Theses of Doctoral (PhD) Dissertation

Genetic assessment of historical Hungarian horse breeds from Mezőhegyes

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1. Introduction and aim of the thesis

The human changes their environment and nature, including the animal and the plant species as well. It is carried out according to his own well- or less well perceived interests (BODÓ, 2002). The function of the animal breeding is to satisfy the human demands for animal-based needs with developing and maintaining animal populations with high genetic merit (BODÓ, 2011; VÍGH et al., 2008). The human demands have been changed over time. Each horse breed was breeding because of the human interest. There was a fact in the past to almost every horse breeds came from the military demands (MIHÓK, 2014).

The human-horse relationship is six thousand years old. From the beginning of human history to the first half of the 20th century the horses were indispensable for the armies. The Mezőhegyes Stud was founded in 1784, in this place three indigenous horse breed were bred: Gidran, Nonius and Furioso-North Star. Each breed had a unique type of use. Gidran and the Furioso-North Star were riding horses, the Gidran was used as light cavalry horse whereas the Furioso-North Star characterized like a heavier type. The breeding aim of the Nonius breed was originally to produce draft and driving horses especially for military purposes (SZ. BOZSIK, 1985).

Nowadays the utilization of horses has been changed. Horses not important for the military, due to the motorization horses were lose ground in the agriculture, public and personal transport. They became from farm animal to a popular pet animal (BODÓ és HECKER, 2013). The Hungarian indigenous horse breeding was influenced by a lot of things in the past centuries. Their population decreased and suffered from the bottleneck-effect. Their breeding aims were changed from the military purposes to a hobby usage that changed them characterize too. But these decisions led to the current population genetic structure of the breeds, which have to assessment and clarification. This work is becoming urgent, because we have to maintain our horse breeds for the next generations.

In the last decades the population genetic were highly used method. These analyses will suggest appropriate strategies to monitor mating and manage genetic variability to enlarge the selection basis useful or a selection program.

The 32/2004. (IV. 19.) decision of parliament were declared these three indigenous Hungarian horse breeds – with other Hungarian indigenous breeds as well – to national treasure.

The recorded pedigrees were provided information's about the animals for quantitative genetic calculations (ČAČIĆ et al., 2014). The method of pedigree analysis is being more popular and spread. There are a lot of published research articles about world breeds and also local breeds.

Aim of the research:

- Assessment of the population genetic status of the three indigenous horse breeds from Mezőhegyes using pedigree analysis.
- Assessment of the genetic diversity of the active populations. Determining the most influential individuals for the current population and their responsibility of the genetic diversity.
- Quantification of the bottleneck effect that was suffered the breeds several times.
- Determination of the inbreeding with difference calculation methods for each three breeds.
- Identification of the ancestors that have the greatest influence on the genetic diversity of the studied breeds.
- Identification of the partial inbreeding rate of the stallions that will produce the variety or line.

2. Material and methods

2.1. Material

The base pedigree information for each breed was given by the appropriate breeding associations. These three databases were connected to each other, and after that completed with the missing data from Hungarian and international online databases, studbooks and literature sources. For the Hungarian breeds the OLIR (Országos Lótenyésztési Információs Rendszer) and the http://www.meneskonyv.hu site were used. For the Shagya-Arabian breed Shagya-Arabian Horses Directory (https://shagyadata.ch/shagya/) was used.

Altogether, there were the pedigree data of 47,682 animals in our database

The active populations in 2019 were chosen as reference population for each breed. The population genetic coefficients were calculated for these reference populations.

2.2. Methods

2.2.1. Pedigree completeness

It could be measured in three different ways:

- Number of full generations traced
- Maximum number of generations
- Complete generations equivalent (CGE)

2.2.2. Generation Interval (GI)

The generation interval was average age of the parents at the birth of their offspring kept for reproduction (JAMES, 1977). Generation intervals were estimated on 4 different pathways separately in this study: sire–daughter, sire–son, dam–daughter and dam–son ways. (VALERA et al., 2005). The four pathways were compared pairwise for each using paired samples t-test, for each breed. The confidence interval was 95% ($p<0.05$).

2.2.3. Number of founders (Nf)

The number of animals having both parents unknown (POSTA et al., 2016). They were the known founders. (BOKOR et al., 2010). Each animal within the reference population could be traced back to their founder ancestors, which are responsible unequal for the genetic variability of the population (VÍGH et al., 2008).

2.2.4. Number of ancestors (Na)

The minimum number of (not necessary founder) animals in the pedigree which explains the total genetic variability of the reference population (BOKOR et al., 2010). The indicator takes into consideration the decreasing factors of the number of founders and corrects them (BOICHARD et al., 1997).

2.2.5. Effective number of founders (f_e)

The number of equally contributing founders that would beexpected to produce the same genetic diversity as in the population under study (LACY, 1989, 1995). The effective number of founders was lower than the number of founders because of the calculating method (NAGY, 2016).

2.2.6. Effective number of ancestors (f_a)

The marginal contributions of ancestors that would be expected to produce the same genetic diversity as in the population under study (BOICHARD et al., 1997).

2.2.7. Ratio of effective number of ancestors and effective number of founders (f_a/f_e)

The ratio of effective number of ancestors and effective number of founders implies the bottleneck effect suffered. If the difference between the effective and the total number was high the bottleneck effect was considerable (NEI et al., 1975).

2.2.8. Founder genome equivalent (f_g)

It can be defined as the number of founders that would be expected to produce the same genetic diversity as in the population under study if the founders were equally represented and no loss of alleles occurred (CHEVALET és DE ROCHAMBEAU, 1986). The value was directly comparable with the effective number of founders and the effective number of ancestors.

2.2.9. Ratio of founder genome equivalent and effective number of founders (f_g/f_e)

The ratio of founder genome equivalents and the effective number of founders indicated whether the analysed population was affected by genetic drift. Genetic drift is a random change in the frequency of an existing gene variant – allele – in a population from generation to generation (VÍGH et al., 2008).

2.2.10. Average relatedness (AR)

The average relatedness coefficient shows the likelihood of an allele randomly chosen from the pedigree covering the whole population belonging to an individual (VÍGH et al., 2008). If the value of the coefficient was higher than the half of the Wright coefficient there were mating between relatives in the breeding.

2.2.11. Inbreeding coefficient (F)

The inbreeding coefficient is the probability that two alleles were identical by descent. That is possible if they had at least one common ancestor (SZABÓ et al., 2011). The value of the inbreeding coefficient is between 0 and 1, but there is convertible to percentage form.

- Wright method:

It was calculated following WRIGHT (1922), where the inbreeding coefficient of an individual (X) is:

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

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 common ancestor A on the paternal side (n) and the maternal side (n'), and FA is the inbreeding coefficient of the common ancestor

- Ballou method

The probability that any allele of an individual has been homozygous in previous generations at least once (BALLOU, 1997).

- Ancestral History Coefficient (A_{HC})

Quantifies the frequency that a randomly taken allele has undergone identical by descent status in the past (BAUMUNG et al., 2015).

- Kalinowski and new Kalinowski method

The inbreeding coefficient was split into two parts following method of Kalinowski et al. 2000, whether identical alleles were inbred in the past (Kalinowski coefficient) or became inbred in recent generations (new Kalinowski coefficient).

- Partial inbreeding coefficients (pf)

Generally, the partial inbreeding coefficient is the probability that an individual is autozygous for an allele descended from a specified founder. The partial inbreeding coefficient which calculated for every ancestor is the Wright coefficient (LACY et al., 1996, BAUMUNG et al., 2015).

The partial inbreeding coefficients were measured these breed founder and line founder stallions: Gidran Senior, Nonius Senior, Furioso Senior xx, North Star Senior xx, Gidran XXXI (1863) – Gidran "A" line founder, Gidran XXXIII (1868) – Gidran "B" line founder, Gidran XXI (1863) – Gidran "C" line founder, Nonius XXIX (1880) – Nonius "A" line founder, Nonius XXXI (1880.) – Nonius "B" line founder, Nonius XXXVI (1883) – Nonius C" line founder, Nonius XLII (1847) – Nonius "D" line founder, Furioso I (1850) – Furioso "A" line founder, Furioso X (1851)– Furioso "B" line founder, North Star IV (1899) – North Star "A" line founder, North Star VI (1877) – North Star "B" line founder.

2.2.12. Effective population size (Ne)

The real population inbreeding level is similar to a smaller but ideal structured population. The number of the individuals in this populations was the effective population size (PIRCHNER, 1968). It was defined as the number of breeding animals that would lead to the actual increase in inbreeding if they contributed equally to the next generation (GUTIÉRREZ és GOYACHE, 2005).

Based on the breeders experience the critical effective population size is 50 (FRANKHAM et al. 2002). That was assessed same by FAO (1998) and HILL (2000) too. To necessary interval to maintain the genetic diversity was between 50 and 100 (HALL, 2016), although under 100 the fitness properties were decreased (MEUWISSEN, 1999).

2.3. Presentation of the software used for the analyses

The research work was based on a Microsoft Access database, in which the name and sex of each horse, name of sire and dam, date of birth, breed and identification number were registered. The pedigree file was checked with a Pedigree Viewer 6.0 (KINGHORN, 1994). Databases were analysed by using the ENDOG (GUTIÉRREZ és GOYACHE, 2005). The pedigree completeness by year was computed using PopRep (GROENEVELD et al., 2009). The inbreeding coefficients with different measurements were calculated by Grain software (BAUMUNG et al., 2015), the number of replicates was one million.

3. Results

3.1. Pedigree completeness

Table 1 presents the main indexes for pedigree quality.

Table 1

Pedigree completeness is the reference populations (generations)

Coefficient	Gidran	Nonius	Furioso-North Star
Maximum number of generations	36.32	36.53	36.56
Number of full generations traced	6.10	4.95	4.69
Complete generations equivalent	16.45	12.64	15.18

The average maximum generations were close to 36 generations for each breeds. The highest (36.56) was the Furioso-North Star and the lowest (36.32) was the Gidran population. There were 31 individuals with more than 40 generations length pedigree. In the active populations almost every horses (99.3%) had ancestors at least 30 generations back

The mean number of complete generations was 6.1 for the Gidran, and 4.69 for the Furioso-North Star. The Nonius (4.95) were close to the Furioso-North Star. At least five generations were completely known for the 78.6% of the animals in the three reference populations

The complete generations equivalent varied between 12.64 and 16.45. The Gidran was the highest and the Nonius was the lowest. The mean number was 15.18 for Furioso-North Star reference population.

3.2. Generation Interval

The generation interval was measured in four different pathways (sire–to-daughter, sire–to-son, dam– to-daughter, dam– to-son).

The longest generation interval (12.77) was computed for sire pathways, and the shortest (10.83) to the dam- to-son pathway for the Gidran reference population. The average generation interval was 11.93.

The longest generation interval (12.54) was computed for sire- to-son, and the shortest (10.63) to the dam- to-daughter pathway for the Nonius reference population. The average generation interval was 11.61.

The longest generation interval (12.64) was computed for sire- to-son, and the shortest (10.75) to the dam- to-son pathway for the Furioso-North Star reference population. The average generation interval was 11.78.

The four pathways were compared pairwise for each breed, using independent samples t-test. There were significant differences between the mare and the sire pathways ($P<0.05$) for the Furioso-North Star and the Nonius breed as sire pathways were approximately two years longer than those of broodmares. Besides the significant different between the sire and dam pathways, dam-to-son and dam-to-daughter pathways was also significantly different for the Gidran breed. The longer breeding time was caused to longer generation interval, in this time the genetic diversity still constant.

3.3. Effective number of founders, effective number of ancestors, ratio of the effective number of founders and the effective number of ancestors, the founder genome equivalent, and the ratio of the founder genome equivalent and the effective number of founders

The effective numbers of founders were both 99 for the Gidran and the Furioso-North Star, and 95 for the Nonius reference population. The effective number of ancestors was similar (22 and 24) for the Gidran and Nonius, and almost double, 43 for the Furioso-North Star.

The ratio between the coefficients was reasonable, each breed suffered the bottleneck effect. The values were lower for the Gidran and the Nonius breeds, and higher for the Furioso-North Star.

The value of founder genome equivalent was lower than the effective number of founders and the effective number of ancestors. The Gidran and the Nonius were close to each other, the calculated founder genome equivalent was estimated at 7.84 for Gidran, and 7.97 fort the Nonius reference population. The value for the Furioso-North Star was higher than that, 11.75 The ratio between the founder genome equivalent and the effective number of founders was affected by genetic drift. The level of the genetic drift was in the same tendency, the lowest (7.9%) for the Gidran and the highest (12%) for the Furioso-North Star. The Nonius population were close to the Gidran (8.4%).

3.4. Genetic variability

The concentration of the genetic variability was different for each breed. The Gidran was the most concentrated for the total and the reference population too. The active Gidran population in 2019 (367 horses) was described with 138 ancestors, but the total population was described with 1724. The Nonius total population was covered by 4246 horses, while a reference population was described only 239. Only 9-9 animals cover the 50% of the genetic variability for Gidran and Nonius breeds, respectively. In the Furioso-North Star population that was a bit higher, 17 horses. The total population of the Furioso-North Star was described with 3123 and the reference population was described with 311 ancestors.

The 10 most important ancestors were covered different parts of the variability for each total and reference populations. The Gidran and the Nonius were narrowed in the 10 most influential ancestors. For the total population the 10 most important individual were covered the 45.9% of the genetic diversity, for the reference population that increased to 54.7%. For the Nonius that was increased from 38% to more than 55%. The value of the genetic variability for the Furioso-North breed was decreased. The 10 most important ancestors covered more than 43% fort the total population and just under 40% for the reference population.

The three most influential ancestors were same for each breed: Herod xx and Eclipse xx English Thoroughbreds and Godolphin Arabian one of the founder stallion of the English Thoroughbred breed. In the ten most important ancestors were English Thoroughbreds and English Thoroughbred founders for the Gidran and Furioso-North Star total populations. However for the Nonius total population there were Nonius breeding stallions too.

There were just stallions in the ten most important ancestors for the Gidran reference population. The genetic variability was covered with 138 individuals, there were 25 horses with 1% impact. Besides the Gidran stallions there were two English Thoroughbred (Herod xx, Eclipse xx) and one Arabian (Godolphin Arabian). The most important ancestor was Gidran XI. This stallion covered 10.34% of the genetic diversity, it had 62 progenies in our database.

There were eight Nonius breeding stallions, one English Thoroughbred (3185 Akitos xx) and one Holsteiner (311 Aldato) in the ten most important ancestors for the Nonius reference population. There were 22 horses with 1% impact among the all ancestor. The most important ancestor was Nonius VI, only that breeding stallion covered 13.81% of the genetic variability. This Breeding Stallion had 80 progenies in our database, there were 6 breeding stallions among these horses.

There were 23 horses with 1% impact among the all ancestors for the Furioso-North Star reference population. There were just stallions in the ten most important ancestors for the Furioso-North Star reference population. One of them was Arabian, three of them English Thoroughbred and 6 were Furioso-North Star Breeding Stallions. Among these horses there were five from the Furioso line and only one from the North Star line. The most important ancestor was Herod xx, it covered 7.75% of the genetic diversity. The first breeding stallion from the Furioso-North Star breed was in the fourth most important ancestor with 4.7% impact.

This stallion (Furioso VI) had 12 stallion progenies 3 were breeding stallions (Furioso XI, Furioso XIII, Furioso XV) among these horses.

3.5. Average Relatedness

Figure 1 presents the average relatedness for the total and the reference populations for each breed. The average relatedness for the total populations was the highest for Gidran (4.5%), and lowest for the Nonius (3.4%), The value of the Furioso-North Star breed was close to the Gidran (4.32%). The average relatedness was the highest for the Furioso-North Star (4.08%) and the lowest for the Nonius breed (3.68%), but the value was approximately 4% for each reference populations.

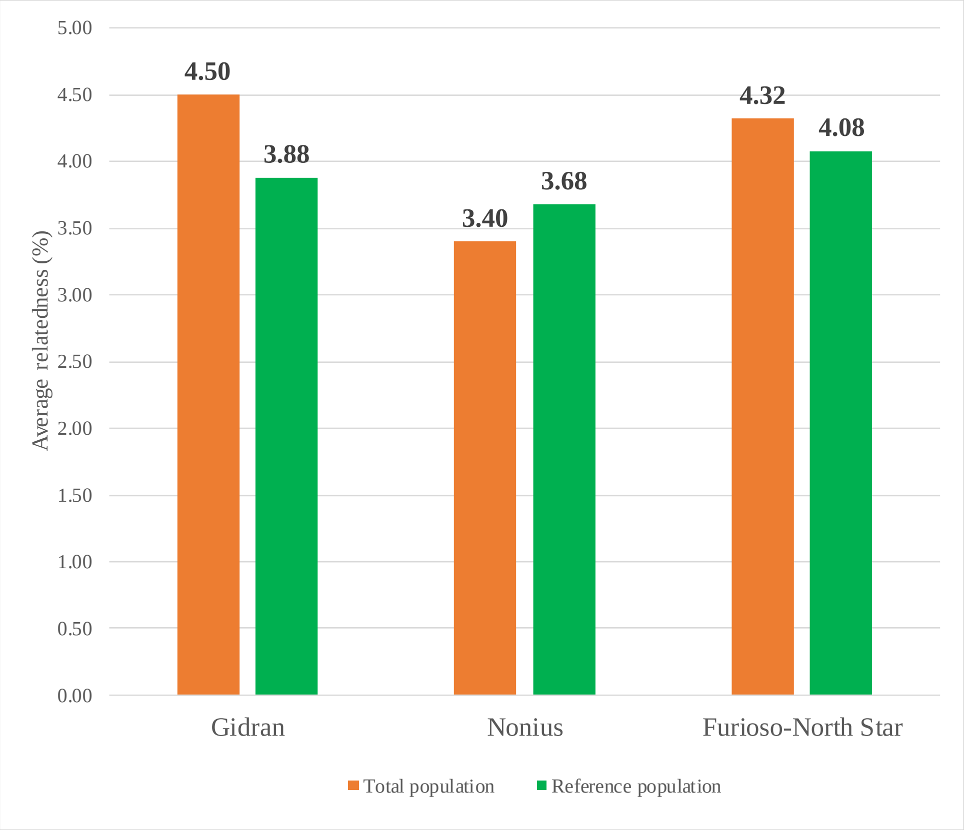

Figure 1: **Average relatedness for the total and the reference populations**

Compared to the value of the total population the Gidran and the Furioso-North Star were decreased, the Nonius slightly increased. Because the value of the coefficient was higher than the half of the Wright coefficient there were mating between relatives in the breeding.

3.6. Inbreeding

3.6.1. Inbreeding for the all ancestors

The different inbreeding coefficients for the total and reference populations were shown in Table 2.

Table 2

Comparison of the inbreeding values based on different approach (%)

Method	Gidran		Nonius		Furioso-North Star	
	total population	reference population	total population	reference population	total population	reference population
Wright	5.02	4.95	3.82	5.59	4.70	4.31
Kalinowski	3.15	3.48	2.23	3.29	3.10	3.07
New Kalinowski	1.86	1.48	1.59	2.40	1.60	1.24
Ballou	22.43	39.30	17.94	28.87	23.04	34.39
A_{HC}	35.49	73.64	27.27	45.45	38.30	66.90

The traditional Wright coefficient for the total populations was the highest for the Gidran and the lowest fort the Nonius breed. For the reference population there were inverse, the mean Wright inbreeding coefficient was the highest for the Nonius (5.59). The inbreeding level was higher in the total population for the Gidran and the Furioso-North Star, than in the references. Only for the Nonius breed was higher the value of the reference population, so the current population was more inbred. The inbreeding coefficient was the lowest (4.31) for the active Furioso-North Star population.

The Ballou coefficient was higher than the other estimated inbreeding coefficients especially for the Gidran breed. The value for the reference populations was increase, from the total populations. There were the lowest (28.87) for the Nonius and the highest (39.3) for the Gidran reference populations. The probability that an allele was homozygous in the previous generations was more than 30% for the Furioso-North star and almost 40% for the Gidran breed.

The Wright inbreeding coefficient was split into two parts using Kalinowski's method: alleles which had undergone inbreeding in the past and alleles identical by descent for the first time. The higher the value of Kalinowski coefficient means that the inbreeding was from the past, if the new Kalinowski coefficient was higher the alleles identical by descent for the first time. The Kalinowski and the new Kalinowski coefficients were lower than the other measured parameters for each population. The estimated new Kalinowski values were smaller then

Kalinowski values, so inbreeding originated mostly from the past, ant these level was similar in each breed. The mean value of Kalinowski coefficient was the lowest for the Nonius, and the highest for the Gidran total population. The new Kalinowski coefficient was the lowest for the Furioso-North Star and the highest for the Gidran population. The Kalinowski and the new Kalinowski inbreeding coefficient for the reference population was the lowest for the Furioso-North Star breed. The Kalinowski was 3.07 the new Kalinowski was 1.24.

The A_{HC} coefficient was the number that tells how many times during pedigree segregation a randomly taken allele has been in identical by descent status. The value was the lowest for the total population for Nonius and the highest for the Furioso-North Star breed. For the reference populations the value of the Gidran breed was the highest mean coefficient. There was a huge difference between the total and the reference populations. The value of the reference populations was higher than the total, especially in the Gidran breed where more than double.

In the Gidran reference population there were 22 individuals with more then 10% Wright inbreeding coefficient. The five most inbred horses with their Wright and Kalinowski coefficient were shown in Table 3.

Table 3

Animals with highest inbreeding coefficient within the Gidran reference population

Individual	Birth year	Sire	Dam	Wright (%)	Kalinowski (%)
Gidran XXX-47 (Holdfény)	2014	Gidran XXX (2002)	Gidran XXX-44 (Harmat)	29.37	14.80
Gidran XXX-60 (Hozomány)	2015	Gidran XXX (2002)	Gidran XXX-44 (Harmat)	29.37	14.80
Gidran XXIV-126 (Sirály)	2007	Gidran XXIV (1983) (XXXIX R)	Gidran XIX-63 (Moldika)	19.07	11.00
Gidran Mersuch-22 (Virág)	2010	4888 Mersuch XXII Gidran-46	Mersuch XXII Gidran-42 (Vera)	18.46	6.77
Déva Gidran-18 (Linda)	2000	Déva Gidran II (1993)	148 Déva Gidran-3 (Kincses)	18.16	12.80

There were just mares in the Table. The two highest inbred animal – Gidran XXX-47 (Holdfény), Gidran XXX-60 (Hozomány) – originated from the same father-daughter mating. Their Wright coefficient was 29.37%, and their Kalinowski coefficient (14.8%)was the highest too. so the half of the inbreeding originated from the past.

The next horse Gidran XXIV-126 (Sirály) originated from the grandfather-granddaughter mating. There were accumulated English Thoroughbred stallions (Naum xx, 2394 Déva xx) in last two individual's pedigree. Among these horse Déva Gidran-18 (Linda) had the third highest Kalinowski coefficient. But the ratio between the Wright and the Kalinowski coefficient was more than 70%.

In the Nonius reference population there were 46 individuals with more than 10% Wright inbreeding coefficient. The five most inbred horses with their Wright and Kalinowski coefficient were shown in Table 4.

Table 4

Animals with highest inbreeding coefficient within the Nonius reference population

Individual	Birth year	Sire	Dam	Wright (%)	Kalinowski (%)
4341 Nonius-142 (Saci)	2009	2819 Makó Nonius-9	3238 Nonius-10 (Emma)	27.99	9.53
4709 Nonius IV-126 (Dáma)	2009	Nonius IV (1996)	3826 Nonius XVII-11 (Melitta)	19.70	10.48
4708 Nonius IV-129 (Csoda)	2016	Nonius IV (1996)	4031 Nonius XVII-133 (Panka)	18.49	9.52
Nonius-217	2009	2556 Nonius XV-3	2271 Tündér	18.24	9.79
4250 Nonius IV-142 (Vonzó)	2012	Nonius IV (1996)	273 Nonius XVII-73 (Dudus)	18.01	8.28

There were just mares in the Table. The highest inbred horse 4341 Nonius-142 (Saci) was originated from father-daughter mating. The other individual's coefficient was 10% lower. The Kalinowski coefficient for this horse was one of the highest in the breed respectively. The two grandfathers were the same for the second and the third mare, so they were originated from half siblings mating. The Kalinowski inbreeding coefficient was the highest for 4709 Nonius IV-126 (Dáma), the value was more than 10.4%. In the fourth animal pedigree several horses were accumulated. The fifth horse originated from half siblings mating.

In the Furioso-North Star reference population there were 35 individuals with more than 10% Wright inbreeding coefficient. The five most inbred horses with their Wright and Kalinowski coefficient were shown in Table 5. There were just mares in the Table. The highest inbred horse The Bart Furioso III-84 (Boglár), was originated from father-daughter mating, it's had more than 30% Wright coefficient. The Kalinowski coefficient for this horse was 16.64%, so the half of the inbreeding coefficient was from the previous generations.

Table 5

Animals with highest inbreeding coefficient within the Furioso-North Star reference population

Individual	Birth year	Sire	Dam	Wright (%)	Kalinowski (%)
The Bart Furioso III-84 (Boglár)	2014	The Bart Furioso III (2003)	Furioso-106	30.01	16.64
Hadfi Furioso-61 (Mira)	2012	3233 Szentes Hadfi-5 Mandarin	Furioso-110 (Mici)	27.76	11.94
Furioso Hadfi-16 (Dórika)	2014	3233 Szentes Hadfi-5 Mandarin	Furioso-63 (Levendula)	27.68	11.83
Hadfi Furioso-37 (Lenke)	2013	3233 Szentes Hadfi-5 Mandarin	Furioso-63 (Levendula)	27.68	11.83
The Bart Furioso II-92 (Büszke)	2016	The Bart Furioso II (1996)	Furioso XLVIII-101	18.95	11.66

The first four individuals were originated from father-daughter mating, Furioso Hadfi-16 (Dórika) and Hadfi Furioso-37 (Lenke) had same parents. The value of the Kalinowski coefficient was in the same level exceptionally the first horse.

3.5.2. Partial Inbreeding

Up to now, the total inbreeding coefficients were analysed. The stallions for which partial inbreeding was estimated were listed in the 2.2.11. chapter.

Three genealogical lines were kept by the Gidran Breeding Association, it was started in the late XIX. century. Table 6 shows the Wright coefficient and the partial inbreeding for the breed founder and the line founder stallions in each Gidran stallion lines.

The average Wright inbreeding coefficient was the highest for the ”A” line, almost 5%, there were less than 0.05% the partial inbreeding from that. The values were almost the same for the ”B” and ”C” lines. The sum of the partial inbreeding was 0.39% for the ”B” line, and a bit higher 0.49% for the ”C” line, but both value were low. For each genealogical line the partial inbreeding was the highest for the ”A” line founder stallion and the lowest was the ”C” line founder stallion. The partial inbreeding value for Nonius Senior was 0.02% for each genealogical line, proven that these three originated from Mezőhegyes.

Table 6

The Wright coefficient and the partial inbreeding for the breed founder and line founder stallions of each Gidran stallion lines (%)

	Wright coefficient	**Gidran Senior**	**"A" line founder**	**"B" line founder**	**"C" line founder**
"A" line stallions	4.87±1.92	0.03±0.01	0.32±0.17	0.11±0.07	0.02±0.01
"B" line stallions	3.51±2.10	0.02±0.02	0.27±0.19	0.07±0.08	0.03±0.04
"C" line stallions	3.52±1.33	0.02±0.01	0.34±0.10	0.11±0.04	0.01±0.01

Table 7 shows the Wright coefficient and the partial inbreeding for the breed founder and the line founder stallions of each Nonius stallion lines.

Table 7

The Wright coefficient and the partial inbreeding for the breed founder and line founder stallions of each Nonius stallion lines (%)

	Wright coefficient	**Nonius Senior**	**"A" line founder**	**"B" line founder**	**"C" line founder**	**"D" line founder**
"A" line stallions	6.09±3.16	0.05±0.02	1.12±0.61	0.69±0.35	0.60±0.35	0.01±0.01
"B" line stallions	4.01±2.24	0.03±0.03	0.62±0.29	0.46±0.19	0.29±0.12	0.01±0.01
"C" line stallions	4.30±3.05	0.03±0.03	0.73±0.55	0.46±0.30	0.42±0.31	0.01±0.01
"D" line stallions	7.96±4.45	0.10±0.06	1.07±0.43	0.62±0.25	0.64±0.30	0.02±0.02

Four genealogical lines were kept by the Nonius Breeding Association, but they were not in balance. There were only 9 stallions in the ”D” line, the most individuals (26) were in the ”A” line. For each genealogical line the partial inbreeding was the highest for the ”A” line founder stallion and the lowest was the ”D” line founder stallion. Moreover the value of the

”D” line founder stallion was lower than Nonius Senior’s value. The mean Wright coefficient was higher than the Gidran breed’s value. The highest was for the ”D” line, where the average value was almost 8%, so the partial inbreeding coefficients were high as well.

There were four traditional stallion lines for the furioso-North Star breed, but nowadays one (North Star ”B”) extinct. Table 7 shows the Wright coefficient and the partial inbreeding for the breed founder and the line founder stallions in each Furioso-North Star stallion lines. Each stallion lines partial inbreeding were the lowest for the North Star ”B” line founder stallion.

One of the most important about the Furioso-North Star stallion's character was their line. However the partial inbreeding was higher in the Furioso ”A” and Furioso ”B” line in the North Star Senior than Furioso Senior. For each genealogical line the partial inbreeding was the highest for the Furioso ”A” line founder stallion. The Wright coefficient was lower than the in Nonius breed, The highest value was in Furioso ”B” and North Star ”A” lines, their inbreeding coefficient were above 4%.

Table 8

The Wright coefficient and the partial inbreeding for the breed founder and line founder stallions of each Furioso-North Star stallion lines (%)

	Wright coefficient	**Furioso Senior**	**North Star Senior**	**Furioso "A" line founder**	**Furioso "B" line founder**	**North Star "A" line founder**	**North Star "B" line founder**
Furioso "A" line stallions	3.11±1.87	0.02±0.02	0.07±0.06	0.16±0.14	0.07±0.06	0.12±0.14	0.12±0.10
Furioso "B" line stallions	4.06±1.46	0.02±0.01	0.10±0.06	0.23±0.10	0.09±0.05	0.17±0.09	0.04±0.09
North Star "A" line stallions	4.01±1.55	0.02±0.01	0.07±0.04	0.19±0.09	0.06±0.04	0.14±0.09	0.11±0.07

3.7. Effective population size

The effective population size was crucial part in the endangered populations. The coefficient for each reference population was above the critical 50. The lowest effective population size (70.35) was characterised the Furioso-North Star population. The value of the Gidran and the Furioso-North Star were both 77.67. Each population was between 50 and 100, these level is necessary to maintain the genetic diversity.

4. New scientific results

1. The values of the average relatedness were between 3.68 and 4.08% for the three indigenous horse breed from Mezőhegyes. The effective number of founders was 95–99 individuals, the effective number of ancestors was 22–24 for the Gidran and the Nonius, and 43 for the Furioso-North Star.

2. The genetic variability of the reference populations of the three indigenous horse breed's from Mezőhegyes were covered mostly by their own breeding stallions, respectively. The number of individuals whose covered the genetic variability were decreased for each breed for the Gidran 1724 to 138, for the Nonius 4246 to 239, for the Furioso-North Star breed 3123 to 311.

3. The three indigenous horse breed form Mezőhegyes were suffered from bottleneck effect. The ratio of the effective number of ancestors and the effective number of founders was 0.24 for the Gidran, 0.23 for the Nonius and 0.43 for the Furioso-North Star breed.

4. The inbreeding coefficient of the three indigenous horse breed from Mezőhegyes was measured with different methods. The values of the Wright coefficients were between 4.31 and 5.59% for the reference populations. Based on the Kalinowski method, the inbreeding originated from the past for each breed, and was lower nowadays.

5. The most influential ancestors in the three indigenous horse breed from Mezőhegyes were Herod xx, Godolphin Arabian and Eclipse xx

6. The partial inbreeding coefficient were identified for stallions of the three indigenous horse breed from Mezőhegyes. The values of the partial inbreeding for each founder stallion was 0.01–0.06 for the Gidran 0.01–2.36 for the Nonius and 0,01–0,18 for the Furioso-North Star.

5. Important results of the thesis for practice

1. This study would help to the breeding associations to develop appropriate strategies and modifies selection programs.
2. There was some highly inbred animal in the three reference populations. Our data could help to mating these horses with an appropriate breeding partner to decreasing the Wright inbreeding coefficient for the population.
3. The long generation interval is preferable for the gene preservation. Our generation interval values help to maximize this coefficient for each breed. In case of maximized generation interval, the decreasing to the genetic diversity is slower.
4. In our database the pedigree of the breeding stallions from other breeds were longer and more complex than the national database. The breeding associations could make a more precise decision to choose a breeder animal based on our data.
5. Because of the really depth English Thoroughbred pedigrees we can see the value of the English Thoroughbred gene percentage for each breed. There are more precise data which animals were in the breeds in the past centuries. It is a useful help to choose a breeder animal.

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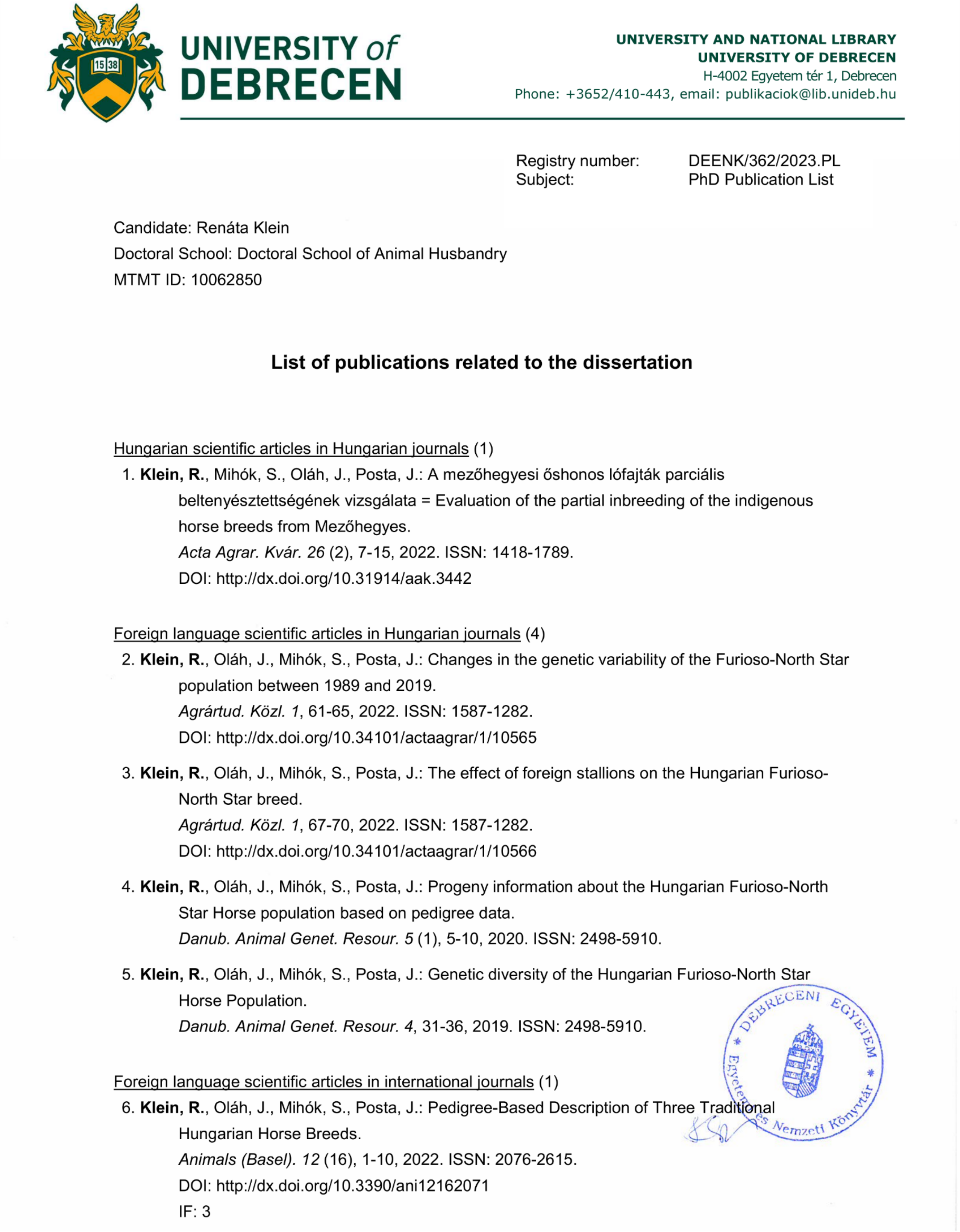
7. List of publications



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List of publications related to the dissertation

Hungarian scientific articles in Hungarian journals (1)

1. **Klein, R.**, Mihók, S., Oláh, J., Posta, J.: A mezőhegyesi őshonos lófajták parciális beltenyésztettségének vizsgálata = Evaluation of the partial inbreeding of the indigenous horse breeds from Mezőhegyes.
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