

The effect of foreign stallions on the Hungarian Furioso-North Star breed

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SUMMARY

The most common aim of animal conservation programs is to maintain genetic diversity. Furioso-North Star is an indigenous Hungarian horse breed originated from Mezöhegyes Stud. The breed is based on two founder stallions, Furioso Senior and North Star Senior. The aim of this research study was to analyze the effect of the foreign breeding stallions to the genetic structure of Hungarian Furioso-North Star breed. The genetic structure of the breed was studied from pedigree data what was received from the Furioso-North Star Horse Breeding Association. Foals born between 2015–2018 were chosen as reference population. Every breeding stallion was marked by nationality (Austrian, Czech, German, Hungarian, Romanian or Slovak) according to their birth place. The population was described with genetic variability, what was calculated using Endog software. The Furioso-North Star breed is popular in Central Europe and nearby countries. The stallion imports and the stallion transfers were necessary and useful as they made changes in the composition of the genetic variability. The new genes and the new lines have refreshed the genetic structure. There were several breeds, like the Nonius, Shagya Arabian and English Thoroughbred, whose had an impact on the genetic structure of the Furioso-North Star breed.

Keywords: Furioso-North Star; pedigree analysis; stallions; genetic diversity

INTRODUCTION

The most common aim of animal conservation programs is to maintain genetic diversity. Similarly, to some other indigenous Hungarian horse breeds, the Furioso-North Star (FNS) was developed on the Mezöhegyes State Stud Farm. The breed based on two determining founder English Thoroughbred stallions, Furioso Senior and North Star Senior (Edwards and Geddes, 1991). These two stallions founded two lines that completed each other really good in the breeding (Bodó and Domokos, 2016). The FNS horses regularly featured in equestrian disciplines over the years. Nowadays the breed widespread in the countries of the Carpathian Basin. Besides Hungary, there are considerable populations also in Slovakia and Romania.

Pedigree analysis is a useful method for describing genetic diversity in animal populations (Cole et al., 2004). Small population size and directed selection are known to reduce genetic variability. The FNS population in Hungary is endangered. The results of pedigree analysis give expected values of the increase in homozygosity and decrease in heterozygosity for the analyzed population. (Falconer and Mackay, 1996). The results of pedigree analysis will support appropriate strategies for managing mating plans and illustrating genetic diversity and enlarge the selection basis useful for a selection program (Valera et al., 2005).

In recent decades, a number of studies have been carried out on the population structure and genetic variability of different horse breeds. These methods have been applied to the genetic characterization of different populations, including the Lippizan (Zechner et al., 2002), Hanoverian (Hamann and Distl, 2008),

Polish Arabian (Głazewska and Jezierski, 2004), Lusitano (Faria et al., 2018a) and English Thoroughbred (Bokor et al., 2013).

There were many imported stallions during the almost 200 years breeding history, which resulted the changing of the genetic diversity. The aim of this research study was to analyze the effect of the foreign FNS stallions to the genetic structure of Hungarian Furioso-North Star breed.

MATERIALS AND METHODS

The genetic structure of FNS horse breed was studied from pedigree records. The base pedigree information was given by the Furioso-North Star Horse Breeding Association. That was corrected and expanded from online databases, studbooks and literature sources. The pedigree information was traced back from current population back to the founder animals. The pedigrees were started in the early 1700s years, because of the English Thoroughbred individuals. There were 31,888 animals in the corrected database. The following information was collected by each animal in the built database: name, sex, name of the sire, name of the dam, birth date, and breed. Every breeding stallion (282 horses) was marked by nationality (Austrian, Czech, German, Hungarian, Romanian or Slovak) according to their birth place. All foals between 2015 and 2018 (450 individuals) were chosen as reference population when needed.

The genetic diversity was computed using Endog 4.8 software (Gutiérrez and Goyache, 2005). Before the analysis the database was graphically checked with the Pedigree Viewer 6.5 software (Kinghorn, 1994).

RESULTS AND DISCUSSION

Table 1 presents the concentration of genetic variability in the reference and the total population. The whole population could be covered with much more ancestors than the reference, obviously acceptable the gene loss during the almost two centuries breeding history. The half of the genetic diversity was described by 15 horses in the reference population, there were 3 English Thoroughbred, 1 Arabian and 11 FNS horses. Because of the breed English Thoroughbred background there were horses with quite deep pedigrees, which started in the 1700s years.

There was one broodmare (126 Catalin III-72) among these horses. The total population was described by 20 ancestors.

The variability was decreased (Table 1). Only 255 horses covered all of the genetic variability in the reference population, whereas it was 3478 for the total population. There were 15 horses responsible for the 50% of the genetic variability of the reference population and it was 20 horses for the total population. Bokor et al. (2013) reported smaller numbers for the Hungarian English Thoroughbred population. This confirms the difference between breeds having opened or closed studbooks.

Table 2 shows ancestors having greatest impact in the reference population. Every individual was stallion among the most important ancestors, most of them belonged to the breed. There were three English Thoroughbreds and one Arabian horse (Godolphin

Arabian was one of the founder animals of the English Thoroughbred breed). These ten horses covered more than 40% of the diversity. Only four broodmares were found among the 25 horses which were responsible for at least 1% of the genetic diversity. Herod xx had the biggest proportion of the genetic variability for the reference population. This stallion appeared several times in Furioso Senior's and North-Star Senior's pedigree. This sire was appeared in numerous pedigrees, merely the covering of the variability was almost negligible in each. It can be seen easily, how remarkable was that quantity for that variability. There were 6 FNS breeding stallions (4 Hungarian and 2 Slovak) among these ten ancestors. The ten most important ancestors described 22.48% in the Brazil Quarter Horse population (Faria et al., 2018b).

Table 1: Concentration of genetic variability

Percentage of genetic variability	Individuals	
	Reference population	Total population
50%	15	20
60%	23	43
70%	34	94
80%	51	253
90%	82	945
100%	255	3478

Table 2: Ancestors with greatest impact in the reference population

Ancestor	Birth year	Breed	Ratio of the genetic variability (%)
Herod xx	1758	English Thoroughbred	7.23
Godolphin Arabian	1724	Arabian	5.71
Furioso VI	1969	Furioso-North Star	5.25
Furioso X	1967	Furioso-North Star	4.73
Furioso XX	1987	Furioso-North Star	4.18
Eclipse xx	1764	English Thoroughbred	3.95
Furioso "A" XXVIII	1902	Furioso-North Star	3.46
North Star X	1992	Furioso-North Star	2.58
Snap xx	1750	English Thoroughbred	2.35
Furioso XXIII	1889	Furioso-North Star	2.15

Table 3 shows the ten most important ancestors from the FNS breed with greatest impact in the reference population. There were 5 Hungarian and 5 Slovak stallions, these 10 animals covered almost 30% of the variability. Every Slovak stallion was imported to Hungary. The first Romanian sire was in the 38th position. Furioso VI had the greatest impact (5.25%) in the reference population as there were 40 progenies of this stallion in this database. FNS The most of horses born after 1960, moreover Furioso L from Slovakia in the 7th position born after 2000.

The distribution of the 255 ancestors who covered the complete genetic diversity in the reference

population is illustrated in Figure 1. FNS horses covered 64.8% of the genetic variability from that 42.4% was breeding stallion and the further 22.4% was other FNS sires (not breeding stallions) and mares. There were 91 horses from other breeds with 35.2% of the genetic diversity. The most individuals (27) of them were English Thoroughbred whose covered 24.3%, but Shagya Arabian, Holsteiner, Kisber Halfblood, Hanoverian, Hungarian Sport Horse and Hungarian Warmblood etc. horses as well, but their number was really few.

There were 43 FNS breeding stallions covered the 42.4% of the genetic variability. Most of the stallions

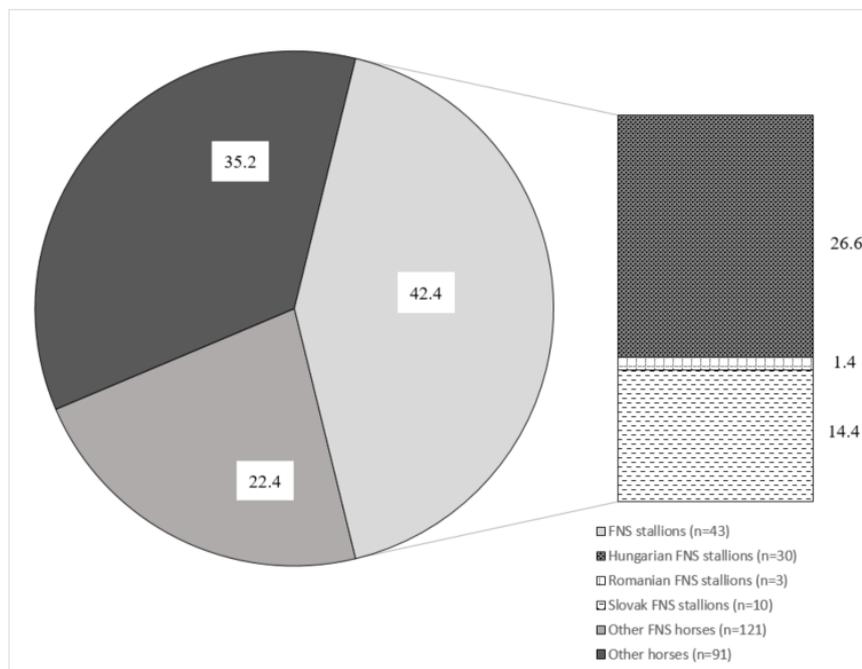
were Hungarian, these 30 animals covered the 26.6% of the genetic diversity. Ten Slovak stallions 14.4% and the Romanian stallions covered just 1.4%. The foreign stallions had an impact to the genetic variability. The Furioso-North Star breed is popular in Central Europe and the nearby countries, the stallion import and the

stallion transfer from that countries is available. The new genes and the new lines refreshing the genetic structure. The Romanian stallions' role were really low, so this population was separate. For the next generations this breeding stock will be an important gene resource.

Table 3: FNS Stallion ancestors with greatest impact in the reference population

Ancestor	Birth year	Nationality	Ratio of the genetic variability (%)
Furioso VI	1969	Hungarian	5.25
Furioso X	1967	Hungarian	4.73
Furioso XX	1987	Slovak	4.18
Furioso "A" XXVIII	1902	Hungarian	3.46
North Star X	1992	Slovak	2.58
Furioso XXIII	1889	Hungarian	2.15
The Bart Furioso II	1996	Hungarian	2.00
Furioso L	2002	Slovak	1.87
Furioso XL	1993	Slovak	1.67
North Star III	1985	Slovak	1.54

Figure 1: The distribution of the ancestors in the reference population (%)



CONCLUSIONS

The reference population could be described with much less ancestors which show reasonable gene loss during the breeding history of the Furioso-North Star horses. Only 15 individuals covered the half of the genetic variability and 255 horses covered the whole.

The most important ancestor was the English Thoroughbred Herod xx for the reference population. This stallion several times appeared in two founder's pedigree. The first ten horses covered more than 40%

of the diversity. 25 horses had at least 1% of the genetic diversity, there were just only four broodmares from them. The stallions role were more significant.

There were five Slovak and five Hungarian stallions among the ten most important FNS breeding stallion ancestors. The imported new genes and the new lines refreshing the genetic structure. Foreign stallions covered more than 15% for the genetic variability in the reference population. The Romanian FNS horse population is a notable gene resource, because of the separation.



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REFERENCES

- Bokor, Á.–Jónás, D.–Bart, D.–Nagy, I.–Bokor, J.–Szabari, M. (2013): Pedigree analysis of the Hungarian Thoroughbred population. *Livestock Science*, 151, pp. 1–10.
- Bodó, I.–Domokos, G. (2016): A mezőhegyesi félvér. Magyar Lótenyésztők Országos Szövetsége, 365 p.
- Cole, J.B.–Franke, D.E.–Leighton, E.A. (2004): Population structure of a colony of dog guides. *Journal of Animal Science*, 82, pp. 2906–2912.
- Edwards, E.H.–Geddes, C. (1991): *The complete horse book*. Ward Lock, London, 344 p.
- Falconer, D.S.–Mackay F.C.T. (1996): *Introduction to quantitative genetics* (Fourth ed.), Longman Group Ltd., Harlow, Essex, 380 p.
- Faria, R.A.S.–Vicente, A.P.A.–Duarte Guedes dos Santos, R.I.–Maiorano, A.M.–Curi, R.A.–Loyola Chardulo L.A.–Vasconcelos Silva, J.A (2018a): Genetic Diversity of Lusitano Horse in Brazil Using Pedigree Information. *Journal of Equine Veterinary Science*, 69, pp. 149–158.
- Faria, R.A.S.–Maiorano, A.M.–Bernardes, P.A.–Pereira, L.G.–Silva, M.G.B.–Curi, R.A.–Vasconcelos Silva, J.A (2018b): Assessment of pedigree information in the Quarter Horse: Population, breeding and genetic diversity. *Livestock. Science*, 214, pp.135–141.
- Glazewska, I.–Jeziński, T. (2004): Pedigree analysis of Polish Arabian horses based on founder contributions. *Livestock Production Science*, 90, 2–3, pp. 293–298.
- Gutiérrez, J.P.–Goyache, F. (2005). A note on ENDOG: a computer program for analysing pedigree information. *J. Anim. Breed. Genet.*, 122, pp. 172–176.
- Hamann, H.–Distl, O. (2008): Genetic variability in Hanoverian warmblood horses using pedigree analysis. *Journal of Animal Science*, 86, 7, pp. 1503–1513.
- Kinghorn, B.P. (1994): Pedigree Viewer—a graphical utility for browsing pedigreed datasets. *Fifth World Congress on Genetics Applied to Livestock Production*. Guelph, 7–12 August 1994., 22, pp. 85–86.
- Valera, M.–Molina, A.–Gutiérrez, J.P.–Gómez J.–Goyache, F. (2005): Pedigree analysis in the Andalusian horse: population structure, genetic variability and influence of the Carthusian strain. *Livestock Production Science*, 95, pp. 57–66.
- Zechner, P.–Sölkner, J.–Bodó I.–Druml, T.–Baumung, R.–Achmann, R.–Marti, E.–Habe, F.–Brem, G. (2002): Analysis of diversity and population structure in the Lipizzan horse breed based on pedigree information. *Livestock Production Science*, 77, pp. 137–146.