

Test-Day Model for National Genetic Evaluation of Somatic Cell Count in Italian Simmental Population

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Introduction

Since 1994 herd testing in Italy is done not only for milk, fat and protein but also for somatic cell count (SCC). Currently, routine genetic evaluation for the Italian Simmental population is focussed on milk, fat and protein yield but not on SCC. This study has been carried out in order to implement a system for genetic evaluation for SCC. As known, this trait is a very good indicator of mastitis. Many surveys in Italy showed that Simmental dual purpose cows seem to be more resistant to mastitis than other breeds, as reported in table 1. Nevertheless, ANAPRI (Italian Simmental breeders association) decided to take into account also SCC in the breeding program, due to its very high economic value both at incomes level (effect on milk price) and at costs level (treatments, vet costs, milk loss, etc.). Moreover, animal welfare is another aspect to take care of when reducing mastitis incidence.

Table 1. Somatic cell count in Simmental and Holstein cows observed in herds having cows of both breeds under official milk recording in 2002.

	<i>n.test-days</i>	<i>SCC</i> (*1000)	<i>Milk yield</i> kg	<i>DIM</i>
Simmental	43,463	291	24.0	149
Holstein	56,796	456	28.0	168

Test day models (TDm) have been proposed for genetic evaluation programs of dairy cattle, in particular for SCC.

Similarly to milk production traits, we have chosen to develop a fixed regression (FD) repeatability test-day model (TD), because of very small size of Simmental herds in Italy (around 10 TD records per herd test-day). Simmental herds are located especially in North-east regions of Italy whereas farms are smaller, especially in mountain areas of such regions.

Materials and Methods

Size of initial data set was **1,527,011** SCC records, of **263,466** lactations and **107,708** cows. LINEAR SCORE of SCC was computed by logarithmic transformation $[\log_2(\text{SCC}/100.000)+3]$, in order to get a normal distribution. Simple statistics on this dataset are reported in Table 2.

Table 2. Descriptive statistics for the data set (1,527,011 TD records).

	<i>Mean</i>	<i>SD</i>	<i>Min</i>	<i>Max</i>
SCC (.000)	288	725	1	74,850
SCS log	2.93	1.45	-1.61	9.62
Milk kg	19.4	6.7	0.2	87.2
% fat	3.91	0.71	0.50	7.50
% protein	3.42	0.38	1.50	5.30
DIM (days in milk)	153	90.1	6.00	360
Parity	2.9	1.9	1	15

Fixed effects analysis

A major fixed effect in test-day models is the herd-test day effect (HTD), which is the best way to consider herd effect over time. Moreover, age at calving, parity of lactation, calving season and lactation stage have been taken into consideration.

Data editing was performed in order to get reliable estimates of model effects.

Records out of following ranges were excluded:

- age at the 1st calving less than 22 and greater than 42 months;
- age at the 2nd calving less than 34 and greater than 54 months;
- age at the 3rd calving greater than 45 months;
- days in milk less than 6 and greater than 360 d ;
- cows with no records in the first lactation;
- HTD classes with at least 5 observations and lactations with at least 2 observations.

Size of dataset after editing was **867,566** records of **63,027** cows and **2,179** herds.

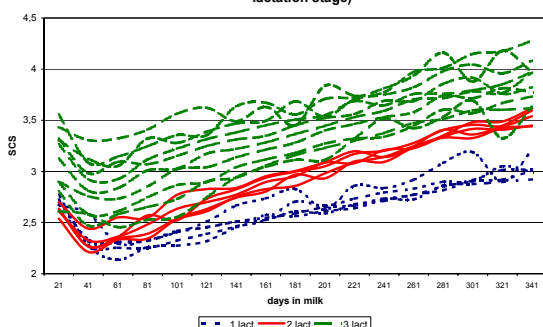
Parity of lactation, age at calving and lactation stage were combined in order to consider also their interaction effect. Interaction factor among these three effects was called PAD (Parity-age-days in milk). PAD levels were 340, divided on 5 age classes of first parity, 5 age classes of second parity, 10 age classes of third or higher parity, each of them with 17 classes of days in milk (DIM).

In order to carry out variance components estimation, dataset size had to be reduced by sampling. Sampling was done on herds in order to keep the same data structure by previous editing avoiding losses of females relationships.

Thus, size of the sample was **204,127 records from 524 herds, 16,341 HTD, 15,017 cows and 36,051 lactations.**

Least Squares means for each level of PAD effect were computed and plotted getting ability of fitting over parity, age and days in milk (figure 1). As expected, SCC increases in following parities after the first and within parities over age and over days in milk. Some discrepancies of fitting ability were observed at bounding classes because of less reliable estimates due to fewer observations in such classes.

Figure 1: LS means of fixed effect PAD (Parity by age at calving by lactation stage)



Variance components estimation

Because of the small size of herds (13.6 tests per HTD), a simple model like as a fixed regression repeatability testday model was chosen. It is described as follows:

$$SCS_{ijklmno} = HTD_i + PAD_j + CM_K + a_l + pec_m + pel_n + e_{ijklmno}$$

where:

- $SCS_{ijklmno}$ = log transformation of $ijklmno$ SCC TD record
- HTD_i = fixed effect of i-th herd-test day (i=1-16,341)
- PAD_j = fixed effect of j-th PAD interaction factor parity(1-3) by age at calving (1-20) by days in milk (1-17 class) (j=1-340)
- CM_K = fixed effect of k-th calving season (k=1-12)
- a_l = random additive genetic effect of l-th animal (l=1-47,037)
- pec_m = random non-additive genetic and permanent environment effect of m-th animal (m=1-15,017)
- pel_n = random permanent environment effect of n-th lactation (n=1-36,051)
- $e_{ijklmno}$ = random error

Taking into consideration permanent environment effect, three models have been tested:

1. cow effect (permanent environment effects related to entire cow productive life)
2. lactation effect (permanent environment effects related to each lactation)
3. cow and lactation effects.

Variance components were estimated by AI-REML (BLUPF90 package) written by I. Mistral e S. Tsuruta under Linux environment.

Pedigree information included five generations and total number of animals was 47,037.

Computing time was quite short, i.e. some hours, and convergence was reached after 9-10 rounds.

Estimations of variance components are reported in table 3. Results from models 1 and 3 are very comparable, whereas those from model 2 are quite different. Heritabilities from models 1 and 3 are around 8%. By model 2 heritability value is 3 times greater, due an overestimation of the additive genetic variance.

Explanation of this difference may be that non genetic factors related to a cow (chronic matitis, teat injuries, etc.) may affect SCC along entire productive life and not only one lactation.

Table 3. Variance estimation results in the three different models.

	σ^2_a	σ^2_e	σ^2_{pec}	σ^2_{pel}	h^2	r
MODEL 1 (pe=COW)	0.13	1.05	0.43		0.08	0.35
MODEL 2 (pe=LACTATION)	0.39	0.81		0.44	0.23	0.51
MODEL 3 (pe=COW+ LACTATION)	0.12	0.82	0.23	0.44	0.08	0.48

Moreover, looking at simple statistics of random effects solutions, it was found that the mean of additive genetic animal effect estimated by model 2 is very different from 0.

The closest to 0 is that from model 3. (figures 2-3-4). The distribution of residual has a zero mean in all models as well as a normality pattern(fig. 5).

figure 2: distribution of random effects solution (model 1)

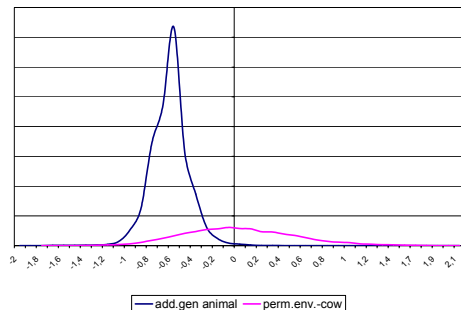


Figure 3: distribution of random effects solution (model 2)

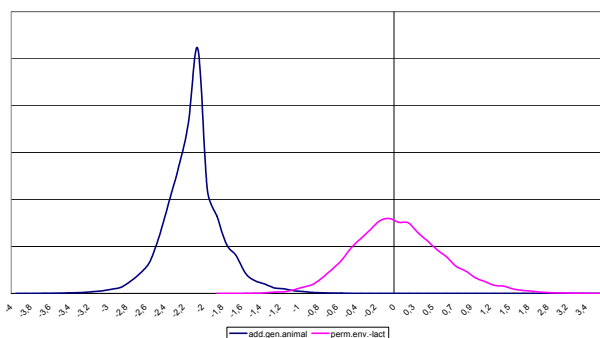
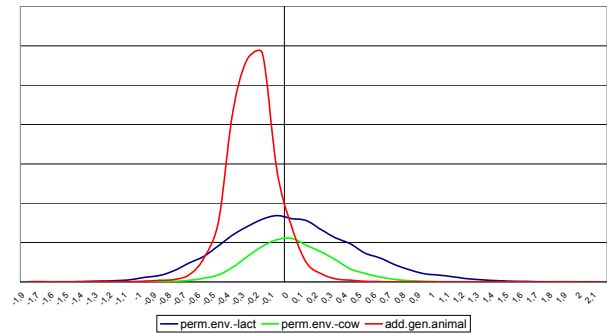
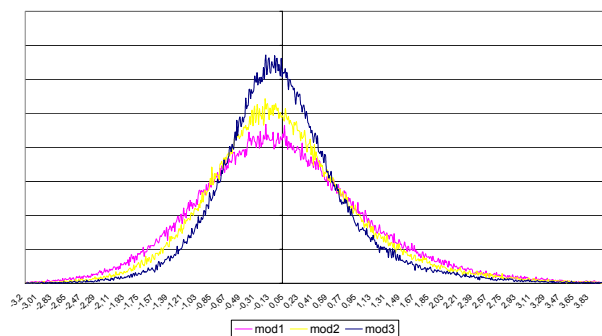


Figure 4: distribution of random effects solution (model 3)



Model residuals were computed and statistics on them were obtained in order to discover possible biases. Mean equal to 0 and normality of distribution were checked either on whole dataset as within classes of fixed effects without finding any biases (figure 5).

Figure 5: residual distribution with different models



Cross comparison between animal solutions by computing simple correlations show that estimations by model 2 are significantly different from the others (table 4). Correlations of 0.99 between solutions by models 1 and 3 show that they can be considered quite the same.

Table 4. Correlations between animal solutions computed by different models.

	$N^{\circ} obs$	$Ebv1-ebv2$	$Ebv1-ebv3$
All animals in pedigree	47,037	0.92	0.99
Cows with records	15,017	0.88	0.99

In conclusion, model 3 looks like the most suitable to get reliable estimations of variance components and breeding values as well.

National breeding values estimation

Model 3 was chosen to compute breeding values. Herd test SCC data was extracted from ANAPRI database. **1,902,538** test-day records were extracted from 1994 to February 2004.

The same editing as that applied for variance estimation has been used, except for the minimum number of records within HTD class which is reduced from 5 to 3. A total of **1,123,772** records was available for genetic evaluation after editing, corresponding to **77,326 cows**, **189,814 lactations**, and **111,838 herd-testdays (HTD)**.

Total number of animals in pedigree was **171,466**. Ninety seven **unknown parent groups** have been defined according to sex, offspring origin and estimated year of birth. If some of these groups had less than 50 observations, they were grouped.

Average distribution of data by cows and HTD classes is reported in Table 5. On average, cows had approximately 14.5 testdays and HTD classes had about 10 observations.

Table 5. Distribution of data by cows and by HTD.

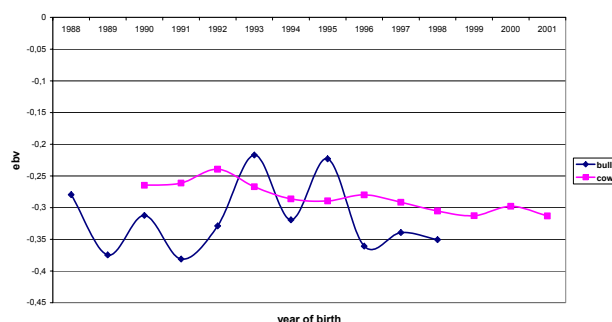
	<i>n.levels</i>	<i>mean</i>	<i>Std.dev</i>	<i>min</i>	<i>max</i>
N° TD /cow	77,326	14.5	10.5	2	79
N° TD /HTD	111,838	10.1	10.5	3	208

Breeding values were computed by BLUPF90 software developed by I. Mistral (Georgia University, USA), under LINUX environment.

Approximated reliabilities were computed as suggested by Harris and Johnson (1998).

Genetic trends for bulls and cows have been analyzed and are reported in Figure 6. Sign of solutions has been reversed in order to have a desirable meaning. An heterogeneous pattern is observed, especially for bulls, probably because no selection for this traits has ever been practiced. Anyway, a small negative trend over time is observed for cows.

Figure 6: GENETIC TREND FOR MILK SOMATIC CELL COUNT IN ITALIAN SIMMENTAL BREED



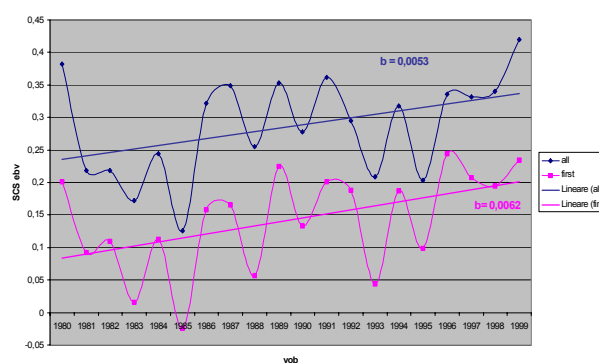
As in the Italian Simmental population a large number of foreign bulls is used, mostly coming from Germany, Austria and France (Montbeliarde), simple correlations between ebvs computed in Italy and those from countries of origin were estimated.

Correlation on 73 german-austrian bulls evaluated in Italy with at least 80% reliability was .82. For French bulls (Montbeliarde) correlation was .75. Since the models are quite different across countries and the number of daughters is strongly unbalanced because most of them are second crop proven bulls, these correlations can be considered higher than expected.

International evaluation

The Italian Simmental association provided Interbull, in September 2004, with data of SCC breeding values in order to submit them to a test run for this trait in the Simmental breed. As known, before to send data to Interbull a trend validation must be done in order to discover possible biases in national ebvs. Method 1 has been chosen to validate the genetic trend. Genetic trends on AI bulls born since 1980 were computed separately on test-days from first lactations only and on from all lactations. Figure 7 shows comparison between two trends which have clearly the same pattern.

Figure 7: bulls genetic trend of SCS on all lactations vs. first lactations only



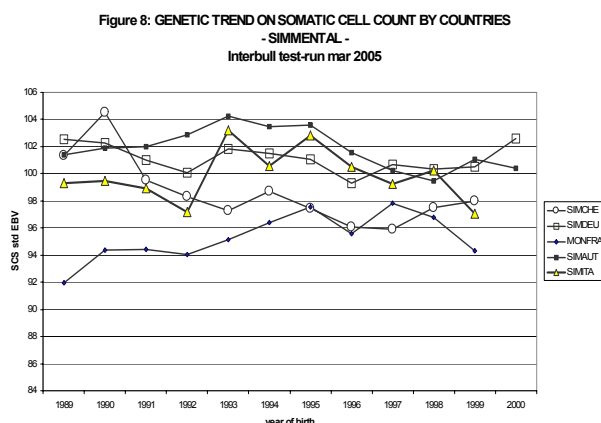
Slope difference between the two trends (all lactations vs. first) is -.00086 that means -.02% of the genetic standard deviation.

Genetic correlations between countries estimated in March 2005 test-run are pretty good. At the moment genetic correlations are higher than those estimated for production traits, as shown in table 6.

Table 6. genetic ties between countries in the SCC international evaluation from May 2005 test-run.

	SCC		PROTEIN	
	common bulls	Gen. Corr.	common bulls	Gen. Corr.
FR mon	100	0.93	98	0.86
FR sim	37	0.92	33	0.87
DEA	230	0.93	254	0.85
CHE	42	0.87	45	0.86

Figure 8 shows bull genetic trend by countries with reversed sign to give a desirable meaning. That for the Italian bulls is slightly decreasing albeit they are on average in middle level. In terms of average genetic level it seems that German and Austrian bulls are a little bit higher than the others, albeit since 1993 they are showing a slightly decreasing pattern as well. French and Swiss bulls seem to have a lower genetic level for this trait, but for French ones it is slightly increasing over time.



Results and Discussion

A genetic evaluation program for SCC in the Italian Simmental breed has been successfully performed.

It is very simple being a repeatability test-day model using data from all lactations. A simple model like this is more suitable to a data structure based on small herds, i.e. 10 records per herd-testday. Considering the permanent environment animal effect, it has been shown that accounting for cow and lactation gives better results. Estimated heritability was not high, i.e. around 8%. As the high economic value of this trait, ANAPRI (the Italian Simmental breeders association) decided to provide national official ebvs for this trait starting from February 2005. Starting from August 2005, Interbull proofs will be released. Genetic trend validation by method 1 was successful, showing no bias in the national evaluation. High genetic correlations between countries have been found in the first Interbull test-run. Slightly decreasing genetic trend was observed for cows and bulls. Starting from August 2005, SCS will be also introduced in the selection index of the Italian Simmental population (IDA) with a weight of 5%.

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