

Change of Genetic Parameters for National Evaluations of Italian Holstein and Effect on International Proofs

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Introduction

Reliable international evaluations of bulls are a basic tool in dairy cattle improvement, not only because of international trade of semen and embryos, but also to address selection on sire of bulls performed by AI organisations.

In 1995 INTERBULL released the first official international comparison of dairy bulls. The official method used by INTERBULL is MACE (Multiple-trait Across Country Evaluations) proposed by Shaeffer and Zhang (1993) which improved other methods previously used to rank bulls across country (Wilmink, 1986, Goddard 1985).

Since MACE was officially applied some changes to the procedure have already been introduced based on results of a study conducted by Shaeffer et al. (1993) aimed to detect factors affecting international evaluation performed with MACE.

Input used by MACE are genetic proofs estimated in each participating country: parameters involved in national genetic evaluation could have a direct impact on international proofs. Selection programs of various countries could affect differently genetic parameters of each population. Population size, number of bulls sampled, number of daughters per bull, efficiency of progeny testing schemes define differently the selection programme of each country. Genetic parameters should be monitored in order to update their value if necessary. Actually heritability values used in genetic evaluation procedures of country participating to INTERBULL evaluations are heterogeneous with values from .25 to .35 estimated with different models and data editing. Parameters used in Italian national evaluation were estimated by Bagnato et al (1991) with a sire

model.

Objective of this study was to estimate heritability and genetic correlations of productive traits in the Italian Holstein with different data sampling criteria. Moreover the aim was to detect a possible impact of heritability values on international ranking.

Material and Method

First productive records of 17,267 cows were used to estimate heritabilities and genetic correlations of milk kg (MK), fat kg (FK), protein kg (PK), fat % (F%) and protein % (P%). Mature equivalent productions were used. Records were sampled from the national data base on a herd basis from 1991 to 1995 (data set S1). Only lactations that have reached at least 305 days were included in the analysis. Two generations were included in the pedigree and phantom groups were assigned according to the birth year of the animal. A multiple trait animal model was used in order to obtain estimates of genetic parameters. Fixed factor included in the model was herd-year-season effect. Four different seasons of three months were defined starting from January. Only herd-year-season with at least 2 records were included in the analysis. Additive genetic effect was included as random factor with 45,369 levels and was assumed $N(0, A\sigma_a^2)$. Residual effect was assumed $N(0, I\sigma_e^2)$.

Other estimates for heritabilities were obtained with the same model from a data set including only animals of herds with at least 150 first parity cows from 1990 (S2). A third data set (S3), sampled as S1, was also used to estimate heritabilities for milk kg, fat kg, and protein kg. With S2 and S3 data sets

heritabilities were estimated with a single trait procedure.

Impact of heritability used in national evaluation on international sire ranking for protein kg was evaluated estimating genetic sire variances according to the true beta method (INTERBULL, 1986). Only sire sampled in Italy and born in the last ten years were included in the analysis. Heritabilities used were .25 and .35.

Results and Discussion

In table 1 are shown arithmetic means and standard deviations of traits used in the analysis for all sampling criteria.

Samples S1 and S3 have means and standard deviations comparable to all first parity cow data set, while S2 show lower values.

In table 2 are shown heritabilities, phenotypic and genetic correlations of production traits considered in data set S1.

Heritability estimates for milk kg, fat kg and protein kg, .33, .33, and .31 respectively, are higher of those obtained in a previous study on the same population (Bagnato et al., 1991) which showed values of .26, .27, and .24 for milk kg, fat kg and protein kg respectively. Heritability values obtained in other studies show values for milk fat and protein kg comparable to those obtained in this analysis (Boichard and Bonaiti 1987, Wade and Van Vleck 1988, Van der Werf and De Boer 1989). Also genetic correlations estimated by Kennedy (1982), Teeepker and Swalve (1988), Boichard and Bonaiti (1987) are comparable with those calculated in this study. Genetic correlation between protein kg and protein percentage show a value of .08, greater than one obtained in the study of Bagnato et al. (1991) that show a value of zero.

Heritabilities obtained with samples S2 and S3 with a single trait analysis are in table 3. Estimates obtained with S2 data set are greater of those estimated with S1 and S3 data set, showing values of .36 for milk kg .33 for fat kg and .38 for fat kg. Greater heritabilities obtained with S2 data set are

probably due to the different sampling criteria.

In table 4 are shown sire standard deviation within years for protein kg. As shown values of sire standard deviations are higher when heritability is .35. A different time trend in sire standard deviations with different heritability can also be observed. Weighted average is 7.3 with heritability of .35 and is 7.1 when heritability is .25. As a consequence different heritabilities can affect variance ratios and international ranking of bulls may change.

Conclusions

Estimates obtained with S3 data set for milk kg, fat kg, and protein kg data set are considered not representative of the population given the sampling criteria used to build the data set.

Heritabilities for milk kg, fat kg and protein kg found in this study indicate that is necessary to update heritabilities (.25) actually used in national genetic evaluation. Values obtained in this study suggest to set heritability of milk kg, fat kg and protein kg in national genetic evaluation to .30 for milk kg, fat kg and protein kg. This value is recommended for Italian national genetic evaluation because protein heritability resulted .31 both with S1 and S3 data set and same heritability values were considered desirable for all three traits used in estimating proofs. According with criteria given by INTERBULL validation of genetic trend with heritability of .30 has been carried out successfully.

Although effect of heritability on international proofs was here estimated with the true beta model and not with the official model adopted by INTERBULL, results indicate that heritability values might affect international comparisons. These findings suggest to further investigate the effect of genetic parameters used in national evaluation on international sire ranking. Genetic parameters of populations should be periodically monitored. Guidelines for genetic parameters estimation and some validation

criteria on estimates obtained should be suggested to make easier comparisons of genetic parameters of different populations.

It is possible that other assumptions, parameters or preadjustments, as adjustment for heterogeneity of herd variance, involved in national genetic evaluation could affect international comparisons.

Further investigation is necessary in order to verify the effects of different national genetic evaluation methods on international comparisons.

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References

- Bagnato, A., Jansen, G., Cerutti, F. and Pagnacco, G. 1991. Production traits in Italian Holstein Friesian: heritabilities and correlations. *Zoot. Nutr. Anim. Supplement ASPA Conference 1991*, pp. 595-601.
- Boichard, D. and Bonaiti, B. 1987. Genetic parameters for first lactation dairy traits in Friesian, Montbéliarde and Normande breeds. *Genet. Sel. Evol.* 19(3), 337.
- Goddard, M. 1985. A method of comparing sires evaluated in different countries. *Livest. Prod. Sci.*, 13, 321.
- INTERBULL 1986. Procedures for international comparisons of dairy sires - Current practice and evaluation of methods., Bulletin No. 1.
- Kennedy, B. 1982. Reducing fat in milk and dairy products by breeding. *J. Dairy Sci.* 65, 443.
- Shaeffer, L.R. and Zheng, W. 1993. Multi-trait Across Country Evaluation of dairy sires. INTERBULL Bulletin No. 8, Aarhus, Denmark.
- Shaeffer, L.R., Reents, R. and Jamrozik, J. 1993. Factors influencing international comparisons of dairy sires. *J. Dairy Sci.*, vol. 78, Supplement 1, 221.
- Van der Werf, J.H.J. and De Boer, W. 1989. Estimation of genetic parameters in a crossbred population of black and white dairy cattle. *J. Dairy Sci.* 72, 2615.
- Teepker, G. and Swalve, H.H. 1988. Estimation of Genetic parameters for milk production in the first three lactations. *Livest. Prod. Sci.* 20, 193.
- Wade, K.M. and Van Vleck, D.L. 1989. Genetic parameters for production traits of Holsteins in California, New York, and Wisconsin. *J. Dairy Sci.* 72, 1280.
- Wilmink, J.B.M., Meijering, A. and Engen, B. 1986. Conversion of breeding values for milk from foreign populations. *Livest. Prod. Sci.*, 14, 223.

Table 1. Means and standard deviations of the traits used in the analysis for the three sample and for all first lactation from 1991 before sampling

	All 1st parity (from 1991)	S1	S2	S3
MK	9,142±1843	9,224±1894	8,968±1695	9,021±1852
FK	320±66	323±68	312±59	333±61
K	279±57	281±58	272±52	300±61
F%	3.52±.40	3.52±.39	3.50±.39	3.43±.40
P%	3.05±.18	3.05±.18	3.04±.18	3.08±.17
records n.	385,462	17,267	5,467	5,362

Table 2. Heritabilities (diagonal), genetic correlations (above diagonal), phenotypic correlation (below diagonal) estimated with sample S1. Heritabilities standard errors less then .02

	MK	FK	PK	F%	P%
MK	.33	.53	.86	-.41	-.43
FK	.68	.33	.68	.55	.17
PK	.90	.74	.31	-.12	.08
F%	-.34	.45	-.14	.51	.60
P%	-.36	.02	.07	.48	.44

Table 3. Heritabilities for MK, FK and PK obtained for sample S2 and S3

	S2	S3
MK	.36	.33
FK	.33	.31
PK	.38	.31

Table 4. Sire standard deviation within year of birth for protein kg and weighted average across years

	1982	1983	1984	1985	1986	1987	1988	1989	1990	All ¹
h ² .25	9.0	8.9	8.2	7.7	6.8	6.3	7.4	7.1	6.6	7.1
h ² .35	9.6	7.8	8.2	7.8	6.9	6.3	7.3	7.3	7.3	7.3

¹ Weighted average across years.