

Some population genetics parameters of the present Hungarian Hucul Horse population

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SUMMARY

We examined the Hungarian population of the Hucul horse breed, under genetic protection, based on population genetic indicators until the year 2014 included. The evaluation was performed using the Endog programme based on the following indicators: inbreeding coefficient, average relatedness, the maximum number of generations, the number of full generations traced and offspring number. Our findings were as follows: the average inbreeding coefficient of the total population was 5.99%, average relatedness was 11.82%, the maximum number of generations was, on the average, 16.04%, and the number of full generations traced with reference to the whole population was 4.15% on the average. 40% of the whole population (723 individuals) did not have any offspring; 42% (759 individuals) attained an offspring of 1 or 2, while 3.4% (88 individuals) had a surviving offspring of 3. The highest offspring number according to the national database (92) was attained by one stallion.

Keywords: Hucul Horses, genetic diversity, genetic relationship

ÖSSZEFOGLALÁS

A génvédelem alatt álló hucul lófajta magyarországi állományát populációgenetikai mérőszámok alapján vizsgáltuk 2014-ig bezárólag. Az értékelést Endog programmal végeztük a következő indikátorok alapján: beltenyésztési koefficiens, átlagos rokonsági fok, maximálisan ismert nemzedékek száma, ismert teljes ősi sorok száma és az ivadékszám. Az általunk kapott eredmények: a teljes állomány átlagos beltenyésztettsége 5,99%; átlagos rokonsági fok 11,82%; a maximálisan ismert nemzedékek átlagos száma 16,04%; a teljes állományra vetített teljes ősi sorok számára átlagosan 4,15%-os értéket kaptunk. A teljes állomány 40%-ánál (723 egyed) nem született ivadék, 42%-nak (759 egyed) 1–2 ivadéka lett, 3,4%-ának (88 egyed) 3 megszületett ivadéka van. Az országos adatbázis szerint a legnagyobb ivadékszámot (92 utód) egy mén érte el.

Kulcsszavak: hucul, genetikai diverzitás, genetikai kapcsoltság

INTRODUCTION

The purpose of our examinations was to evaluate the genetic structure of the Hungarian Hucul population based on pedigree data, using population genetic methods. The performance of such examinations has been increasingly justified and frequent in the case of endangered breeds whose population has shrunk to a small size. These calculations may be of great help when designing or making necessary modifications to the breeding programmes. They may set the directions or even the extent of the modifications. They may imply ways for and prove the necessity of sustaining diversity within the populations, may help avoid close breeding or suggest mating systems. They may play a huge role in the necessary and most often essential exchange of breeding stock for blood refreshment. The exploration of the population genetic structure of the breeds may help breeders avoid mistakes that could arise from adapting breeding methods causing genetic imbalance.

Literature review

The theoretical bases of pedigree analysis were first discussed by Wright (1931), followed by James (1962, 1971, 1972), Maccluer et al. (1986) and Lacy (1989). Since the method of Boichard et al. (1997), several pedigree analyses have been published with reference to various species.

Thanks to the development of computer science, today there is opportunity for performing pedigree analyses using various programmes. The programme package PEDIG written in the Fortran programming language by Boichard in 2002 made the analysis of bigger pedigrees possible. Three years later the ENDOG programme enabling the pedigree analysis of smaller populations was released, written in Visual Basic (Gutiérrez and Goyache 2005). In 2006, Sargolzaei et al. designed a programme written in Visual C++ and the following year (2007) Cole wrote PyPedal in Python. In 2009, Groeneveld et al. published the programme Poprep, creating the opportunity of comparing populations as well.

In the course of pedigree analyses, characteristically for populations, the inbreeding coefficient, pedigree completeness (complete generation equivalent, the number of full generations traced, the maximum number of generations) and average relatedness are calculated. Using the ENDOG programme designed and further developed by Gutiérrez and Goyache (2005), these characteristics, too, can be calculated.

Inbreeding coefficient (F_X)

Inbreeding means reproduction from mating based on close genetic relationship. In the case of this breeding technological method gene flow is not applied, as a consequence of which the number of alleles of the same origin grows. Accordingly, the proportion of

heterozygotes and the frequency of rare alleles fall and the proportion of homozygotes rises, so the genetic variability of the progeny population decreases, while phenotypic variance grows. Through the rise in the proportion of harmful homozygous recessive alleles the population's physiological buffer capacity and thus their environmental adaptability weaken, which is reflected in inbreeding degeneration (Dohy 1989). This is why due attention is paid to ensure that the female individuals representing the population have a greatly heterozygous genetic composition (Dohy 1999).

There are numerous references of inbreeding coefficients with regard to various horse breeds, which usually varies between 0.66 and 15.7. The lowest value, 0.66 was specified by Bartolomé et al. (2011) with reference to Spanish Sport Horses; a similar value (0.7) was published by Moureaux et al. (1996) for Selle Français; values between 2.1–7.8 were recorded by Gharahveysi and Irani (2011) with reference to Iranian Arab horses, while a higher one, 9.4 was published by Delgado et al. (2014). With regard to Lipizzan horses, Pjontek et al. (2012) published a value of 4.02 and

Zechner et al. (2002) a much higher one, 10.81. With reference to English–Irish Thoroughbred, Cunningham et al. (2001) published 14, which is the highest value among those specified for English Thoroughbred. Considering all values published, the second highest inbreeding coefficient, 15.7, was recorded by Sevinga (2004) for Friesian horses. For further data relevant in this respect cf. *Table 1*.

Average relatedness (AR)

With regard to average relatedness, in the reviewed literature values between 0.16 and 12.25 were reported. The lowest value (0.16) was published with reference to Spanish Sport Horses by Bartolomé et al. (2011). Bokor et al. (2013) published 10 with reference to Hungarian Thoroughbreds, while Álvarez et al. (2010) published 10.1 for Mallorquí horses. The highest figure, 12.25 was calculated by Valera et al. (2005) in the case of Andalusian horses. Further data on average relatedness are summarised in *Table 2*.

Table 1.

Inbreeding coefficient		
Reference	Breed	Inbreeding coefficient
Moureaux et al. (1996)	Anglo-Arab	1.17
	Arab	3.08
Pjontek et al. (2012)	Shagya Arabian horses	3.95
Gharahveysi and Irani (2011)	Iranian Arab Horse	2.1–7.8
Cervantes et al. (2008)	Spanish Arab Horse	7
Delgado et al. (2014)	Spanish Arabian horse	9.4
Moureaux et al. (1996)	Thoroughbred	1.02
Bokor et al. (2013)	Hungarian Thoroughbred	9.58
Cunningham et al. (2001)	English–Irish Thoroughbred	14
Pjontek et al. (2012)	Lipizzan horses	4.02
Zechner et al. (2002)	Lipizzan horse	10.81
Bartolomé et al. (2011)	Spanish Sport Horse	0.66
Pjontek et al. (2012)	Slovak Sport Ponies	2.67
Posta et al. (2006)	Hungarian Sport Horses	7.9
Moureaux et al. (1996)	Selle Français	0.7
Hamann and Distl (2008)	Hanoverian warmblood horses	mare 1.29 stallion 1.19
Pjontek et al. (2012)	Hucul horses	6.26
Sevinga et al. (2004)	Friesian horses	15.7

Table 2.

Average relatedness		
Reference	Breed	Average relatedness
Bartolomé et al. (2011)	Spanish Sport Horse	0.16
Pjontek et al. (2012)	Shagya Arabian horses	3.08
	Lipizzan horses	3.73
Dunner et al. (1998)	Asturcon pony	6.80
Pjontek et al. (2012)	Slovak Sport Ponies	7.19
Cervantes et al. (2008)	Spanish Arab Horse	9.10
Royo et al. (2007)	Asturcón pony	9.20
Pjontek et al. (2012)	Hucul horses	9.34
Bokor et al. (2013)	Hungarian Thoroughbred	10.00
Álvarez et al. (2010).	Mallorquí horse	10.10
Valera et al. (2005)	Andalusian horse	12.25

Pedigree completeness

The maximum number of generation

The maximum number of generations published in various references varies between 3.1 and 24.56. These are summarised in *Table 3*. The lowest values include 3.1 calculated by Medeiros et al. (2014) for Brazilian Sport Horses and 4.55 (Teegen et al. 2008) for Trakehner Horses. Medium values (17.54) were published by Pjontek et al. (2012) in the case of Hucul horses. Higher values, 29.96, were calculated by Bokor et al. (2013) for Hungarian Thoroughbreds and Pjontek et al. (2012), 34.82, for Shagya Arabian horses.

The number of full generations traced

Findings as regards the number of full generations traced have been relatively low (between 1.25 and 6.69). Medeiros et al. (2014) recorded 1.25 for Brazilian Sport Horses and Teegen et al. (2008) reported a similar value, 1.86, for Trakehner Horses. The highest value (6.69) was published by Bokor et al. (2013) with reference to Hungarian Thoroughbreds. Relevant data including the former are presented in *Table 4*.

Table 3.

The maximum number of generation

Reference	Breed	The maximum number of generation
Medeiros et al. (2014)	Brazilian Sport Horse	3.10
Teegen et al. (2008)	Trakehner Horse	4.55
Pjontek et al. (2012)	Slovak Sport Pony	5.76
Pinheiro et al.(2013)	Sorraia horse	8.17 (back to 1937 it is 13)
Siderits et al. (2013)	German Paint Horse	(2000–2009 original pedigree) 12 (2000–2009 improved pedigree) 14 (1990–1999 improved pedigree) 15
Pjontek et al. (2012)	Hucul horses	17.54
Hamann and Distl (2008)	Hanoverian warmblood horses	23.00
Pjontek et al. (2012)	Lipizzan horses	24.56
Bokor et al. (2013)	Hungarian Thoroughbred	28.96
Pjontek et al. (2012)	Shagya Arabian horses	34.82

Table 4.

The number of full generations traced

Reference	Breed	The number of full generations traced
Medeiros et al. (2014)	Brazilian Sport Horse	1.25
Teegen et al. (2008)	Trakehner Horse	1.86
Pjontek et al. (2012)	Hucul horses	4.29
Pjontek et al. (2012)	Slovak Sport Pony	4.31
Pjontek et al. (2012)	Shagya Arabian horses	5.58
Hamann and Distl (2008)	Lipizzan horses	5.90
Bokor et al. (2013)	Hungarian Thoroughbred	6.69

MATERIAL AND METHODS

In our study we analysed one of the indigenous Hungarian horse breeds, the Hucul, which is included in today's genetic protection programme. The Hungarian Hucul population was analysed until 2014 included. The database was drawn up on the basis of the broodmares, stallions and their foals up to the year 2014 included, recorded in the stud book (Mihók 2014) and held under herd book control. The 153 300 ancestors in the pedigree can be traced back to 1774 different individuals. These 1774 individuals formed the basis of the population genetic calculations. In the course of the study we calculated the inbreeding coefficient, the two indicators of pedigree completeness, i.e. the number of generations traced and the maximum number of generations, as well as average relatedness and the number of offspring. These characteristics were calculated using the Endog programme developed by Gutiérrez and Goyache (2005).

Several indicators can be used for characterising homozygosity in the population. The widely known inbreeding coefficient expresses the likelihood of the occurrence of alleles of the same origin at a given locus. The precision of the inbreeding coefficient depends on the length and completeness of the pedigree (Boichard et al. 1997).

Endog calculates using Wright's formula (1922) where the inbreeding coefficient of a given individual (X) is:

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

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 ancestor "A" on the father's side (n) and the mother's side (n'), and F_A is the inbreeding coefficient of the common ancestor. "Σ" means the

summary of all common ancestors and ancestry roads in the chains of origin of the individual X's father and mother.

Endog calculates average relatedness with an algorithm made by Colleau (2002). It shows the likelihood of an allele randomly chosen from the pedigree characterising the whole population belonging to an individual. It can be evaluated together with the inbreeding coefficient but in the case of defective and/or short pedigrees in characterises population structure in itself. In addition, average relatedness can be used for comparing the inbreeding levels of sub-populations. If it is higher than half of the inbreeding coefficient, the mating of related individuals could not be avoided (Gutiérrez et al. 2003).

Pedigree completeness expresses for how many complete generations we are totally familiar with the origin of individuals. The equivalent complete generations is an adjusted indicator characterising the completeness of the pedigree. The equivalent complete generations is 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).

Pedigree completeness can be characterised by the values of the number of full generations traced, the maximum number of generations and the equivalent complete generations. The first is defined as the furthest generation in which all the ancestors are known. Ancestors with no known parent were considered as founders (generation 0). The second is the number of generations separating the individual from its furthest ancestor.

The offspring number in the pedigree shows the number of offspring born to a certain individual. It is important by how many offspring it contributes to the construction of the next generation. In the selection of individuals chosen for further breeding effort should be made to ensure that the breeding specimen should originate from as many different mating combinations as possible, thereby avoiding either parent's overweight, preventing inbreeding and preserving sustainable genetic diversity.

RESULTS AND DISCUSSION

In what follows we analysed the attained values of the inbreeding coefficient, average relatedness and of the two indicators of pedigree completeness, i.e. the

number of generations traced and the maximum number of generations, as well as offspring number.

Inbreeding coefficient

The mares and stallions with the ten highest inbreeding coefficients are summarised in *Table 5*. Number one is Hroby Bogrács with an inbreeding coefficient of 33.47%. In the case of the parents Hroby Szellő and 3486 Hroby Haragos, the mating was between a father and daughter. There are further factors contributing to the high inbreeding coefficient, i.e. the multiple occurrence of 162 Ousor 02-7 Turek (Murány) in the generation 4–4 in the maternal ancestry of 3486 Hroby Haragos and Hroby Szellő, as well as the multiple occurrence of 136 Gurgul V (Top) in the generation 5–5. The following two high values were once again calculated for two offspring of 3486 Hroby Haragos: Hroby Szilaj 2012 (29.17%) and Hroby Cseppecske (29.07%).

The average inbreeding coefficient of the whole population is 5.99%, which is significantly higher than those specified by Bartolomé et al. (2011) for Spanish Sport horses (0.66%), Moureaux et al. (1996) for Selle Français (0.7) and Anglo-Arab (1.17%). At the same time it is lower than the 6.26% specified by Pjontek et al. (2012) for Hucul horses and Sevinga et al. (2004) for Friesian horses (15.7%).

Average relatedness

The highest average relatedness value, 19.69%, was calculated for the stallion 3804 Hroby XXI-32 (Lu). This stallion is followed by his father, breeding stallion Hroby XXI (Lu) with a value of 18.66%. Next to follow are the offspring of 3804 Hroby XXI-32 (Lu) with values between 18.20–18.33%. The professional explanation for the latter is that the stallion had an offspring of 92, including 8 from the mares Pietrosu X-3 Füles and Ousor IX-22 Gacsos (Lu) (*Table 6*).

The average relatedness of the whole population is 11.82%. This value is significantly higher than the indicators published by the known authors. Bartolomé et al. (2011) published 0.16% for Spanish Sport Horses, Pjontek et al. (2012) 3.08% for Shagya Arabian horses and 3.73% for Lipizzan horses. The highest value in the references was found in Valera et al. (2005) with reference to Andalusian horses, the value being 12.25%.

Table 5.

The 10 individuals in the population with the highest inbreeding coefficients

Animal	Sire	Dam	Gender	Inbreeding coefficient
Hroby Bogrács	3486 Hroby Haragos	Hroby Szellő	stallion	33.47
Hroby Szilaj 2012	3486 Hroby Haragos	Hroby Szöcske	stallion	29.17
Hroby Cseppecske	3486 Hroby Haragos	Hroby Patak	mare	29.07
Hroby II	1342 Hroby I-3-5	Csöpi HL	stallion	28.22
Ousor Félős	2028 Ousor-26 (Sk)	Ousor Edina	mare	27.88
Ousor Gyémánt Fanni	2028 Ousor-26 (Sk)	Ousor Ében	mare	27.88
Ousor Detty	1623 Ousor-13 (Sk)	Ousor Zsályá	mare	27.68
Goral IX (Lu)	Goral VII (Top) Go. V-6 (Lu)	223 Ousor-11 (Lu)	stallion	27.10
Goral Ulrika	392 Goral X-24	3622 Goral Sáríka	mare	26.54
Pietrosu Sámán HL	5001 Pietrosu XI-1 (Lu)	Pietrosu XI-2 (Lu) Stea	mare	23.65

Table 6.

The 10 individuals reflecting the highest average relatedness in the population

Animal	Sire	Dam	Gender	Average relatedness
3804 Hroby XXI-32 (Lu)	Hroby XXI (Lu)	450 Pietrosu VIII-23 (Lu)	stallion	19.69
Hroby XXI (Lu)	Hroby XVI (Lu)	323 Goral X-83 (Lu)	stallion	18.66
Hroby Füles Csacsi	3804 Hroby XXI-32 (Lu)	Pietrosu X-3 Füles	mare	18.33
Hroby Tasli	3804 Hroby XXI-32 (Lu)	Pietrosu X-3 Füles	mare	18.32
Hroby Fáklya	3804 Hroby XXI-32 (Lu)	Pietrosu X-3 Füles	mare	18.31
Hroby Szikra	3804 Hroby XXI-32 (Lu)	Ousor IX-22 Gacsos (Lu)	mare	18.29
Hroby Farkas	3804 Hroby XXI-32 (Lu)	Pietrosu X-3 Füles	stallion	18.28
Hroby Kajla	3804 Hroby XXI-32 (Lu)	Pietrosu X-3 Füles	mare	18.28
Hroby Legenda	3804 Hroby XXI-32 (Lu)	Pietrosu X-3 Füles	stallion	18.28
Hroby Galóca	3804 Hroby XXI-32 (Lu)	Ousor IX-22 Gacsos (Lu)	mare	18.20

The maximum number of generations

The New Age history of the breed has been ongoing since the end of World War I, but the documents of origin of the two stallion stocks go back to the last third of the 19th century. Unsurprisingly there are relatively long pedigrees in the Hungarian population, too; in our case, the maximum number of generations is 24, in the case of the individual Pietrosu Békás.

6% of the stock, 120 individuals, demonstrate 22–23 generations; the individuals Hroby Csinos born in 2006 and Hroby Ádáz born in 2007 are worth mentioning by name. 53% of the stock examined have 18–21 generations traced. Only 91 individuals belong to the zero generation group, which in population genetics (the parents are unknown on both sides) are considered as founders (*Figure 1*).

The average of the maximum number of generations is 16.04. This value is much higher than the value of 3.1 published by Medeiros et al. (2014) with reference to Brazilian Sport Horses or the relatedness published by Teegen et al. (2008), 4.55, with reference to Trakehner Horses, which latter gives rise to doubts. Similarly surprising is the value of 5.76 published by Pjontek et

al. (2012) with reference to Slovak Sport Ponies, which are one of the youngest breeds. Naturally, however, the average of the maximum number of generations of the Hucul breed is lower than the value 28.96 recorded by el Bokor et al. (2013) for Hungarian Thoroughbreds and the 34.82 generation number registered by Pjontek et al. (2012) for Shagya Arabian horses.

The number of full generations traced

The longest complete pedigree in the population examined is 7 generations. This was reached by 101 individuals, i.e. 5.69% of the complete stock. Such individuals are e.g. Pietrosu Tiha or Ousor Gesztenye. 48% of the stock have a complete pedigree of five or six generations.

The differences between the maximum number of generations traced and the number of pedigrees with full generations are due to genetic loss, the immigration demanded in order to increase the genetic diversity of the breed where individuals of unknown origin which are, from a population genetic point of view, considered as founders, were added (*Figure 2*).

Figure 1: The maximum number of generations in the population examined

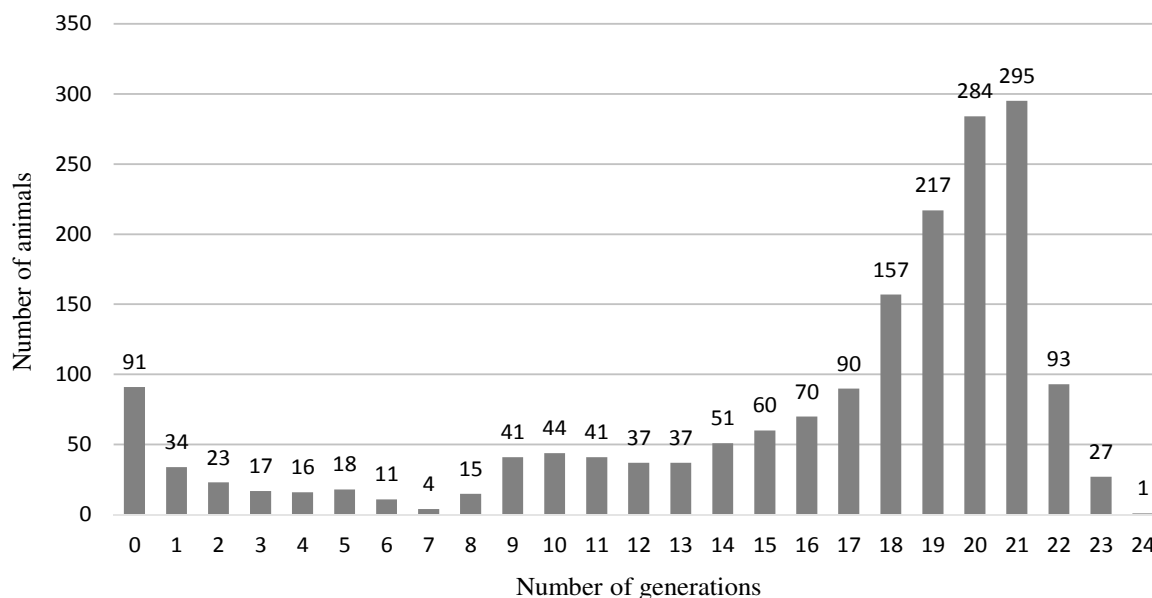
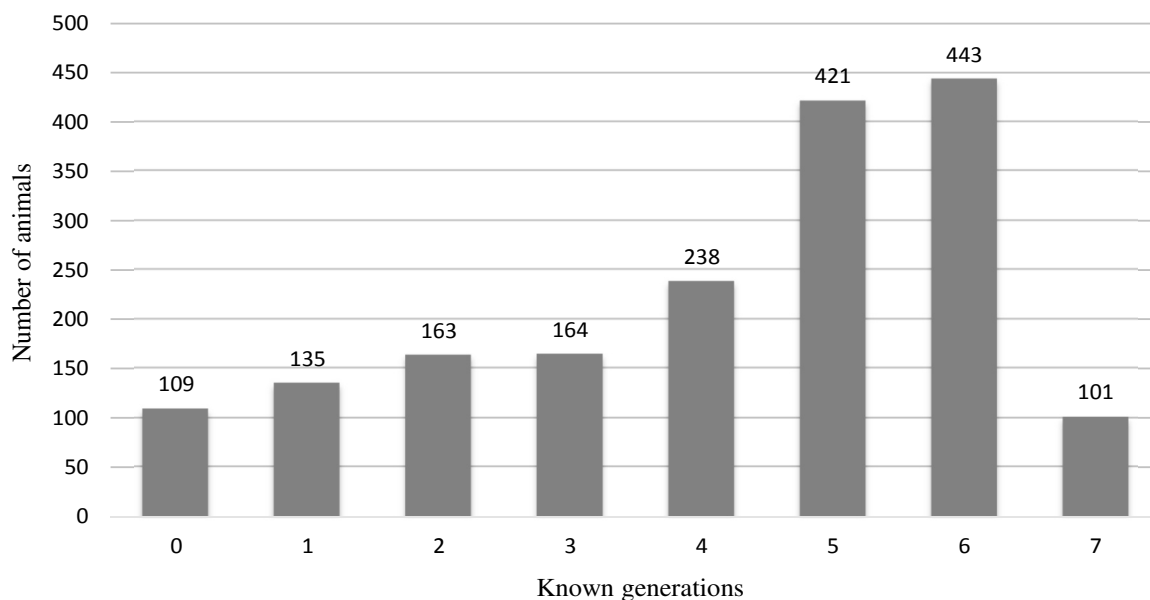


Figure 2: The number of full generations traced in the Hungarian Hucul population



The average number of full generations traced with reference to the whole stock is 4.15. A lower figure than this (1.25) was calculated by Medeiros et al. (2014) for Brazilian Sport Horses and Teegen et al. (2008) for Trakehner Horses (1.86). Higher figures were recorded for Shagya Arabian horses by Pjontek et al. (2012) (5.58) and Hamann and Distl (2008) for Lipizzan horses (5.9). In the reviewed literature, the highest value (6.69) was published by Bokor et al. (2013) with reference to Hungarian Thoroughbreds.

The number of offspring in the pedigree

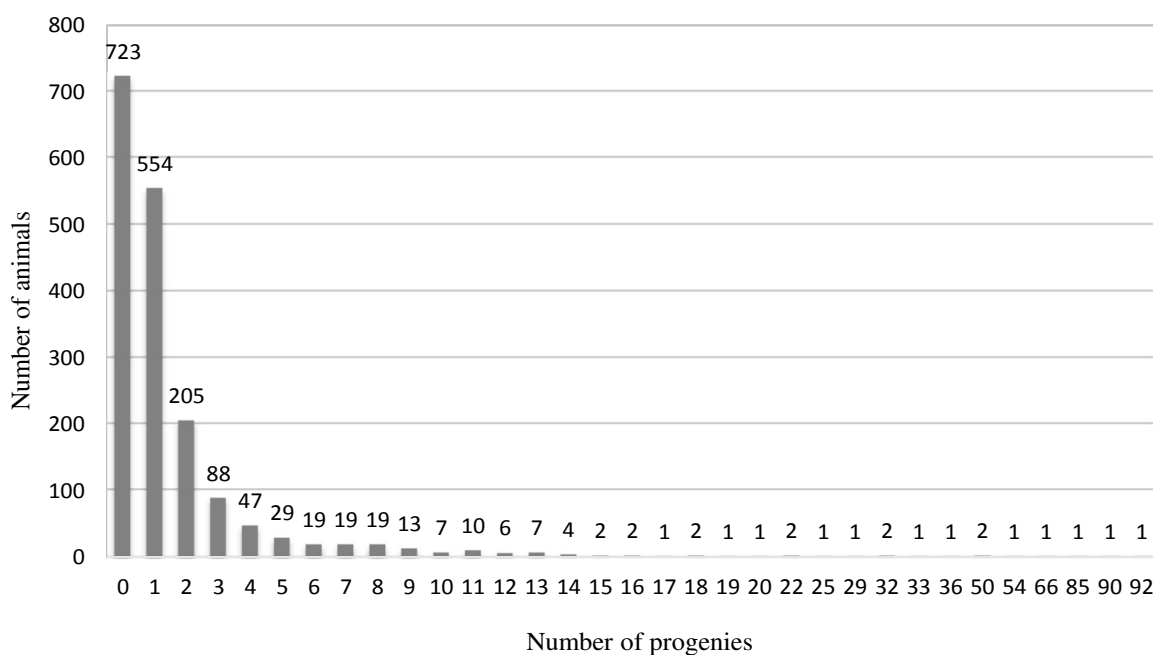
In the case of endangered breeds the aim is, for the sake of the retained genetic diversity, to have as many breeding stock as possible to contribute to the next

generation without any single one having outstandingly many offspring.

Our research shows that 40% of the total population (723 individuals) did not have any offspring. This population genetic indicator can be misleading from the points of view of sustaining genetic diversity or the inevitably growing inbreeding rate because the population examined also includes offspring under the breeding maturity age as well as individuals capable of reproduction that may contribute to genetic diversity in future. In any case, the calculated values reflect a specific state.

Parents with an offspring of 1 or 2 represent the same percentage as the above indicator (42 percent, 759 individuals). 88 individuals in the population (3.4%) have 3 surviving offspring (Figure 3).

Figure 3: The genetic diversity of the population as reflected in the number of offspring



Quite naturally, stallions have abundant offspring. In our case, number one is 3804 Hroby XXI-32 (Lu), with an offspring of 92 recorded in the national database. Stallions' sometimes outstandingly high number of offspring should not be put down to a breeding principle meeting the principle of genetic preservation but, in the majority of cases, to the fact that the owner lacks the means to use numerous stallions in the breeding process.

Here it is worth noting a productive mare (Ousor Detty) that contributed to Hucul breeding in Hungary by an offspring of 15.

CONCLUSIONS

The inbreeding coefficient value we obtained was 5.99, which is higher than half of the average relatedness

(5.91), on the basis of which it can be established that close breeding could not be avoided. In comparison with other breeds (English-Irish Thoroughbreds or Friesian horses), however, this value can be considered low. The maximum number of generations is 24 generations, which is not surprising since the pedigree can be traced back to the time before World War I. The average of the maximum number of generations is 16.04, which is lower in comparison to Shagya Arab and Hungarian Thoroughbreds. The longest complete pedigree extends over 7 generations, which can be considered a high value: this means 256 known ancestors in the pedigree. The mean value of the latter is 4.15, which is lower than those of the Hungarian Lipizzan, Shagya Arab and Hungarian Thoroughbred populations.

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