

PRELIMINARY RESULTS OF BIVARIATE ANALYSIS IN JOINT SLOVENIAN AND CROATIAN EVALUATION FOR MILK TRAITS IN HOLSTEIN BREED

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ABSTRACT

The objective of this study was to estimate genetic parameters for milk traits (daily milk, fat, and protein yield) for a joint genetic evaluation in Holstein breed in Croatia and Slovenia and to compare results from the joint and national evaluation systems. Test-day records from Croatian (CRO) and Slovenian (SVN) routine genetic evaluation in May 2012 were used. A joint data set included 1,840,816 CRO and 2,680,001 SVN test-day records of 111,218 CRO and 127,774 SVN cows. The total number of animals included in the joint pedigree was 382,991. Genetic parameters for milk traits were estimated using bivariate model. SVN data were evaluated with a model which included fixed effects of calving season and stage of lactation fitted by the Ali-Schaeffer's lactation curve nested within parity. Random part of the model consisted of a common herd environment, direct additive genetic, and permanent environment effect within lactation. In addition to these, fixed class effect of region and covariate age at the first calving were included in the model for CRO data. In the random part, the contemporary group was defined as an interaction between the herd and year of testing for CRO data and as herd effect in SVN data. The estimated heritabilities of daily milk, fat, and protein yield were 0.19, 0.15, and 0.17 for CRO and 0.23, 0.19, and 0.21 for SVN data. Genetic correlation between countries was medium to high (0.78, 0.64, and 0.63) indicating some differences between countries. Correlations between inferred breeding values from the joint and national evaluations were high (0.997 for CRO and 0.999 for SVN evaluation). On SVN scale, genetic trend obtained from the joint evaluation was higher compared to the national evaluation. On CRO scale, the national genetic trend for daily protein yield was similar to the trend from joint model.

Key words: cattle / Holstein / milk traits / heritability / correlations / genetic trends / Slovenia / Croatia

1 INTRODUCTION

Breeding values (BV) estimated for the economically important production traits are the most important tools for selection. Slovenia and Croatia have been using common Holstein bulls for improvement of female population as well as selection of domestic sires via progeny testing in both countries. The use of the same bulls across countries leads to sufficient genetic ties between populations that could be utilized for joint evaluation. International evaluations of bulls from different countries are performed at INTERBULL using the MACE (multiple across country evaluation) system (Schaeffer, 1994).

Joint evaluation is of interest as it leads to higher genetic progress due to the enlarged population size used for selection (Lohuis and Dekkers, 1998). Similar joint genetic evaluation as explored here is already implemented in Austria and Germany in Simmental and Brown Swiss cattle, which started in 2000 for type traits in Simmental breed. Since February 2002, Italian Simmental population has been included in the type evaluation as well. Other traits were added as follows: somatic cell score and milkability (Sprengel *et al.*, 2001), longevity (Fuerst and Egger-Danner, 2002a), fertility (Fuerst and Egger-Danner, 2002b), calving ease and stillbirth (Fuerst and Egger-Danner, 2003), and beef traits (Schild *et al.*, 2003). The

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inclusion of the milk traits was completed in November 2002 (Emmerling *et al.*, 2002). Nordic countries (Sweden, Denmark, Norway, and Finland) also developed a joint evaluation model for milk production traits in Holstein and Red cattle (Finnish Ayrshire, Swedish Red and White, Red Danish, and Norwegian Red Cattle; Pedersen *et al.*, 2001) and for udder health traits (Negussie *et al.*, 2010).

The objective of this study was to estimate genetic parameters using bivariate model for milk traits in Holstein breed based on Croatian (CRO) and Slovenian (SVN) data and to compare inferred BV from the joint and national evaluation.

2 MATERIAL AND METHODS

Test-day records from CRO and SVN routine genetic evaluation in May 2012 were used for joint evaluation. CRO data were taken from the central database of the Croatian Agricultural Agency, while the SVN data were provided by the Slovenian Agricultural Institute. CRO data included test-day records between January 2003 and April 2012, while SLO data contained test-day records between January 2000 and April 2012. Records from the first to the tenth parity between five and 400 days in milk were included in the analysis. Additionally, parities from the seventh to the tenth were joined into a common class (parity 7+) due to the small number of records. SVN data consisted of test-day records from the first to the fifth parity between six and 305 days in milk. The ratio of test-day records from CRO to SVN was 41:59. A joint data set included 1,840,816 CRO and 2,680,001 SVN test-day records of 111,218 CRO and 127,774 SVN cows. Data editing was performed in each country separately (Potočnik, 1999; Špehar, 2010). Descriptive statistics for milk traits are presented in Table 1. Average daily production was larger in SVN compared to CRO cows. Furthermore, SVN cows also had larger maximum daily milk, fat, and protein yields. Despite a wider range of SVN records standard deviations were smaller for SVN.

Remaining data preparation was related to the

construction of a joint pedigree file with national and international identities. This process involved checking and comparing pedigrees from both sources since the number of generations involved in the national evaluations varied. The structure of constructed pedigree file is shown in Table 2. For CRO data, pedigree is fairly incomplete as almost one third of animals belonged to the base population. The average number of progeny per sire was 8.7, while dams had on average 1.2 progenies. Low number of progeny resulted from the large number of imported bulls during the past two decades. SVN data had better pedigree structure and the proportion of base animals was only 6%. Bulls in Slovenia had larger average number of progeny (85.3) compared to Croatia. The total number of animals included in the joint pedigree was 382,991 with intermediate values for other statistics.

In Slovenia, BV estimation for milk traits is based on the single-trait fixed regression repeatability test-day model (Potočnik, 1999). The same methodology is used for genetic evaluation of milk traits in Croatia (Špehar, 2010). For joint analysis, a bivariate model was used based on national single trait test-day models for milk traits (Eq. 1 and 2). In the bivariate analyses, separate evaluation was carried out for daily milk, fat, and protein yields. The traits were chosen based on INTERBULL guidelines (Interbull, 2000) for international genetic evaluation. SVN data were evaluated with a model which included fixed effects of calving season modelled as interaction between year and month of calving (S_{j}) and stage of lactation fitted by the Ali-Schaeffer's lactation curve (Ali and Schaeffer, 1987) nested within parity. Random part of the model consisted of a common herd environment (h_k), direct additive genetic (a_m), and permanent environment effect within lactation (p_{ilm}). An additional fixed class effect included in the Croatian model was region (R_j), while calving season was modelled as interaction between year of calving and trimester (S_k). The effect of age at first calving ($x_{ijklmno}$) was additionally included as covariate in the model. The effect was modelled as quadratic regression in the first parity. Statistical model for later parities did not include the effect of age at first calving. In the random part, the contemporary group was

Table 1: Descriptive statistics for daily milk (DMY), fat (DFY) and protein (DPY) yield for CRO and SVN data

Trait	Country	N	Avg	Std	Min	Max
DMY (kg)	CRO	1831627	21.79	8.26	3.00	50.00
	SVN	2680001	23.38	7.55	1.50	69.50
DFY (kg)	CRO	1724245	0.878	0.364	0.051	3.458
	SVN	2680001	0.941	0.325	0.031	4.547
DPY (kg)	CRO	1762094	0.727	0.261	0.063	2.620
	SVN	2680001	0.762	0.232	0.046	3.129

Table 2: Pedigree structure by country and jointly

Item/Country	CRO		SVN		Jointly	
	n	%	n	%	n	%
Animal with records	111,217	54.3	127,774	71.4	238,991	62.4
Non base animals	142,879	69.8	168,171	93.9	310,623	81.1
- both parents known	133,787	65.3	155,574	86.9	288,991	75.5
- only sire known	2,439	1.2	7,050	3.9	9,439	2.5
- only dam known	6,653	3.2	5,547	3.1	12,193	3.2
Base animals	61,952	30.2	10,922	6.1	72,368	18.9
Total number of animals	204,831	100.0	179,093	100.0	382,991	100.0
Average number of progenies per sire	8.7	/	85.3	/	17.4	
Average number of progenies per dam	1.2	/	1.5	/	1.4	
No of common bulls in the pedigree	11,772	/	4,602	/	668	
No of common bulls with recorded daughters	11,772	/	1,435	/	251	

defined as an interaction between the herd and year of testing (hy_{jm}).

$$y_{ijklmn} = \mu + \sum_{q=0}^4 b_q t_{qijklmno} + S_j + h_k + a_m + p_{ilm} + e_{ijklmn} \quad (1)$$

$$y_{ijklmno} = \mu + \sum_{q=0}^4 b_q t_{qijklmno} + R_j + S_k + b_5(x_{ijklmno} - \bar{x}) + b_6(x_{ijklmno} - \bar{x})^2 + hy_{jm} + a_n + p_{imn} + e_{ijklmnc} \quad (2)$$

The structure of covariance for the random effects (Eq. 3) involves traits in bivariate analysis. Matrix I_{c_i} is an identity matrix for the herd-year of test (c_1), or the herd effect (c_2), while I_{p_i} and I_{e_i} are identity matrices for the permanent environmental effect (p_1 and p_2) within lactation and residual, respectively. The assumption was that herd-year and herd effects, permanent effects and re-

siduals were not correlated. Genetic covariances among animals were obtained through the additive genetic covariance matrix

$G_A = G_0 \otimes A$ where G_0 is additive genetic covariance matrix between CRO and SVN scale, A is nu-

merator relationship matrix, and \otimes is the direct or Kronecker product. Genetic groups were not accounted in this work.

Variance components were estimated by the Residual Maximum Likelihood method as implemented in the VCE-6 software package (Groeneveld *et al.*, 2010). Prediction of BV was obtained using the same software

$$= \begin{bmatrix} I_{c_1} \sigma_{c_1}^2 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & I_{c_2} \sigma_{c_2}^2 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & I_{p_1} \sigma_{p_1}^2 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & I_{p_2} \sigma_{p_2}^2 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & A \sigma_{a_1}^2 & A \sigma_{a_{12}} & 0 & 0 \\ 0 & 0 & 0 & 0 & A \sigma_{a_{12}} & A \sigma_{a_2}^2 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & I_{e_1} \sigma_{e_1}^2 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & I_{e_2} \sigma_{e_2}^2 \end{bmatrix} \quad (3)$$

Table 3: Covariance component estimates \pm standard error for additive genetic effect (σ^2_a), herd-year of testing (CRO) or herd effect (SVN) (σ^2_c), permanent environmental effect (σ^2_p), and residual (σ^2_e) of milk traits from joint evaluation

Trait*	Country	σ^2_a	$\sigma_{a,CRO,SVN}$	σ^2_c	σ^2_p	σ^2_e
DMY (kg)	CRO	9.0150 \pm 0.0940	7.5850 \pm 0.6860	7.3280 \pm 0.1110	10.3590 \pm 0.0550	19.8640 \pm 0.0220
	SVN	10.4760 \pm 0.0890		9.8250 \pm 0.2850	11.3570 \pm 0.0390	13.5440 \pm 0.0120
DFY (kg)	CRO	0.0152 \pm 0.0002	0.0103 \pm 0.0020	0.0156 \pm 0.0002	0.0155 \pm 0.0001	0.0554 \pm 0.0001
	SVN	0.0171 \pm 0.0002		0.0189 \pm 0.0005	0.0169 \pm 0.0001	0.0367 \pm 0.0001
DPY (kg)	CRO	0.0087 \pm 0.0001	0.0059 \pm 0.0010	0.0099 \pm 0.0001	0.0092 \pm 0.0001	0.0235 \pm 0.0001
	SVN	0.0102 \pm 0.0001		0.0135 \pm 0.0001	0.0103 \pm 0.0001	0.0154 \pm 0.0001

*DMY – daily milk yield; DFY – daily fat yield; DPY – daily protein yield

package conditional on the estimated variance components. The general assumption of a joint evaluation is that the obtained results should have higher accuracy than the national evaluation. To investigate differences between the joint and national evaluation, Pearson and rank correlations of inferred BV from both scales (for all animals, as well as for sires and dams) were computed and comparison of genetic trends was performed. The later were calculated as the average BV by the year of birth. All data preparation and processing was performed with statistical package SAS (SAS, 2009).

3 RESULTS AND DISCUSSION

Estimates of (co)variance components in bivariate analyses (Table 3) were larger for SVN than for the CRO data. Estimates from the bivariate model were very similar to those estimated with univariate analysis in SVN national system¹. For CRO data, larger additive genetic variance was estimated with bivariate model in comparison to univariate national model (Špehar, 2010). The larger estimates in this study could be attributed by the additional relationships among animals used in the joint pedigree. Surprisingly, common herd environmen-

tal variance was larger in SVN than variance for herd-year of testing in CRO data. This is unexpected since the major advantage of test-day model is accounting for the temporary environmental effects on test-days (Ptak and Schaeffer, 1993).

The estimated heritabilities for daily yield traits (Table 4) were moderate and in agreement with the studies based on similar test-day models. For daily milk yield, the estimated heritability was 0.19 for CRO and 0.23 for SVN data. The estimated heritabilities of daily fat and protein yields were 0.15 and 0.17 in CRO and 0.19 and 0.21 in SVN data. Lower heritabilities found for CRO data could be attributed to unfavourable pedigree structure. In fact, most of the sires have small number of sons (Table 2). Estimated heritabilities of daily yield traits were comparable to the estimates in member countries of INTERBULL (Interbull, 2000; 2008) which use fixed regression test-day models. Medium to high genetic correlations between countries for daily milk (0.78), fat (0.64), and protein (0.63) yield indicates some differences between analysed traits in CRO and SVN.

Herd effect used as contemporary group in SVN data explained higher proportion of phenotypic variation for daily yield traits in comparison to herd-year of testing used for CRO data sets as already mentioned. As expected, permanent environmental effect accounted a large proportion of the phenotypic variance in both data

¹ http://www.bfro-uni-lj.si/zoo/org/centre/doc/variance_1.rtf

Table 4: Covariance components ratios estimates \pm standard error for additive genetic (h^2), herd-year of testing (Croatia) or herd (Slovenia) (c^2), permanent environmental effect (p^2) and residual (e^2) of milk traits in joint evaluation for Holstein breed

Trait*	Country	h^2	$r_{a,CRO,SVN}$	c^2	p^2	e^2
DMY (kg)	CRO	0.19 \pm 0.002	0.78 \pm 0.070	0.16 \pm 0.002	0.22 \pm 0.002	0.43 \pm 0.003
	SVN	0.23 \pm 0.002		0.22 \pm 0.005	0.25 \pm 0.002	0.30 \pm 0.001
DFY (kg)	CRO	0.15 \pm 0.001	0.64 \pm 0.001	0.15 \pm 0.002	0.15 \pm 0.001	0.55 \pm 0.004
	SVN	0.19 \pm 0.001		0.21 \pm 0.005	0.19 \pm 0.001	0.41 \pm 0.001
DPY (kg)	CRO	0.17 \pm 0.002	0.63 \pm 0.001	0.17 \pm 0.003	0.18 \pm 0.002	0.46 \pm 0.004
	SVN	0.21 \pm 0.001		0.27 \pm 0.005	0.21 \pm 0.002	0.31 \pm 0.001

*DMY – daily milk yield; DFY – daily fat yield; DPY – daily protein yield

Table 5: Pearson (r_p) and Spearman rank (r_s) correlations between inferred breeding values from the joint and national evaluations for all animals, bulls, and cows

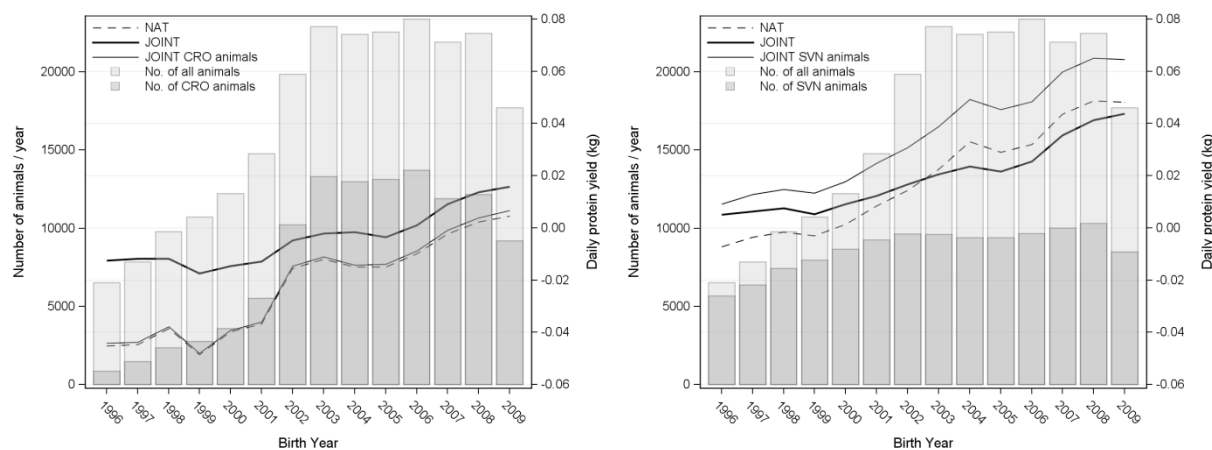
	Daily milk yield		Daily fat yield		Daily protein yield	
	r_p	r_s	r_p	r_s	r_p	r_s
All animals						
CRO	0.991	0.989	0.981	0.976	0.985	0.983
SVN	0.996	0.995	0.994	0.993	0.995	0.994
Bulls						
CRO	0.961	0.966	0.945	0.954	0.950	0.956
SVN	0.949	0.943	0.946	0.947	0.940	0.934
Cows						
CRO	0.993	0.991	0.983	0.978	0.987	0.985
SVN	0.997	0.996	0.995	0.994	0.996	0.995

sets. The variance ratio for permanent environmental effect covered larger proportion of phenotypic variance of daily milk, fat, and protein yields in SVN (25%, 19%, and 21%) compared to CRO (22%, 15%, and 18%) data. The proportion of unexplained variance was higher in CRO than in SVN data.

Pearson correlations ($P < 0.01$) showed that BV for daily milk, fat, and protein yields from the joint evaluation were highly correlated with the BV from the national evaluation (> 0.981 for CRO and > 0.994 for SVN data) for all animals and cows (Table 5). For bulls, Pearson correlations between inferred BV from the joint and national evaluation were lower for both data sets. Correlations were a bit higher for CRO in comparison to SVN data. In Nordic evaluations, Pedersen *et al.* (2001) obtained larger correlations (0.99) between joint and national evaluation of milk traits. Spearman rank correlations (≥ 0.976) indicate that there is a high correlation

between the rankings of all animals and cows for joint and national evaluation for all daily yield traits. However, the ranking of sires was more affected by the evaluation in comparison to cows.

Genetic trend based on BV from the joint and national evaluation for daily protein yield was computed for animals with official BVs (minimum accuracy of 0.50). Since the genetic trends for all analysed traits showed similar pattern, daily protein yield was chosen as an example based on its economic importance. Overall genetic trend obtained from the joint and national was positive for both populations (Figure 1). On the CRO scale genetic trend was virtually the same for national and joint evaluation (Figure 1, left), while there has been increase in genetic trend for SVN scale in joint evaluation in comparison to national evaluation (Figure 1, right). Observed changes should be explored further in detail. On average genetic level (mean) was lower for CRO ani-

**Figure 1:** Genetic trend and number of animals for daily protein yield on the CRO scale (left) and SVN (right) scale evaluated with national model (NAT) and joint model (JOINT)

mals than for SVN animals as indicated by lower values for CRO animals in comparison to joint population on CRO scale and larger values for SVN animals. If observed changes in genetic trends are solely due to the improved data structure use of joint bivariate model is warranted.

4 CONCLUSION

A joint bivariate evaluation model for milk production traits in Croatia and Slovenia has been tested. Medium to high genetic correlations are indicating some differences between studied traits in these two countries. However, correlations between inferred BV from national and joint model were high. For CRO scale, national genetic trend for daily protein yield was similar to the trend observed from joint model. More changes in genetic trends were observed between the joint and national evaluation in SVN scale possibly indicating improvement in the data structure. Further research is warranted to explain observed changes to improve both national and joint evaluations and to share development and routine costs of evaluations.

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