i>	27,47	5,12	10	48
<i>Foot Angle (FA)</i>	24,26	6,00	2	50
<i>Fore Udder (FU)</i>	24,68	6,20	4	48
<i>Body Depth (BD)</i>	27,34	5,21	3	48
<i>Udder Depth (UD)</i>	26,88	6,46	3	46
<i>Udder Support (US)</i>	27,38	5,97	2	48
<i>Teat Length (TL)</i>	22,39	5,86	2	45
<i>Teat Placement (TP)</i>	24,24	5,91	2	50

Table 2. Heritabilities (diagonal) and correlations (genetic above and phenotypic below the diagonal) of Jersey type traits.

	FS	ST	CW	RA	ANG	RW	RUW	RUH	RLSW	FA	FU	BD	UD	US	TL	TP
FS	0,23	0,34	0,00	-0,02	0,57	0,16	0,63	0,70	-0,22	0,32	0,58	0,10	0,27	0,43	-0,06	0,53
ST	0,28	0,37	0,59	0,30	0,16	0,70	0,09	-0,11	-0,18	0,31	0,03	0,56	0,05	-0,41	0,44	-0,12
CW	0,22	0,47	0,22	0,18	-0,36	0,87	-0,05	-0,32	-0,42	0,25	-0,15	0,90	-0,09	-0,23	0,47	-0,41
RA	0,00	0,14	0,09	0,29	0,01	0,05	-0,01	-0,05	0,10	-0,30	0,07	0,15	-0,07	-0,11	0,01	0,31
ANG	0,39	0,11	-0,10	0,02	0,28	-0,15	0,56	0,36	0,09	-0,22	0,02	-0,06	-0,35	-0,01	0,03	0,22
RW	0,23	0,35	0,48	0,03	0,00	0,17	0,21	-0,11	-0,38	0,28	0,02	0,79	-0,05	-0,25	0,43	-0,33
RUW	0,48	0,10	0,18	0,04	0,29	0,25	0,29	0,73	-0,22	0,12	0,14	0,02	-0,33	0,21	-0,14	0,16
RUH	0,52	0,06	0,03	-0,03	0,28	0,09	0,45	0,17	0,14	0,10	0,50	-0,34	0,21	0,56	-0,37	0,39
RLSW	-0,20	-0,07	-0,10	0,01	0,04	-0,03	-0,11	-0,06	0,10	-0,47	-0,01	-0,31	0,17	0,12	-0,52	-0,07
FA	0,30	0,14	0,20	-0,01	0,00	0,19	0,18	0,17	-0,24	0,09	0,36	0,05	0,42	-0,16	0,00	0,01
FU	0,51	0,05	0,07	-0,04	0,08	0,11	0,23	0,42	-0,04	0,16	0,28	-0,20	0,82	0,48	-0,34	0,71
BD	0,27	0,46	0,74	0,08	0,09	0,43	0,19	0,06	-0,07	0,15	0,03	0,25	-0,22	-0,19	0,38	-0,31
UD	0,23	0,01	-0,09	-0,08	-0,14	-0,05	-0,13	0,15	-0,01	0,08	0,44	-0,18	0,41	0,41	-0,34	0,47
US	0,45	0,01	0,02	-0,01	0,13	0,07	0,27	0,33	-0,02	0,12	0,32	0,02	0,26	0,12	-0,50	0,53
TL	0,11	0,19	0,18	0,01	0,08	0,18	0,13	0,07	-0,07	0,09	0,01	0,19	-0,11	0,03	0,20	-0,43
TP	0,43	0,00	0,02	0,02	0,10	0,03	0,15	0,29	-0,03	0,10	0,39	0,01	0,28	0,38	-0,10	0,14

Table 3. Correlations between single- and multiple-trait indexes for Jersey type traits (all the animals).

	FS	ST	CW	RA	ANG	RW	RUW	RUH	RLRW	FA	FU	BD	UD	US	TL	TP
	0,934	0,955	0,852	0,954	0,909	0,810	0,937	0,830	0,822	0,767	0,867	0,926	0,939	0,765	0,819	0,750

Table 4. Correlations between single- and multiple-trait indexes for Jersey type traits (only bulls with at least 20 daughters).

	FS	ST	CW	RA	ANG	RW	RUW	RUH	RLRW	FA	FU	BD	UD	US	TL	TP
	0,968	0,983	0,930	0,975	0,958	0,915	0,974	0,902	0,903	0,883	0,939	0,973	0,979	0,873	0,905	0,858

Table 5. Mean reliability for final score EBVs.

	single-trait	multiple-trait
all animals	0,20016	0,2382
bulls with >= 20 daughters	0,632	0,67157