

Animal welfare, etológia és tartástechnológia



Animal welfare, ethology and housing systems

Volume 2

Issue 3

Gödöllő
2006



PEDIGREE ANALYSIS OF HUNGARIAN SPORT HORSES

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Abstract

Authors analysed the Hungarian Sport horse Studbook (contains ancestors at least 3 generations back) comprising a total of 11.286 individuals in order to ascertain the genetic structure of the breed and to evaluate its genetic variability. The numbers of founders based on this pedigree between birth years 1994 and 2003 were 2459 and 3222 individuals for stallions and mares, respectively. The effective numbers of founders were 376.3 and 512.9, respectively. Only 102 ancestors for stallions and 156 ancestors for mares were necessary to explain 50% of the genetic variability of the breed. One ancestor with the largest influence contributed 2.71% to the stallions' and 2.15% to the mares' genetic variability. There were 42 inbred individuals in the analysed population with mean inbreeding coefficient of 0.079.

Keywords: Hungarian Sporthorse; pedigree analysis; population structure; inbreeding; genetic variability

MAGYAR SPORTLÓ PEDIGRÉ-ANALÍZISE

Összefoglalás

A szerzők az összesen 11286 egyed adatait tartalmazó magyar sportló méneskönyvben található tenyészállatok (amely a származást legalább 3 generációra visszamenően tartalmazza) genetikai szerkezetét és a genetikai variabilitását elemezték. A méneskönyvben szereplő származási adatok alapján az 1994 és 2003 között született méncsikók esetében az alapítók száma 2459, az effektív alapítók száma 376,3; kancacsikók esetében az alapítók száma 3222, az effektív alapítók száma 512,9. Méncsikókra vonatkozóan mindösszesen 102, kancacsikók esetében 156 ős felelős a fajta genetikai variabilitásának 50 százalékáért. A fajta genetikai variabilitásából a legjelentősebb ős a méncsikók esetében 2,71%-kal, a kancacsikók esetében 2,15%-kal részesedett. Az elemzett állományban 42 beltenyésztett egyedet találtunk, Ezek átlagos beltenyésztési koefficiense 0,079.

Kulcsszavak: magyar sportló; pedigré-analízis; populáció szerkezet; beltenyésztés; genetikai variabilitás



Introduction

The assessment of the within-population genetic variability and gene flow is necessary before the implementation of selection programs to establish appropriate management of the genetic stock. Some simple demographic parameters, largely dependent on the management and mating policy, have a large impact on the genetic variability. Additionally, the study of the population structure and demography can highlight important circumstances affecting the genetic history of the population.

Hungarian Sporthorse is a noble riding and harness horse with a good constitution and an aesthetical and functional conformation. Its principal breeding goal invokes a horse for riding and show-jumping (MSLT, 2000).

In recent years, many publications have described the genetic structure of different horse breeds (Głażewska, I., Jezierski, T., 2004; Valera et al., 2005; Zechner et al., 2002).

Hungarian Sporthorse breeders are interested in the implementation of a selection program. The aim of this work is to analyse the information of the Hungarian Sporthorse studbook to contribute to the knowledge of the structure of the population and to evaluate its genetic variability in terms of inbreeding and genetic representation. This analysis will suggest appropriate strategies to monitor matings and manage genetic variability to enlarge the selection basis useful for a selection program.

Materials and methods

Information from all the individuals registered in the Hungarian Sporthorse studbook from its foundation (contains ancestors at least 3 generations back), comprising a total of 11.286 (7.517 females) animals. The pedigree data came from The Association of Hungarian Sporthorse Breeders (MSLT).

The pedigree completeness level was characterised by computing generation lengths. This is the average age of parents at the birth of their offspring. We computed generation interval for the 4 pathways (father–son, father–daughter, mother–son and mother–daughter) using birth dates of registered animals together with those of their fathers and mothers.

The genetic variability of the population was characterised with the effective number of founders, effective number of ancestors and inbreeding coefficient. Effective number of founders (Lacy, 1989) was defined as the number of equally contributing founders that would be expected to produce the same genetic diversity as in the population under study. The inbreeding coefficients of these animals were estimated with the use of VanRaden's method (VanRaden, 1992). All parameters were estimated using PEDIG software (Boichard, 2002).



Results and discussion

Average generation interval for descendants in the range of 1994 and 2003 was 10.24 years. *Table 1* shows generation lengths for the four pathways parent–offspring. In any case the stallion pathways were similar but longer than those involving mares.

Table 1: Generation intervals for the four pathways parent–offspring for the whole pedigree of the Hungarian Sporthorses born between 1994 and 2003. Number of progeny within brackets.

Birth year (1)	Stallion-son (4)	Mare-son (5)	Stallion-daughter (4)	Mare-daughter (5)
1994	10.79 (210)	8.69 (188)	11.03 (312)	9.28 (255)
1995	10.85 (234)	9.17 (229)	10.99 (375)	9.00 (316)
1996	11.71 (286)	9.02 (259)	11.51 (411)	8.70 (347)
1997	10.37 (316)	8.69 (299)	11.37 (437)	8.86 (366)
1998	11.29 (299)	9.13 (282)	10.92 (430)	8.94 (396)
1999	9.90 (423)	8.49 (408)	10.10 (479)	8.50 (424)
2000	10.92 (350)	8.95 (339)	11.19 (420)	8.54 (398)
2001	11.50 (298)	8.64 (290)	12.42 (383)	8.96 (368)
2002	13.61 (275)	8.79 (270)	13.41 (316)	9.23 (312)
2003	14.20 (321)	9.18 (322)	13.86 (288)	8.94 (297)
Average (6)	11.47 (3012)	8.86 (2886)	11.55 (3851)	8.87 (3479)

1. táblázat: A generációs intervallumok a négyféle szülő–ivadék csoportosítás esetében az 1994 és 2003 között született magyar sportlovakra vonatkozóan. Zárójelben az adott évben született ivadékok száma.

Születési év(1), Ménnevelő mén(2), Ménnevelő kanca(3), Kancanevelő mén(4), Kancanevelő kanca(5), Átlag(6)

From a demographic point of view generation intervals computed for the breed are consistent with those reported before for other horse breeds. It is usually admitted that generation intervals in horses are long (*Mihók, Jónás, 2005*). Generation intervals found for Hungarian Sporthorses are consistent with those previously reported for race or riding horses. *Langlois (1982)* found average generation interval 10.5 for Thoroughbred horses. Other average generation intervals were found in Polish Arabian horses in the range of 10.24 to 12.60 years for mares, and in the range of 8.64 to 13.94 years for stallions, respectively (*Głażewska, I., Jezierski, T., 2004*).

Table 2 shows major information on the concentration of gene origin in the Hungarian Sporthorse.

**Table 2: Parameters characterising the concentration of gene origin in the Hungarian Sporthorse population born between 1994 and 2003**

Parameter (1)		1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	All (10)
Stallions (2)	Number of animals (4)	229	264	302	341	314	432	352	299	277	327	3137
	Number of founders (5)	465	553	630	702	698	895	760	686	644	753	2459
	Effective number of founders (6)	203.2	198.9	213.6	242.2	245.2	236.5	207.8	186.5	97.1	168.1	376.3
	Number of ancestors explaining 100% (7)	327	381	433	474	452	573	471	398	372	433	-
	Number of ancestors explaining 70% (8)	142	166	179	188	184	200	158	139	129	136	445
	Number of ancestors explaining 50% (9)	57	68	63	68	71	66	51	49	44	47	102
Mares (3)	Number of animals (4)	434	485	508	514	501	508	430	391	319	299	4389
	Number of founders (5)	803	920	941	986	973	1021	894	778	727	714	3222
	Effective number of founders (6)	297.9	273.9	360.4	390.9	357.2	246.0	246.2	169.8	140.4	178.2	512.9
	Number of ancestors explaining 100% (7)	627	688	706	720	692	694	585	487	430	417	-
	Number of ancestors explaining 70% (8)	301	322	305	313	290	256	199	157	149	140	537
	Number of ancestors explaining 50% (9)	128	128	114	118	108	87	68	50	53	46	156

2. táblázat: Az 1994 és 2003 között született magyar sportló állomány populációgenetikai mérőszámaiért felelős ősök száma. Paraméter(1), Méncsikó(2), Kancacsikó(3), Egyedek száma(4), Alapítók száma(5), Alapítók effektív száma(6), 100% lefedettséget adó ősök száma(7), 70% lefedettséget adó ősök száma(8), 50% lefedettséget adó ősök száma(9), Összesen(10)

Number of founders for stallions and mares were in the range of 229 and 432, and 299 and 514, respectively. Effective number of founders for stallions and mares broken down into yearly figures were in the range of 97.1 and 245.2, and 140.4 and 390.9, respectively. The numbers of founders based on the studbook for birth years between 1994 and 2003 were 2459 and 3222 individuals for stallions and mares, respectively. The effective numbers of founders for the complete population were 376.3 and 512.9, respectively. Number of ancestors explaining 50% of the genetic variability for stallions and mares in yearly details were in the range of 44 and 71, and 46 and 128, respectively. Only 102 ancestors for stallions and 156 ancestors for mares were necessary to explain 50% of the genetic variability of the examined population. 70% of the genetic variability can be explained with 445 ancestors for stallions and 537 ancestors for mares. The complete genetic variability of the



population for stallions and mares in yearly details can be described in the range of 327 and 573, and 417 and 720, respectively. These numbers show high heterogeneity in the Hungarian Sporthorse population with wide variability of gene origin. Large number of stallions indicates that too many stallions are in the breeding stock. In this way the population can not be influenced by superior stallions so preferring of these stallions and using of fewer stallions may be recommended.

Table 3 and 4 detail the 10 ancestors contributing the most in the case of stallions and mares, respectively. All selected ancestors were stallions. Most of them were born in the 1980s and 1990s. The ancestor (2533 Goliath) contributing the most explained 2.71% and 2.15% of the genetic variability in the case of stallions and mares, respectively. The most important founders were imported Holsteiner and Dutch Warmblood stallions. This indicates that traditional Hungarian breeds might be disregarded. Low values of explained genetic variability show the heterogeneity of the analysed population. This can help in preservation of high variability but also prevent the population from the influence of superior stallions.

Imported founders also indicate the importance of inter-country handling of pedigrees.

Table 3: Description of 10 ancestors contributing the most to the genetic variability of the Hungarian Sporthorse stallions born between 1994 and 2003

ID (1)	Name (2)	Sex (3)	Year of birth (4)	Breed (5)	Explained variability (%) (6)
IM884830000	2533 Goliath	stallion (7)	1988	Dutch Warmblood (8)	2.71
IM912340094	2972 Justboy	stallion (7)	1991	Dutch Warmblood (8)	2.14
IM921190095	3001 Koppány	stallion (7)	1992	Dutch Warmblood (8)	1.80
IM75000To00	1117 Toborzó	stallion (7)	1975	Holsteiner (9)	1.59
IM880022001	3866 Ginus	stallion (7)	1988	Dutch Warmblood (8)	1.42
IM885460000	2534 Gringo	stallion (7)	1988	Dutch Warmblood (8)	1.31
IM79001Mo00	1551 Merano-1	stallion (7)	1979	Holsteiner (9)	1.22
HB820010000	1861 Hatalom	stallion (7)	1982	Hannoverian (10)	1.11
IM58000A100	311 Aldato	stallion (7)	1958	Holsteiner (9)	0.99
IM920070098	3481 Stauffenberg	stallion (7)	1992	Holsteiner (9)	0.97

3. táblázat: Az 1994 és 2003 között született magyar sportló ménék genetikai változékonyságához legnagyobb arányban hozzájáruló ősök leírása

Azonosító(1), Név(2), Ivar(3), Születési év(4), Fajta(5), Variabilitás lefedettségének aránya(6), mén(7), holland félvér(8), holsteini(9), hannoveri(10)

Table 4: Description of 10 ancestors contributing the most to the genetic variability of the Hungarian Sporthorse mares born between 1994 and 2003

Horse ID (1)	Name (2)	Sex (3)	Year of birth (4)	Breed (5)	Explained variability (%) (6)
IM884830000	2533 Goliath	stallion (7)	1988	Dutch Warmblood (8)	2.15
IM75000To00	1117 Toborzó	stallion (7)	1975	Holsteiner (9)	1.66
IM912340094	2972 Justboy	stallion (7)	1991	Dutch Warmblood (8)	1.49
IM921190095	3001 Koppány	stallion (7)	1992	Dutch Warmblood (8)	1.14
IM885460000	2534 Gringo	stallion (7)	1988	Dutch Warmblood (8)	1.11
IM79001Mo00	1551 Merano-1	stallion (7)	1979	Holsteiner (9)	1.05
IM58000A100	311 Aldato	stallion (7)	1958	Holsteiner (9)	1.00
IM930410096	3114 Colorado	stallion (7)	1993	Holsteiner (9)	0.96
IM890220099	3648 Laurenz	stallion (7)	1989	Holsteiner (9)	0.91
IM880022001	3866 Ginus	stallion (7)	1988	Dutch Warmblood (8)	0.84

4. táblázat: Az 1994 és 2003 között született magyar sportló kancák genetikai változékonyságához legnagyobb arányban hozzájáruló ősök leírása

Azonosító(1), Név(2), Ivar(3), Születési év(4), Fajta(5), Variabilitás lefedettségének aránya(6), mén(7), holland félvér(8), holsteini(9)



Table 5 shows the description of the most inbred animals. Forty-two horses were inbred from the 11286 individuals with mean inbreeding coefficient of 0.079. Highest inbreeding coefficient was 0.25. These values show that inbreeding is not typical in the examined population.

Table 5: Description of horses with at least 0.125 inbreeding coefficients

Horse ID (1)	Sex (2)	Sire ID (3)	Dam ID (4)	Inbreeding coefficient (5)
MF961000000	mare (6)	SV74003Si00	M 890880000	0.2500
MF032600000	stallion (7)	IM912340094	MF993520000	0.2500
MF013370000	stallion (7)	ZA910500000	ZA920200000	0.1875
MF030960000	stallion (7)	ZA910500000	ZA920200000	0.1875
MF001150000	mare (6)	ZA910500000	SO83081Hm00	0.1250
MF933230000	mare (6)	M 82065K100	M 88086K100	0.1250
MF013590000	stallion (7)	E 830130000	BA900150000	0.1250
MF944580000	stallion (7)	M 82065K100	M 88086K100	0.1250
MF981840000	mare (6)	ZA910500000	ZA881020000	0.1250
MF034830000	mare (6)	IM895430000	CD982260000	0.1250
SS87073Ma00	mare (6)	IM71000Ma00	SS82017Mc00	0.1250
MF992160000	mare (6)	M 890890000	SY911820000	0.1250
MF004730000	stallion (7)	MF952150000	IM906120000	0.1250

5. táblázat: A legalább 0,125 beltenyésztettségű együthathatójú egyedek leírása

Azonosító(1), Ivar(2), Mén azonosítója(3), Kanca azonosítója(4), Beltenyésztettség mértéke(5), Kancacsikó(6), Méncsikó(7)

Inbred horses could be separated into six groups by inbreeding coefficients. There were 13 horses with inbreeding coefficient between 0 and 0.05. Inbreeding coefficients of sixteen animals were between 0.05 and 0.10. Nine horses' inbreeding coefficients were between 0.10 and 0.15. There were inbreeding coefficient of two horses between 0.15 and 0.20 and between 0.20 and 0.25, respectively. Inbreeding was directed not only for animals most responsible for genetic variability in the examined population.

Acknowledgements

This work was carried out within "4/057/2004 NKFP" research theme. The Association of Hungarian Sport Horse Breeders is gratefully acknowledged for providing pedigree information for the study.



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