GENETIC PARAMETERS FOR PRODUCTION TRAITS AND SOMATIC CELL SCORES ESTIMATED WITH A MULTIPLE TRAIT RANDOM REGRESSION MODEL IN ITALIAN HOLSTEINS

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INTRODUCTION
In Italy a random regression (RR) test day (TD) model, analogous to the one adopted in Canada for breeding value estimation (Schaeffer *et al.*, 2000), is under study for genetic evaluation of Holstein dairy cows. Italian and Canadian Holstein populations have similar size, and comparable selection objectives and recording systems. Nevertheless, in Italy, specific covariance parameters need to be estimated to be used in a RR TD model that will substitute the lactation model actually in use. The objectives of this study were: 1) the estimation of (co)variance parameters for production traits and somatic cell scores in Italian Holstein to be used in a national RR TD model; and 2) the comparison of TD RR (co)variance estimates from Italian and Canadian Holstein populations.

MATERIAL AND METHODS
Data. Italian data consisted of TD records on milk (kg), fat(kg), protein(kg) and SCS (on log2 scale) from the first three lactation of Holstein Friesian cattle. A sample of data was created by random selection of herds with at least 1000 records. Year of calving was required to be between 1990 and 1998. All four traits had to be recorded on each TD. For each lactation, two classes of age by four seasons of calving were created. Thresholds for two classes of age for each parity are 28 months for first, 41 months for second, and 55 months for third lactation, and seasons were defined as: January to March, April to June, July to September, October to December. The sample included 82,368 test day records from 5,675 cows. Data were distributed 51% of TD in first, 32% in second and 17% in third lactation. The corresponding levels of herd-test-day (HTD) were 2,544 for first, 2,197 for second, and 1,725 for third lactation. Data used for the Canadian analysis are described in Jamrozik *et al*. (1998).

Model. The model of TD analysis was an animal model with multiple trait (MT) RR. Traits were considered across lactations. The model for trait i in lactation j was: $y_{ijtlmno} = HTD_{ijl} + \sum b_{ijnp}z_{tp} + \sum a_{ijmp}z_{tp} + \sum p_{ijmp}z_{tp} + e_{ijtlmno}$, where $y_{ijklmno}$ was the record o on cow m made on day t within herd-test day effect l, for a cow in the subclass n for season-age of calving, HTD_{ijl} was fixed HTD effect, b_{ijnp} were fixed regression coefficients specific to subclass n, a_{ijmp} were random regression coefficients specific to cow m, p_{ijmp} were random permanent environmental coefficients specific for cow m, $e_{ijtlmno}$ was the residual effect for each observation, and z_{tp} were covariates assumed to be the same for both fixed and random regressions.

Shapes of lactation curves were modelled using Wilmink's function (1987) as: $W(t) = w_0 + w_1 t + w_2 \exp(-0.05t)$.

Vectors a_m and p_m included 36 elements (4 traits, 3 lactations, 3 covariates) with random regression coefficients for animal m. Covariance matrices were G for genetic and P for permanent environmental. Residual effects on different days in milk (DIM) were considered uncorrelated within and between cows. Residual covariances differed across 4 stages in each lactation: 5 to 45 DIM, 46 to 115 DIM, 116 to 265 DIM, and 266 to 305 DIM.

In total the model estimated 666 genetic, 666 permanent environmental, and 120 residual (co)variances. A Bayesian approach, as described in Jamrozik *et al*. (1998), was used to obtain the means of the posterior distributions for all parameters of the model. For the Italian data set two chains of 55,000 samples were generated. The first 5,000 samples were discarded as the burn-in period. Values obtained were averaged across the chains.

Canadian data had been previously analysed using the same model.

RESULTS AND DISCUSSION

Italian parameters. Covariance estimates were used to calculate average daily heritabilities, genetic and permanent environmental correlations. These values are shown in Table 1.

Table 1. Average values, from 5 to 305 days from calving, of additive genetic variance (on diagonal), genetic (above the diagonal) and permanent environmental (below) correlation coefficients (x100) for milk (M), fat (F), protein (P), and SCS (S), in first (1), second (2), and third (3) lactation. Correlations are with the corresponding parameter for the same day from calving

	M1	F1	P1	S1	M2	F2	P2	S2	M3	F3	P3	S3
M1	**7.88**	56	89	-2	59	29	50	4	51	27	43	4
F1	75	**0.01**	36	-4	24	44	28	-2	17	37	21	-1
P1	94	45	**0.01**	-2	48	32	52	0	42	30	45	1
S1	-18	-11	-11	**0.50**	0	-4	0	29	1	-4	1	26
M2	37	17	28	-9	**13.24**	56	80	-16	65	44	60	-5
F2	28	29	26	-11	78	**0.02**	46	-14	25	51	31	-6
P2	37	20	33	-9	93	51	**0.01**	-14	54	46	60	-5
S2	-7	-6	-4	28	-29	-19	-19	**0.67**	-9	-14	-10	40
M3	25	12	17	-10	43	23	31	-12	**17.24**	53	75	-14
F3	15	22	14	-9	33	34	27	-14	68	**0.03**	43	-12
P3	20	14	18	-8	41	26	33	-12	81	50	**0.02**	-14
S3	-5	-5	-3	20	-14	-10	-9	41	-23	-16	-24	**0.96**

Heritabilities increased for all traits from first to third lactation (Table 2). Lowest values were for SCS, from 0.15 to 0.25, but estimates for this trait were higher than results obtained with a TD fixed regression analysis in Italian data (Samoré *et al.*, 2001). Production traits had heritabilities (0.30-0.38) comparable to 0.30 used in national evaluation with a lactation model. Genetic correlations between production traits were high, especially between milk and protein. Differing from most of the literature (Mrode and Swanson, 1995), also in first parity, SCS had

favourable or null genetic correlations with production traits. From these results, genetic selection for production should not be expected to cause unfavourable increase in SCS level in Italian Holstein.

Comparison of Italian and Canadian variances. Additive genetic variances in Italy and Canada showed a similar trend over DIM, but at different levels (Figure 1). Generally, for all traits and lactations, variances initially decreased at the beginning of lactation (5-45 DIM), remained constant in the central period, and tended to increase at the end (after 255 DIM).
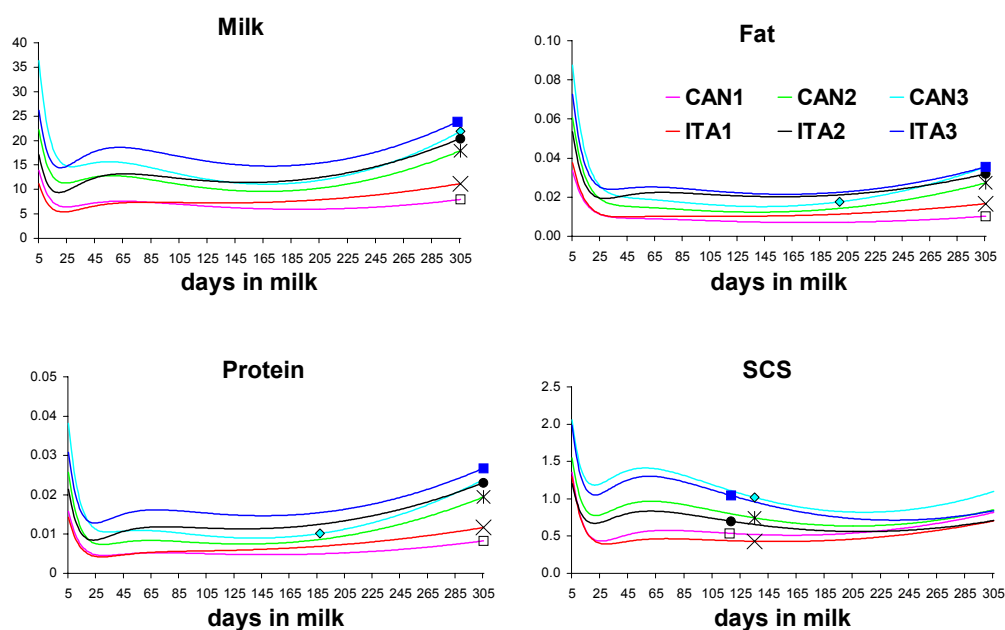

Figure 1. Trend of additive variances for milk, fat, protein, and SCS, in first (1), second (2), and third (3) lactations, in Canadian (CAN) and Italian (ITA) Holsteins. Symbols:ITA1=X, ITA2=•, ITA3 =■, CAN1=□, CAN2=✳, CAN3=◆

Similar shapes of the curves between the two populations were also observed for permanent environmental variances (no figure). Residual variances resulted in higher values in Italy than in Canada. Average heritabilities, from 5 to 305 DIM, tended to be higher in Canada than in Italy (Table 2), with the exception of fat and protein in second lactation. Greatest differences between the two populations were observed for SCS. Similar results had been previously observed based on estimates from lactation models (INTERBULL, 2000) for production traits.

Table 2. Average values, from 5 to 305 days from calving, of heritabilities (x100) for milk (M), fat (F), protein (P), and SCS (S), in first (1), second (2), and third (3) lactation in Canadian and Italian Holstein

	M1	F1	P1	S1	M2	F2	P2	S2	M3	F3	P3	S3
Canada	38	33	34	25	36	28	34	27	41	35	38	35
Italy	33	30	30	15	34	34	35	19	37	32	38	25

CONCLUSION

Estimates of (co)variances obtained in this study for the Italian Holstein will be used as parameters for multiple trait random regression model that will be soon adopted for genetic evaluations of production traits and SCS in Italy. Estimates of (co)variances for Italy and Canada followed the same trend across lactations, but at different levels. This result seems to suggest that the two populations are genetically comparable but the differences in (co)variance parameters should be accounted for in international comparisons.

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