Pedigree analysis of Thoroughbred horses in Slovakia

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The aim of this paper was to evaluate the breeding population of Thoroughbreds in Slovakia using pedigree analysis. Examined population consisted of 123 mares and 10 stallions registered in Slovak Stud Book. Three stallions linked to Nasrullah line (30 %) and 2 stallions linked to Northern Dancer (20 %) and Native Dancer (20 %) lines. Over a half of mares were represented by Northern Dancer line (50.41 %). The average inbreeding coefficient was 0.86 % in whole reference population (133 individuals) and increase in inbreeding per generation was 0.17 %, in stallions 0.25 %. The number of founders in investigated population was 949. The effective number of founders was 202, while the effective number of ancestors was 67. These results point out unbalanced contributing of founders and ancestors into reference population as well as the bottleneck effect occurance. The Northern Dancer (CAN) was the most important ancestor in investigated population with individual contribution IC = 7.88 %.

Keywords: genetic diversity, inbreeeding, pedigree analysis, racing, Thoroughbred

1. Introduction

The Thoroughbred (TB) is typical representative of modern type of race horse. Achievement of maximal speed and earliness in races is main criterion in Thoroughbred selection. TB horse breed was established in England in the early 1700s based on crosses between stallions of Arabian origin and poorly defined, possibly indigenous, groups of mares. The founder population was small; all contemporary males trace back to one of three stallions (the Godolphin Arabian, the Byerley Turk and the Darley Arabian), whilst on the female side about seventy foundation mares have been identified (Binns et al., 2010; Willett 1970). TB performance testing is provided by racing. Flat races have the highest selection level, while the selection level of hurdle races is negligible. The very first race on the teritory of today´s Slovakia took place on 22ⁿᵈ May 1814 in Urmín (Mojmírovce) organized by earl Jozef Hunyady (Gressner, 1995). Nowadays, TB breeding and racing in Slovakia is controlled by Turf Direktorium, s.e. Bratislava, which is responsible for Stud Book keeping as well. The quality of Slovak races is on very high level in central European region. However Slovak TB breeding passes through the stagnation and decline in recent years, as evidenced by decreased number of born and registered foals as well as by performance quality of horses born in Slovakia. There have been some positive results of Slovak TB breeding in recent years which proved that right system of mating and rearing of young horses can lead to production of good class horses in Central European region. Except the genetic predisposition, the horse performance is significantly influenced by many environmental factors. The success of a TB racehorse is determined by a multitude of factors such as age, sex, nutrition (Gálik et al., 2011; Gálik et al., 2012) of which many are impossible to evaluate.

The aim of our work was to assess breeding population (stallions and mares) of Thoroughbred in Slovakia by the methods of pedigree analysis.

2. Material and methods

The input information was obtained from the Slovak Stud Book for Thoroughbred (SSB), volume IV. (2006–2009) and from the 2ⁿᵈ supplement of SSB issued in 2011 by Turf Direktorium Bratislava. Breeding stallions having mating licence in 2012 and breeding mares presented in the 2ⁿᵈ supplement of SSB issued in 2011, were involved in the analysis. Mares, which died or were euthanized or exported abroad in 2011, were excluded from the analysis. There were 10 breeding stallions and 123 breeding mares included in the analysis. The paternal lineage structure and structure according to sires and dam-sires in investigated population were evaluated.

In further analysis, we focussed on evaluation of genetic diversity measures in given population by the methods of pedigree analysis. The 133 individuals (10 stallions, 123 mares) set up the reference population.

Acta fytotechn. zootechn., 17, 2014(4): 122–126

Ivan Pavlík, Zuzana Schubertová, Ondrej Kadlečík, Juraj Candrák, Radovan Kasarda: Pedigree analysis of Thoroughbred horses in Slovakia

These animals represented whole active breeding population of TB in Slovakia. The program ENDOG v.4.8 (Gutiérrez and Goyache, 2005) was used for computation of diversity parameters. Index of pedigree completeness (PEC) according to McCluer et al. (1983) was calculated as well.

Parameters based on probability of identity-by-descent were used as follows:

- Individual inbreeding coefficent (F_i), defined as the probability that two individuals recieved two identical alleles by descent (Gutiérrez and Goyache, 2005).
- Individual increase in inbreeding (ΔF_i), calculated as the difference of inbreeding coefficient of individual i and its parents (Kaerney et al., 2004).
- Average relatedness coefficient (AR), defined as the probability that an allele randomly chosen from the whole population belongs to a given animal (Gutiérrez and Goyache, 2005).

Parameters based on probability of gene origin were used as follows:

- Number of founders (f). Founder is defined as animal with unknown genetic connections to other animals in pedigree except its own progeny (Lacy, 1989).
- Effective number of founders (f_e), defined as the number of equally contributing founders that will produce the same genetic diversity as in the assessed population (Boichard et al., 1997).
- Effective number of ancestors (f_a), defined as the minimal number of ancestors necessary to explain the genetic diversity in the reference population (Boichard et al., 1997).
- Number of ancestors explaining 50 % of the genetic diversity.

In the final part, marginal individual contributions (IC) of the most important ancestors were calculated in given breeding population of TB in Slovakia. The marginal contribution of an individual quantifies its contribution to the reference population, which has not previously been explained by greater contributing individuals (McParland et al., 2007).

3. Results and discussion

The pedigree completeness has been evaluated at the beginning of our analysis. McCluer´s index of pedigree completeness was 100 % (Figure 1) in the first five generation, hence presented results have high reliability. Higher pedigree completeness has been confirmed by Cunningham et al. (2001), Pjontek et al. (2012) and Druml et al. (2009) in several horse breeds.

The overview of the lineage structure in TB population is presented in Table 1. There were 6 paternal lineages found in the stallions. Three stallions linked to Nasrullah line (30 %) and 2 stallions linked to Northern Dancer
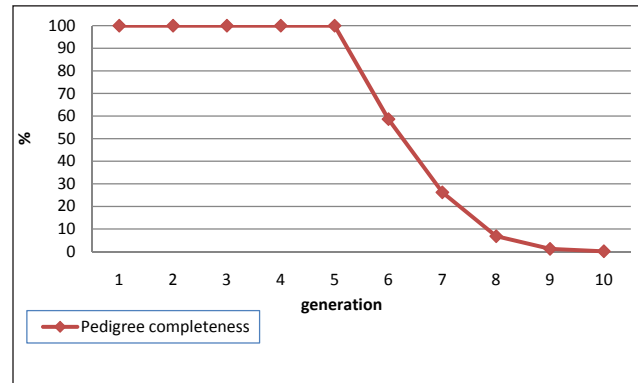
Figure 1   Pedigree completeness index in evaluated population

(20 %) and Native Dancer lines (20 %). Lineages Blenheim, Ribot and War Relic were represented by only 1 stallion. Over a half of mares were represented by Northern Dancer line (50.41 %). This paternal lineage is considered as the most important in recent years. Further important paternal lineages were Nasrullah (11.38 %), Birkhahn (6.5 %), Turn-To (5.69 %) and Native Dancer (4.88 %) in mares´ population.

The lineage structure of populations is mainly used in horse breeding. In our study, Northern Dancer was the most influential lineage in Slovak TB population. Moreaux et al. (1996) state, that line variability in TB is dropping off and stresses the increasing tendention of Northern Dancer line within global TB population, mainly in the European countries. Vlček (2006) claims that the main reason of monopolization of lines Northern Dancer, Nasrullah, Native Dancer and Turn-To is the effort of the breeders to react the increasing demand on international racing horse markets. Cunnigham et al. (2001) presented while other stallions were responsible for paternal lineages early in the history of Thoroughbred, by the mid-1800s only three remained: the Byerley Turk, the Darley Arabian and the Godolphin Arabian. The percentage of paternal lineages attributable to the Darley Arabian line has been increasing for nearly 175 years, and is now responsible for 95 % of paternal lineages in the modern population. Each of these three foundation stallions is linked to the population in paternal lineage through contributions of only one of their male-line descendants. The influance of the Byerley Turk is carried on through his great great grandson Herod (1758), the Darley Arabian through his great great grandson Eclipse (1764) and Godolphin Arabian through his grandson Matchem (1748).

Each stallion originated from different sire (Allaged, Alrayed, Dictator´s Song, Green Desert, High Estate, King´s Best, Local Suitor, Raut, Sadler´s Wells a Stimul). Two of them had the same dam-sire (Mill Reef). There were 93 sires identified in mares´ popoulation. Sebastian had the largest number of daughters (7 mares; 5.69 %), Solarstern and Najoom had five daughters (4.07 %),

Acta fytotechn. zootechn., 17, 2014(4): 122–126

Ivan Pavlík, Zuzana Schubertová, Ondrej Kadlečík, Juraj Candrák, Radovan Kasarda: Pedigree analysis of Thoroughbred horses in Slovakia

Table 1 Paternal lineages structure of mares and stallions

Line	Mares		Stallions	
	n	%	*n*	%
Birkhahn	8	6.50		
Blenheim	1	0.81	1	10
Crepello	1	0.81		
Dante	2	1.63		
Dschingis khan	3	2.44		
Hyperion	5	4.07		
Nasrullah	14	11.38	3	30
Native dancer	6	4.88	2	20
Never bend	4	3.25		
Northern dancer	62	50.41	2	20
Ribot	5	4.07	1	10
Teddy	1	0.81		
Tourbillon	1	0.81		
Turn-to	7	5.69		
War relic	3	2.44	1	10

Muscatite and Platini had four daughters (3.25 %) and Czas had three daughters (2.44 %). The rest of sires had two or only one daughter. There were 113 dam-sires found in mares pedigrees as well. The 3 mares (2.44 %) had Nebos as dam-sire, the rest of dam-sires had two or one granddaughter.

The TB is the breed created by using of inbreeding. The International Agreement on Breeding, Racing and Wagening prohibits using of artificial insemination in TB breeding what positively influences the number of offsprings per superior animals especially stallions. This fact helps to maintain inbreeding on acceptable level. The genetic diversity parameters based on probability of identity-by-descent are presented in Table 2.

The average inbreeding coefficient was 0.86 % in whole reference population (133 individuals), whereby in mares 0.85 % and stallions 1.10 %. Increase in inbreeding per generation was 0.17 %, in stallions 0.25 %. The averege relatedness was 0.91 % in whole population (mares 0.91, stallions 0.85 %).

The number of founders in investigated population was 949. The effective number of founders was 202, while the effective number of ancestors was 67. The difference between these values indicates unbalanced using of small number of ancestors, especially breeding stallions. Given results show the bottleneck effect as well. In recent years, the total TB breeding population has decreased and many former important breeders disappeared (Motešice, Šamorín). These results point out unbalanced contributing of founders and ancestors in reference populations as well as the bottleneck effect occurance. The overview of parameters based on probability of gene origin is presented in Table 3.

Pedigree analysis as a tool for diversity evaluation has been published by many authors. Using of genealogical analysis for diversity assessment in Slovak Sport Pony population was published by Kadlečík et al. (2012). Cunningham et al. (2001) calculated inbreeding coefficient in British Thoroughbred horses born between 1976–1996. Its value was 0.130 % ±0.014. Gołębiewska et al. (2013) presented higher inbreeding coefficient (F = 1.93 %) of Sztumski mares in Poland than in our TB population (average F = 0.86 %). Sztumski breed is involved in genetic resources conservation programme in Poland. The inbreeding coefficients were calculated by Cervantes et al. (2008a) in Spanish Arabian horse (9.8 %, 6240 animals born between 1995–2004), Druml et al. (2009) in Austrian Noriker draught horse (5.01 % for all available generations), Valera et al. (2005) in Spanish Andalusian horse (8.48 %) and Dunner et al. (1998) in Spanish Asturcon pony (2.7 %) as well.

Pjontek et al. (2012) found the highest F-value in Slovak Hucul horse (6.26 %, ΔF_i = 1.06 %), while the lowest in Slovak Sport Pony (2.67 %; ΔF_i = 0.62 %). Cervantes et al. (2008b) computed ΔF_i = 0.2 % in Spanish Anglo-arab horse, lower than 1 % in Andalusian horse and around 2 % in Carthusian subpopulation of Andalusian horse.

Cunningham et al. (2001) analyzed pedigrees of 211 British Thoroughbreds (representative sample of horses born from 1770 to 1990) with effective number of founders 28.15 (in our case 202). Cervantes et al. (2008a) presented f_e = 39.5 in Spanish Arab horse and Moureaux et al. (1996) calculated f_e = 70 in French Trotter. The fe as well as the other divesity measures, significantly depends on the pedigree depth. Pjontek et al. (2012) evaluated

Table 2 Genetic diversity parameters based on probability of identity-by-descent

Measure	Reference population (*n* = 133)		Mares (*n* = 123)		Stallions (*n* = 10)	
	mean	s.d.	mean	s.d.	mean	s.d.
F_i	0.8647	1.0418	0.8453	1.0187	1.1026	1.3357
ΔF_i	0.1726	0.2097	0.1659	0.1980	0.2548	0.3240
AR	0.9064	0.2087	0.9109	0.1902	0.8515	0.3810

s.d. – standard deviation

Acta fytotechn. zootechn., 17, 2014(4): 122–126

Ivan Pavlík, Zuzana Schubertová, Ondrej Kadlečík, Juraj Candrák, Radovan Kasarda: Pedigree analysis of Thoroughbred horses in Slovakia

Table 3   Genetic diversity parameters based on probability of gene origin

Measure	Reference population ($n = 133$)	Mares ($n = 123$)	Stallions ($n = 10$)
f	949	931	249
f_e	202	200	145
f_a	67	64	10
50 % of diversity	35	35	5

n – number of animals

Table 4   The most important ancestors in the reference population

No	Ancestor	Born	Sex	IC in %	CC in %	DI	CD
1	Northern Dancer (CAN)	1961	1	7.8830	7.8830	3.00	0.69
2	Nasrullah (GB)	1940	1	3.2542	11.1372	1.95	0.46
3	Surumu (GER)	1974	1	2.4906	13.6278	0.29	-0.65
4	Sebastian (GB)	1992	1	2.3261	15.9540	0.96	0.16
5	Muscatite (IRE)	1980	1	2.0677	18.0216	7.80	1.32
6	Princequillo (IRE)	1940	1	1.5889	19.6106	0.78	-0.21
7	Solarstern (FR)	1979	1	1.5508	21.1613	2.38	0.73
8	Hyperion (GB)	1930	1	1.5052	22.6665	0.33	-0.75
9	Native Dancer (USA)	1950	1	1.4803	24.1468	2.20	0.47
10	Masshtab (RUS)	1995	1	1.4626	25.6094	0	-2.00

IC – individual contributions, CC – cummulative contributions, 1 – male, DI – Dosage index, CD – Center of distribution

diversity measures based on probability of gene origin in Slovak endangered horses populations. They calculated $f_e = 160$ ($f_a = 20$) in Shagya Arab, 94 (32) in Lipizzan, 75 (15) in Original Arab, 47 (7) in Slovak Sport Pony and 26 (16) in Hucul.

Cunningham et al. (2001) state that 45 % of cummulative contributions, in British Thoroughbreds, is represented by 10 founders. The most significant founders were Godolphin Arabian (13.8 %), Darley Arabian (6.5 %), Curwen Bay Barb (4.2 %), Ruby Mare (4.2 %) and Byerley Turk (3.3 %). Over than 25 % of cummulative contributions was explained by 10 ancestors in our study.

In the final part of our work, marginal individual contributions (IC) of the most important ancestors were computed. The list of most important ancestors according to their IC is presented in Table 4. Individual contributions express the gene proportion of given ancestor in the population. The stallion Northern Dancer born in Canada was the most important ancestor (IC 7.88 %). This stallion is considered as the most important ancestor in global TB populations. The second most important ancestor was Nasrullah (IC 3.25 %) which is relative with Northern Dancer in paternal side of pedigree. The 10 most important ancestors explained 25.6 % of diversity.

4.   Conclusions

The Thoroughbred is unique horse breed spread all over the world. Slovak TB population is small. Slovak breeding population can not provide enough horses to make Slovak horse racing self sufficient. The breeding population consisted of 133 horses of those 10 stallions and 123 mares. The paternal lineage structure is satisfying; modern lineages are represented sufficiently. The state of genetic diversity within the population is satisfying. It points out unbalanced using of small number of ancestors. The most important ancestor is the stallion Northern Dancer which represents the most popular paternal lineage world wide. FAO (2007) states the critical value of $\Delta F = 1$ %, whereby in our case it was not higher than 0.5 %.

5.   Acknowledgements

6.   References

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Acta fytotechn. zootechn., 17, 2014(4): 122–126

Ivan Pavlík, Zuzana Schubertová, Ondrej Kadlečík, Juraj Candrák, Radovan Kasarda: Pedigree analysis of Thoroughbred horses in Slovakia

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