

Changes in the genetic variability of the Furioso-North Star population between 1989 and 2019

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SUMMARY

The Furioso-North Star (FNS) is one of the indigenous Hungarian horse breeds, originated from Mezőhegyes Stud. The aim of this work was to analyze the pedigree diversity and inbreeding of the registered Hungarian Furioso-North Star population in two different time points: the first was the active population in 1989, the second was the active population in 2019. Pedigree data was analyzed using Endog 4.8 software. The pedigree completeness was calculated in three different ways. In the past 30 years the pedigrees became more complete. In the population 2019 were 5 horses with ancestor in the 40th generation. Only 17–17 animals covered the 50% of the genetic variability for the two population. The most important ancestor was Herod xx in both reference populations. The FNS breed has English Thoroughbred background, that might be the reason of having several horses from this breed in the database. There were six animals among the ten most important ancestors in both reference populations. The average inbreeding coefficient was 3.31 in 1989 and 4.22 in 2019. Animals with highest inbreeding coefficient were born from the mating of close relatives (typically father-daughter). The Bart Furioso III-84 Boglár had the highest inbreeding coefficient (0.299) in the population 2019.

Keywords: Furioso-North Star; pedigree analysis; inbreeding; genetic variability

INTRODUCTION

Maintaining genetic diversity is the most common goal of animal conservation programs. Collecting pedigree information is considered very important in the animal breeding, especially in horse breeding. The demand to get to know the genetic variability of breeding animals has been continuously increasing (Woolliams et al., 2002). In pedigree analysis, information about the individual's founders, ancestors, relatives and progenies is used to carry out analyses to estimate parameters, which characterize the genetic structure and variety of the populations (Maignel et al., 1996). These data may reveal appropriate strategies for managing and monitoring mating programmes and maintain genetic variability (Valera et al., 2005).

Many publications in the past few years have described the genetic variability of different breeds of horses based on analysis of levels of inbreeding and founder contributions. There were studies about world breeds like English Thoroughbred (Bokor et al., 2013) and Quarter Horse (Faria et al., 2018a) breeds. Moreover, local breeds like Old Kladruber (Vostrá-Vydrová et al., 2016), Tuigpaard (Schurink et al., 2012) and Franches-Montagnes (Poncet et al., 2006) as well.

The Furioso-North Star (FNS) horse breed is an indigenous Hungarian breed, which originated from Mezőhegyes Stud (founded in 1785). The breed based on two founder stallions, Furioso Senior and North Star Senior. The FNS breed is an important gene resource in Hungary. In the past two centuries the breed was popular in the Austro-Hungarian Monarchy's territory, used mainly as heavy riding horse. In turn after the historical changes (first and second World War,

changes on state borders) nowadays FNS horses are competing in show-jumping events in several Central European countries (Hungary, Slovakia, Romania).

The goal of this research study was to analyze the pedigree diversity and inbreeding of the registered Hungarian Furioso-North Star population in 1989 and 2019.

MATERIALS AND METHODS

The studbook data of the registered Hungarian FNS horse population up to 2019 were analyzed. The recent pedigree information was given by the Furioso-North Star Horse Breeding Association, and old studbooks were also used. The pedigree information was traced back from current horses back to the founder animals. Because of the English Thoroughbred background, the pedigrees were started in the early 1700s years. There were the pedigree data of 32,624 individuals in the built database. The following information was stored for each horse in the developed database: name of the individual, the sex of the individual, name of the sire, name of the dam, birth date, and breed. In this work, two reference populations were considered: the first was the active population in 1989 (293 horses), the second was the active population in 2019 (646 horses).

The pedigree analysis was carried out using Endog 4.8 software (Gutiérrez and Goyache, 2005). Before the analysis, the database was checked for errors with the Pedigree Viewer 6.5 software (Kinghorn, 1994).

The following parameters were estimated to describe the population structure: pedigree completeness, genetic variability and inbreeding. The

pedigree completeness could measure in three different ways:

- The maximum number of generations: the number of generations separating the individual from its furthest ancestor.
- Number of full generations traced: the furthest generation where all ancestors of the individual are known.
- Equivalent complete generations: computed as the sum over all known ancestors of the terms computed as the sum of $(1/2)^n$ where n is the number of generations separating the individual to each known ancestor (Maignel et al., 1996).

The homozygosity of the population was characterized using the inbreeding coefficient (Wright, 1922). The inbreeding coefficient was defined as the probability of an individual having two genes identical by descent.

The formula used for calculation of the inbreeding coefficient is the following:

$$F_X = \sum \left(\frac{1}{2}\right)^{n+n'+1} \times (1 + F_A)$$

where A is the common ancestor in the chains of origin of the father and mother of the individual X, n and n' are the number of generations between the individual X and the common ancestor A on the paternal side (n) and the maternal side (n'), and F_A is the inbreeding coefficient of the common ancestor.

RESULTS AND DISCUSSION

Pedigree quality

The quality of the pedigree is a crucial part, because the results are greatly affected by the depth and completeness of the pedigree (Gutiérrez et al., 2008). Table 1 presents the main indexes for pedigree quality.

Table 1: The main indexes of the pedigree quality

Indicator	Value	
	1989	2019
Maximum number of generations	31.78	36.05
Number of full generations traced	3.19	4.69
Equivalent complete generations	12.21	15.03

The average of maximum number of generations back to the founder animals was 31.78 for the first and 36.05 for the second reference population. The value varied between 27 and 36 generations in 1989, and 28 and 40 generations in population 2019. There were two horses having known ancestors 36 generations back in the first reference population, whereas five horses had known ancestor in the 40th generation. This might be due to the impact of English Thoroughbred. Results of Bokor et al. (2013) where the Thoroughbred was examined in Hungary, were lower (28.96) than the first reference population's average. Our findings for the population 2019 was quite similar to Pjontek et al.

(2012) reported for the Polish Shagya Arabian population.

The average number of full generations traced in the population 1989 was above 3 generations of which value varied between 1 and 8 generations. In the population 2019 every individual had on average 4.69 known generations. At least five generations were completely known for the 68.6% of the animals. The 10.4% of the horses in the population 2019 were born before 2000 while 43.8% born after 2010. The eldest born in 1991 and the youngest in 2018. The values in the two reference populations is not as high as in old breeds with good documentation background like Lipizzan (5.9 – Pjontek et al., 2012) and English Thoroughbred (6.69 – Bokor et al., 2013).

The value of the average equivalent complete generations was 12.21 generations in 1989, the values varied between 4.1 and 19.8 generations. The average is almost the same like in the Noriker population's 12.28 (Druml et al., 2009).

In the 2019 population the average was 15.03 generations the lowest 4.5 and the highest value was 22.8 generations. The recent equivalent complete generations average was lower than it was found for the Old Kladruber population (Vostrá-Vydrová et al., 2016).

Genetic diversity

Table 2 gives information about the genetic variability of the two reference populations. Only 17–17 animals cover the 50% of the genetic variability for the two population, respectively. There were 8 same horses (Table 3), 3 English Thoroughbred, 4 FNS and 1 Arabian (Godolphin Arabian, one of the English Thoroughbred founders). The variability was decreased. In 1989, 81 horses cover 80% of the genetic variability, but in 2019 that was just only 62 horses. It can be seen easily, that the population in 2019 could be covered with much less ancestors which show reasonable gene loss during the breeding history of the FNS horses. There was a slight expansion between 90% and 100%. In 1989, 251 ancestors covered the 90% of the variability, however in the 2019 population that covered 308. In this reference population the last 10% covered by 204 individuals with almost negligible variability, the average contribution was 0.05%, the values varied between 0.002% and 0.148%.

Table 2: Concentration of genetic variability

Ratio of the genetic variability	Individuals	
	1989	2019
50%	17	17
60%	28	26
70%	48	40
80%	81	62
90%	136	104
100%	251	308

Table 3 shows ancestors with greatest impact in the two reference populations. In the first reference population there was only one broodmare (230 Przedswit) among the ten most important ancestors. Most of them were FNS horses. There were three English Thoroughbreds among the ten most important ancestors, and Godolphin Arabian which is one of the founders of the breed. These ten horses were responsible for more than 40% of the total genetic diversity. There were 20 horses took part at least 1% of the genetic variability. The most important ancestor was Herod xx in both reference population, its impact grows in the last 30 years, like the Godolphin Arabian's

in the 2nd place as well. In the population 2019, the ten greatest ancestors covered more than 39% of the total genetic variability. Every horse was stallion; the first broodmare was in the 19th positions with 1.2% impact. Six of them from the FNS breed, three of them from English Thoroughbred, moreover the English Thoroughbred founder Godolphin Arabian. The last two stallions were imported from Slovakia in the 1990's. They had considerable breeding effect, as North Star III had 95, and Furioso XL had 51 progenies in our database. The two stallions together covered cca. 4% of the genetic variability.

Table 3: Ancestors with greatest impact in the two reference populations

1989 population			2019 population		
Ancestor	Birth year	Ratio of the genetic variability (%)	Ancestor	Birth year	Ratio of the genetic variability (%)
Herod xx	1758	7.12	Herod xx	1758	7.60
Godolphin Arabian	1724	5.64	Godolphin Arabian	1724	6.00
Furioso "A" XXVIII	1902	5.25	Furioso VI	1969	5.03
Furioso VI	1969	4.60	Eclipse xx	1764	4.65
Eclipse xx	1764	4.09	Furioso "A" XXVIII	1902	3.76
North Star XXV	1929	3.67	Furioso XXIII	1889	3.19
Furioso XXIII	1889	3.35	Furioso X.	1967	2.81
Furioso II	1961	2.78	Snap xx	1750	2.58
3000 Blokád xx	1949	2.30	North Star III	1985	2.09
230 Przedswit	1937	2.02	Furioso XL	1993	1.98

Inbreeding

Horses having highest inbreeding coefficient in the 1989 population are shown in Table 4 and the 2019 population in Table 5. Every horse in the table was mare. The most inbred animal is 1494 Tüнемény in the first reference population with 25.2% inbreeding coefficient. This mare was born from a father-daughter mating. Also highly inbred 365 North Star "A" XXII

Csinos too. In its pedigree there were three ancestors (North Star XVII, Furioso XL/Sütvény Furioso VII, Furioso "A" XXVIII) accumulated and could be found among the ancestors of maternal and paternal side. The average inbreeding of this reference population was 3.31%. Own results were higher compared to Moureaux et al. (1996) and Vostrý et al. (2011) findings.

Table 4: Horses with the ten highest inbreeding coefficient in the population 1989

Individual	Birth Year	Sire	Dam	Inbreeding coefficient (%)
1494 Tüнемény	1985	117 North Star "A" XXI-11	1441 Tündér	25.2
365 North Star "A" XXII Csinos	1969	North Star "A" XXII tm	364 North Star "A" XIX Vám	15.4
38 Honos	1984	1595 Láttam III	7 Hágó	12.7
23 Gyepes	1980	Haljad I	Gyopár	11.5
Arcpír xx	1977	360 Primás (e.Primstep) xx	Aruna xx	11.1
8 Orsolya	1982	599 Furioso II-9	47 Linka	11.1
22 Illem	1979	1595 Láttam III	Ildomos	9.7
20 Lenge	1970	1594 Piros III	Liget	9.5
34 Látvány	1983	1594 Piros III	4 Látnok	9.5
38 Cica-2	1981	526 Krózus-35	2 Cidrus	9.0

The most inbred animal is The Bart Furioso III-84 Boglár in the 2019 reference population with 29.9% inbreeding coefficient. The first four animals were born from father-daughter mating, the 3rd and the 4th had the same parents. There was just one stallion (5335 The Bart Furioso II-35 Titán) in the ten highly inbred

individual. There were 34 animals with at least 10% inbreeding coefficient. Interestingly, almost every father belonged the line from The Bart xx. The average inbreeding of this reference population was 4.22%. Our results are similar to the data of like Mackowski et al. (2015) and lower than Faria et al. (2018b) finding.

Table 5: Horses with the ten highest inbreeding coefficient in the population 2019

Individual	Birth Year	Sire	Dam	Inbreeding coefficient (%)
The Bart Furioso III-84 Boglár	2014	The Bart Furioso III	Furioso-106	29.9
Hadfi Furioso-61 Mira	2012	3233 Szentes Hadfi-5 Mandarin	Furioso-110 Mici	27.6
Furioso Hadfi-16 Dórika	2014	3233 Szentes Hadfi-5 Mandarin	Furioso-63 Levendula	27.4
Hadfi Furioso-37 Lenke	2013	3233 Szentes Hadfi-5 Mandarin	Furioso-63 Levendula	27.4
The Bart Furioso II-92 Büszke	2016	The Bart Furioso II	Furioso XLVIII-101	18.9
Furioso XXXVI-96 Gyöngy	2012	Furioso XXXVI	Gyümölcs	18.3
The Bart Furioso II-86 Irgalom	2015	The Bart Furioso II	Furioso-38	18.3
The Bart Furioso III-89 Dilemma	2015	The Bart Furioso III	Furioso-43 Dicső	17.0
5335 The Bart Furioso II-35 Titán	2004	The Bart Furioso II	Furioso-131 Fintor	16.3
The Bart Furioso II-94 Félének	2006	The Bart Furioso II	Furioso-31 Fátyol	15.7

CONCLUSIONS

The pedigree completeness increased in the last 30 years all the three measure ways as five more maximum generations were known nowadays and the number of full generations increased by 1.5 generations. There were a few horses with really long 40 generations pedigree, because of the English Thoroughbred background.

In the last 30 years there was a slightly expansion in the genetic diversity, number of animals covering the total genetic variability has been increased from 251 to 308.

Most important ancestor was the English Thoroughbred stallion, Herod xx, for both populations.

Six animals were the same among the ten most important ancestors in both reference populations.

Unfortunately, the inbreeding coefficient increased in the recent population. The highest inbred animals born from matings of close relatives – typically father-daughter.

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