Impact of New Genetic Parameters from a Three Trait Model on the Italian Holstein Genetic Evaluation for Production

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Abstract

In November 2004 the first Italian genetic evaluation based on Test day random regression model (TDRRM) was published. The model is a Multiple-Trait-Multiple-Lactation model including four traits and three lactations for each trait. The four traits evaluated are milk, fat and protein kg and somatic cell counts. Genetic parameters used in the current model were estimated in 2003 (Muir *et al.,* 2007). New parameters were estimated in 2006 (Canavesi,2007) with a model including only the three production traits. The estimated parameters resulted in a lower heritability and a higher within trait across lactations genetic correlations compared to the four traits model. This research investigated the impact of the three traits genetic model genetic parameters on the stability of genetic proofs. Data from November 2002 and from May, August and November 2006 and February 2007 were used to estimate genetic proofs with the new parameters. The stability of those proofs, measured in terms of simple and rank correlations, was compared with the stability of the corresponding official proofs computed using the four traits model. Correlations among proofs were from 1% to 4% for certain group of bulls. Correlations were also very high for cows, few top cows changed because of extreme values for protein and fat kg. Further research is ongoing to investigate other changes in the model that may improve stability over time.

Introduction

The RRTDM is official in Italy since November 2004.

From that day onward a big amount of time has been devoted to meet farmers and industry people to explain the advantages of the new system and of all the additional information that can be used to better the selection of bulls that will help them increase their profit.

In the meantime research has started in order to improve the system and to address the many questions that users are raising while getting acquainted with the new system.
One of the big issues is the overall stability of proofs from run to run which in Test day model is perceived as much lower compared to the lactation model. One of the reasons of the higher variation from run to run is linked to the fact that RRTDM assumes a more dynamic way of expressing genetic superiority, along the lactation and across lactations, that brings with itself more variation over time in bull proofs.

Among the many factors that were investigated since may 2005, one test was related to the exclusion of somatic cells from the multiple traits setting. Estimations of genetic parameters of variances and covariances for the two models were carried out in 2006 (Canavesi, 2007) by Bayesian methods using the Gibbs sampler as described by Jamrozik and Schaeffer (1997). The three traits analysis resulted in a higher correlation within traits across lactations, very similar to correlations from single trait analysis (Muir *et al.,* 2004). The four traits analysis confirmed a decrease in heritability but similar correlations among traits and lactations to estimates from Muir *et al.* (2007).

Material and Methods

Table 1 reports the genetic parameters currently used in genetic evaluation. Table 2 presents the parameters estimated using only the three production traits. Genetic correlations between first and second, and second and third lactations within trait increased depending on the trait and lactation from 0.04 to 0.10.

Data from November 2002 and data from May, August and November 2006 along with February 2007 were used to compute genetic proofs with a three lactations three traits RRTDM. Fixed effects were the same as for the official model.

Proofs were compared in terms of simple and rank correlations among bulls and on differences from run to run

Results and Discussion

Simple correlations for all proofs increased by 1-4% especially for bulls in the first two years after publication compared with the official proofs for the corresponding period. As an example Table 3 reports the correlation for bulls published the first time in May 2006, May 2005 and May 2004. For bulls published the first time in May 2004, official proofs computed based on four traits have the same stability of proofs based on the three traits setting . For bulls published later, the difference in terms of correlation varies depending on traits, going from 0.003 to almost 0,03.

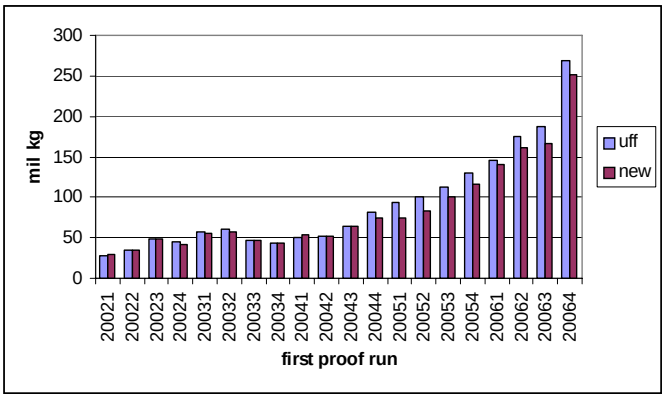
The comparison of correlations among second crop bulls proofs between the November 2002 and the February 2007 genetic evaluations shows no difference in simple correlations but an increase of 1% of rank correlation for all traits with the three traits model.

The average variation of bulls proofs in two subsequent runs by date of first publication is not very different between the two models. The standard deviation of the variation shows an interesting reduction with the three traits model which confirms the overall greater stability that was observed through the correlations.

Table 3. Simple correlations among subsequent by class of bull publication date (below diagonal in red the difference from the corresponding correlation in the official proofs).

Date of publication: February 2006				
	Milk0605	Milk0608	Milk0611	Milk0702
Milk0605		0,93208	0,91738	0,88947
Milk0608	**0.00460**		0,95574	0,92055
Milk0611	**0.02026**	**0.01156**		0,95524
Milk0702	**0.02834**	**0.02328**	**0.01132**	
Date of publication: February 2005				
	Milk0605	Milk0608	Milk0611	Milk0702
Milk0605		0,98383	0,97177	0,96282
Milk0608	**0.00312**		0,98710	0,97507
Milk0611	**0.00344**	**0.00266**		0,98480
Milk0702	**0.01044**	**0.00692**	**0.00471**	
Date of publication: February 2004				
	Milk0605	Milk0608	Milk0611	Milk0702
Milk0605		0,99147	0,98458	0,97764
Milk0608	**-0.00051**		0,99120	0,98610
Milk0611	**0.00001**	**0.00097**		0,99411
Milk0702	**-0.00010**	**0.00118**	**0.00019**	

Figure 1. Standard deviation of differences (milk yield) by class of bull publication date.



Conclusions

The model considering only three traits instead of four, taking away somatic cell score, did show an improved stability over time. This is due to the increased genetic correlations within trait across lactations defined by the estimated parameters.

Although this is very important it is still a small improvement and more research is ongoing in order to verify if other aspects of the model have larger impact on stability. The final aim of all this work is to apply all changes together in order to improve significantly the overall stability of the system.

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Table 1. 305 days parameters for the Italian RRTDM, heritability (average daily) on the diagonal, 305 days genetic correlations below the diagonal, 305 days PE correlations above the diagonal (Muir, 2003).

	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. 305 days parameters estimated with three traits RRTDM, heritability (average daily) on the diagonal, 305 days genetic correlations below the diagonal, 305 days PE correlations above the diagonal (Muir, 2003).

	m1	f1	p1	m2	f2	p2	m3	f3	p3
m1	**,26**	,85	,97	,45	,37	,45	,33	,26	,34
f1	,47	**,26**	,88	,37	,48	,42	,31	,40	,36
p1	,84	,59	**,24**	,45	,41	,49	,34	,30	,38
m2	,81	,42	,68	**,27**	,88	,97	,43	,35	,46
f2	,38	,86	,48	,60	**,28**	,90	,39	,47	,45
p2	,68	,55	,82	,87	,72	**,26**	,45	,40	,50
m3	,75	,31	,64	,84	,43	,74	**,30**	,89	,97
f3	,39	,76	,51	,54	,85	,66	,64	**,27**	,91
p3	,59	,42	,73	,71	,54	,84	,88	,76	**,29**