The estimation of the genetic parameters for conformation traits in the Romanian Spotted cattle breed

H. Grosu, M.C. Rotar and M.A. Gras

National Research&Development Institute for Biology and Animal Nutrition,Calea
Bucuresti, 077015, Balotesti, Romania
Corresponding Author: rotar.mircea.catalin@gmail.com

Abstract

Improving the global genetic potential of cattle, involves the consideration of several groups of characters, such as milk production, longevity, conformation, reproduction and others. An economical milk and meat production are sustained by superior longevity which is influenced by a harmonious conformation. Among the character groups enumerated above, in the present paper were analysed the conformation traits from the genetic point of view (heritability, genetic and environmental correlations). The genetic parameters were estimated for a number of 18 conformation traits, using as phenotypic information the linear score from the conformation traits appreciation of cows at first calving from the Romanian Spotted breed. In total, 2387 animals were analysed, of which 1193 were parents and 1194 were animals with performance. In order to optimize the running time and genetic parameters computation, we used the canonical transformation method, applied to a multi-trait animal model. The fixed effects of the model were: year-month, age at first calving and stage of lactation, and random effects were herd-year-season and animal. The obtained results revealed that the values of heritability, and genetic and environmental correlations are within the normal range of variation, specific to the conformation traits, similar for other cattle populations.

Keywords: canonical transformation, conformation, genetic parameters.

Introduction

For a more productive cattle population and a long and productive life, we must be sure of what animals will be removed from the herd. For that we try to preserve animals with good conformation and that will ensure us a sustainable production (Bertipaglia *et al.*, 2012). The exterior of an animal is associated with the production and in that case, it is necessary for us to make a conformation evaluation (Liu *et al.*, 2014). The purpose of the conformation evaluation is to discover the ideal animal. The managerial target of a herdsmen is to be efficient from financial point of view, and from that perspective, the conformation evaluation not imply high costs (Zink *et al.*, 2014; Satola *et al.*, 2017). It can be done very easy, also being good for exterior traits inclusion in total breeding value evaluation. All the country in the world were cattle breeding have an important share in economy, estimate genetic parameters for conformation traits, estimates that will help in cattle genetic evaluation (Mindur *et al.*, 2014; Akinsola *et al.*, 2018). Because the exterior evaluation includes a lot of traits, and also the number of evaluated animals is high, mathematical methodology must be involved into solving the mixed model equation in a short time and with fewer computer resources (Misztal

I. *et al*., 1995). In the presenting paper canonical transformation was applied. This procedure analyses traits one by one and in the end gives results like in simultaneous analysis.

Material and methods

2387 animals were analysed, 1193 of them were parents and 1194 were offspring with measured performances. Each animal with records had scores for all 18 analysed traits, resulting a total number of 21492 scores, used in the analysis. For this study, all the data were provided by Romanian Spotted Simmental-type Breeding Association from Brasov, Romania. Like any other evaluation system found in other countries, the classical visual evaluation was performed, by 5 referees. For each trait the score was between 1 and 9 scores. In the genetic evaluation, in order to have a fare hierarchy, scores were transformed in points from 50 to 90, each trait being adequately customized.

In order to solve the mixed model equation, finalized with genetic parameters, the traits were grouped in four categories: height at cross, rump length, hip width, rump angle, body depth were introduced in type traits group. Muscularity was introduced in muscle group. Hook angularity, hook development, pasterns, height hoof traits were introduced in feet and legs group. Udder traits: fore udder length, rear udder length, fore udder attachment, central ligament, udder depth, teat placement, teat length, teats thickness traits were introduced in udder group.

For estimating genetic parameters, was applied B.L.U.P. methodology to a multi-trait animal model with canonical transformation. The analysis was performed by R software, version 3.5.1. (R Core Team (2018). R: A language and environmental for statistical computing. R Foundation for Statistical Computing, Vienna, Austria (URL *https://www.R-project.org/*).

The biometric model used was:

$$y_{ijklm} = B_i + DIM_j + AGE_k + YM_l + HYS_m + a_{ijklm} + e_{ijklm} \qquad (1)$$

Where,

y_{ijklm} - recorded performances;
B_i - fixed effect of the referee;
DIM_j - fixed effect of days in milk for each cow in the scoring moment;
AGE_k - fixed effect of age;
YM_l- fixed effect of the combination month-year of calving;
HYS_m - random effect of the combination herd-year-season;
a_{ijklm} - random effect of the animal;
e_{ijklm} - error.

Results and conclusions

First step was to perform an analysis for descriptive statistics, for both scores and points. For each trait mean, mean error and standard deviation were calculated (Table 1). Scores ranged from 3.84 up to 7.08 with the general average 5.62, it can be observed. The traits from feet and legs group has majority of values around the average. If we look at the points number, we can observe that the means ranged between 75.8

and 87.2, with the general average of 82.39. In terms of standard deviation, for scores was obtained values from 0.87 to 1.66. On the other hand, for points number, the variation was between 3.75 and 9.18. For both scores and points the trait with the highest standard deviation was in udder group and the lower value was in feet and legs group, also for both scores and points.

Table 1. Standard deviation, Mean and standard error of mean for conformation traits.

Body region	Trait	Mean + Standard Error		Standard Deviations	
		Scores	Points	Scores	Points
Type traits	Height at Cross	6.41 + 0.04	79.1 + 0.40	1.47	6.77
	Rump Length	5.09 ± 0.05	76.2 ± 0.34	1.58	6.51
	Hip Width	4.95 ± 0.04	75.8 ± 0.34	1.45	5.78
	Rump Angle	5.30 + 0.03	85.6 + 0.25	0.97	3.95
	Body Depth	5.73 ± 0.04	78.9 ± 0.25	1.22	4.86
Muscle	Muscularity	5.14 + 0.04	83.6 + 0.31	1.24	5.83
Feet and Legs	Hock Angularity	5.28 ± 0.03	84.5 ± 0.28	0.93	4.04
	Hock Development	6.73 + 0.03	86.2 + 0.21	1.04	4.24
	Pasterns	5.74 + 0.03	81.5 + 0.24	0.87	4.05
	Hoof Height	6.14 ± 0.03	82.3 ± 0.20	0.95	3.75
Udder Traits	Fore Udder Length	6.58 + 0.04	80.1 + 0.24	1.55	6.19
	Rear Udder Length	5.87 ± 0.05	79.8 ± 0.23	1.66	6.64
	Fore Udder Attachment	5.95 + 0.03	83.6 + 0.21	1.14	4.55
	Central Ligament	6.20 + 0.04	87.2 + 0.31	1.36	6.40
	Udder Depth	7.08 ± 0.03	86.8 ± 0.26	1.09	4.53
	Teat Placement	5.16 + 0.03	83.6 + 0.26	1.14	5.29
	Teat Length	3.93 + 0.03	86.6 + 0.37	1.15	8.03
	Teat Thickness	3.84 ± 0.03	81.7 ± 0.36	1.07	9.18

The purpose of this study was to estimate genetic parameters and in table 2 it can be observed genetic variance, phenotypic variance and heritability. In terms of genetic variance, table 2 shows that the values ranged from 2.01 up to 16.64. Feet and legs group has the lowest values for genetic variance and the biggest value was 38.37 for teat thickness trait. Also, for the phenotypic variance it can be observed that the highest value was for the same trait like the genetic variance. The values for phenotypic variance ranged between 11.94 and 89.51.

In term of heritability we can observe that the values ranged from 0.13 up to 0.54, with the lowest value for fore udder length trait and the highest for rump length. Other authors show similar values for heritability (Nemcova *et al.*, 2011). Higher heritability for conformation traits was observed by other authors (Rotar *et al.*, 2019), but in general terms all the values ranged from 0.12 to 0.60.

It can be observed in Figure 1 that for one animal all 18 breeding values were grouped in four major groups and in the end, all of that was centralized in a global index. If the animal were retained at reproduction only by hierarchy from one group, the evaluation can be biased. Animal 4 had the highest breeding value for group Muscle and if the hierarchy were performed only by that group, in the end the evaluation is not correct. When the global index was calculated, animal 4 was disqualified because for udder traits and type traits it obtained low breeding values.

Table 2. Heritability for conformation traits.

Trait	Genetic Variance	Phenotypic variance	h^2
Type traits			
Height at cross	16.28	38.87	0.42
Rump length	10.29	37.85	0.54
Hip width	9.99	30.06	0.33
Rump angle	4.34	16.85	0.26
Body depth	7.55	24.98	0.30
Muscle			
Muscularity	12.31	31.27	0.39
Feet and legs			
Hock angularity	2.11	14.37	0.15
Hock development	2.31	15.92	0.15
Pasterns	2.76	14.34	0.19
Hoof height	2.01	11.94	0.17
Udder traits			
Fore udder length	3.94	31.03	0.13
Rear udder length	7.68	37.16	0.21
Fore udder attachment	2.48	18.17	0.14
Central ligament	14.24	36.31	0.39
Udder depth	4.57	20.05	0.23
Teat placement	6.85	27.82	0.25
Teat length	16.64	62.51	0.27
Teat thickness	38.37	89.51	0.43

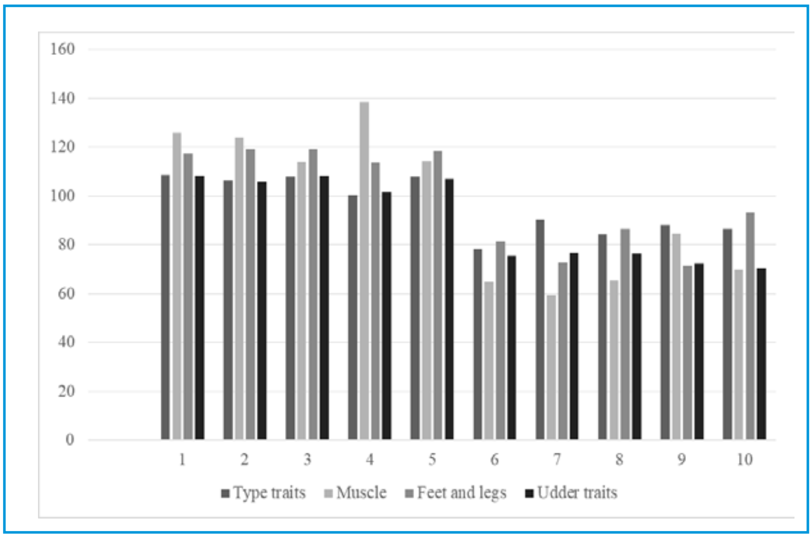

Figure 1. Relative Breeding Values for best/worst five cows

In terms of genetic and environmental correlation, in the presenting paper correlation were from highly negative to highly positive. In table 3 it can be observed that the lowest genetic correlation was obtained between teat length and rump length (-0.13), also negative correlation was obtained in general terms between udder traits and type traits. At the opposite, the highest genetic correlation was obtained between rump length and hip width (0.69). Regarding environmental correlation, the trend was similar with that from genetic correlations.

Table 3. Genetic correlation (above diagonal) and Environmental correlation (below diagonal).

Trai	HC	RL	HW	RA	BD	M	HA	HD	P	HH	FU	UL	UA	CL	UD	TP	TL	TT
HC		0.47	0.49	-0.02	0.47	0.2	0	-0.01	-0.03	0.08	0.13	0	0.03	0.03	-0.12	-0.07	0.07	0.11
RL	0.45		0.69	-0.08	0.51	0.17	-0.02	0.07	0.04	0.1	0.25	0.2	0.12	0.09	0.02	-0.07	-0.13	-0.04
HW	0.48	0.71		-0.01	0.49	0.26	0	0.06	0.02	0.11	0.27	0.22	0.16	0.12	-0.04	-0.09	-0.06	0.03
RA	-0.04	-0.1	-0.03		0	0.02	0.01	0.01	0	-0.04	-0.05	-0.06	0.01	0.04	0.04	0.06	0.07	-0.02
BD	0.47	0.5	0.5	0.03		0.21	0.02	0.08	0.06	0.13	0.23	0.19	0.17	0.06	-0.02	0	-0.08	-0.02
M	0.23	0.15	0.25	0	0.24		0.1	0.18	0.1	0.18	0.4	0.35	0.32	0.36	0.09	0.06	0.23	0.38
HA	-0.01	-0.02	-0.02	0.02	-0.03	0.15		0.23	0.16	0.11	0.05	0.04	0.11	0.12	0.16	0.07	0.06	0.07
HD	0.07	0.12	0.09	0.05	0.13	0.19	0.3		0.26	0.25	0.2	0.3	0.32	0.26	0.29	0.11	0.08	0.09
P	0.01	0.08	0.05	-0.02	0.08	0.12	0.26	0.32		0.31	0.11	0.16	0.14	0.15	0.28	0.14	0.03	0.01
HH	0.15	0.14	0.15	-0.04	0.19	0.2	0.2	0.3	0.37		0.26	0.23	0.18	0.2	0.21	0.11	0.09	0.13
FU	0.22	0.3	0.31	-0.04	0.26	0.41	0.07	0.24	0.15	0.29		0.68	0.5	0.51	0.16	0.13	0.1	0.26
UL	0.07	0.25	0.27	-0.07	0.22	0.31	0.05	0.31	0.16	0.26	0.73		0.59	0.57	0.24	0.16	0.07	0.22
UA	0.11	0.16	0.21	0.03	0.21	0.34	0.11	0.35	0.14	0.23	0.59	0.67		0.5	0.25	0.2	0.11	0.2
CL	0.06	0.09	0.11	-0.02	0.01	0.35	0.11	0.26	0.12	0.21	0.54	0.58	0.54		0.33	0.18	0.18	0.31
UD	-0.07	0.05	0.02	0.02	0.01	0.07	0.14	0.3	0.24	0.19	0.19	0.28	0.3	0.34		0.22	0.06	0.05
TP	-0.05	-0.08	-0.1	0.04	0	0.14	0.1	0.11	0.14	0.12	0.16	0.16	0.23	0.13	0.23		0.14	0.05
TL	0.05	-0.14	-0.08	0.08	-0.08	0.18	0.09	0.05	0.01	0.05	0.05	0.02	0.08	0.18	0.05	0.16		0.61
TT	0.08	-0.09	-0.03	0	-0.07	0.32	0.12	0.08	0	0.11	0.23	0.18	0.2	0.33	0.08	0.07	0.64	

As resulting from the presented study, the values of heritability, and genetic and environmental correlations are within the normal range of variation, specific to the conformation traits, similar for other cattle populations.

Genetics an environmental correlations are stronger inside the grouped traits, especially in udder traits group.

Acknowledgement

This study was funded by Romanian Breeding Association Baltata Romaneasca Simmental-type and Romanian Ministry of Research and Innovation through Program 1 – Developement National Research-Developement, Sub-program 1.2 – Institutional Performance - Projects funding excellence in R & D, Contract no.17 PFE/ 17.10.2018.

List of references

Akinsola, Oludayo Michael, Ishaya Bawa Atang, Adekola Omololu Atanda, Louis Ugwu, Danladi Shuaibu Bunjah, Dorcas John Jirgi, and Muizzat Onozasi Bello, 2018. Genetic Parameter Estimates for Milk and Conformation Traits of Multi-genotype Cattle. Asian Journal of Advances in Agricultural Research: 1-8.

Bertipaglia T.S., Carreno L.O.D., Machado C.H.C, Andrighetto C., Ricardo da Fonseca, 2012. Estimates of genetic parameters for visiual scores and their correlation with production and reproduction and reproductive traits in Brahman cattle. Revista Brasileira de Zootecnia, v. 41 (6):1407-1411.

Liu, Songbai, Huize Tan, Lu Yang, and JianMing Yi, 2014. Genetic parameter estimates for selected type traits and milk production traits of Holstein cattle in southern China. Turkish Journal of Veterinary and Animal Sciences 38, (no. 5): 552-556.

Misztal I., Weigel K., Lawlor T.J., 1995. Approximation of Estimates of (Co)variance Components with Multiple-Trait Restricted Maximum Likelihood by Multiple Diagonalization for More Than One Random Effect. J. Dairy Sci 78:1862-1872.

Nìmcová, E., M. Stípková, and L. Zavadilová, 2011. Genetic parameters for linear type traits in Czech Holstein cattle. Czech J. Anim. Sci 56, (no. 4): 157-162.

Otwinowska-Mindur, Agnieszka, Ewa Ptak, Wojciech Jagusiak, and Andrzej Zarnecki, 2014. Genetic parameters of conformation traits in younG polish holstein-friesian bulls. Annals of Animal Science 14, (no. 4): 831-840.

Rotar M.C., Grosu H., Gras M.A., Pelmus Rodica Stefania, Lazar Cristina, Popa F., 2019. Using Canonical transformation to estimate breeding values for conformation traits for Montbeliarde breed. Animal Science and Biotechnologies 52(2).

Satola, Alicja, Ewa Ptak, Wojciech Jagusiak, and Agnieszka Otwinowska-Mindur, 2017. Genetic relationship of conformation traits with lactose percentage and urea concentration in milk of Polish Holstein-Friesian cows. Animal Science Papers & Reports 35, (no. 3).

Zink, V., L. Zavadilová, J. Lassen, M. Stípková, M. Vacek, L. Stolc, J. Zídková *et al.*, 2014. Analyses of genetic relationships between linear type traits, fat-to-protein ratio, milk production traits, and somatic cell count in frst-parity Czech Holstein cows. Czech J. Anim. Sci 59, (no. 12): 539-547.