

From a Repeatability to a Random Regression Test Day Model Evaluation for Somatic Cells: Evaluation of Results in the Italian Holstein Population

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Abstract

With the introduction of a random regression multiple trait multiple lactation test day model in 2004 the official genetic evaluation for somatic cell score will move from a repeatability test day to a random regression test day. Furthermore the new model will use test day from parity 1,2 and 3 and it will adjust for heterogeneity of variance across herds while the current model uses only test day records from first parity cow and does not consider heterogeneous variances. The correlations among proofs from the two models is very low, around 0.70 both for bulls and cows. Estimated trend of bulls and cows is clearly affected. Bull estimated trend from increasing became decreasing and cow genetic trend from increasing changed to a flat trend. Checks on residuals on the new model did not show any significant trend over time.

Possible reasons for the change may relate to: 1) additional information from later lactations; 2) correlated effect from production traits on SCS; 3) heterogeneity of variances across herds and over time; 4) different “genetic model” that leads to different estimated BV. Looking at trends by lactation did not show any significant difference across lactations.

Two runs with correlations set to zero among production traits and SCS (run 1) and correlations set to zero among production traits and SCS and among different parities for SCS (run 2) did not show any significant change in genetic trend estimation. The average SD within herd is increasing over time by 4% in total, it's not too big but it may have affected the trend if not accounted for along with the different genetic parameters and the different genetic assumptions of the two models.

Introduction

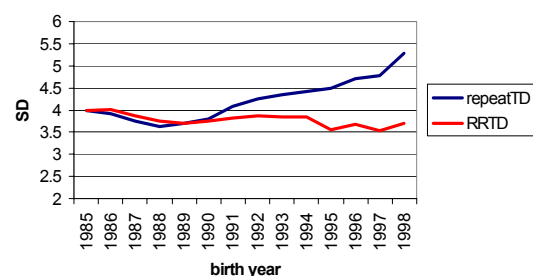
Since 2002 the Italian Holstein is developing a genetic evaluation for production traits and somatic cell score based on a multiple trait multiple lactation Random Regression Test Day Model (RRTD) based on Legendre polynomials using the same approach and the programs of the Canadian Test Day Model (Jamrozik *et al.*, 1997; Jamrozik *et al.*, 1998; Schaeffer *et al.*, 1999; Kistemaker, 2003).

This project is at the final stage of its development and the first official publication is foreseen before the end of year 2004.

Correlations for bulls proofs between lactation Animal Model and RRTDM are very high between 0.97 and 0.98 for production proofs. For SCS official evaluation the current model is a Repeatability Test Day Model

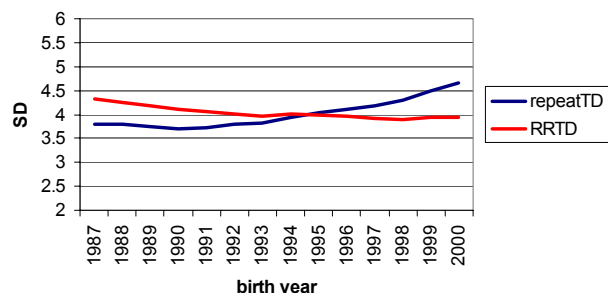
(RepeatTD) based on first parity information only (Samorè *et al.*, 2001; Samorè *et al.*, 2002). The correlations between estimated genetic proofs in this case between the RRTD and the current model are very low, around 0.70 both for cows and bulls.

Figure 1. Estimated bull genetic trend.



In particular estimated genetic trend for bulls and cows are very different between the two models (Figure 1 and 2).

Figure 2. Estimated cow genetic trend.



Possible reasons for the different trend are:

1. additional information from later lactations;
2. correlated effect from production traits on SCS;
3. heterogeneity of variances across herds and over time;
4. different “genetic model” with different heritability that leads to different estimated BV.

The objective of the present study was to investigate further the issue to:

- validate the results obtained with the RRTD;
- verify the difference in the different lactations;
- verify the impact of genetic correlations of SCS with production traits and among different lactations for SCS;
- investigate other possible reasons for differences.

Materials and Methods

In order to verify the quality of the RRTD evaluation residuals were analysed. Expectation was for a mean of zero with normal distribution and particular attention was devoted to trend in residuals over year of production. Interbull Method 3 was applied to verify the effect of new daughters in subsequent evaluations.

Total genetic merit for SCS is computed as follows for bulls and cows:

$$SCS_{TOT} = 1/3 SCS_{1st} + 1/3 SCS_{2nd} + 1/3 SCS_{3rd}$$

Genetic trend in first, second and third parity was analysed and compared with the general trend that results from the sum of the EBVs in the three lactations.

To evaluate the effect of genetic correlations with production traits and among different lactations two additional runs were performed using the same test-day record data used for the evaluation provided to the test run of Interbull in March 2004:

1. correlations with production traits were set to zero;
2. correlations with production traits and across lactations for SCS were set to 0.

The estimated genetic trend was compared for bulls and cows.

Heterogeneity of variance across herds in first parity test day records was also analysed and the differences in genetic parameters and in the genetic assumptions between the two models are discussed.

Results and Discussion

Table 1 illustrates the differences in parameters between the two model. Higher heritabilities in the RRTD implies that a very different information is derived on average from phenotypic records that may lead to very different results in terms of genetic trend. Average genetic correlations across lactations for SCS are moderate and positive. Average genetic correlations with production traits do change over lactations and are positive in first and negative in thirds lactations but generally speaking very low.

Table 1. Genetic parameters used in the two models.

	repeafTD	RRTD*
Heritability 1 st lact.	0.08	0.17
Heritability 2 nd lact.	-	0.21
Heritability 3 rd lact.	-	0.25
Repeatability	0.44	-
Average r_g across lact.		0.26/0.44
r_g with M,F,P (1 st lact)		-0.04 / .12
r_g with M,F,P (2 nd lact)		-0.09/-0.01
r_g with M,F,P (3 rd lact)		-0.17 /-.21

* Muir, 2003

Figure 3 reports bull genetic trend and the trend for each of the three lactation. It is clear that the general trend does not differ from first to third lactation and it is decreasing overall although the trend for first parity cows is higher compared to later lactations.

Figure 3. Bull genetic trend in total and in different lactations.

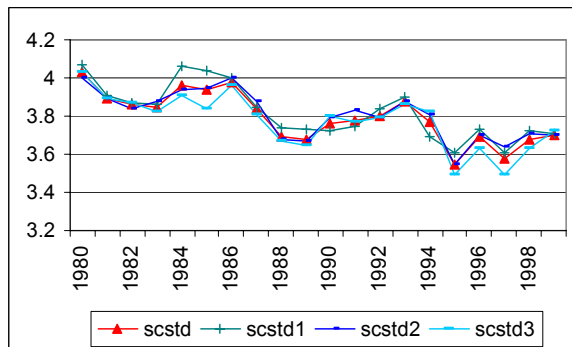


Figure 4 shows bull genetic trend in the RRTD compared with results from the run where genetic correlations among production traits and SCS were set to zero. The trends are very similar and there is no difference in the pattern across lactations (Figure 5). The general pattern when genetic correlations are set to zero is that the trend tends to become even more negative. The same results are obtained when all genetic correlations are set to zero (run 2, results not shown).

Figure 4. Genetic trend in the complete parameter run compared with the run where genetic correlations among production traits and SCS were set to zero.

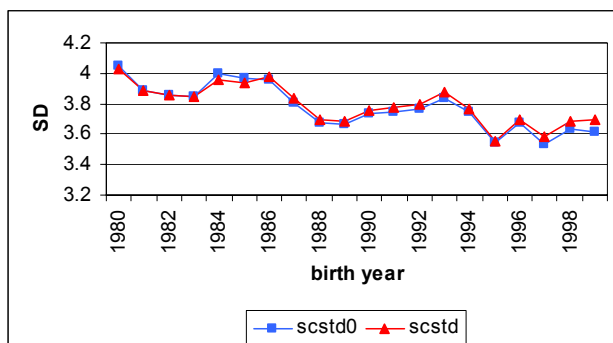


Figure 6 report the observed trend in the average SD for SCS within herd over time. From 1994 when the majority of milk recording agencies started to keep SCS records the average increase over time has been around

4%. If we consider earlier data the increase is around 10%. The average variability across within year seems to be stable. This heterogeneity it is accounted for in the RRTD model but not in the current model and together with the difference in genetic parameters may explain the difference in the estimated genetic trend.

Figure 5. Genetic trend in different lactations when genetic correlations among production traits and SCS were set to zero.

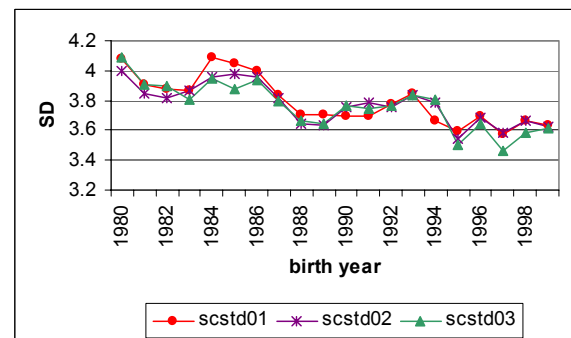
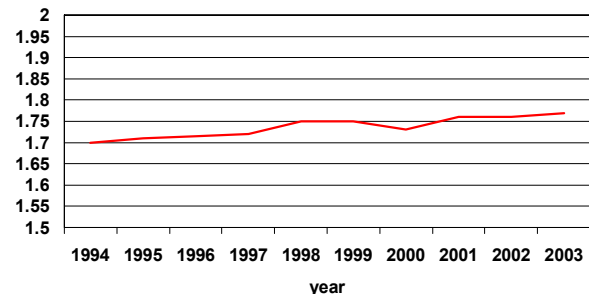


Figure 6. Within herd average SD for SCS over time.



The best bulls for SCS remain the same with both models. It is more the general pattern and the scale of the differences especially for bulls that is changing due to changes in parameters and in genetic assumptions.

The current official model (repeatTD) was validated applying Interbull method 2 to check changes over time in DYD and resulted in an estimated effect of -0.0026 on a standardized scale with change of sign, although the trend seems rather high for a traits with such a low heritability.

The new RRTD was validated using Interbull method 3 and did not show a significantly different from zero effect from new daughters equal to $+0.0146$ on the original scale.

Figure 7 reports the residual distribution that has mean zero and seems to be normally distributed and Figure 8 shows the trend of the residuals over time. Test day records from 1994 to 1998 are incomplete.

Figure 7. Residual distribution for SCS in RRTD.

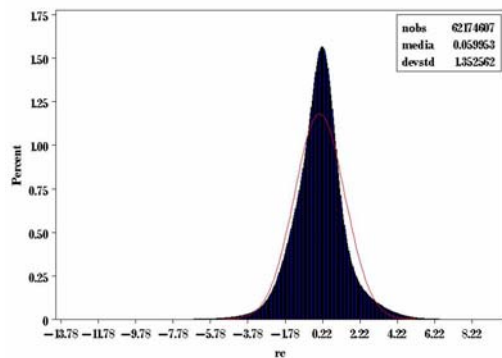
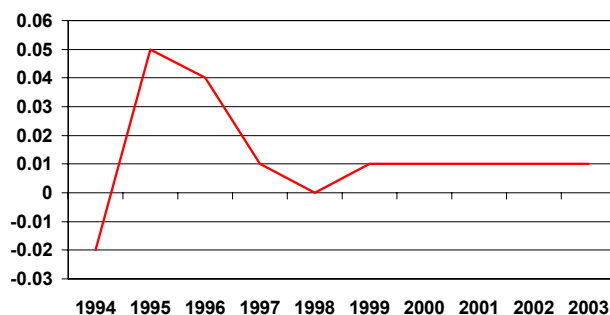


Figure 8. Residuals in RRTD over time.



Conclusions

The estimated genetic trend with the RRTD is correct. No bias have been detected either with Interbull Method 3 or through the analysis of residuals.

The difference in trend is not due to the additional information coming from later parities nor from the indirect selection effect from production traits.

There is a certain amount of heterogeneity of variance across herds which is accounted for in RRTD and not in the repeatability model. This may be partially responsible of the resulting difference in estimated genetic trend along with the different genetic parameters (heritability is much higher in RRTD than in

the current repeatTD) and the difference in genetic assumptions by the two models.

Acknowledgments

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