Genetic Evaluation In Half-Bred Stallions

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Introduction

Genetic evaluation of livestock species is usually based on objectively measured production traits. However, in case of horses, the performance traits recorded are quite different. For instance, in Poland the routine procedure for half bred stallions includes a standardized test at Training Centers. Thus several categorical, subjectively scored traits are registered. More details on the methodology were described by Lewczuk et al. (2004). Similar procedures are applied in several European countries (Koenen and Aldridge, 2002; Hellsten et al., 2008).
The main objectives of the present study were to predict the breeding values of half-bred stallions undergoing the stationary performance test as well as to estimate the heritabilities and genetic correlations among conformation and performance traits during these trials. The inbreeding level of the population studied was examined. Genetic and phenotypic and environmental trends were derived as well.

Material and methods

The data were extracted from the database of the Polish Horse Breeding Association. The performance of 494 half-bred stallions (whereas pedigree data comprised 8512 individuals) during 100-days test in 2002-2008 were analyzed. Three basic biometrical traits were also recorded. Moreover, nine traits were subjectively scored during 100-days test: seven of them were evaluated by a breeding commission, all nine by head of training centre and three traits by test rider. Moreover, four combined traits were expressed as indexes. More details on the recording system and brief statistical description of these traits are given in Table 1.

Statistical analyses. The following linear model was employed for the statistical analysis:
$\mathbf{y} = \mathbf{X}_1\boldsymbol{\beta}_1 + \mathbf{X}_2\boldsymbol{\beta}_2 + \mathbf{X}_3\boldsymbol{\beta}_3 + \mathbf{X}_4\boldsymbol{\beta}_4 + \mathbf{Za} + \mathbf{e}$, where $\mathbf{y}$ is the observation vector; $\boldsymbol{\beta}_1$, $\boldsymbol{\beta}_2$, $\boldsymbol{\beta}_3$ and $\boldsymbol{\beta}_4$ are the vectors of fixed effects of age of stallion (3 levels), breed group (6 levels), year of performance test (7 levels) and place of performance test (2 levels), respectively; $\mathbf{a}$ is the vector of additive genetic effects; $\mathbf{e}$ is the vector of residuals; $\mathbf{X}_1$, $\mathbf{X}_2$, $\mathbf{X}_3$, $\mathbf{X}_4$ and $\mathbf{Z}$ are the respective design matrices. The computations were performed using ASREML program (Gilmour et al., 2008). Genetic trends were derived from averaging annual predicted genetic effects, whereas environmental trends were estimated from solutions of year effects.
Inbreeding coefficients were obtained using modified algorithm by Colleau (2002) based on additive relationship matrix in the CFC 1.0 program by Sargolzaeia et al. (2006).

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Table 1. Mean and standard deviation (SD) for the studied traits

Trait		Mean	SD	Trait		mean	SD
HW	height at withers (cm)	166.56	3.10	JRD	jumping under rider	6.85	0.95
ChC	chest circumference (cm)	191.76	4.56	WD	walk	7.03	0.93
CaC	cannon circumference (cm)	21.69	0.76	TD	trot	6.98	0.91
TY	type	13.47	0.62	CD	canter	7.24	0.82
HN	head-neck	4.01	0.36	FJC	free jumping	7.06	0.85
BO	body	13.15	0.66	JRC	jumping under rider	6.85	0.85
FL	forelegs	6.68	0.56	WC	walk	7.14	0.66
HL	hind legs	6.83	0.57	TC	trot	6.98	0.79
HO	hoofs	6.99	0.51	CC	canter	7.15	0.69
LW	locomotion walk	7.18	0.65	SC	strength canter	6.79	0.99
LT	locomotion trot	7.46	0.63	GM	general mark	7.07	0.71
GI	general impression	13.24	0.54	RA	rideability	6.06	1.77
CS	conformation score	79.07	1.16	DA	dressage-ability	5.65	1.93
TA	training-ability	7.16	1.00	JA	jumping-ability	5.89	1.89
CH	character	8.55	1.08	TI	total index	99.98	19.67
HF	health and feed intake	9.44	0.79	DI	dressage index	100.00	19.66
TE	temperament	7.78	0.76	JI	jumping index	100.02	19.60
FJD	free jumping	7.17	0.91				

Score range: 0.0-5.0 for HN; 0.0-15.0 for TY, BO, GI; 0.0-100 for CS; 0.0-10.0 for other traits, except of TI, DI and JI;
Scores: TY, HN, BO, FL, HL, HO, LW, LT, GI, FJC, JRC, WC, TC, CC, SC, GM (by breeding commission); TA, CH, HF, TE, FJD, JRD, WD, TD,CD (by head of training centre); RA, DA, JA (by test rider)

Results and discussion

The heritability estimates were shown on Figures 1-3. The estimates for basic biometrical measurements (HW, ChC, CaC) were moderate. They ranged from 0.3 to 0.5. In general, these results are in agreement with ones reported by Gomez et al. (2009) for Spanish Purebred Horses and by Torzynski et al. (2005) for Polish half-bred horses.

For conformation traits the heritability estimates varied from 0.23 (TY) to 0.44 (LT). However, in case of three of traits (HN, FL, HL) no REML estimates were found. It is strongly affected by a negligible variability of these characters and non-normality of their distributions. The heritabilities for the next group of traits scored by the head of training centre and breeding commision were quite high, except for CH. It should be stressed that approximated standard deviation of the estimates were relatively large. From theoretical point of view high heritability estimates indicate considerable opportunity for their genetic improvement. On the other hand, more sophisticated statistical methodology could have been employed to analyze the data. For instance, Oki et al. (2007) found that heritability of horse temperament using Bayesian approaches under a threshold animal model equaled 0.23 whereas repeatability for this traits was 0.98. So, further comparative studies including different statistical models are necessary to estimate genetic parameters for the subjectively scored traits. Moreover, some revision of the current recording system can be also considered. In general, the phenotypic, genetic and environmental trends for studied traits were negligibly positive. It also suggests a some modification on performance and genetic evaluation methodology.

Nonzero inbreeding coefficients were estimated for 88 recorded stallions as well as for 458 unrecorded ancestors. Average inbreeding level for the stallions recorded was 0.29%, whereas for all inbred individuals – 1.69%. From methodological perspective it is too small sample to estimate inbreeding effects on the measured traits.

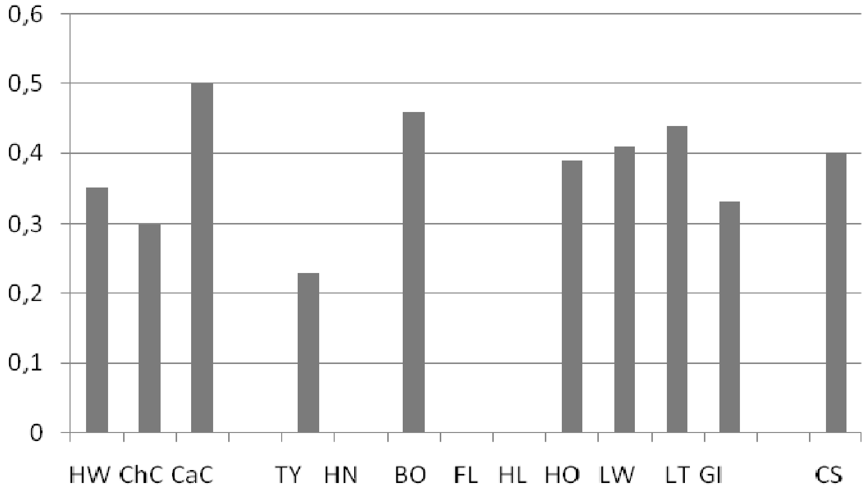

Figure 1. Heritability estimates for the conformation traits.

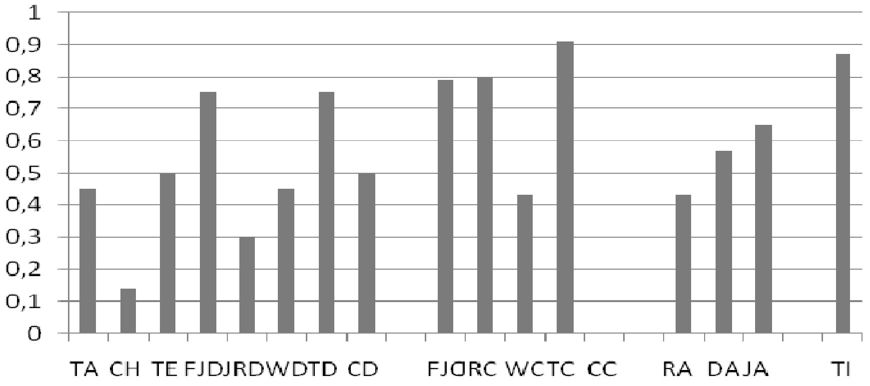

Figure 2. Heritability estimates for the performance traits.

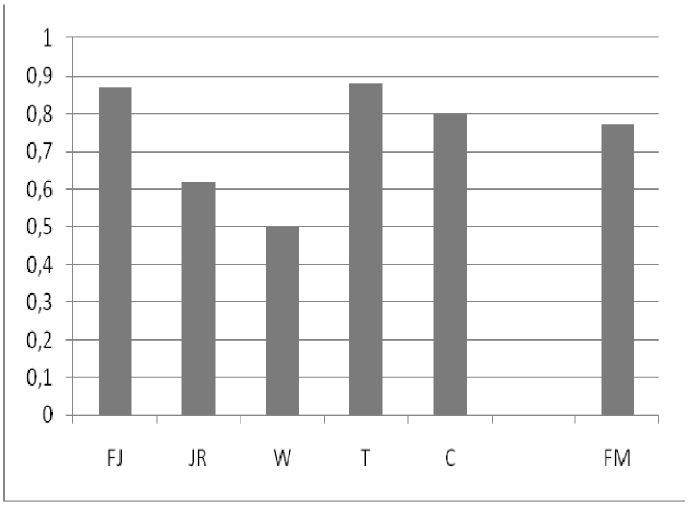

Figure 3. Heritability estimates for the traits summarized traits

Conclusion

The heritability estimates for majority of the analyzed traits were high. However, the results from linear model require verification by other statistical tools.

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