Population genetic parameters and phenotypic trends based on some performance tests data of native Gidran broodmares

Populációgenetikai paraméterek, fenotípusos és genetikai trendek gidrán tenyészkancák teljesítményvizsgálati adatai alapján

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ABSTRACT

Body measurement and some conformation data recorded in the national breeding mare performance test of the Hungarian Association of Gidran Horse Breeders were processed. The initial database contained the data of the entire Hungarian active (living) breeding mare stock (N = 293), which were born between 1994-2016 and were offspring of 44 breeding stallions. During the study, eight traits - height at withers measured with stick and tape (HWS, HWT), chest girth (CHG), cannon circumference (left fore/front) (CAC), pedigree score (PES), conformation score (COS), movement score (MOS), total score (TOS) - were evaluated. One- and multi-trait analysis of variance (GLM) and weighted linear regression analysis were used to process the data. The corrected mean values (± SE) of the examined traits were as follows: HWS 161.6 ± 0.4 cm, HWT 169.6 ± 0.5 cm, CHG 188.4 ± 0.7 cm, CAC 19.9 ± 0.1 cm, PES 29.1 ± 0.3 points, COS 72.8 ± 0.5 points, MOS 40.5 ± 0.4 points, TOS 142.4 ± 0.7 points. The heritability of HWS, HWT, COS and TOS was moderate and high (0.37-0.47), CHG and CAC proved to be moderate (0.29-0.31), while low h² values were estimated for MOS (0.20). In the case of body measurements, moderate, decreasing trends (b = -0.25, -0.33, -0.35 and -0.08 cm/year, respectively; *P* < 0.01), for the other traits while stagnant (NS) phenotypic trends were observed. It can be concluded that the average body measurements as well as the results of the other examined traits for the Gidran breeding mares did not change essentially over time.

Keywords: Gidran, brood mare, performance test, heritability, breeding value, trends

ÖSSZEFOGLALÁS

A Szerzők a Gidrán Lótenyésztők Magyarországi Egyesületének országos tenyészkanca sajátteljesítmény-vizsgálati adatbázisát dolgozták fel. A kiindulási adatbázis lényegében a teljes magyarországi aktív (élő) tenyészkanca állomány (N = 293) adatait tartalmazta, melyek 1994-2016 között születtek és 44 tenyészmén ivadékai voltak. A munka során nyolc tulajdonságot - marmagasság bottal (HWS), marmagasság szalaggal (HWT), övméret (CHG), szárkörméret (CAC), származási pontszám (ORS), küllemi pontszám (COS), mozgásbírálati pontszám (MOS), összpontszám (TOS) - értékeltek. Az adatok feldolgozására egy és többtényezős variancia-analízist (GLM), valamint súlyozott lineáris regresszió-analízist használtak. A vizsgált tulajdonságok korrigált főátlaga (\pm SE) a következő volt: HWS 161,6 \pm 0,4 cm, HWT 169,6 \pm 0,5 cm, CHG 188,4 \pm 0,7 cm, CAC 19,9 \pm 0,1 cm, ORS 29,1 \pm 0,3 pont, COS 72,8 \pm 0,5 pont, MOS 40,5 \pm 0,4 pont, TOS 142,4 \pm 0,7 pont. A HWS, a HWT, a COS és a TOS öröklődhetősége jónak bizonyult (h² = 0,37-0,47). A CHG és a CAC esetén közepes (0,29-0,31), míg a MOS esetén kis (0,20) h² értékeket becsültek. A testméretek esetén kismértékű,

csökkenő irányú (b = -0,25, -0,33, -0,35 and -0,08; P < 0,01), míg a többi tulajdonság esetén stagnáló (NS) fenotípusos trendeket állapítottak meg. Valamennyi tulajdonság esetén a "C" geneológiai vonalba tartozó apák lányai érték el a legjobb eredményeket. Megállapítható, hogy a gidrán tenyészkancák sajátteljesítmény-vizsgálatokon mutatott átlagos teljesítménye a vizsgált időszakban lényegében nem változott.

Kulcsszavak: gidrán fajta, tenyészkanca, teljesítményvizsgálat, öröklődhetőség, tenyészérték, trendek

INTRODUCTION

Among the indigenous gene reserve horse breeds bred in Hungary, the Gidran can be considered the most endangered (Klein et al., 2022). The number of active mares ranges from 250-300 with 25-30 breeding stallions used. For the breeding of the Gidran breed, the guidelines for gene preservation play a decisive role, although, if there is an opportunity, sports-oriented selection (mainly aimed at improving jumping ability) is also carried out. Therefore, the evaluation of pedigree is a primary consideration, but the mares to be registered are also classified based on their performance.

The qualification of Gidran breeding mares takes place after the age of three years. For the certification, a performance test (so-called "mare exam") is organized, during which the pedigree, conformation and movement of the mares are evaluated. Based on the results achieved, the mares are classified into pedigree classes. The procedure of performance testing is described in detail in the Horse Performance Testing Guideline (Zámbori, 2007).

Very few data can be found in the relevant literature sources on the performance results and qualification of breeding mares of different Hungarian breeds (Posta et al., 2014; Rudiné et al., 2015). In Hungary, Posta and Komlósi (2007) and Posta et al. (2007a, 2007b) studied in detail the performance test of Hungarian Sport Horse mares, their genetic parameters and heritability for certain traits. For the breeding of non-Hungarian breeds, some sources of data (Dietl et al., 2004, 2005; Thorén Hellsten et al., 2006; Ducro et al., 2007) can also be found in the literature, the results of which were described in detail in our previous work (Bene et al., 2012).

Much more information can be found in the literature about the examination of characteristics related to

conformation, movement, or jumping ability, which are an integral part of performance tests (Bruns, 1981; Philipsson et al., 1990; Lewczuk et al., 2006). The aforementioned and other sources of literature deal with the relationship between conformation and movement (Koenen et al., 1995; de Oliveira Bussiman et al., 2022), the characteristics and modeling of jumping (Jónás et al., 2007, 2008), the gait of the horse, the kinematic description of movement (locomotion) (Ripollés-Lobo et al., 2022), with different competitive performances (Langlois and Blouin, 2004; Halo et al., 2008) and their genetic parameter estimation (Tavernier, 1988; Bugislaus et al., 2004; Bokor et al., 2007) for horses. Several studies of this range of subjects have also played a role in the further development of performance testing systems (Rovere et al., 2017).

The jumping ability of different horse breeds was previously presented: Dutch Warmblood (Huizinga et al., 1990; Ducro et al., 2007), Trakehner (Preisinger et al., 1991), Mecklenburger (Dietl et al., 2005), Haflinger (Samoré et al., 1997). There is often a discussion about the horse's performance evaluation at different ages and moreover, the age of the animals is inserted into the statistical models (Koenen et al., 1995; Bugislaus et al., 2004; Posta et al., 2007a). There are some references on the effect of gender in several literature sources (Langlois and Blouin, 2004; Lewczuk et al., 2006; Poncet et al., 2006), as well as on the differences in vintages of the animals (Ricard and Touvais, 2007).

Except for our previous research (Bene et al., 2014), certain information on the conformation and performance of Gidran horses can be found almost exclusively in Hungarian-language sources. Nagy et al. (2009) reported the following data on the body measurements of adult Gidran broodmares (in parentheses are the values from

Central European Agriculture ISSN 1332-9049 the Horse Performance Testing Guideline (2007): height at withers measured by stick 162.5 cm (minimum 163 cm), height at withers measured by tape 167.6 cm (minimum 173 cm), chest girth 192.7 cm (186-195 cm) and cannon circumference 19.9 cm (20.5-21.5 cm). In the analysis of the movement of the Gidran breed, Jónás et al. (2007) reported data. In our previous research (Bene et al., 2013), the heritability of the conformation parameters recorded during the performance test of the stallions was moderate ($h^2 = 0.4$ -0.5), that of the movement evaluation parameters was low to moderate ($h^2 = 0.2$ -0.4). The number of foreign publications about the conformation of the Gidran breed is extremely modest. In the work of Cighi et al. (2020) in Romania, the height at withers,

the chest girth and the cannon circumference of adult Gidran broodmares were 161.8 cm, 184.2 cm and 20.4 cm, respectively.

There are four different stallion groups, or lines distinguished in the Gidran breed. The different mare lines play an important role in avoiding inbreeding and maintaining genetic variability. Three genealogical lines ("A", "B" and "C" lines) were the founders of the breed which was designated before the turn of the twentieth century. There is a fourth stallions group includes nonpure Gidran stallions, which were used to improve the performance of the Gidran breed and to avoid inbreeding, in addition to observing the rules of gene preservation (Mihók and Janászik, 2020).

In light of the above, our study aimed to investigate the performance tests on the breeding mares of the native Gidran breed based on the data recorded during performance tests. We were curious to see the phenotypic trend in the past period, and the heritability values of the studied traits. We wanted to estimate the breeding values of the stallions (sires) on the investigated traits, as well as to compare the performances of broodmares of different stallion groups. In the case of the Gidran breed, population genetic studies of this kind are largely absent from the domestic literature and completely absent from the international literature.

MATERIALS AND METHODS

The database

This study is based on the pedigree, conformation and performance data of living breeding mares from the mare register of the Hungarian Association of Gidran Horse Breeders were collected at the end of 2021. The data was verified according to the Gidrán Stud Book (Mihók, 2005). In this way, almost the entire, living Hungarian Gidran mare population was included in the tests. The initial database contained the data of 293 broodmares, which were born as offspring of 44 stallions between 1994-2016. Datas collected from mares that had at least one half-sibling on the paternal side were only included the examination. It can be seen from the above that the native Gidran is a breed bred in very small population. Therefore, we had the opportunity to process a fairly modest database during this study.

The project to save the Gidran breed started in year of 1974, the starting herd consisted of 22 mares and 3 stallions. Mare performance tests were organized from the beginning of the 1980s, but they covered only a few mares, and their results were kept on a paper basis and were very difficult to find and process. In 1989, the system for conducting the mare performance tests changed somewhat, so the results of the previous years cannot be directly compared to the later data.

The studied traits

During the study a total of eight traits were examined which were as follows: There were four body measurement traits of broodmares, namely height at withers measured by stick and tape (HWS, HWT), chest girth (CHG) and left front/fore cannon circumference (CAC). Furthermore, there were another four, scored traits, such as pedigree score (PES), conformation score (COS), movement score (MOS) and total score (TOS). The methodology for recording body measurements was previously described in detail (Bene et al., 2007, 2009). The PES was the basic value of breed identity. It was calculated in the fourth ancestral/generation row (great-grandparents). Among the 16 great-grandparents, 2 points could be given for each Gidran breed ancestor, 1 point for a parent accepted in breeding but not a Gidran, while 0 points could be given for all other or unknown parents. The base value of the PES could thus be 32. An extra point (maximum 8 points) could be given in the case of outstanding great-grandparents, so the maximum value of the pedigree score could be 40 (32+8) (Zámbori, 2007).

The COS was determined using a classic 100-point evaluation system. During the type "B" judging, a total of 18 conformation traits were judged (overall impression, gender, proportionality, development, head, head set, neck joint, neck curve, top line, shoulder blade, front legs from the side, withers, front legs from the front, front hooves, rump, hind legs from the side, hind legs from behind, hind hooves).

The MOS was determined based on the length, momentum and regularity of the walk, canter and gallop. 10 points could be given for each of the six evaluated parameters, so the maximum value of the movement score could be 60 points.

The TOS of the mares was determined by adding the pedigree score, the conformation score and the movement score. A total of 200 points (40+100+60) could be obtained during the basic qualification (Zámbori, 2007).

Examining the effects of different factors

The processing of the data was begun with the calculation of the basic statistical indicators (mean, standard deviation, cv% etc.) of the examined traits. To check the normality of the data the Kolgomorov-Smirnov test and Levene's test were used to test the homogeneity (Table 1).

Multifactor analysis of variance (General Linear Model - GLM) was used to evaluate the performance test database of the Gidran mares. The sire (stallion) of the examined broodmares was included in the models as a random effect, and the birth year of the mares as a fixed effect. In the study, all eight examined traits were treated separately and model calculations (runs) were performed separately, too. The general form of the applied estimation models is described as follows:

$$\hat{y}_{hi} = \mu + S_h + Y_i + e_{hi}$$

where \hat{y}_{hi} = the trait of the mare, born in year "i" from sire "h"; μ = average for all observations; S_h = effect of the sire; Y_i = effect of the birth year; e_{hi} = random error.

The significance tests of the effects were also carried out for all traits.

Calculating phenotypic trends

During the calculation of the phenotypic trends, the data of the mares born in the same year were averaged for all eight traits, and then linear lines were fitted using the one-factor linear regression analysis weighted to the averages. The evaluated trait was considered as the dependent variable, the birth year of the mare as the independent variable, and the number of animals per year as the weighting factor.

Estimation of population genetic parameters and breeding values

During the estimation of the population genetic parameters, four values were determined for each trait: the (genetic) variance between progeny groups (σ_d^2), the (environmental) variance within the progeny group (σ_e^2), the phenotypic variance (σ_p^2) and the heritability value (h^2). For the estimation, the simple GLM procedure described above (with ANOVA Type III method) was used. The estimated variance components and the process of their calculation were described in detail by Willham (1972), Szőke and Komlósi (2000) and Lengyel et al. (2004), so we do not repeat them here.

Also, in this study, the breeding value (BV) of the sires was estimated for all traits. The predicted transmitting ability (TA) was defined as the difference between the average performance of the sire's offspring group and the average performance of the contemporary offspring population.

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Traits	HWS	HWT	CHG	CAC	PES	COS	MOS	TOS
	(cm)	(cm)	(cm)	(cm)	(pts)	(pts)	(pts)	(pts)
Ν	278	278	278	278	293	293	293	293
Mean	161.2	169.0	187.6	19.8	29.9	72.6	40.2	142.7
SD	4.5	5.1	7.5	0.9	3.7	4.9	3.6	7.8
CV%	2.8	3.0	4.0	4.5	12.4	6.7	9.0	5.5
Min	148.0	154.0	161.0	17.0	21.0	54.5	24.5	105.5
Max	175.0	183.0	211.0	22.0	38.0	84.5	49.0	166.5
Median	161.1	169.0	188.0	20.0	30.0	73.0	40.5	142.5
Normality test*	0.00	0.01	0.01	0.00	0.00	0.07	0.00	0.06
Homogenity test [#]	0.58	0.87	0.18	0.06	0.01	0.64	0.10	0.35
Breeding regulation ^{&}	Min. 163	Min. 173	186-195	20.5-21.5	Max. 40	Max. 100	Max. 60	Max. 200

Table 1. Descriptive statistics of the examined traits

HWS, HWT = height at withers measured with stick and tape; CHG = chest girth; CAC = cannon circumference; PES = pedigree score; COS = conformation score; MOS = movement score; TOS = total score; pts = points; *if P > 0.05, the normal distribution is confirmed; #if P > 0.05, the homogenity is confirmed; &Mihók and Janászik (2020)

The BV was estimated as twice the transmitting ability ($BV = 2 \times TA$). For the reasons of limited space, the BV is presented in Table 6 only for the 10 sires with the most offspring number.

In the case of the PES - due to the nature of the trait - neither population genetic parameters nor breeding values were estimated.

Comparison of the performance of different stallion groups

A total of 44 examined stallions and their offspring were divided into 4 categories based on their pedigree. The performance of the groups was considered as the mean value of the trait for the daughters of the sires belonging to a certain group.

The groups were compared in two ways. On the one hand, the eight traits recorded during the performance examination of the mares according to the stallion groups were statistically compared separately. On the other hand, the BV of the stallions belonging to the four different stallion groups was averaged per group. Oneway analysis of variance was used to compare the stallion groups. In cases where the F-test showed a significant difference, the Tukey test for homogeneous variance was used, and the Tamhene test for non-homogeneous variance to detect differences between groups.

The used software

The data were prepared using MS Excel 2003 and Word 2003. The evaluation of the database was performed with the statistical software package SPSS 27.0 (2020).

RESULTS

The effect of the birth year of mare and the phenotypic trends

The corrected main mean values (\pm SE) of the examined traits were as follows: HWS 161.6 \pm 0.4 cm, HWT 169.6 \pm 0.5 cm, CHG 188.4 \pm 0.7 cm, CAC 19.9 \pm 0.1 cm, PES 29.1 \pm 0.3 points, COS 72.8 \pm 0.5 points, MOS 40.5 \pm 0.4 points and TOS 142.4 \pm 0.7 points (Table 2a and Table 2b).

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Didle up of more	N	HWS (cm)	HWT (cm)	CHG (cm)	CAC (cm)			
Birth year of mare	Ν	Mean ± SE						
- 1994	2	158.5 ± 4.2	164.2 ± 4.7	195.1 ± 7.2	19.9 ± 0.8			
- 1995	6	162.5 ± 2.2	172.6 ± 2.4	192.6 ± 3.7	20.5 ± 0.4			
- 1996	5	164.9 ± 2.4	171.6 ± 2.7	195.7 ± 4.2	20.9 ± 0.5			
- 1997	6	165.1 ± 2.2	172.4 ± 2.5	189.6 ± 3.8	20.9 ± 0.4			
- 1998	7	164.4 ± 2.1	174.8 ± 2.3	190.0 ± 3.6	20.7 ± 0.4			
- 1999	4	166.0 ± 2.6	178.0 ± 2.9	189.1 ± 4.5	20.8 ± 0.5			
- 2000	8	163.0 ± 1.8	172.2 ± 2.0	190.1 ± 3.0	20.7 ± 0.3			
- 2001	14	164.0 ± 1.8	172.9 ± 2.0	189.5 ± 3.1	20.5 ± 0.3			
- 2002	12	160.3 ± 1.7	169.1 ± 1.9	186.5 ± 2.9	20.0 ± 0.3			
- 2003	10	161.0 ± 1.7	167.2 ± 1.9	187.1 ± 2.9	20.3 ± 0.3			
- 2004	10	161.5 ± 1.7	170.3 ± 1.9	186.3 ± 2.9	19.7 ± 0.3			
- 2005	18	162.4 ± 1.3	169.0 ± 1.4	190.6 ± 2.2	19.3 ± 0.2			
- 2006	10	163.4 ± 1.5	170.0 ± 1.7	190.0 ± 2.6	19.5 ± 0.3			
- 2007	21	161.4 ± 1.2	168.9 ± 1.3	182.2 ± 2.0	19.8 ± 0.2			
- 2008	8	160.0 ± 1.6	168.9 ± 1.8	188.0 ± 2.8	19.9 ± 0.3			
- 2009	16	158.6 ± 1.4	166.1 ± 1.5	185.3 ± 2.4	19.1 ± 0.3			
- 2010	19	161.3 ± 1.2	168.6 ± 1.4	187.2 ± 2.1	19.3 ± 0.2			
- 2011	18	159.1 ± 1.2	166.8 ± 1.3	187.1 ± 2.1	19.2 ± 0.2			
- 2012	30	159.9 ± 1.0	167.3 ± 1.2	188.0 ± 1.8	19.3 ± 0.2			
- 2013	16	160.2 ± 1.3	167.6 ± 1.4	187.4 ± 2.2	19.3 ± 0.2			
- 2014	28	159.6 ± 1.2	166.8 ± 1.3	186.4 ± 2.1	19.1 ± 0.2			
- 2015	8	159.2 ± 2.3	166.8 ± 2.6	185.9 ± 4.0	19.7 ± 0.4			
- 2016	2	159.8 ± 3.2	168.2 ± 3.5	183.7 ± 5.5	19.6 ± 0.6			
Corrected grand mean (± SE)	278	161.6 ± 0.4	169.6 ± 0.5	188.4 ± 0.7	19.9 ± 0.1			
Effect of birth year (p)		NS (0.516)	NS (0.139)	NS (0.426)	<0.05 (0.023)			

Table 2a. Effect of birth year of the mare on the examined traits

HWS = height at withers measured with a stick; HWT = height at withers measured with tape; CHG = chest girth; CAC = cannon circumference

In terms of body measurements, the highest HWS $(166.0 \pm 2.6 \text{ cm})$ and HWT $(178.0 \pm 2.9 \text{ cm})$ were obtained in mares born in 1999. The lowest were the mares born

in 1994, their withers height was almost 8 cm lower than that of the previous group. CHG (195.7 \pm 4.2 cm) and CAC (20.9 \pm 0.5) were the largest in mares born in 1996.

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Distlesson of more	N	PES (points)	COS (points)	MOS (points)	TOS (points)			
Birth year of mare	Ν		Mean ± SE					
- 1994	3	31.1 ± 2.1	78.7 ± 3.8	43.4 ± 2.8	153.1 ± 5.8			
- 1995	7	28.7 ± 1.3	71.6 ± 2.3	41.4 ± 1.8	141.7 ± 3.6			
- 1996	5	28.2 ± 1.4	71.8 ± 2.6	46.3 ± 2.0	146.1 ± 4.1			
- 1997	7	29.6 ± 1.2	71.4 ± 2.3	39.4 ± 1.7	140.3 ± 3.5			
- 1998	8	26.9 ± 1.2	69.3 ± 2.2	41.7 ± 1.6	138.3 ± 3.4			
- 1999	5	27.9 ± 1.6	77.6 ± 2.9	39.8 ± 2.2	145.2 ± 4.5			
- 2000	9	28.9 ± 1.0	68.9 ± 1.8	38.0 ± 1.4	135.7 ± 2.9			
- 2001	15	28.6 ± 1.0	71.2 ± 1.9	39.9 ± 1.4	139.6 ± 2.9			
- 2002	12	29.4 ± 1.0	71.2 ± 1.9	39.6 ± 1.4	140.2 ± 2.9			
- 2003	10	31.9 ± 1.0	70.5 ± 1.9	39.4 ± 1.4	141.8 ± 2.9			
- 2004	10	30.3 ± 1.0	74.5 ± 1.9	39.4 ± 1.4	144.1 ± 2.9			
- 2005	18	28.6 ± 0.8	74.9 ± 1.4	40.2 ± 1.1	143.5 ± 2.2			
- 2006	10	27.1 ± 0.9	75.5 ± 1.7	40.1 ± 1.3	142.5 ± 2.6			
- 2007	21	25.9 ± 0.7	74.3 ± 1.3	40.0 ± 1.0	140.1 ± 2.0			
- 2008	8	26.6 ± 1.0	75.8 ± 1.8	41.7 ± 1.4	144.0 ± 2.8			
- 2009	17	27.2 ± 0.8	70.2 ± 1.5	40.6 ± 1.1	138.0 ± 2.3			
- 2010	19	29.4 ± 0.7	73.5 ± 1.4	40.1 ± 1.0	143.3 ± 2.1			
- 2011	18	30.6 ± 0.7	68.0 ± 1.3	39.4 ± 1.0	138.0 ± 2.1			
- 2012	30	30.9 ± 0.6	70.0 ± 1.2	39.6 ± 0.9	140.5 ± 1.8			
- 2013	18	30.4 ± 0.7	71.5 ± 1.4	38.4 ± 1.0	140.3 ± 2.1			
- 2014	33	30.0 ± 0.7	71.8 ± 1.3	40.4 ± 1.0	142.3 ± 2.0			
- 2015	8	31.0 ± 1.4	74.2 ± 2.6	39.9 ± 2.0	145.2 ± 4.0			
- 2016	2	30.4 ± 1.9	78.3 ± 3.6	42.8 ± 2.7	151.6 ± 5.5			
Corrected grand mean (± SE)	293	29.1 ± 0.3	72.8 ± 0.5	40.5 ± 0.4	142.4 ± 0.7			
Effect of birth year (p)		<0.01 (0.000)	<0.01 (0.001)	NS (0.260)	NS (0.101)			

Table 2b. Effect of birth year of the mare on the examined traits

PES = pedigree score; COS = conformation score; MOS = movement score; TOS = total score

The effect of birth year of the mare was found to be statistically reliable (P < 0.05 and P < 0.01) for three traits: CAC, PES, and COS. The average COS of mares born in 1994, 1999 and 2016 exceeded 76 points (78.7 ± 3.8 points, 77.6 ± 2.9 points, 78.3 ± 3.6 points, respectively). The smallest COS (68.0 ± 1.3 points) was observed in

mares born in 2011. The mares born in 1994, in addition to their outstanding COS value, were much bigger than the average MOS (43.4 \pm 2.8 points), moreover we also obtained the highest TOS (153.1 \pm 5.8 points) for these mares.

The phenotypic trends estimated based on the annual average results of the traits are summarized in Table 3.

For all examined body measurements, the fitting value of the phenotypic trend lines was quite high ($R^2 = 0.54$ -0.72; P < 0.01). For all four body measurements, a small but statistically verifiable (P < 0.01) downward trend was experienced. The rate of annual decrease turned out to be rather small, in the case of HWS -0.25 cm/year, in the case of HWT -0.33 cm/year, in the case of CHG -0.35 cm/year, while in the case of CAC, it was -0.08 cm/year.

In the case of additional parameters recorded in the performance tests, the fitting value of the trend lines was not found to be statistically reliable in any case. Both the R^2 values and the slope (b) values were very close to zero, so we could establish a stagnant tendency for these traits.

Population genetic parameters, breeding values

The population genetic parameters of the estimated traits in this study are presented in Table 4. The heritability of HWS, HWT, COS and TOS proved to be moderate

Table 3. The phenotypic trend of the examined traits

Traits —		Slope (bX)			Intercept (a)	Fitting		
	b	SE	Р	а	SE	Р	R ²	Р
HWS (cm)	-0.25	0.05	<0.01	672.55	91.81	<0.01	0.60	<0.01
HWT (cm)	-0.33	0.05	<0.01	835.52	102.22	<0.01	0.67	<0.01
CHG (cm)	-0.35	0.07	<0.01	889.84	139.90	<0.01	0.54	<0.01
CAC (cm)	-0.08	0.01	<0.01	188.67	22.79	<0.01	0.72	<0.01
PES (pts)	+0.05	0.05	NS	-79.90	103.73	NS	0.05	NS
COS (pts)	-0.04	0.09	NS	163.26	181.13	NS	0.01	NS
MOS (pts)	-0.03	0.04	NS	96.47	73.31	NS	0.03	NS
TOS (pts)	+0.02	0.09	NS	103.43	190.65	NS	0.00	NS

HWS, HWT = height at withers measured with stick or tape; CHG = chest girth; CAC = cannon circumference; PE = pedigree score; COS = conformation score; MOS = movement score; TOS = total score; pts = points; b = slope; SE = standard error; P = significance; a = constant; R^2 = fitting

Table 4. Population genetic parameters of	of the examined traits
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Traits	σ^2_{d}	σ_{e}^{2}	σ^2_{p}	$h^2 \pm SE$
HWS	13.40	15.43	28.83	0.47 ± 0.25
HWT	16.22	19.00	35.22	0.46 ± 0.25
CHG	20.59	45.30	65.89	0.31 ± 0.22
CAC	0.25	0.61	0.86	0.29 ± 0.22
COS	11.49	19.33	30.82	0.37 ± 0.22
MOS	2.79	11.32	14.11	0.20 ± 0.19
TOS	43.49	46.82	90.31	0.48 ± 0.24

 σ_d^2 = additive direct genetic variance; σ_e^2 = residual variance; σ_p^2 = Phenotypic variance; h^2 = heritability; HWS, HWT = height at withers measured with stick or tape; CHG = chest girth; CAC = cannon circumference; COS = conformation score; MOS = movement score; TOS = total score

($h^2 = 0.37-0.47$). Low to moderate h^2 values (0.29-0.31) were estimated for CHG and CAC, and low values ($h^2 = 0.20$) for MOS.

stallion used for crossbreeding with registration number 4694.

The phenotypic performance of different stallion groups

The estimated BV of the sires included in the study based on the performance of their daughters can be seen in Table 5. The effect of sires was observed significant (P < 0.05 and P < 0.01) for all traits except the MOS. Among the tested sires, the breeding stallion of registration number 4889 proved to be outstanding. For this stallion the highest breeding values were estimated for five of the evaluated traits (compared to the corrected overall mean value of the population, HWS +4.02 cm, HWT +4.46 cm, COS +4.66 points, MOS +0.68 points, TOS +11.66 points). In the case of CHG and CAC, the highest BV (+3.78 cm and +0.56 cm) was obtained for stallion of registration number 3833. The BV of this stallion was above the average for all the traits. In terms of body measurements, the smallest BV's (HWS -5.68 cm, HWT -5.74 cm, CHG -4.54 cm) were found in the case of the Thoroughbred

The effect of the stallion groups was statistically verifiable (P < 0.05 and P < 0.01) in six cases of the eight examined traits (HWS, CHG, PES, COS, MOS, TOS) (Table 6). In the case of two body measurements, there were smaller differences between the stallion groups, than for aforementioned six traits. However, in the case of the performance evaluation parameters, the daughters of the stallions belonging to the genealogical line "C" achieved significantly (P < 0.05 and P < 0.01) better results for all four traits than the offspring of the sires belonging to the other three groups. The performance of the daughters of the stallions belonging to the "A" and "B" genealogical

lines was similar. The daughters of the stallions from the

"for breeding used group" had lower HWS, HWT, CHG

and PES than those of the other three groups.

Reg. number of sire (group)#	N*	HWS (cm)	HWT (cm)	CHG (cm)	CAC (cm)	COS (pts)	MOS (pts)	TOS (pts)		
	000	161.6	169.6	188.4	19.9	72.8	40.5	142.4		
Corrected mean	293			Difference f	rom corrected	mean (± SE)				
- 1624 (line-A)	20	-0.64 ± 1.15	+1.36 ± 1.27	-0.56 ± 1.61	+0.34 ± 0.18	+2.20 ± 1.13	-0.30 ± 0.49	+4.68 ± 1.93		
- 2550 (line-B)	12	+2.86 ± 1.12	+2.06 ± 1.23	-1.82 ± 1.58	-0.10 ± 0.18	-0.26 ± 1.15	-0.20 ± 0.49	-2.38 ± 1.95		
- 3782 (FBU)	8	+2.34 ± 1.26	+3.72 ± 1.39	+2.70 ± 1.72	+0.40 ± 0.20	+2.78 ± 1.29	+0.48 ± 0.51	+2.24 ± 2.24		
- 3833 (line-A)	12	-0.22 ± 1.08	+0.08 ± 1.19	+3.78 ± 1.55	+0.56 ± 0.18	-1.26 ± 1.10	+0.66 ± 0.48	+2.32 ± 1.85		
- 4053 (line-C)	15	+3.50 ± 1.04	+4.02 ± 1.14	-0.00 ± 1.50	+0.40 ± 0.17	+0.14 ± 1.09	+0.14 ± 0.48	+7.90 ± 1.83		
- 4103 (line-B)	26	-0.30 ± 0.93	+0.54 ± 1.03	+3.32 ± 1.37	+0.02 ± 0.16	+0.22 ± 0.98	+0.34 ± 0.46	+8.34 ± 1.64		
- 4473 (line-A)	9	+2.36 ± 1.14	+0.78 ± 1.26	+2.00 ± 1.61	+0.26 ± 0.18	+1.24 ± 1.19	-0.42 ± 0.50	+4.48 ± 2.02		
- 4659 (line-A)	27	-2.50 ± 0.87	-2.50 ± 0.96	+3.06 ± 1.29	-0.08 ± 0.15	+0.76 ± 0.91	-0.64 ± 0.45	+2.62 ± 1.52		
- 4694 (FBU)	13	-5.68 ± 1.06	-5.74 ± 1.17	-4.54 ± 1.53	+0.00 ± 0.17	+2.48 ± 1.10	+0.18 ± 0.48	-1.58 ± 1.85		
- 4889 (line-C)	13	+4.02 ± 1.06	+4.46 ± 1.17	+1.12 ± 1.53	+0.36 ± 0.17	+4.66 ± 1.11	+0.68 ± 0.48	+9.99 ± 1.88		
Effect of sire (p)		<0.010.000	<0.010.001	<0.050.022	<0.050.033	<0.010.004	NS 0.101	<0.010.000		

"breeding values are presented only for the 10 sires with the most offspring; N^* = number of progeny; FBU = "for breeding used"; HWS, HWT = height at withers measured with stick or tape; CHG = chest girth; CAC = cannon circumference; COS = conformation score; MOS = movement score; TOS = total score; pts = points

Group of sire		Genealogical line				P-value
	"A"	"B"	"C"	- "FBU"	Mean ± SE	
Ν	95	50	34	99	278	
- HWS (cm)	°160.8 ± 4.3	^{ab} 162.0 ± 4.6	^b 162.9 ± 4.2	°160.7 ± 4.6	161.2 ± 4.5	<0.05
- HWT (cm)	168.5 ± 5.1	169.7 ± 5.0	170.9 ± 4.2	168.7 ± 5.4	169.0 ± 5.1	NS
- CHG (cm)	°189.3 ± 6.4	^b 186.5 ± 8.4	^{ab} 188.2 ± 7.9	^b 186.3 ± 7.5	187.6 ± 7.5	<0.05
- CAC (cm)	19.8 ± 0.9	19.6 ± 0.7	19.9 ± 0.7	19.7 ± 0.9	19.8 ± 0.9	NS
Ν	105	50	35	103	293	
- PES (pts)	°31.5 ± 2.3	^b 29.8 ± 4.0	^a 32.6 ± 3.8	°27.3 ± 3.2	29.9 ± 3.7	<0.01
- COS (pts)	°71.7 ± 5.0	^{ab} 73.1 ± 4.4	^b 74.7 ± 4.6	^a 72.6 ± 4.8	72.6 ± 4.9	<0.05
- MOS (pts)	°39.4 ± 3.7	^{ab} 40.4 ± 3.9	°42.2 ± 2.5	^b 40.4 ± 3.5	40.2 ± 3.6	<0.01
- TOS (pts)	°142.6 ± 7.1	°143.3 ± 8.6	^b 149.6 ± 6.2	°140.3 ± 7.2	142.7 ± 7.8	<0.01

Table 6. The effect of a group of sires on the examined traits

FBU = "for breeding used" sires; HWS, HWT = height at withers measured with stick or tape; CHG = chest girth; CAC = cannon circumference; PES = pedigree score; COS = conformation score; MOS = movement score; TOS = total score; treatments without the same superscript differ significantly (P < 0.05)

Regarding the differences between different stallion's progeny groups, there were differences not only in phenotypic performances, but in breeding values, too (Table 7). The average BV of the stallions belonging to the "C" genealogical line was positive and exceptionally high for all traits. This is especially true in the case of the

MOS and TOS traits, where the effect of the stallion line was statistically verifiable on the average of the breeding values. The average BV of the stallions from the "for breeding used group" was below the population average for all body measurement traits.

		Genealogical line					
Group of sire	"A"	"B"	"C"	"FBU"	Corrected mean (± SE)	P-value	
	Av	verage difference f	rom corrected mea	an			
- HWS (cm)	-0.09	+0.36	+0.65	-0.27	161.6 ± 0.4	NS	
- HWT (cm)	-0.34	+0.11	+0.71	-0.06	169.6 ± 0.5	NS	
- CHG (cm)	+1.19	-2.02	+4.59	-1.18	188.4 ± 0.7	NS	
- CAC (cm)	+0.00	-0.23	+0.50	-0.02	19.9 ± 0.1	NS	
- COS (pts)	-0.88	-0.55	+2.26	+0.13	72.8 ± 0.5	NS	
- MOS (pts)	ª-1.13	°-0.86	^b +2.60	ª+0.28	40.5 ± 0.4	<0.05	
- TOS (pts)	^a -0.38	ª-1.52	^b +8.23	ª-1.27	142.4 ± 0.7	<0.01	

Table 7. The average breeding values of sire groups

FBU = "for breeding used" sires; HWS, HWT = height at withers measured with stick or tape; CHG = chest girth; CAC = cannon circumference; COS = conformation score; MOS = movement score; TOS = total score; treatments without the same superscript differ significantly (P < 0.05)

DISCUSSION

The body measurement results obtained during this study were very similar to what we reported in our previous work (Nagy et al., 2009; Bene et al., 2014). Regarding the HWS, HWT and CAC, both the results of our mentioned previous tests and the average values observed in this study were smaller than those of the minimum values indicated in the breeding regulations (Zámbori, 2007; Mihók and Janászik, 2020). The results obtained in this study for the CHG were similar to both of the data we experienced during our previous tests and the data in the regulations.

Since no literature data on the heritability of the examined traits in the Gidran breed were found, we were able to compare our results with data from research conducted for other breeds. Posta et al. (2007a) reported similar h² values to our results for both conformation and movement traits in the Hungarian Sport Horse breed. Most of the relevant literature sources (Preisinger et al., 1991; Koenen et al., 1995; Samoré et al., 2007) also reported moderate or high heritability values for conformation parameters. Dietl et al. (2004) and Huizinga et al. (1990) estimated h² values between 0.1 and 0.3 in the case of movement traits in Mecklenburger and Dutch warmblood herds, which results were similar to our results.

The downward phenotypic trends observed in the case of body measurements are somewhat different from the guidelines found in the breeding regulations (Mihók and Janászik, 2020). According to the guideline, in the case of HWS, a value below 160 cm is insufficient for the Gidran breed. The average HWS of the Gidran mares observed in this study was only by 1.6 cm higher than the mentioned value. In the recent period, the BV of the "for breeding used" group stallions (registration number 4694, 4717, 5091, 5220, etc.) used for crossing in the Gidran breed was almost, without exception, below the population average in terms of body measurements, which can partially explain the experienced negative phenotypic trends in the trait group. Contrary to our results, Posta et al. (2007b) found that the genetic trend of the conformation traits of the breeding mares of the Hungarian Sport Horse breed was increasing.

No data were found in the international or Hungarian literature about the BV of the stallions used for breeding in the Gidrán breed in the tested traits, so we did not have the opportunity to compare our results with the data of previous tests. Following this idea, the breeding values estimated during our work can be considered novel.

The good performance of the daughters of stallions belonging to the "C" genealogical line was more or less subjectively recognized during practical work. Our research presented here was able to prove this good performance with data on the one hand, and with the average breeding value of stallions belonging to different lines on the other hand.

CONCLUSIONS

The finding that the conformation and movement traits of the Gidran mares did not change significantly during the examined period highlights that gene preservation is being successfully carried out in this breed.

Based on the moderate and high heritability experienced in the case of the eight examined traits, it can be concluded that by selecting a suitable sire, significant genetic progress can be achieved even within a few generations, if that were the goal.

The finding, that the conformation and movement scores due to the stallions used for drop blood crossing were improved, suggests that the performance of the breed can be improved in this way.

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