

GENETIC PARAMETERS OF THE TYPE TRAITS OF HOLSTEIN-FRIESIAN PRIMIPAROUS DAIRY COWS

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The aim of this study was to determine the level and variability of type traits in primiparous Holstein-Friesian cows, as well as to assess the additive genetic variance of type traits and heritability coefficients. The research was conducted on a data set of linearly evaluated primiparous Holstein-Friesian cows, which is ceded by the Main dairy cattle breed organization in the Province of Vojvodina, which is a unit of the Department of Animal Science, at the Faculty of Agriculture in Novi Sad. Data of 24226 primiparous Holstein-Friesian cows, refer to the period 2012-2015, were analysed. The phenotypic variability of the type traits, as well as effects of systemic factors affecting these traits, were analyzed using standard statistical methods in the Statistica software 13.2, and the general linear model (GLM). A Statistically highly significant effect for most of the type traits had the farm size, interaction of the year and the season of evaluation, age at linear evaluation, lactation stage and a genetic group formed by the year and country of bull/sires birth. The total type traits score (final score), which represents an evaluation of the overall primiparous cow exterior, is calculated for the 24226 linearly evaluated primiparous cows. Estimation of variance components and heritability coefficient calculation is done in the software package WOMBAT. Heritability coefficient values for the primiparous cow's type traits in the Province of Vojvodina were low to middle, ranged

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from 0.08 for the rear legs - side view up to 0.38 for the stature. Due to the fact that the value of the heritability coefficient depends on the variability of the traits and previous selection, lower heritability may be a consequence of the low genetic variability, or, a higher degree of variability which is a consequence of the effect of the systematic factors. Heritability coefficients indicate a genetic variability of the type traits, and its evaluation is important for the breeding value estimation for the type traits.

Key words: Holstein Friesian primiparous cows, type traits, variance components, additive genetic variance, heritability.

INTRODUCTION

Current trends in milk production require constant work to improve the genetic potential of cattle. In addition to increasing the milk yield, milk fat, and protein, modern dairy cows are also expected to have good reproductive traits, a long productive life using high-energy meals for nutrition, and to endure other efforts related to modern management requirements. In order to achieve these goals, in modern breeding programs, the emphasis is on the functional compliance and productive life efficiency of the cow and more attention is paid to the constitution, body development and characteristics of the dairy cow type (JANKOVIĆ, 2017). A significant number of scientific studies found that the reasons for productivity, but also for the culling of dairy cows, are very closely related to the genotype of the animal (MARTINEZ *et al.*, 2004; PÁCHOVÁ *et al.*, 2005; CHIRINOS *et al.*, 2007; MÉSZÁROS *et al.*, 2008), as well as with the type traits of dairy cows (BOOTH *et al.*, 2004; ESPEJO *et al.*, 2006; SANDERS *et al.*, 2009; FORSBÄCK *et al.*, 2010; STOJIC *et al.*, 2012; SOLANO *et al.*, 2015). It has been found that cows with a lower level of milk production have a higher risk of culling from herd than cows with average milk production, and that diseases of the legs and udder are among the most common causes of unplanned culling of cows from the herd, but also that cullings can be prevented by improvement of those type traits. Deficiencies in type traits have been found to lead to lower production and poorer animal health status and, therefore, premature culling of cows from the herd.

As an objective and unbiased method for determining the physical ability for milk production and evaluation of the body development of cows, linear assessment of type traits is used. Linear assessment is the basis of modern classification systems and the basis of all cow description systems, but also an integral part of the dairy cow evaluation systems in many countries (ICAR, 2016). It is based on the measurement of individual type traits without giving opinions about them and describes the degree of expression of the trait rather than its desirability. Thanks to clearly defined scores, two different cows with the same scores for type traits are similar, regardless of the farm or location they come from. Scores are on a linear scale from 1 to 9. The score depends on the expression of the trait, which is, in addition to genetic factors, influenced by various systematic factors. The estimates of systematic factors are important, because they have a substantial share of total variation in milk production (JANKOVIĆ *et al.*, 2016). Accordingly, the average values of the linear scores in the studied populations vary over a wide range.

The primary reason for collecting information about type traits is to assist the breeders in the objective selection of a profitable, functional and long-lived cow. Type traits are important for dairy farmers because, in addition to the quantity of produced milk, milk fat and protein

produced, they are a common criterion for the selection of dairy cows. Linear assessment is important because it makes possible to examine the phenotypic and genotypic variability of type traits, the calculation of heritability coefficient and the association of type traits with productive traits, as well as other studies related to the body development, reproduction, productive life and longevity of dairy cows. At the same time, thanks to linear assessment, type trait evaluation is a relatively inexpensive selection criterion because type traits can be reliably evaluated once during the life of a cow.

Currently, a number of methodologies are used in genetic evaluation of type traits of cows, but the most commonly used methods for estimation of genetic parameters are ML (Maximum Likelihood) and its derivatives (REML, AI-REML, DF-REML, AS-REML), and BAYESIAN using GS (Gibbs sampling). It should be borne in mind that the value of the heritability coefficient refers to a specific type trait, measured on animals in a given population and at a particular time. Type traits have low to moderate heritability (PANTELIĆ *et al.*, 2010; SAMORE *et al.*, 2010; PTAK *et al.*, 2011; DADPASAND *et al.*, 2012; TAPKI and GUZEY, 2013; ZINK *et al.*, 2014; BOHLOULI *et al.*, 2015; BILAL *et al.*, 2016; SUSANTO *et al.*, 2018) and may be included in selection indices that are formed for various purposes in dairy cow selection. Heritability is important for an answer on question which traits could be included in estimation of an animal breeding value (SPASIĆ *et al.*, 2012).

The aim of this study is to determine the manifestation and variability of type traits of the primiparous Holstein-Friesian dairy cows, as well as to evaluate the additive genetic component of type traits, which will contribute to a fuller understanding of the inheritance of these traits.

MATERIALS AND METHODS

The research included 24226 primiparous Holstein-Friesian dairy cows that have calved for the first time in the territory of AP Vojvodina, Republic of Serbia, from 2011 to 2015. The cows originate from 585 bull-sires: The average number of daughters evaluated per bull-sires was 41. In the period from 2012 to 2015, primiparous dairy cows were evaluated by 22 evaluators who completed professional training according to the Guidelines for linear assessment of the type and body development of Holstein-Friesian cows (JANKOVIĆ, 2012). The average number of cows per farm was 10 and cows calved for the first time at an average age of 27 months. The average age of primiparous dairy cows at assessment was 30 months, while the realized average number of days in lactation on the day of assessment was 95 days for primiparous cows for which the data were analyzed. The type traits were analysed on a data set provided by the Main Animal Breeding Organization in AP Vojvodina, which is part of the Department of Animal Science, Faculty of Agriculture, University of Novi Sad.

Calculation of phenotypic parameters

Phenotypic parameters, that is, average values of linear scores of type traits and their variability, were calculated using descriptive statistics in Statistica 13.2 software (STATSOFT, 2017). For this purpose, standard statistical parameters were calculated: mean (\bar{x}), standard error of the mean ($S_{\bar{x}}$), minimum (Min), maximum (Max), standard deviation (SD), and coefficient of variance (CV).

Calculation of genetic parameters

To form a model for the estimation of the additive component of variance and heritability, the impact of each systematic factor (farm size, estimator, year and calving season, age at first calving, age and season of assessment, age on assessment, lactation phase, genetic group) was first individually examined by one-way ANOVA, as well as their interactions of variance on type traits in Statistica 13.2 software package (STATSOFT, 2017), while variance components and heritability values, calculated by the restricted maximum likelihood (REML), using the algorithm of average informations (AI), in the WOMBAT software package (MEYER, 2007). The impact of the animal was included as a random effect in the variance component evaluation model, and the model for the estimation of the additive component of variance and heritability had the following structure:

$$Y_{ijklm} = \mu + F_i + O_j + GSO_k + L_l + GG_m + b_2(x_2 - x_2) + e_{ijklm}$$

Where:

Y – linear scores for type traits;

μ – the average value of linear scores;

F_i – fixed farm size impact;

O_j – the fixed influence of the assessee;

GSO_k – fixed impact of the interaction of year and season of evaluation;

L_l – fixed influence of lactation phase;

GG_m – genetic group (year x country of birth of the father of primiparous cow);

$b_2(x_2 - x_2)$ – linear regression effect of age on evaluation;

e – other uncontrollable factors (random error).

Additive genetic variance σ_a^2 and variance of the rest σ_e^2 were evaluated by solving the following equations in matrix form:

$$y(\sigma_a^2) = A * P y = (1/\sigma_a^2) Z \hat{a}$$

$$y(\sigma_e^2) = P y = (1/\sigma_e^2) \hat{e}$$

Where:

P – designed matrix $V^{-1} - V^{-1}X(X'V^{-1}X)^{-1}X'V^{-1}$, a $(X'V^{-1}X)^{-1}$ represents the inversion of $(X'V^{-1}X)$

y – number of measurements

A – matrix of relationship

RESULTS AND DISCUSSION

Phenotypic expression and variability of type traits

The calculation of average values for type traits in a particular population is very important and gives an insight into the state of the population when it comes to the expression of type traits, but also shows the deviations of the scores of individual traits relative to the recommended ideal scores for given traits of a particular breed. In order to obtain insight into the population status of HF breed cows for type traits in AP Vojvodina, a descriptive statistical analysis was conducted for the evaluated type traits (Table 1).

Table 1. Descriptive statistical analysis of type traits of HF breed in AP Vojvodina; the average and ideal scores for the primiparous Holstein-Friesian cows defined by the World Holstein Friesian Federation (WHFF), 2008.

Type traits	N	\bar{x}	Average scores HF	Ideal scores HF	S_x	SD	CV (%)	Min	Max
1 - ST	24226	5.98	5	8	0.010	1.61	26.84	1	9
1 - TL	24226	6.22	5	7	0.007	1.07	17.27	1	9
1 - CW	24226	5.95	5	7	0.008	1.22	20.47	1	9
1 - BD	24226	6.22	5	7	0.008	1.22	19.60	1	9
1 - RP	24226	5.90	5	5	0.008	1.25	21.18	1	9
1 - RW	24226	6.21	5	8	0.008	1.20	19.28	1	9
2 - AN	24226	6.55	5	9	0.009	1.37	20.91	1	9
3 - RLSrv	24226	6.32	5	8	0.009	1.37	21.64	1	9
3 - RLSsv	24226	5.15	5	5	0.007	1.06	20.50	1	9
3 - FA	24226	4.81	5	7	0.007	1.15	24.01	1	9
4 - FUA	24226	5.79	5	9	0.009	1.41	24.26	1	9
4 - FTP	24226	4.99	5	6	0.007	1.14	22.78	1	9
4 - FTL	24226	5.16	5	5	0.007	1.10	21.23	1	9
4 - UD	24226	5.93	5	5	0.008	1.19	20.07	1	9
4 - RUH	24226	6.29	5	9	0.009	1.33	21.14	1	9
4 - SL	24226	5.97	5	9	0.009	1.41	23.69	1	9
4 - RTP	24226	5.75	5	5	0.009	1.33	23.10	1	9
4 - RTL	24226	4.46	5	5	0.007	1.10	24.72	1	9

N- total number of primiparous cows used in research; \bar{x} - average scores for type traits of primiparous cows; S_x - standard error; SD- standard deviation; CV(%)-coefficient of variation (%); Min- minimum score; Max- maximum score .1- body traits; 2- dairy character; 3- leg and hoof features; 4- udder properties. ST- stature; TL- top line; CW- chest width; BD- body depth; RP- rump position; RW- rump width; AN-angularity; RLSrv- rear legs set – rear view; RLSsv- rear legs set – side view; FA- foot angle; FUA- fore udder attachment; FTP- front teats placement; FTL- front teats length; UD- udder depth; RUH-rear udder height; SL- suspensory ligament; RTP- rear teats position; RTL- rear teats length.

The mean values of the type trait scores, calculated for the primiparous Holstein-Friesian cow's population, ranged from 4.46 for the rear teat length to 6.55 for the angularity.

Variance components and heritability of type traits

The division of variance into components contributes to an objective view of how much of the total variability in type traits is caused by hereditary factors, and the estimation of variance components allows the estimation of genetic parameters, such as heritability. The determined values of the variance components, heritability coefficients, and their errors are shown in Table 2.

Table 2. Variance components and values of heritability coefficients and heritability errors of type traits

Type traits	Animal				
	V_a	V_e	V_p	h^2	SE
ST	0.749	1.232	1.980	0.378	0.028
TL	0.140	0.880	1.020	0.137	0.021
CW	0.184	0.934	1.118	0.165	0.022
BD	0.941	0.188	1.129	0.166	0.022
RP	0.224	1.087	1.311	0.171	0.022
RW	0.223	0.986	1.209	0.185	0.023
AN	0.376	1.189	1.565	0.240	0.025
RLSrv	0.248	1.274	1.522	0.163	0.021
RLSsv	0.080	0.936	1.016	0.078	0.016
FA	0.178	0.967	1.144	0.155	0.023
FUA	0.313	1.346	1.659	0.189	0.024
FTP	0.165	1.034	1.199	0.138	0.020
FTL	0.180	0.897	1.077	0.167	0.023
UD	0.196	1.184	1.379	0.142	0.020
RUH	0.166	1.314	1.480	0.112	0.019
SL	1.436	0.202	1.638	0.123	0.020
RTP	0.294	1.246	1.539	0.191	0.022
RTL	0.723	0.235	0.958	0.245	0.025

V_a – additive variance; V_e – residual variance; V_p – phenotypic variance; h^2 – heritability; SE – standard error. ST- stature; TL- top line; CW- chest width; BD- body depth; RP- rump position; RW- rump width; AN-angularity; RLSrv- rear legs set – rear view; RLSsv- rear legs set – side view; FA- foot angle; FUA- fore udder attachment; FTP- front teats placement; FTL- front teats length; UD- udder depth; RUH-rear udder height; SL- suspensory ligament; RTP- rear teats position; RTL- rear teats length.

The stature, relative to other type traits, shows mainly higher genetic variability in studies performed by other researchers. The obtained value of the heritability coefficient of 0.38 is approximate to the value of 0.37 obtained for stature by TAPKI and GUZEY (2013) and 0.39 obtained by ZINK *et al.* (2014). Lower value of heritability coefficient for stature (0.24) was obtained by TOGHIANI (2011), while higher value (0.45) was obtained by VAN DER LAAK *et al.* (2016).

The top line is not a standard type trait and is included as an optional trait in the linear assessment program of primiparous Holstein-Friesian cows in AP Vojvodina. The estimated value of the heritability coefficient for the top line of the primiparous cows in AP Vojvodina is low (0.14), and is close to the value 0.17 obtained by CAMPOS *et al.* (2015) in the Holstein population in Brazil, while a lower value of 0.09 was obtained by DADPASAND *et al.* (2012) for the Holstein population in Iran.

An identical value of the heritability coefficient of 0.17 for the chest width trait primiparous cows in AP Vojvodina was obtained by ZINK *et al.* (2014). A lower value (0.12) was

obtained by CASSANDRO *et al.* (2015). A higher coefficient value of 0.22 was obtained by BOHLOULI *et al.* (2015).

For the trait of body depth in primiparous cows in AP Vojvodina, the value of the heritability coefficient is 0.17. The identical value was obtained by CASSANDRO *et al.* (2015). A lower value of 0.11 was obtained by DADPASAND *et al.* (2012), while the highest values of 0.29 were obtained by VAN DER LAAK *et al.* (2016).

Within the functional trait of the frame i.e. the body is also evaluated for the rump traits (position and width of the rump). The values of heritability coefficients for these traits in the population of primiparous Holstein-Friesian cows in AP Vojvodina are 0.17 for rump position and 0.19 for rump width. A similar value of the heritability coefficient for the rump position of 0.19 was obtained by DADPASAND *et al.* (2012), while CASSANDRO *et al.* (2015) obtained a lower value (0.12). A higher coefficient value of 0.24 was obtained by BOHLOULI *et al.* (2015).

For the rump width trait, the heritability coefficient value of 0.19 is the closest to the value of 0.17 obtained by BOHLOULI *et al.* (2015). A lower value of 0.10 was obtained by CASSANDRO *et al.* (2015), while a higher value of heritability coefficient for rump width was 0.27 obtained in the studies of CAMPOS *et al.* (2015).

Within the system of linear assessment, angularity is a trait that is evaluated as an indicator of the dairy character of cows. The obtained value of the heritability coefficient for the angularity trait in the population of primiparous Holstein-Friesian cows in AP Vojvodina is 0.24, and it is close to the value 0.23 obtained by TOGHIANI (2011). A lower heritability coefficient value of 0.07 for angularity was obtained by RABBANI-KHOURASGANI *et al.* (2014). A higher value of the coefficient, compared to the heritability coefficient for the angularity characteristic of the primiparous cows in AP Vojvodina, was obtained by ZAVADILOVA *et al.* (2014) with a value of 0.30.

The values of heritability coefficients obtained in this study for the traits of the legs and hooves, for the population of primiparous Holstein-Friesian cows in AP Vojvodina, are low and are 0.16 for traits of the rear legs set – rear view and the foot angle, and 0.08 for the rear legs set – side view.

For the rear legs set – rear view, the heritability coefficient of 0.16 approximates the value of the coefficient of 0.14 obtained by VAN DER LAAK *et al.* (2016). Lower heritability coefficients of 0.03 were obtained by CASSANDRO *et al.* (2015). A higher heritability coefficient of 0.22 for the rear legs set – rear view was obtained by TAPKI and GUZEY (2013).

For the rear legs set – side view, the coefficient of heritability is identical to the coefficient value of 0.08 obtained by TOGHIANI (2011). A lower coefficient of 0.02 was obtained by CASSANDRO *et al.* (2015), while higher values of 0.15 were obtained by BOHLOULI *et al.* (2015).

The value of the heritability coefficient for the foot angle of 0.16 is identical to the value obtained by TAPKI and GUZEY (2013), while the lower value of coefficient was obtained by 0.06 JAGUSIAK *et al.* (2015). A higher heritability coefficient of 0.21 was obtained by VAN DER LAAK *et al.* (2016).

The obtained heritability coefficients in the conducted research primiparous Holstein-Friesian cows in AP Vojvodina for udder traits were low to medium and ranged from 0.11 for rear udder height to 0.25 for rear teats length. For the fore udder attachment, the heritability coefficient value of 0.19 is identical to the value obtained by CAMPOS *et al.* (2012). Lower

heritability coefficients of 0.10 were obtained by 0.16 LIU *et al.* (2014). Higher heritability coefficients were obtained in the value of 0.21 ZAVADILOVA and ŠTIPKOVA (2012).

For the trait of front teats placement, the heritability coefficient value of 0.14 obtained in this study is close to the value of 0.13 obtained by DADPASAND *et al.* (2012). A lower coefficient of 0.12 was obtained by CASSANDRO *et al.* (2015), while in other research heritability coefficients are higher than 0.22 in BOHLOULI *et al.* (2015) and 0.23 MIKHCHI *et al.* (2013).

The front teats length is not a standard trait of the type and is included as an optional trait in the linear assessment program of primiparous Holstein-Friesian cows in AP Vojvodina. The value of the heritability coefficient for the front teats length in primiparous Holstein-Friesian cows in AP Vojvodina is 0.17 and is identical to the value obtained by DADPASAND *et al.* (2012) for the Holstein population in Iran.

For the udder depth trait, the heritability coefficient value of 0.14 obtained in this study is closest to the value of 0.11 obtained by LIU *et al.* (2014). A lower value of 0.09 was obtained by DURU *et al.* (2012), while for other researchers the coefficients obtained are higher and range from 0.23 at BOHLOULI *et al.* (2015) to 0.41 in TAPKI and GUZEY (2013).

The heritability coefficient value of 0.11 for the trait of rear udder height in primiparous Holstein-Friesian cows in AP Vojvodina obtained in the conducted research is close to the value of 0.10 obtained by TOGHIANI (2011). A lower coefficient of 0.08 was obtained by RABBANI-KHOURASGANI *et al.* (2014), while higher coefficients of 0.20 were obtained by ZAVADILOVA and ŠTIPKOVA (2012).

For the central ligament trait, the value of the heritability coefficient 0.12 obtained in the primiparous Holstein-Friesian cows in AP Vojvodina was similar to the value of 0.11 obtained by TOGHIANI (2011). A lower coefficient of 0.03 was obtained by MIKHCHI *et al.* (2013), while the coefficients obtained by other researchers are higher: 0.18 by VAN DER LAAK *et al.* (2016); 0.19 TAPKI and GUZEY (2013); 0.26 by DURU *et al.* (2012).

The heritability coefficient value of 0.19 for the rear teats position trait obtained in the present study in the primiparous Holstein-Friesian cows in AP Vojvodina is close to the value of 0.18 obtained by DADPASAND *et al.* (2012). Lower coefficients of 0.10 were obtained by DURU *et al.* (2012), while higher coefficients were obtained by VAN DER LAAK *et al.* (2016) worth 0.24. For the trait of rear teats length, the heritability coefficient value of 0.25 obtained in this study in the primiparous Holstein-Friesian cows in AP Vojvodina is approximate to the value of 0.26 obtained by ZINK *et al.* (2014). The lower coefficients were obtained by CASSANDRO *et al.* (2015) 0.12. Higher heritability coefficients for the trait of rear teats length were obtained by ZAVADILOVA *et al.* (2014) 0.28.

All of the aforementioned researchers used the REML method in different software packages (e.g. MTDFREML, WOMBAT, VCE 6.0, REMLF90, ASREML) to evaluate variance components. The reported results of the values of heritability coefficients for type traits are of different values, varying over a wide interval. Their variability may also be due to the application of different models for the estimation of genetic parameters, as well as the volume of data included in the analysis.

According to DJEDOVIĆ *et al.* (2013) it is important, when investigating the heritability, to use a great number of animals produced by a greater number of bull-sires, by which it may be possible, in overall variability, to decrease the share of variability caused by external factors, and

to increase the variability caused by genetic effect, what altogether leads to a more precise evaluation of heritability.

The values of heritability coefficients in the population of the primiparous Holstein-Friesian cows in AP Vojvodina are low for almost all type traits and are in the range 0.10 to 0.20, except for the trait of rear legs - side view on the side, for which obtained value was 0.08. Medium-high values of heritability coefficients were obtained for traits rear teats length, angularity, and stature, and ranged from 0.20 to 0.40 (Table 2). Since the height of heritability coefficients depends on the variability of traits, low and medium heritability coefficients may be due to lower genetic variability, that is, more variability influenced by systematic factors.

CONCLUSIONS

The values of heritability coefficients in the population of primiparous Holstein-Friesian cows in AP Vojvodina are low for almost all type traits, except for traits of stature, angularity, and rear teats length, for which the value is medium. Since the values of heritability coefficients depend on the variability of traits and previous selection, low heritability may be a consequence of lower or higher genetic variability, caused by the influence of systemic factors. Heritability coefficients indicate the genetic variability of type traits, and their assessment is important for the assessment of breeding values of type traits, which will be the subject of further scientific work.

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GENETSKI PARAMETRI OSOBINA TIPRA PRVOTELKI HOLŠTAJN-FRIZIJSKE RASE

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Izvod

Cilj ovog istraživanja bio je da se utvrdi nivo i varijabilnost osobina tipa kod prvotelki holštajn-frizijske rase, kao i procena aditivne genetske varijanse osobina tipa i koeficijenta heritabilnosti. Istraživanje je sprovedeno na setu podataka linearno ocenjenih prvotelki holštajn-frizijske rase, koji je ustupljen od strane Glavne odgajivačke organizacije za govedarstvo u Vojvodini, sa Departmana za stočarstvo Poljoprivrednog fakulteta u Novom Sadu. Analizirani su podaci za 24226 prvotelki, ocenjenih u periodu 2012–2015. Fenotipska varijabilnost osobina tipa, kao i efekti sistemskih faktora koji utiču na ove osobine, analizirani su korišćenjem standardnih statističkih metoda u softveru Statistica 13.2 i opštim linearnim modelom (GLM). Statistički vrlo značajan efekat za većinu osobina tipa imala je veličina farme, interakcija godine i sezone ocenjivanja, starost pri linearnom ocenjivanju, faza laktacije i genetska grupa koja je formirana prema godini i zemlji rođenja bika/oca. Procena komponenata varijanse i izračunavanje koeficijenta heritabilnosti vršila se u softverskom paketu WOMBAT. Vrednosti koeficijenta heritabilnosti za osobine tipa prvotelki u Vojvodini bile su niske do srednje, kretale su se od 0.08 za položaj zadnjih nogu sa strane do 0.38 za visinu krsta. Zbog činjenice da vrednost koeficijenta heritabilnosti zavisi od varijabilnosti osobina i prethodne selekcije, niža naslednost može biti posledica niske genetske varijabilnosti, ili većeg stepena varijabilnosti koji je posledica efekta sistemskih faktora

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