THREE VERSUS FOUR TRAITS RANDOM REGRESSION TEST DAY MODEL GENETIC EVALUATION FOR THE HOLSTEIN BREED IN ITALY

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ABSTRACT

Genetic evaluation for production traits in the Holstein breed in Italy is based on a Random Regression Test Day Model (RRTDM) since November 2004. More specifically the model is a multiple lactation, multiple traits (milk, fat , protein and somatic cell count) RRTDM, similar to the model used in Canada for official genetic evaluation. Fixed regression curve effects include time, region, age at calving, parity and season of calving. An improved model uses test days pre-adjusted for number of days pregnancy and include the effect of year of production instead of time in the fixed effects definition. A new set of genetic parameters was estimated in December 2006 without somatic cell count. As a result genetic correlations across lactations within trait increased by 0.06-0.10. Data from February 2007 and November 2002 evaluation were used to assess the different ability of the two systems (four traits versus three traits) to predict future breeding values. Correlations among proofs on the same data set ranged from 0.99 to 0.98. Rank correlation was also very high. Rank correlations of the top 250 bulls comparing November 2002 and February 2007 proofs in the three traits model were 0.01-0.02 higher than with the four trait model. Research is still ongoing in order to evaluate the impact of the three trait evaluation system when new lactation test day records are added from run to run.

Objective:
to compare a four trait to a three trait system in term of genetic parameters and stability of proofs over time

MATERIAL AND METHODS

Genetic parameters estimation. Data were randomly sampled from the first 3 lactations test day records of Italian Holsteins collected between 1998 and 2006. A total of 220000 test day records of around 15000 cows, distributed in 51 herds, was used to estimate genetic parameters with a program kindly supplied by J. Jamrozik. A chain of 100000 samples were generated from the marginal posterior distribution using Gibbs sampling. The first 10000 samples were discarded as a burn in period. Only milk, fat and protein yield were considered. Model was a multiple trait, multiple lactation TDM. The model considered as fixed effects the interaction of age, parity, region and season of calving effects and the random part of the model was a fourth order Legendre polynomial for additive and permanent environmental effects for a total of 45 parameters each (5 parameters for 3 lactations and 3 traits). Four different residual matrices among traits were estimated depending on DIM, Covariances among residuals for records made on different DIM were assumed to be zero. Resulting genetic parameters were compared to the official 4 traits model estimated by Muir et all, in 2003 (Muir et al, 2007).

Breeding value estimation. Data from the official genetic evaluation of February 2007 and from November 2002 were used to compute EBVs with the new parameters and results were compared with official proofs in terms of correlations and bull ranking. Interbull Method III was also applied.

CONCLUSION

These results show that there is an effect of somatic cell count on estimated genetic correlations within traits across lactations. This may have an impact on stability of proofs over time when bull daughters add new lactation records. The higher rank correlation for second crop bulls seems to suggest a superior ability of the three traits model in estimating bull ranking. Effect of cow ranking and on stability of proofs show that the three trait system is more stable than the actual four trait model.

RESULTS AND DISCUSSION

Genetic parameters estimated from the three trait model resulted in higher genetic correlations within trait across lactations compared to the four trait model (Table 1 and 2) . Genetic correlations across traits were very similar to estimates from single traits analysis from other countries and from a study done in Canada by Muir in 2004 (Table 3) with a single trait model.

Heritability estimates were lower than previously estimated probably due to an higher level of misidentification on more recent data.

Somatic cell count as an additional trait in the four trait model seem to be the responsible of the change in genetic correlations across traits. This may be due to some selection effects in the data or to the fact that the correlation of somatic cell score with the other traits is not constant across lactations and more over it changes direction.

The estimated EBVs had a very high correlations (0.98-0.99) with official proofs on February 2007 data. Rank correlation for second crop bulls between November 2002 and February 2007 EBV was 0.01 higher with the three trait model.

Interbull Method III trend validation results showed a non significant effect of new daughters over time, as it is for the official model

Table 3. Estimates of genetic parameters in different set/countries

		ITA new	ITA off	CAN off	CAN ST	NLD	DEU	GBR
milk	1-2	0.85	0.79	0.81	0.84	0.85	0.84	0.75
	1-3	0.81	0.70	0.73	0.77	0.80	0.84	0.68
	2-3	0.86	0.86	0.88	0.89	0.87	0.97	0.95

Table 1. Average 305 genetic parameters (genetic below diagonal, permanent environmental above, daily heritability on the diagonal)

	m1	f1	p1	sc1	m2	f2	p2	sc2	m3	f3	p3	sc3
m1	**.30**	.86	.97	-.18	.48	.37	.47	-.02	.36	.30	.36	.05
f1	.51	**.27**	.88	-.15	.40	.50	.44	-.02	.27	.40	.33	.02
p1	.88	.62	**.28**	-.15	.47	.41	.50	-.01	.35	.33	.39	.06
sc1	.12	-.04	.12	**.17**	-.09	-.08	-.09	.36	-.07	-.05	-.06	.26
m2	.79	.42	.70	.01	**.30**	.88	.97	-.24	.42	.39	.45	.02
f2	.40	.82	.49	-.09	.63	**.29**	.90	-.27	.33	.48	.40	-.01
p2	.67	.54	.79	.03	.90	.73	**.30**	-.22	.43	.44	.49	.03
sc2	.13	.00	.13	.49	-.03	-.09	-.01	**.21**	-.14	-.16	-.15	.44
m3	.70	.35	.63	.05	.86	.51	.78	-.02	**.33**	.88	.97	-.23
f3	.37	.75	.47	-.03	.51	.84	.63	-.06	.66	**.31**	.91	-.25
p3	.57	.45	.69	.07	.74	.60	.85	-.01	.90	.75	**.33**	-.21
sc3	-.01	-.04	-.01	.43	-.17	-.14	-.16	.52	-.21	-.18	-.17	**.25**

Table 2. Average 305 genetic parameters (genetic below diagonal, permanent environmental above, daily heritability on the diagonal)

	m1	f1	p1	m2	f2	p2	m3	f3	p3
m1	**,25**	,86	,97	,44	,37	,45	,31	,25	,33
f1	,46	**,26**	,88	,37	,48	,41	,30	,38	,33
p1	,83	,59	**,22**	,44	,41	,48	,32	,28	,36
m2	,85	,43	,71	**,25**	,89	,97	,43	,35	,46
f2	,37	,88	,49	,58	**,26**	,90	,40	,47	,46
p2	,70	,58	,86	,86	,71	**,23**	,45	,39	,50
m3	,81	,34	,70	,86	,41	,75	**,27**	,90	,98
f3	,42	,81	,56	,55	,88	,71	,61	**,26**	,90
p3	,62	,46	,80	,71	,54	,87	,86	,76	**,26**