



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



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## Introduction

The purpose of the conformation evaluation is to discover the ideal animal. The managerial target of a herdsman is to be efficient from financial point of view, and from that perspective, the conformation evaluation not imply high costs. 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. 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. 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.

## Results and Conclusion

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.

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	

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.

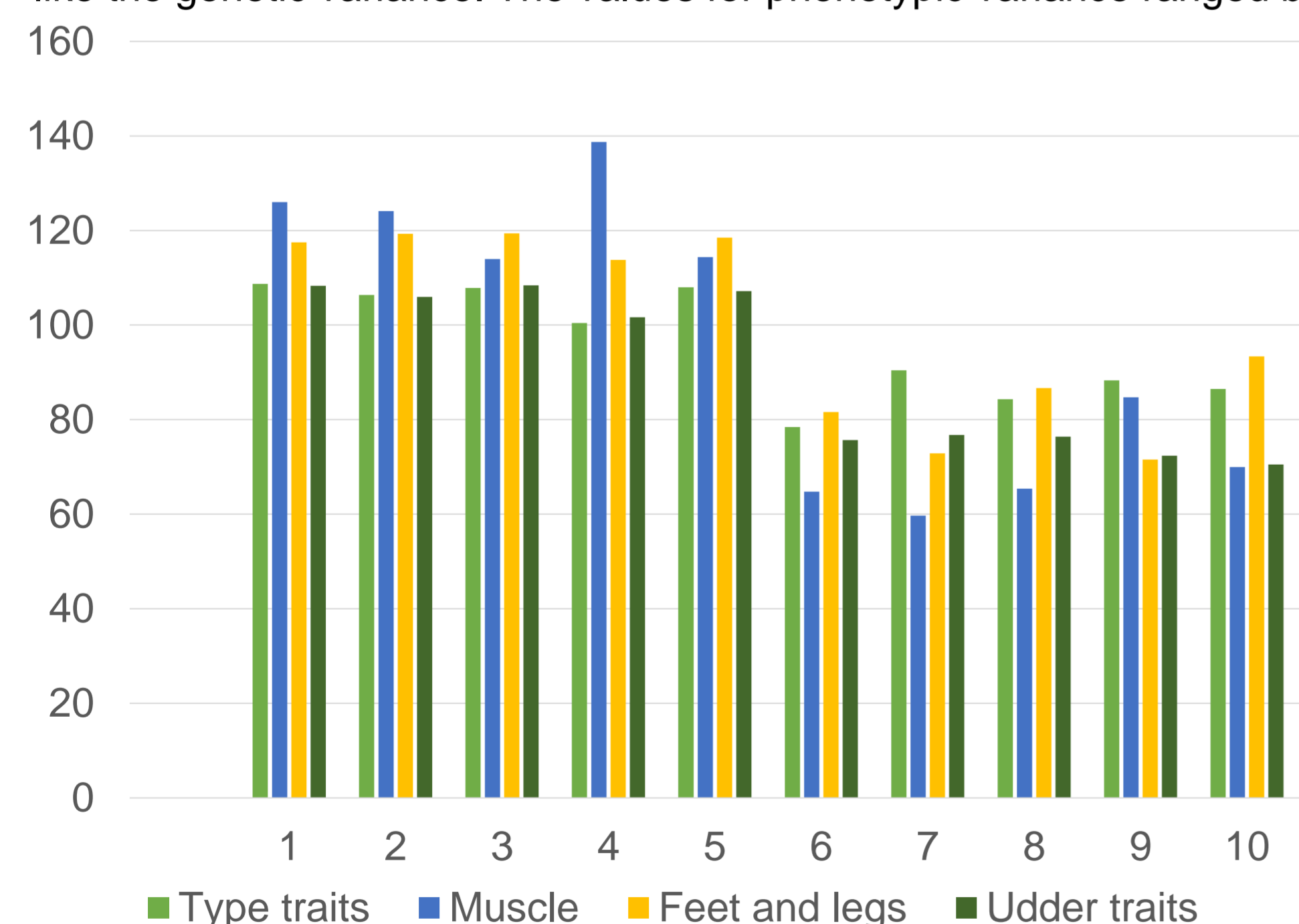


Figure 1. Relative Breeding Values for best/worst five cows

## 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. For each trait the score was between 1 and 9.

Regarding the estimation of 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:

$$y_{ijklm} = B_i + DIM_j + AGE_k + YM_l + HYS_m + a_{ijklm} + e_{ijklm}$$

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.



Table 2. Heritability for conformation traits

Trait	Genetic Variance	Phenotypic variance	h <sup>2</sup>
<b>Type traits</b>			
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
<b>Muscle</b>			
Muscularity	12.31	31.27	0.39
<b>Feet and legs</b>			
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
<b>Udder traits</b>			
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

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

Trait	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	

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.

**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 fact that shows that the genetic progress can be obtained easily if we select for reproduction only the best individuals.**



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