

GENETIC PARAMETERS FOR TYPE TRAITS OF BRAZILIAN HOLSTEIN CATTLE

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INTRODUCTION

Linear scoring of conformation traits is carried out on dairy cows to detect physical deficiencies that affect their expected performance. Several studies (Interbull, 1999) indicated the relationship between conformation traits and longevity which has a significant impact on cow profitability or dairy production efficiency (Essl, 1998; Vollema, 1998). Besides production traits, type traits are an important component of breeding and have a definitive importance for breeders in their selection of bulls.

The Brazilian Holstein Association provides linear type classification services to Holstein cattle breeders in order to guide their decisions for corrective mating and to produce more productive, healthy and trouble-free cows under Brazilian herd environments. The objective of this study was to estimate variance components and genetic parameters of conformation traits of Holstein cows in Brazil.

MATERIAL AND METHODS

Data consisting of 64,075 linear classification records from Holstein cows classified during 1994/2003 in 751 herds were available from The Brazilian Holstein Association. The recording followed the Canadian system which evaluate traits in a 1-9 point scale. Data were edited for herd size, contemporary group, classifier, stage of lactation, number of classifications/cow and availability of milk production in current lactation. After editing, records of 21 linear traits including Final Classification of 21,208 cows, progeny of 842 sires were used to estimate variance components using univariate analyses by REML (Boldman et al., 1995). The model included fixed effects of herd-year, season of calving, classifier, age of calving, stage of lactation at classification, and the random additive genetic animal and residual effects.

RESULTS AND DISCUSSION

Table 1 shows average, standard deviation, additive genetic and residual variances estimates, heritability and respective standard errors for the 21 type traits and final conformation.

Genetic variances ranged from 0.09 for udder texture to 0.58 for stature. Heritability estimates were generally moderate. Estimates were lower for udder texture (0.09), foot angle

(0.11) and chest width (0.15) and larger for stature (0.40), teat length (0.38) and rump width (0.32). Heritability estimates are in agreement with those used by countries participating in Interbull (Interbull, 1996).

Single-trait analyses were used in this study because of limited computing resources available. Biscarini et al. (2004) reported the impact of multiple-trait analysis in breeding values and ranking of Italian Holsteins for type traits. Further studies are needed to verify if multiple-trait analysis can increase accuracy of estimates and prediction of breeding values of type traits for the Holstein cattle in Brazil.

Table 1. Average, standard deviation (SD), additive genetic and residual variances estimates, heritability and respective standard errors (SE) of type traits and final conformation of Holstein cows.

Type trait	Average $\pm$ SD	Genetic	Residual	Heritability $\pm$ SE
Frame / Capacity				
Stature	7,1 $\pm$ 1,4	0,585	0,867	0,40 $\pm$ 0,02
Height at front end	5,4 $\pm$ 1,1	0,131	0,627	0,17 $\pm$ 0,02
Weight	6,7 $\pm$ 1,4	0,366	0,839	0,30 $\pm$ 0,02
Chest width	5,8 $\pm$ 1,3	0,180	0,986	0,15 $\pm$ 0,02
Body depth	6,3 $\pm$ 1,0	0,171	0,603	0,22 $\pm$ 0,02
Loin strenght	6,5 $\pm$ 1,3	0,287	0,998	0,22 $\pm$ 0,02
Rump				
Rump angle	5,0 $\pm$ 0,9	0,221	0,601	0,27 $\pm$ 0,02
Rump width	6,6 $\pm$ 1,3	0,371	0,777	0,32 $\pm$ 0,02
Feet & Legs				
Foot angle	5,2 $\pm$ 1,3	0,122	1,027	0,11 $\pm$ 0,01
Bone quality	6,3 $\pm$ 1,3	0,243	1,110	0,18 $\pm$ 0,02
Rear legs side view	5,6 $\pm$ 1,1	0,230	0,903	0,20 $\pm$ 0,02
Fore Udder				
Fore udder	5,8 $\pm$ 1,5	0,318	1,606	0,17 $\pm$ 0,02
Teat placement	4,3 $\pm$ 1,1	0,276	0,878	0,24 $\pm$ 0,02
Teat lenght	5,2 $\pm$ 1,0	0,386	0,638	0,38 $\pm$ 0,02
Rear Udder				
Udder height	6,4 $\pm$ 1,2	0,226	0,903	0,20 $\pm$ 0,02
Udder width	5,7 $\pm$ 1,5	0,244	1,207	0,17 $\pm$ 0,02
Teat placement	6,3 $\pm$ 1,2	0,217	0,952	0,19 $\pm$ 0,02
Overall Udder				
Udder Depth	4,9 $\pm$ 1,2	0,231	0,822	0,22 $\pm$ 0,02
Texture	6,5 $\pm$ 1,2	0,089	0,935	0,09 $\pm$ 0,01
Udder support	6,3 $\pm$ 1,4	0,350	1,284	0,21 $\pm$ 0,02
Dairy character				
Angularity	6,5 $\pm$ 1,2	0,197	0,718	0,22 $\pm$ 0,02
Final Score	81,1 $\pm$ 3,4	1,188	5,045	0,19 $\pm$ 0,02

CONCLUSIONS

Most of the type traits revealed moderate to high heritability estimates. There is a potential for improving type traits of Holstein cattle under Brazilian herd environments by selection. A multi-trait analysis should be considered to obtain genetic correlations and possibly improve accuracy in future evaluations of type traits.

REFERENCES

- Biscarini, F., Biffani, S. and Canavesi, F. 2004. Does selection for production affect type traits genetic evaluation in Italian Holsteins? Proceedings of the 2004 Interbull meeting. Sousse, Tunisia, 2004. Bulletin no. 32. p.77-81.
- Boldman, K. G.; Kriese, L. A.; Van Vleck, L. D. et al. 1995. **A manual for use of MTDFREML. A set of programs to obtain estimates of variances and covariances.** Lincoln: Department of Agriculture. Agriculture Research Service, 1995.125p.
- Essl, A. 1998. Longevity in dairy cattle breeding: a review. *Livest. Prod. Sci.* 57:79-89.
- Interbull, 1996. Sire evaluation procedures for non-dairy-production and growth & beef production traits practised in various countries 1996. Uppsala, Sweden, 1996. Bulletin No. 13. 201 pp.
- Interbull, 1999. Proceedings International workshop on EU concerted action genetic improvement of functional traits in cattle (GIFT); longevity. Jouy-en-josas, France, 1999. Bulletin No. 21. 208 pp.
- Vollema, A. R. 1998. Selection for longevity in dairy cattle. Phd. Thesis, Animal Breeding and Genetics, WAU, Wageningen, The Netherlands.