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VARIANCE COMPONENTS ESTIMATION FOR TYPE TRAITS IN SLOVENIAN BROWN SWISS CATTLE

Marija ŠPEHAR [1], Miran ŠTEPEC [2], Klemen POTOČNIK [2]

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Variance components estimation for type traits in Slovenian Brown Swiss cattle

The objective of this study was to estimate genetic parameters for 39 (26 official and 13 new) scored type traits in Slovenian Brown Swiss cattle. Data set included records of 35 386 Brown Swiss cows scored from 2000 to 2011 using method 'System 97'. The studied type traits were scored on scale from 1 to 9 (29 traits), measured by stick or tape (five traits) or expressed in points from 60 to 90 (five traits). Multiple-trait analyses based on three models were used for estimates of genetic parameters. Fixed class effects in the models were: classifier and year of scoring interaction, calving season, and time from calving to scoring. Body condition score effect was additionally fitted as linear regression in the second model. The third model included time after milking as fixed class effect instead of condition. Direct additive genetic effect and herd were used in the models as random effects. Estimated heritabilities ranged from 0.13 to 0.46 for frame and from 0.03 to 0.22 for form traits. Low to intermediate heritabilities (from 0.10 to 0.25) were estimated for mammary system traits. The lowest heritability estimates, in range from 0.04 to 0.13, were obtained for foot and leg traits. The variance ratio for herd covered between 0.02 and 0.26 of phenotypic variation. Genetic correlations among type traits ranged from −0.41 between rear legs side view and legs overall to 0.99 between rump height measured by tape and rump height linearly scored for frame traits. High genetic correlations were estimated for the following pairs of traits: rump width measured and rump width linearly scored (0.92), central ligament and central ligament redefined (0.97), body depth measured and body depth linearly scored (0.86). Phenotypic correlations between pairs of traits were similar in direction but smaller in magnitude in comparison to genetic correlations. Measured type traits should be replaced with the scored one since genetic correlations between them were high. The replacement will lead to the same efficient but cheaper scoring system.

Key words: cattle / breeds / Brown Swiss / type traits / heritability / genetic correlations

Ocena komponent variance za lastnosti zunanjosti pri slovenski rjavi pasmi goveda

Cilj študije je bil oceniti genetske parametre za 39 (26 rutinskih in 13 novo definiranih) lastnosti zunanjosti pri slovenski populaciji rjavega goveda. Podatki zajemajo rezultate ocenjevanja zunanjosti 35 386 prvesnic, ocenjenih med letoma 2000 in 2011 po sistemu 97. Proučevane lastnosti zunanjosti so bile ocenjene na skali od 1 do 9 (29 lastnosti), merjene s palico in trakom (5 lastnosti) ali ocenjene na skali od 60 do 90 (5 lastnosti). Za oceno parametrov disperzije so bili uporabljeni trije različni več lastnostni modeli. Sistematski del prvega modela vključuje vplive: ocenjevalec in leto ocenjevanja, sezono telitve in dobo med telitvijo in ocenjevanjem. Drugi model vključuje poleg vplivov v prvem modelu še vpliv linearne regresije kondicije, tretji model pa sistematski vpliv časa od zadnje molže do ocenjevanja. Naključni del modelov v vseh primerih vključuje vpliv črede in aditivni vpliv živali. Dednostni deleži za okvir so ocenjeni z vrednostmi med 0,13 in 0,46 in za oblike med 0,03 in 0,22. Za lastnosti vimena se ocenjeni dednostni deleži gibljejo med 0,10 in 0,25. Majhni dednostni deleži so ocenjeni za lastnosti nog, in sicer med 0,04 in 0,13. Velike razlike v deležu fenotipske variance, le ta se giblje med 0,02 in 0,26, so pojasnjene s čredo. Genetske korelacije med lastnostmi zunanjosti se gibljejo med −0,41 (kot skočnega sklepa in skupna ocena za noge) in 0,99 med oceno in meritvijo za višino križa. Visoke genetske korelacije so bile ocenjene med naslednjimi pari lastnosti: ocenjena in merjena širina križa (0,92); nova in stara definicija centralne vezi (0,97); ocenjena in merjena globina telesa (0,86). Fenotipske korelacije so v primerjavi z genetskimi nekoliko nižje na absolutni skali. Glede na visoke korelacije je smiselno, da novo definirane ocenjevane lastnosti nadomestijo ustrezne merjene lastnosti. Na ta način bo selekcija primerljivo učinkovita, za ocenjevanje posamezne živali pa bo potrebno manj časa.

Ključne besede: govedo / pasme / rjava pasma / lastnosti zunanjosti / dednostni delež / genetske korelacije

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[1] Croatian Agricultural Agency, Ilica 101, 10000 Zagreb, Croatia
[2] Univ. of Ljubljana, Biotechnical Fac., Dept. of Animal Science, Groblje 3, SI-1230 Domžale, Slovenia

1 INTRODUCTION

Linear type scoring is a part of animal evaluation system in many dairy cattle breeds (Mark, 2004; de Haas *et al.*, 2007). Selection emphasis on conformation traits has several purposes. Type traits are used as an early predictor of longevity (Larroque and Ducrocq, 2001; Neuenschwander *et al.*, 2005). Cow of moderate size, with correct feet and legs and functional udder as well will remain in the herd rather than cows that lack these characteristics. Therefore, information about conformation traits can be used as an early predictor of herd life in order to decrease involuntary culling and the increase profitability (Rogers and McDaniel, 1989; Vukasinovic *et al.*, 2002). Conformation traits are recorded relatively early in life, during the first lactation. These traits have moderate to high heritability (Dekkers *et al.*, 1994; de Haas *et al.*, 2007) which makes selection more efficient.

Current genetic evaluation for type traits is based on a multiple-trait analysis for 26 traits (Potočnik, 2005) in Slovenian Brown Swiss breed. These procedures are undergoing revision since scoring of new traits (6 redefined and 7 introduced traits) started in 2009. The traits were included in the evaluation in order to harmonize scoring system with the European type classification for the Brown Swiss breed. The objective of this study was to update genetic parameters for the official 26 and to estimate them for 13 new type traits using multiple-trait analysis within the trait group. However, high genetic correlations between traits could suggest that reduced number of traits will lead to lower costs with the same efficiency of scoring system.

2 MATERIAL AND METHODS

Conformation records were taken from the database of Slovenian Agricultural Institute. Data set included records of Brown Swiss cows scored from 2000 to 2011 using the method 'System 97'. The studied conformation traits (Table 1) were scored on a 9 – point scale (from 1 to 9), measured by stick or tape, or expressed in points (from 60 to 90). The traits were divided into frame (group 1 and group 2) that included 8 traits – rump height measured by stick, and linearly scored, frame overall expressed in points, strength measured by tape, and linearly scored, rump length measured by tape, body depth measured by tape and linearly scored. The form traits were split into group 3 with the following traits: form, top line, rump width measured by tape and linearly scored and group 4 that includes linearly scored rump angle, rump length, thurl position, while rump overall is expressed in points. Feet and legs (group 5) obtained 5 traits: rear legs side view, hock quality, pasterns, foot height linearly scored, and legs overall expressed in points. Muscularity, and points overall were evaluated separately. All together 16 mammary system traits were scored and divided into four groups (udder and teats) as follows: group 8 (udder overall linearly scored, fore udder attachment, fore udder length, udder attachment, and udder overall expressed in points), group 9 (rear udder height and rear udder width), group 10 (udder depth, central ligament, udder balance, central ligament), and group 11 (teats direction, teats diameter, teats length, fore teat placement, and rear teat placement), respectively. Altogether, 39 traits were scored. Among 13 new traits, 6 of them were redefined traits: rump height, body depth, rump width, udder attachment, central ligament that are linearly scored, and udder overall expressed in points. Other 7, so called introduced traits were completely new traits and expressed in points (frame overall, rump overall, legs overall, points overall), or in scores (thurl position, fore udder length, and udder balance). In preliminary study, the normality of traits was tested and the records were homogenised by classifier and year of scoring. The first data restriction was related to age at first calving and age of scoring. The limits for age at calving were between 500 and 1200 days, while age at scoring was in range from 505 to 1 565 days. Calving season was comprised as year-month of calving interaction. In order to have a reasonable number of records in each classifier-year of scoring interaction, subclass of minimum records were required. For udder traits, time after milking was determined as an interval from the last milking to scoring and expressed in hours. Records for cows scored from the first to the fourteenth hour after milking were included in the analysis. Additionally, time after milking from seventh to fourteenth hour was joined into a common class (7+) due to the small number of scored cows. After editing, a total of 35 386 scored cows were used in data analysis. All cows with records and their relatives tracing back for five generations were included in the pedigree file. A total number of animals involved in the pedigree was 55 137.

The mean scores of the linear conformation traits were between 4.73 and 5.86 (Table 1). The means were in general around and a little bit above the mean (5). Similar means were reported for the same Brown Swiss population in Slovenia (Potočnik, 2005) and for Brown Swiss cattle in Switzerland (de Hass *et al.*, 2007). Cows were on average 140 cm high, and were 1 cm taller than Brown Swiss in Switzerland (de Hass *et al.*, 2007). However, Brown Swiss in Switzerland had on average the widest strength (192 cm) compared to cows (190.2 cm) in this study.

All traits were not scored on all cows, since the traits with less than 8 000 records were implemented recently.

Table 1: *Descriptive statistics for conformation traits*
Preglednica 1: *Opisna statistika za ocene zunanjosti*

Name	Unit	N	Mean	Std	Min	Max
Group 1						
Rump height$_c$	cm	31 587	139.8	4.2	119	158
Rump height	1–9	7 357	4.74	1.39	1	9
Frame overall	point	7 349	79.2	3.5	66	89
Group 2						
Strength$_c$	cm	31 455	190.2	7.7	150	232
Rump length	cm	15 487	48.4	3.5	20	80
Body depth$_c$	cm	13 093	76.2	4.4	50	95
Strength	1–9	20 167	5.14	1.18	1	9
Body depth	1–9	7 594	5.66	1.26	1	9
Group 3						
Form	1–9	24 020	5.25	1.05	1	9
Top line	1–9	31 708	4.83	0.86	1	9
Rump width$_c$	cm	13 765	17.59	2.13	11	52
Rump width	1–9	7 591	4.90	1.19	1	9
Group 4						
Rump angle	1–9	31 699	4.81	1	1	9
Rump length	1–9	19 084	5.32	1.09	1	9
Thurl position	1–9	7 525	5.00	1.16	1	9
Rump overall	point	7 514	80.07	3.22	65	89
Group 5						
Rear legs side view	1–9	31 721	5.12	1.04	1	9
Hock quality	1–9	20 114	5.22	1.24	1	9
Pasterns	1–9	31 715	5.14	1.13	1	9
Foot height	1–9	31 621	5.40	1.2	1	9
Legs overall	point	7 586	80.38	3.52	61	89
Group 6						
Muscularity	1–9	31 628	5.08	1.06	1	9
Group 7						
Points overall	point	7 326	79.67	2.03	71	87
Group 8						
Udder overall	1–9	24 002	4.97	1.09	1	9
Fore udder attachment	1–9	24 110	4.97	1.26	1	9
Fore udder length	1–9	7 631	4.88	1.42	1	9
Udder attachment	1–9	7 631	5.01	1.5	1	9
Udder overall$_p$	point	7 618	79.41	2.66	66	88
Group9						
Rear udder height	1–9	31 628	5.23	1.1	2	9
Rear udder width	1–9	31 635	5.05	1.18	1	9
Group 10						
Udder depth	1–9	31 630	5.86	1.26	1	9
Central ligament	1–9	24 108	5.18	1.32	1	9
Udder balance	1–9	7 630	4.73	0.89	1	9
Central ligament$_{rs}$	1–9	7 629	4.84	1.5	1	9
Group 11						
Teats direction	1–9	31 347	5.12	1	1	9
Teats diameter	1–9	31 348	5.09	0.89	1	9
Teats length	1–9	31 256	5.41	1.1	1	9
Fore teat placement	1–9	19 794	4.85	1.04	1	9
Rear teat placement	1–9	19 774	5.77	1.14	1	9

Therefore, traits were combined within subsets in order to include old and new traits (Table 1).

In order to include new traits in the selection index, (co)variances for new traits were estimated, while previous estimates for old traits were updated. Multiple-trait analyses based on three models were used for estimates. The models differed in the fixed part as follows. Fixed class effects in the model were: classifier and year of scoring interaction (AS_i), calving season (C_j), and time from calving to scoring (T_k). Body condition score effect (x_{ijk}) was additionally fitted as linear regression in the second model. The third model included time after milking (M_l) as fixed class effect instead of condition. Random part of the model was defined with herd (h_{ijklm}) and direct additive genetic effect (a_{ijklmn}).

$$y_{ijklm} = \mu + AS_i + C_j + T_k + h_{ijkl} + a_{ijklm} + e_{ijklm} \qquad [1]$$

$$y_{ijklm} = \mu + AS_i + C_j + T_k + b_I\,(x_{ijklm} - \bar{x}) + h_{ijkl} + a_{ijklm} + e_{ijklm} \qquad [2]$$

$$y_{ijklmn} = \mu + AS_i + C_j + T_k + M_l + h_{ijklm} + a_{ijklmn} + e_{ijklmn} \qquad [3]$$

Table 2: *Estimated variance ratios for frame and form traits, muscularity and points overall*
Preglednica 2: *Ocenjeni deleži za lastnosti okvirja, oblike, omišičenost in točke skupaj*

Group	Trait	h^2	c_h^2	e^2
1	* Rump height$_c$	0.46	0.10	0.44
	Rump height	0.43	0.10	0.47
	Frame overall	0.15	0.08	0.78
2	* Strength$_c$	0.21	0.26	0.53
	Rump length	0.15	0.15	0.70
	* Body depth$_c$	0.18	0.17	0.65
	Strength	0.13	0.19	0.68
	Body depth	0.15	0.12	0.73
3	Form	0.07	0.09	0.84
	Top line	0.16	0.04	0.81
	* Rump width$_c$	0.14	0.15	0.71
	Rump width	0.18	0.08	0.74
4	Rump angle	0.22	0.04	0.74
	Rump length	0.09	0.10	0.81
	Thurl position	0.03	0.04	0.93
	Rump overall	0.09	0.07	0.84
5	Muscularity	0.16	0.21	0.63
6	Points overall	0.16	0.10	0.74

*Rump height$_c$ – height measured by stick; strength$_c$ – strength measured by tape; body depth$_c$ – body depth measured by tape; rump width$_c$ – rump width measured by tape; h^2 – heritability; c_h^2 – ratio for herd; e^2 – ratio for residual

(Co) variance components were estimated using VCE-6 software package (Groeneveld *et al.*, 2010) and REML method based on multivariate animal models.

3 RESULTS AND DISCUSSION

The heritabilities of frame traits were moderate to relatively high and ranged from 0.13 to 0.46. The most heritable traits were rump height measured by stick (0.46) and rump height linearly scored (0.43). Since both traits had similar heritabilities, linearly scored rump height can be used for further genetic evaluation instead of the same trait measured by stick. Estimated heritabilities of stature traits in this study were comparable to the estimates in member countries of Interbull (Interbull, 2012) that use fixed regression models. Heritabilities of rump height for Slovenian Brown Swiss cattle were similar to the estimated heritabilities in joint evaluation in Austria and Germany (0.47; Interbull, 2012) and Switzerland (0.43; Interbull, 2012). The lowest heritability (0.13) was estimated for strength linearly scored. Similar heritability (0.145) was estimated for Brown Swiss in the USA (Wiggans *et al.*, 2006) and Italian Brown Swiss population (0.18; Samore *et al.*, 2010). Heritability estimated for strength measured by tape was higher (0.21) in comparison to heritability estimated in research of Potočnik (0.14; 2005) for Slovenian Brown Swiss population. Heritability of body depth estimated in this study (0.15) was lower than heritability obtained for Brown Swiss cattle in Switzerland (0.34; de Hass *et al.*, 2007) and in the USA (0.201; Wiggans *et al.*, 2006). Higher heritabilities were estimated for body depth in joint evaluation for Austria and Germany (0.26; Interbull, 2012), Switzerland (0.37; Interbull, 2012), and in France (0.386; Interbull, 2012) compared to the values for Brown Swiss cows in Slovenia. Nemcova *et al.* (2011) reported higher heritability estimated for body depth (0.24) in Czech Holstein population.

The estimated heritabilities for traits related to the form were low to moderate (from 0.03 to 0.22). The lowest heritability was estimated for thurl position (0.03) which is a new trait. The reason for that could be inconsistent scoring criteria among classifiers. Low heritabilities (between 0.07 and 0.09) were estimated for form, rump length and rump overall (Table 2). The highest estimated heritabilities were obtained for rump angle (0.22) and rump width linearly scored (0.18). Estimated heritabilities were higher in Switzerland (0.39 and 0.42; Interbull, 2012), France (0.326 and 0.392; Interbull, 2012), and joint evaluation in Austria and Germany (0.29 and 0.28; Interbull, 2012) than the heritabilities in this study. Heritabilities for top line, rump width and rump angle were

Table 3: *Estimated variance ratios for feet and legs traits*
Preglednica 3: *Ocenjeni deleži varianc za lastnosti parkljev in nog*

Group	Trait	h^2	c_h^2	e^2
5	Rear legs side view	0.13	0.05	0.82
	Hock quality	0.11	0.08	0.81
	Pasterns	0.12	0.05	0.84
	Foot height	0.04	0.09	0.87
	Legs overall	0.06	0.05	0.89

h^2 – heritability; c_h^2 – ratio for herd; e^2 – ratio for residual

similar to values estimated for Italian Brown Swiss cattle (0.15, 0.15, and 0.22; Samore *et al.*, 2010).

Moderate (0.16) heritability was estimated for muscularity and points overall. Lower heritability (0.08) was estimated for muscularity in the research of Potočnik (2005) for Slovenian Brown Swiss cattle compared to the values in this study. Higher heritability was obtained for Brown Swiss population in Switzerland (0.30; Interbull, 2012). Heritability estimates for the same trait differ among populations due to scales used for scoring, effects used in the model, consistency of classifiers and data structure and editing procedures.

Table 4: *Estimated variance ratios for udder and teats traits*
Preglednica 4: *Ocenjeni deleži varianc za lastnosti vimena in seskov*

Group	Trait	h^2	c_h^2	e^2
8	Udder overall	0.16	0.13	0.71
	Fore udder attachment	0.14	0.14	0.72
	Fore udder length	0.16	0.20	0.64
	Udder attachment	0.16	0.08	0.76
	* Udder overall$_p$	0.25	0.07	0.68
9	Rear udder height	0.10	0.04	0.86
	Rear udder width	0.12	0.17	0.71
10	Udder depth	0.22	0.08	0.69
	Central ligament	0.14	0.03	0.84
	Udder balance	0.12	0.03	0.85
	* Central ligament$_{rs}$	0.14	0.04	0.82
11	Teats direction	0.25	0.02	0.73
	Teats diameter	0.24	0.04	0.72
	Teats length	0.33	0.03	0.64
	Fore teat placement	0.24	0.02	0.74
	Rear teat placement	0.29	0.02	0.69

*Udder overall$_p$ – udder overall expressed in points; central ligament$_{rs}$ – central ligament as redefined trait; h^2 – heritability; c_h^2 – ratio for herd; e^2 – ratio for residual

The variance ratio for herd effect covered between 8% and 26% of phenotypic variation for frame traits. The residual accounted from 44% of phenotypic variation for rump height to 78% for frame overall. The estimated variance ratio for herd effect was lower (from 4% to 15%) for form traits in comparison to frame. A high proportion of phenotypic variance, from 71% to 93% remained an unexplained. Similar variance ratio for herd effect (between 9% and 14%) for frame and form traits was covered in earlier study for Slovenian Brown Swiss cows (Potočnik, 2005). The residual accounted from 66% to 80% for frame and form traits in the mentioned research.

The analysis confirmed the expectation of low heritability for foot and leg traits (Table 3). Estimated heritability ranged from 0.04 (foot height) to 0.13 (rear legs side view). Samore *et al.* (2010) reported similar heritability for heel depth (0.06) and rear leg set (0.12) but lower heritability for pasterns (0.08) in Italian Brown Swiss cattle. Heritabilities of rear legs side view, pasterns, and foot height in this study were similar with estimates of these traits in France (0.108, 0.121, and 0.121, Interbull 2012). Higher heritabilities were estimated in joint evaluation in Austria and Germany (0.22, 0.18, 0.08; Interbull, 2012), and Switzerland (0.21, 0.13, 0.10; Interbull, 2012). Higher heritability (0.19) for rear leg side view was estimated in Spanish Holstein (Perez-Cabalo *et al.*, 2006).

Heritability estimated of hock quality was in the same range as estimates reported for Italian Brown Swiss (0.10, Samore *et al.*, 2010), and Danish Red, Danish Friesian, and Jersey breeds (0.13, 0.19, 0.26; Boelling *et al.*, 2001). However, lower heritability (0.06) was estimated in Slovenian Brown Swiss population (Potočnik, 2005). Herd effect explained low proportion of phenotypic variance (between 5% and 9%), while high proportion of phenotypic variance (from 81% to 89%) remained unexplained.

Low to intermediate heritabilities (from 0.10 to 0.25) were estimated for mammary system traits (group 8 to group 11). The lowest heritability was estimated for udder traits related to the height (0.10) and width (0.12) of rear udder (Table 4). Higher heritabilities for udder height and width were estimated in joint evaluation for Austria and Germany (0.18, 0.20; Interbull, 2012), in Switzerland (0.23, 0.19; Interbull, 2012) as well as for Swiss Holsteins (Neuenschwander *et al.*, 2005). Estimated heritability was the highest for udder overall (0.25) and udder depth (0.22). The heritability estimates for udder depth and central ligament linearly scored in Slovenian Brown Swiss cows were lower compared to the estimated heritability in Austria and Germany (0.37, 0.22; Interbull) and in Switzerland (0.32, 0.21; Interbull). Heritabilities for udder traits were similar to values estimated for Italian Brown Swiss (Samore *et al.*, 2010) and

***Table 5:** Genetic correlations (above diagonal) and phenotypic correlations (below diagonal) among frame traits within groups*
***Preglednica 5:** Genetske (nad diagonalo) in fenotipske (pod diagonalo) korelacije med lastnostmi okvirja znotraj skupin*

Group	*Trait	RH	RH$_p$	FR	ST	RL	BD	ST$_p$	BD$_p$
1	RH	-	0.99	0.64					
	RH$_p$	0.85	-	0.70					
	FR	0.35	0.36	-					
2	ST				-	0.74	0.83	0.85	0.61
	RL				0.45	-	0.76	0.47	0.52
	BD				0.55	0.33	-	0.57	0.86
	ST$_p$				0.63	0.33	0.41	-	0.48
	BD$_p$				0.48	0.26	0.76	0.45	-

*RH – rump height; RHp – rump height linearly scored; FR – frame overall; ST – strength; RL – rump length; BD – body depth; ST$_p$ – strength linearly scored; BD$_p$ – body depth linearly scored

for primiparous Holstein cows (Misztal *et al.*, 1992; Rupp and Boichard, 1999).

Heritabilities in range from 0.24 to 0.33 were estimated for teats traits (group 11). Estimated heritabilities of fore and rear test placement were higher for Brown Swiss population in Switzerland (0.34, 0.32; Interbull, 2012) and joint Austrian and German population (0.35 for both traits; Interbull, 2012). The heritability estimates were between 0.29 (rear teat placement) and 0.38 (fore teat placement) for the first parity Holstein cows in Switzerland (Neuenschwander *et al.*, 2005). Heritabilities for teats direction (0.25), diameter (0.24) and length (0.33) were higher than heritabilities (0.11, 0.18, and 0.28) estimated in the study of Potočnik (2005). Heritabilities reported for teats traits in several studies were similar to the estimates in Slovenian Brown Swiss cows. For Brown Swiss heifers in Italy, the heritability estimates were 0.18 for teats placement and 0.33 for teats length (Samore *et al.*, 2010). Estimated heritability was in range from 0.26 (teat placement) to 0.30 (teats length) for French Holsteins (Rupp and Boichard, 1999).

Heritability estimates for the same trait differ among populations due to scales used for scoring, effects used in the model, consistency of classifiers and data structure and editing procedures. The variance ratio for herd effect covered between 2% and 20% of phenotypic variation for mammary system traits. The residual accounted between 64% and 85% of phenotypic variation (Table 4). Higher proportion of residual variance (between 75% and 93%) was observed in the study of Potočnik (2005).

Genetic correlations among frame traits within groups are shown in Table 5. As expected, largest positive genetic correlation (0.99) was found between rump height expressed in cm and scores. In the group 2, genetic correlations ranged from 0.47 between rump length and strength linearly scored to 0.86 between fore udder attachment body depth and body depth linearly scored. The corresponding phenotypic correlations were in the same direction but smaller in magnitude in compari-

***Table 6:** Genetic correlations (above diagonal) and phenotypic correlations (below diagonal) among form traits within groups*
***Preglednica 6:** Genetske (nad diagonalo) in fenotipske (pod diagonalo) korelacije med lastnostmi oblik znotraj skupin*

Group	*Trait	FO	TL	RW	RW$_p$	RA	RL$_p$	TP	RO
3	FO	-	0.52	0.29	0.27				
	TL	0.21	-	0.03	−0.02				
	RW	0.15	0.01	-	0.92				
	RW$_p$	0.09	0.04	0.22	-				
4	RA					-	0.06	0.65	0.76
	RL$_p$					0.05	-	0.35	0.54
	TP					0.10	0.10	-	0.67
	RO					0.48	0.43	0.47	-

*FO – form; TL – top line; RW – rump width; RW$_p$ – rump width linearly scored; RA – rump angle; RL$_p$ – rump length; TP – thurl position; RO – rump overall

Table 7: *Genetic correlations (above diagonal) and phenotypic correlations (below diagonal) among feet and leg traits*
Preglednica 7: *Genetske (nad diagonalo) in fenotipske (pod diagonalo) korelacije med lastnostmi parkljev in nog znotraj skupin*

*Trait	RLS	HQ	PA	FH	LO
RLS	-	0.06	−0.32	−0.33	−0.41
HQ	−0.02	-	0.11	−0.25	0.36
PA	−0.15	0.10	-	0.62	0.90
FH	−0.07	−0.06	0.35	-	0.66
LO	−0.21	0.32	0.59	0.57	-

*RLS – rear legs side view; HQ – hock quality; PA – pasterns; FH – foot height; LO – legs overall

son to genotypic correlations. Phenotypic correlations ranged from 0.35 between rump height and frame overall to 0.85 between rump height expressed in cm and scores in the group 1. Lower phenotypic correlations were observed in the group 2. The correlations were from 0.26 between rump length and body depth linearly scored to 0.63 between strength and strength linearly scored.

Genetic correlations (Table 6) among form traits in the group 3 were low to moderate (from −0.02 to 0.52) except a high correlation (0.92) between rump width and rump width linearly scored. High and positive genetic correlations were also found between pairs of traits in the group 4: 0.65 between rump angle and thurl position, 0.67 between thurl position and rump overall, and 0.76 between rump angle and rump overall.

Genetic correlations between frame and form traits within groups were consistent with the previous analysis of Slovenian Brown Swiss population (Potočnik, 2005). Samore *et al.* (2010) reported moderate to high genetic correlations between stature traits in Italian Brown Swiss cattle. Positive correlations between frame and form traits indicated that a balanced cow structure was also maintained in an increase in size.

Phenotypic correlations among form traits were lower in comparison to frame (Table 6). In the group 3, phenotypic correlations were from 0.01 estimated between rump width and top line to 0.21 between form and top line. Low to moderate phenotypic correlations were observed in the group 4. The correlations ranged from 0.05 between rump angle and rump length linearly scored to 0.48 between rump angle (RA) and rump overall (RO).

Genetic correlations were in the wide range from very high positive to moderate negative values (from −0.41 to 0.90) in the group of feet and leg traits (Table 7). The genetic correlation between pasterns and legs overall was the highest positive values (0.90) followed by values of 0.66 for genetic correlation between foot height and legs overall, 0.62 between pasterns and foot height. High and positive genetic correlations between pasterns and foot height were estimated by Potočnik (2005) for the same population of Brown Swiss in Slovenia. Moderate negative genetic correlations were in range from −0.41 between rear legs side view and legs overall to −0.25 between hock quality and foot height. It means that cows with straight rear legs set tend to have steeper foot angle. Genetic correlations between rear legs side view and foot height were also negative but higher (−0.63) in French Brown Swiss (Interbull, 2012). Perez-Cabal *et al.* (2006) reported negative correlations (−0.39) between rear leg set and foot angle, and −0.44 between rear leg set and feet and legs for Spanish Holstein.

Estimates of the phenotypic correlations among feet and leg traits were in range from moderate and negative to moderate and positive (Table 7). Moderate and negative phenotypic correlations (−0.21) were estimated between rear legs side view and legs overall. Phenotypic correlations were moderate and positive and ranged from 0.57 between legs overall and foot height (FH), to 0.59 between legs overall and pasterns.

High genetic correlations were estimated between udder traits in the group 8 (Table 7). Genetic correlations ranged from 0.47 between fore udder length and udder overall to 0.88 between udder and udder attachment. Because of the high genetic correlation (0.70) between rear udder height and rear udder width cows have either high or wide udders. Moderate to high positive genetic correlations were estimated between the traits in the group 10. The estimates were from 0.24 between udder depth and central ligament to 0.97 between central ligament and central ligament redefined. Genetic correlations between udder traits were consistent with the previous analysis of Slovenian Brown Swiss population (Potočnik, 2005). Genetic correlations between udder depth and other udder traits were similar to those reported by Misztal *et al.* (1992) for Holstein breed in the USA.

The phenotypic correlations were positive and high (0.65) between udder overall and fore udder attachment, negative and moderate (−0.40) between udder overall and udder attachment and close to zero between udder overall and udder overall expressed in points (−0.06). In the group 10, the phenotypic correlations were all similar too but lower than the corresponding genetic correlations. Estimates of phenotypic correlations ranged from 0.09 between udder balance and central ligament to 0.30 between udder depth and udder balance.

A wide range of genetic correlations from moderate and negative (−0.36) to high and positive (0.90) was estimated between udder traits in group 11 (Table 8). Negative genetic correlations were obtained between the following pairs of traits: −0.36 between teats direc-

Table 8: *Genetic correlations (above diagonal) and phenotypic correlations (below diagonal) among udder traits within groups*
Preglednica 8: *Genetske (nad diagonalo) in fenotipske (pod diagonalo) korelacije med lastnostmi vimena in seskov*

Group	*Trait	UD	FUA	FUL	UA	UO_p	RUH	RUW	UDT	CL	UB	CL_p	TDR	TDM	TL	FTP	RTP
8	UD	-	0.88	0.84	0.76	0.76											
	FUA	0.65	-	0.95	0.81	0.56											
	FUL	0.43	0.47	-	0.76	0.47											
	UA	−0.40	−0.18	0.46	-	0.78											
	UO_p	−0.06	−0.06	0.36	0.60	-											
9	RUH						-	0.70									
	RUW						0.25	-									
10	UDT								-	0.24	0.62	0.45					
	CL								0.20	-	0.25	0.97					
	UB								0.30	0.14	-	0.39					
	CL_p								0.23	0.47	0.09	-					
11	TDR												-	−0.29	−0.36	0.67	0.90
	TDM												−0.11	-	0.39	−0.20	−0.22
	TL												−0.15	0.31	-	−0.34	−0.34
	FTP												0.36	−0.09	−0.16	-	0.79
	RTP												0.56	−0.10	−0.12	0.51	-

* UD – udder overall; FUA – fore udder attachment; FUL – fore udder length; UA – udder attachment; UO_p – udder overall; RUH – rear udder height; RUW – rear udder width; UDT – udder depth; CL – central ligament; UB – udder balance; CL_p – central ligament; TDR – teats direction; TDM – teats diameter; TL – teats length; FTP – fore teat placement; RTP – rear teat placement

tion and teats length, −0.34 between teats length and fore teat placement, and −0.34 between teats length and rear teat placement. The highest positive genetic correlation was estimated between teats direction and rear teat placement. The magnitude and direction of genetic correlations between teats traits in this study were similar to those reported for Brown Swiss breed in France (Interbull, 2012) and to previously estimated correlations from the same population in Slovenia (Potočnik, 2005). The phenotypic correlations ranged from positive and moderate (0.56) between rear teat placement and teats direction to negative and low (−0.16) between fore teat placement and teats length.

4 CONCLUSION

Genetic parameters were estimated in order to update genetic evaluation system of type traits and to analyse the genetic correlations between new defined and old traits. The heritabilities were low to moderate across subsets. Estimated heritabilities ranged from 0.13 to 0.46 for frame traits. In the group of form traits, the lowest heritability (0.03) was estimated for thurl position which is a newly defined trait. This implies that it is considerably difficult to make selection for the trait. However, it is possible that heritability will be improved after some years of scoring for this trait. The highest heritability was obtained for rump angle (0.22). Estimated heritability was low for foot and leg traits and ranged from 0.04 (heel height) to 0.13 (rear legs side view). Low to intermediate heritabilities, from 0.10 to 0.33 were estimated for mammary system traits. Therefore, greater response should be expected for udder traits compared to feet and legs. Genetic correlations were in the wide range from very high positive (0.99) to moderate negative values (−0.41) for frame, form, and feet and leg group of traits. Moderate to high genetic correlations (from 0.24 to 0.97) were estimated between mammary system traits with exception of teats traits. Favourable genetic correlations between measured and scored type traits indicate that new redefined traits can be used for genetic evaluation instead of measured one. The replacement will lead to the same efficient but cheaper scoring system. Estimated parameters for type traits will be used to update the selection index of Slovenian Brown Swiss cattle.

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