

Analysis of genetic structure of Silesian horses from Książ National Stud

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Abstract: *Analysis of genetic structure of Silesian horses from Książ National Stud.* The aim of the study was to analyze the genetic composition of Silesian horses bred in Książ National Stud basing on their pedigrees and to try to answer the following question: is the subdivision of Silesian horse population really necessary to prevent local horse breed? As the material 72 pedigrees of brood mares and stallions, born between 1991 and 2009 were used. On average, 93.1% of animals were inbred, there were 96.55% inbred stallions and 90.70% inbred mares. The mean inbreeding coefficient for all horses was 2.3%, for inbred horses it reached 2.5%. There were more inbred mares (39) than stallions (28). All 72 Silesian horses from Książ State Stud were related with the average relationship coefficient of 8.5%. The total and effective number of founders were 458 and 163, respectively. The total and effective number of ancestors were 64 and 22, respectively. Among the founding breeds Thoroughbred horses predominated, the next were Oldenburg and Silesian horses, whereas among ancestors there were much more Silesian horses than Thoroughbreds. All in all, the genetic diversity of the Silesian horses from Książ National Stud was satisfactory, however its monitoring is required because of both upward inbreeding and 100% related animals. Because the population of Silesian horses is small, less than 2,000 animals and slightly over 1,000 animals included in conservation programme, the artificial subdivision of this population as proposed

in the new breeding programme, which would result in creation of 2 subpopulations: old-type and new-type Silesian horses, is not recommended. For maintaining genetic diversity, it could be also possible to carefully import of semen or stallions of similar breeds, i.e. German Alt-Oldenburger horses or German Heavy Warmblood horses. The plan should also include the matings recommended within the population of all available Silesian horses of both types. The authors consider introducing such a program essential. It should be also clearly stated in the plan how large proportion of the Silesian mares population could be each year mated to Thoroughbred stallions. Division into two types implies that some fraction of new-type Silesian horses and their progeny would not be regarded as potential parents of individuals for the conservation programme.

Key words: inbreeding, relationship, founder, ancestor, Silesian horse breed

INTRODUCTION

The origin of Silesian horses can be traced back to 19th and the beginning of 20th century. Before that time, Silesian region was not considered as that of highly developed horse breeding. Formation of Silesian horses is closely related to National Studs. The State Stud

in Lubiąż was settled in 1817 and moved afterwards to Książ in 1939. The second State Stud was formed in Koźle in 1877 (Lawin 2004a, Tomczyk-Wrona 2014b). Primarily stallions of draft breeds from Belgium, England and France were imported to Koźle, but then breeding was targeted at importation of old-type Oldenburg horses and horses from Ostfriesland (Tomczyk-Wrona 2014b). Lawin (2004a) reports that proportion of those stallions reached 40% of all stallions used in Silesian area in years 1917–1938. Therefore it is believed that those stallions had major impact on creating Silesian horse breed after World War II. After WW II, the majority of the population had gone, especially the most valuable horses and the Ministry of Agriculture issued the decision to settle State Studs in Koźle and Książ. In those places Silesian horses, old-type Oldenburg horses and other stallions were gathered. State Studs with mares were arranged in Strzelce Opolskie (1950), Wojanów (1951) and Strzegom (1955) (Lawin 2004b). In next years 20 old-type Oldenburg stallions, which set up breeding lines, some of which still exist today, were imported from Germany and Denmark (Lawin 2004b, Tomczyk-Wrona 2014b). Later on, the aim of the breeding program was to create a multi-purpose horse breed. Stallions Diebitsch, Rittmeister, Holdek, Firley and Ulan were chosen as the best, to reach this aim (Walkowicz 2009, Tomczyk-Wrona 2014b).

Next, an attempt was made to breed Silesian mares to stallions of warmblood breeds such as Thoroughbred or Malopolska. Therefore National Studs bred also purebred Silesian horses called old-

-type Silesians (Tomczyk-Wrona 2014a, b). New requirements for horse candidates to entry Silesian horse studbook were published in 1996 and updated in 2014 (Wójcik et al. 2014). Only Silesian, old-type Oldenburg and Thoroughbred ancestors can occur in a horse pedigree. With this breeding policy the opportunity both to breed the modern warmblood sport horse and to keep and protect the old-type, traditional Silesian coach horse appeared (Cześniak 1999, Tomczyk-Wrona 2014a).

In 1997 and 1998 National Studs in Strzegom and Strzelce Opolskie were liquidated and most of stud mares were moved to Książ (Rajca-Pisz 2005). Although Książ National Stud in has been operating since 1947, only since 1997 it has been breeding Silesian horses, as the last national stud, which cooperates with many private breeders. According to the latest breeding program for Silesian horses (Tomczyk-Wrona 2014a, Wójcik et al. 2014), the main breeding goal is to keep the population in purebred and to protect local breed (old-type Silesian horses). The part of the population can be used to obtain sport horses through crossbreeding to Thoroughbred horses. With this specific purpose, the Silesian horse breed has been divided in two branches with different requirements for a horse to enter the studbook. At present the active population is composed of slightly more than 1,600 mares and about 230–250 stallions, from which about 56% mares are included in the Genetic Resources Conservation Programme (Tomczyk-Wrona 2014a, Wójcik et al. 2014), which tends to establish two, more or less separated, subpopulations of Silesian horses. Because of the above-

-mentioned conditions and the relatively small population size, which is still leading to the increase in relationship and inbreeding levels (Walkowicz 2009) and also because of the implementation of the above-mentioned conservation programme for Silesian horses, which termed the Książ National Stud as the valuable breeding center influencing the whole Silesian horse population (Tomczyk-Wrona 2014a, b, Instytut Zootechniki PIB 2017), the aim of the study was to analyze the state of the art in Silesian horse breeding, basing on the genetic structure of Silesian horses from Książ National Stud assessed from genealogical data, and to try to answer the following question: Is the subdivision of Silesian horse population really necessary in order to prevent that local horse breed? It should be stressed that in the above-mentioned conservation programme (Instytut Zootechniki 2017) it is assumed that the genetic material should be exchanged with the foreign breeders.

MATERIAL AND METHODS

As the material 72 pedigrees of Silesian horses born in 1991–2009, which were qualified as breeding horses in 2013 or earlier, were analyzed. For the pedigrees of Silesian horses obtained in this way the contribution of ancestors actually existing in a horse pedigree, i.e. equivalent of complete generations (*ECG*), according to Maignel et al. (1996) was calculated.

Based on data from pedigrees of 72 horses classified in the active population, inbreeding coefficients (F_X) were estimated for the whole examined population, for stallions and brood mares,

as well as means for all and for inbred animals. The values of mean kinship coefficients (R_{XY}) were estimated for all pairs of individuals, for pairs within sex (for male and female group separately) and between males and females. The R_{XY} coefficients were computed using the algorithm proposed by Tier (1990) with recursive modification (Gierdziewicz and Kania-Gierdziewicz 2007). The relationship coefficients obtained by tabular method were transformed into classic relationship coefficients (Kania-Gierdziewicz 2008).

The total number of founders and ancestors and also the effective number of founders (f_e) and ancestors (f_a) were analyzed for the reference population including 72 horses from Książ National Stud, using Lacy's method (1989, 1995) with modification accounting for "bottleneck effect", made by Boichard et al. (1996, 1997). The effective number of founders is always higher than the effective number of ancestors. The bigger the difference, the bigger the "bottleneck effect" leading to the loss of genes (Kania-Gierdziewicz 2006).

The effective number of founders (f_e) and the effective number of ancestors (f_a) were estimated as follows:

The effective number of founders (Lacy 1989) was:

$$f_e = \frac{1}{\sum_{k=1}^f q_k^2}$$

where:

- f_e – the effective number of founders;
- f – the number of founders;
- q_k – the probability of gene origin from k -th founder;

and the effective number of ancestors (Boichard et al. 1996, 1997) was computed as:

$$f_a = \frac{1}{\sum_{k=1}^f p_k^2}$$

where:

f_a – the effective number of ancestors;

f – the number of ancestors;

p_k – the marginal contribution of k -th ancestor.

RESULTS AND DISCUSSION

Inbreeding and relationship

The extended pedigrees of 72 Silesian horses had the equivalent of complete generations – *ECG* (Maignel et al. 1996) ranging from 5.57 to 8.45, with mean value of 7.27. However, the Silesian mares had more complete pedigrees than stallions (Table 1).

On average, over 93% Silesian horses from the examined reference population were inbred. In the examined herd there were more inbred stallions than mares (96.6 vs. 90.7%). In the whole analyzed population Silesian mares were more inbred (over 2.5%), than stallions (almost 1.8%). While mean level of F_X for whole reference population reached 2.3%, mean values of inbreeding coefficients for inbred individuals was on average 2.5%. The inbred Silesian mares had higher level of F_X , reaching about 3%, while in the inbred group of Silesian stallions the mean F_X value did not exceed 2%. Maximum inbreeding value for Silesian stallions was almost three times lower than for Silesian mares (Table 1).

TABLE 1. The mean inbreeding (F_X) and relationship (R_{XY}) coefficients for Silesian horses from Książ National Stud

| Item | Sex | | |
|--|-----------|-----------|--------|
| | male | female | |
| Number of animals in active population | 29 | 43 | |
| Number of animals in pedigrees | 560 | 803 | |
| Mean <i>ECG</i> | 7.21 | 7.32 | |
| Range of <i>ECG</i> | 5.93–8.36 | 5.57–8.45 | |
| Number of inbred animals | 28 | 39 | |
| Mean F_X – all animals | 0.0178 | 0.0265 | |
| Mean F_X – inbred animals | 0.0184 | 0.0293 | |
| Maximum F_X value | 0.0464 | 0.1260 | |
| Item | Pairs | | |
| | male | female | mixed* |
| Number of pairs | 406 | 903 | 1 247 |
| Number of related pairs | 406 | 903 | 1 247 |
| Mean R_{XY} – all pairs | 0.0774 | 0.0974 | 0.0784 |
| Mean R_{XY} – related pairs | 0.0774 | 0.0974 | 0.0784 |
| Maximum R_{XY} value | 0.5305 | 0.5419 | 0.5981 |

* male × female pairs.

All animals (100%), in the examined population were related, regardless of the comparison applied. The average relationship coefficient in the whole reference population was 8.5%. The highest mean R_{XY} value was between Silesian mares (almost 10%). In the remaining groups (between stallions and between stallions and mares) these values were almost at the same level: 7.7 and 7.8%, respectively. The maximum relationship values were high, exceeding 50% for all groups, but for male-female pairs it could be much more disadvantageous and lead to serious problems in designing mating plans (Table 1). It should be pointed out that dividing the small Silesian horse population into two smaller

subgroups, assumed in Breeding Programme (Wójcik et al. 2014), will only make the matters worse.

The mean inbreeding coefficients for inbred Silesian stallions and mares from the ancestor group and from the reference population, depending on the year of birth, are illustrated in Figures 1 and 2. In the ancestor group (Fig. 1) the mean inbreeding coefficients of stallions oscillated between 2 and 3% in the consecutive birth periods, however those of mares increased rapidly in last birth period (1991–2001), reaching over 7%. The average inbreeding coefficients for examined Silesian horses (Fig. 2) were slightly lower for stallions (up to 2%) than for older males in all birth periods and for mares they were much lower than in female ancestor group and decreased slightly from over 3% for females born before 2000 year to 2.8% for the youngest mares probably because they had less ancestors of Silesian origin due to occurrence of Thoroughbred ancestors (as fathers).

In the group of 67 inbred Silesian horses from the active population most were born in years 2000–2009. Only 12 individuals were born earlier, from 1991 to 1999. In the inbred group 13 individuals had F_X smaller than 1%: 7 stallions and 6 mares. Inbreeding coefficient ranging from 1 to 3.5% was found in 39 horses (18 stallions and 21 mares). There were 15 horses with inbreeding coefficients higher than 3.5% (3 stallions and 12 mares). In this group five mares were progeny of one Silesian stallion and two other Silesian stallions had two inbred daughters each. The highest F_X in this group, over 12.5%, was that of the Silesian mare born in 2009.

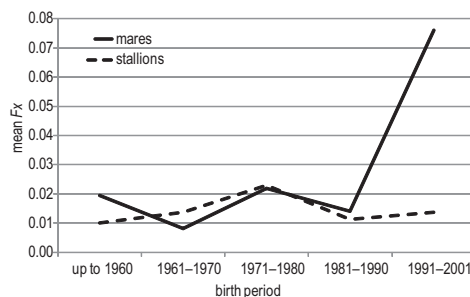


FIGURE 1. Mean inbreeding coefficients (F_X) for mares and stallions from ancestor group

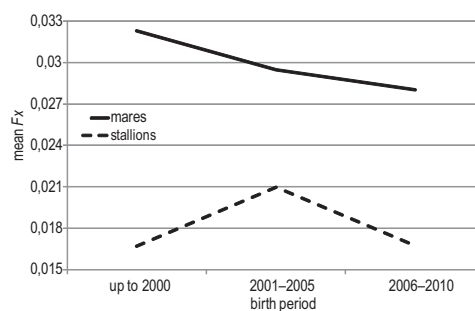


FIGURE 2. Mean inbreeding coefficients (F_X) for mares and stallions from examined herd over birth periods

From the 24 sires of the group of inbred Silesian horses only four sires had $F_X = 0$ and five sires near zero and they produced 21 out of 67 inbred animals (over 31%). Three sires had inbreeding coefficients lower than 0.5% and one slightly above this value and all four sired 17 inbred animals (more than 25%). Among those four sires there was one Silesian stallion with 10 inbred progeny. The remaining 11 sires had F_X values ranging from 1% to over 4.5% and produced 29 out of 67 inbred animals (over 43%).

The 67 inbred Silesian horses had 46 mothers. Only four of those mothers had $F_X = 0$ and seven near zero and they all gave 18 inbred progeny (about 27%).

Next 12 mares, the mothers of 16 inbred Silesian horses, had inbreeding coefficients from about 0.1% to near 1%, but only three had F_X lower than 0.5%. The remaining 23 mothers had F_X values between 1% and more than 8% and produced 33 out of 67 inbred horses (over 49%).

Walkowicz (2009) analyzed inbreeding level in the modern population of 849 Silesian horses and obtained F_X values slightly lower than in presented study, 1.26 and 2.32% for all and for inbred Silesian horses, respectively, but the maximum value of inbreeding coefficient in their study was higher than for Silesian horses from Książ State Stud (18.35 vs. 12.6%). The percent of inbred animals in their study was also much lower, reaching 54%, because of lack of pedigree information for some horses (Walkowicz 2009). The pedigrees in the presented study were more complete and, consequently, much higher percent of inbred animals was detected.

Bokor et al. (2013) investigated the pedigrees of Thoroughbred horses with racing career in Hungary and obtained similar proportion of inbred animals in the population (94.94%) but a higher level of inbreeding coefficient (average 9.58%) compared to the presented study. However, in Bokor's research over 56% horses in the population had F_X value higher than 10% compared to only two mares in the examined Silesian horse group. Hungarian Thoroughbred population had also more complete pedigrees than Silesian horses (average $ECG = 15.64$). In the previous research of Cunningham et al. (2001) the British population of Thoroughbred horses achieved mean inbreeding coefficient

value of about 13.9%, which was significantly higher than that of Silesian horses.

The above-mentioned authors (Bokor et al. 2013) also estimated average R_{XY} for Thoroughbred horses by generation and the calculated mean exceeded 10% from reference population (generation 0) till 24th generation back. For generations 0–5 (used routinely by breeders) the average relatedness mean values were close or higher than 20%. The authors pointed out that the increase of the inbreeding level began because of lack of importation. In comparison to the presented study about Silesian horses, the results for Hungarian Thoroughbreds were higher, which means that inbreeding for the examined population should not be considered at present as a problem.

Zechner et al. (2002) analyzed pedigrees of 565 Lipizzan horses from eight European studs. The inbreeding coefficients ranged from 8.6% to over 14% between studs, whereas the mean inbreeding coefficient for all units reached 10.8%. So the Lipizzan horses were also more inbred than the examined Silesian horses, which lead to decrease in genetic variability in Lipizzan horses. The above mentioned authors found that the population subdivision (male or female lines), in order to preserve gene pool variability, does not necessarily lead to maintenance of such variability. Álvarez et al. (2010) assessed genetic variability in the endangered Mallorquí horse and obtained average F_X values of 2.5% for the whole population and 4.7% for the reference population (animals born between 2005 and 2007). The results were slightly higher than for Silesian horses, but were calculated from less complete pedigrees

($ECG = 1.8$ and $ECG = 2.4$, respectively) than in our study. The R_{XY} coefficients for Mallorquí horses, over 10% for the whole and over 11% for the reference population, were also higher than those for Silesian horses. Álvarez et al. (2010) found that, in order to prevent gene pool variability of the Mallorquí horses, their breeders should not exclude black horses and, especially, heterozygous chestnut horses from stock population.

Recently Kania-Gierdziewicz et al. (2015) examined the pedigrees of the American Quarter horses and found F_X and R_{XY} values almost similar to or slightly lower than those for Silesian horses, whereas the percent of inbred and related Silesian horses were higher than for American Quarter horses. Duru (2017) analyzed pedigrees of 23,668 Turkish Arab horses and found two or four times higher mean inbreeding coefficient values for all and inbred animals and also the maximum F_X values, for almost the same percent of inbred horses, than in our study. The R_{XY} values obtained by the above mentioned author were similar to or slightly higher than for Silesian horses.

Siderits et al. (2013) investigated pedigrees of 2,364 German Paint Horses and found much lower F_X values and also much lower percentage of inbred animals than those for Silesian horses in this study.

Pinheiro et al. (2013) analyzed pedigrees of 653 horses of the endangered Sorraia breed and obtained the mean inbreeding coefficient value of about 0.27 and average relatedness of over 0.46, which were much higher than those obtained for Silesian horses.

Pjontek et al. (2012) examined genetic variability from pedigrees of four endan-

gered Slovak breeds and obtained mean inbreeding coefficients ranging from over 2.5% for Slovak Sport Ponys to over 6% for Hucul horses. Slovak Lipizzan horses and Shagya Arabians had the mean F_X within the above range. All those F_X values were higher than in Silesian horses in the present study, but the ECG values obtained for Silesian horses were similar to those from the cited paper. The relationship coefficient values reported by Pjontek et al. (2012) were similar (Hucul horses, Slovak Sport Pony) or slightly smaller (Lipizzan horses, Shagya Arabians) than for Silesian horses. According to those results, the authors expected inversion of inbreeding trend for Hucul horses and Slovak Sport Ponies in the next generations and recommended monitoring of mating.

Olsen et al. (2010) analyzed pedigrees of two endangered Norwegian horse breeds and estimated that, for the reference population of 1,535 Døle horses, the mean F_X value was 11.8% and for 1,050 Nordland/Lyngen horses – 12.8%. The ECG values were 10.5 and 7.2 for Døle and Nordland/Lyngen horses, respectively. The authors found the considerable loss of heterozygosity in Nordland/Lyngen horse breed and slightly higher genetic variance in the Døle breed due to cross-breeding in the past, and recommended, for both breeds, optimal contribution selection without additional cross-breeding.

Bhatnagar et al. (2011) analyzed pedigrees of 1,659 North American Norwegian Fjord horses and obtained higher F_X values for much lower percentage of inbred animals than in present study. The authors stated that, even though the

inbreeding values for American Norwegian Fjord horses seem to be not very high, the reduction in genetic variability is still possible due to overall small population size.

Hasler et al. (2011) examined genetic variability of Franches-Montagnes horse breed and achieved high mean F_X value (over 5%) for $ECG = 7.8$, i.e. similar to that in presented study. Those authors (Hasler et al. 2011) also obtained higher relationship coefficients for indigenous Swiss horse breed and emphasized that maintenance of genetic variability within a small, endangered population is possible and could be achieved via mating optimization by using pedigree information (relationship) and also performance data.

Sevinga et al. (2004) analyzed inbreeding level and its possible influence on retained placenta in Friesian mares. For Friesian foals born in 1999–2000 the inbreeding coefficient ranged from 15.6 to 15.7%. The authors concluded that the increase of inbreeding level generates problems with retained placenta in mares. Similar fertility problems have been reported by Silesian horse breeders from Książ National Stud (personal communication).

FOUNDERS AND ANCESTORS

The total and effective number of founders and ancestors of the examined Silesian horses are in Table 2.

For the 72 individuals from the reference population the total number of 458 founders and 64 ancestors were found. The effective number of founders (f_e) was 163, whereas the effective number of ancestors (f_a) was 22 and was

about seven times smaller than f_e . The gene pool of the reference population is steadily narrowing down, because 50% of genetic variability was explained by only 8 ancestors, whereas 90% – by about 50% of all ancestors (Table 2). The value of f_a/f_e (0.35) is strongly below 1 and indicates the presence of the “bottleneck effect”, i.e. the downward trend in the level of genetic diversity. Because most mares from Książ National Stud, which is called the Silesian horses breeding center, are considered as the genetic reserve of the Silesian breed, such situation seems to be very harmful to the Stud and also could be troublesome for the whole Silesian horse population.

Table 3 shows breed and sex composition of the groups of 458 founders and 64 ancestors. In the group of founders about 60% were mares. Almost 33% of

TABLE 2. Total number of ancestors and founders, effective number of founders (f_e) and effective number of ancestors (f_a) for reference population from Książ National Stud

| Parameter | Value |
|---|-------|
| Number of animals in reference population | 72 |
| Number of animals in pedigrees | 1 363 |
| Mean ECG | 7.27 |
| Total number of founders | 458 |
| ancestors | 64 |
| Effective number of founders (f_e) | 163 |
| ancestors (f_a) | 22 |
| Explaining 50% of gene pool | |
| founders | 59 |
| ancestors | 8 |
| Explaining 90% of gene pool | |
| founders | 231 |
| ancestors | 33 |

them were Thoroughbreds. The Silesian and Oldenburg female founders constituted about 17 and 16% of all female founders, respectively. Seven other minor breeds were also reported in the group of founder mares with the superiority of the Trakehner breed. In the group of 182 founder stallions, the Thoroughbred horses prevailed as well (over 30% of all male founders). Another most popular breeds in the male founder group were Silesian and Oldenburg breeds, over 16% and more than 22% of all founder stallions, respectively. Also male founders from Trakehner breed (about 4% of all stallions-founders) and three other breeds were shown. However, significant number of founders (over 26%) had missing information about their breed. Most of these horses were born at the beginning of 20th century or even earlier, at the end of 19th century (Table 3). The total number of 64 ancestors included about 47% of mares and 53% stallions. The Silesian breed dominated in this group, because almost all female ancestors belonged to this breed and 59% of male ancestors as well. Oldenburg and Thoroughbred stallions were also in the group of male ancestors. Distribution of sex among founders indicates that mares constituted the majority (60% of all founders), whereas the ancestor group was dominated by stallions (53% of all ancestors) – Table 3.

The Thoroughbred horses were one of the horse breeds that strongly influenced the origin of Silesian breed (founders) but has a little impact on the current Silesian horse population (ancestors), as it has been shown in Table 3. Thus, creating two subpopulations according to the breeding programme for Silesian horses

TABLE 3. Breed and sex of founders and ancestors of the reference population

| Breed | Number of | | Breed contribution (%) |
|-------------------------------|-----------|-----------|------------------------|
| | mares | stallions | |
| Founders (N = 458) | 275 | 182 | × |
| Thoroughbred | 86 | 57 | 31.22 |
| Arabian horse | 0 | 1 | 0.22 |
| Silesian horse | 48 | 30 | 17.03 |
| Oldenburg horse | 44 | 41 | 18.56 |
| Holsteiner horse | 0 | 1 | 0.22 |
| Trakehner/East-Prussian horse | 9 | 7 | 3.49 |
| Wielkopolski horse | 3 | 1 | 0.87 |
| Friesian horse | 3 | 0 | 0.66 |
| Ostfriesen horse | 1 | 0 | 0.22 |
| Anglo-Norman horse | 1 | 0 | 0.22 |
| Half-blood Anglo-Arabian | 1 | 0 | 0.22 |
| Warmblood horse | 2 | 0 | 0.44 |
| Without breed designation | 78 | 44 | 26.64 |
| Ancestors (N = 64) | 30 | 34 | × |
| Thoroughbred | 0 | 5 | 7.81 |
| Silesian horse | 29 | 20 | 76.56 |
| Oldenburg horse | 0 | 8 | 12.50 |

seems to be unnecessary or even harmful for the population. The alternative way of maintaining the genetic diversity of a whole population, very important for Silesian breed, is probably to look for phenotypically similar horse breed of possibly similar origin, as for example the Alt-Oldenburger in Germany (<http://www.ostfriesen-alt-oldenburger.de>). In the pedigrees of some stallions of this breed we found, to some extent,

the same ancestors (Oldenburg or Ostfriesen stallions) as in the pedigrees of Silesian horses. The possibility of taking advantage of such breeding has also been mentioned in the conservation programme of Silesian horse breed (Instytut Zootechniki PIB 2017). And it should be pointed out that Eckermann, a grey stallion of German Heavy Warmblood breed, which is in one-half of Silesian breed, has been recently used for mating in Książ National Stud.

Cunningham et al. (2001) obtained, for the reference population of 211 Thoroughbred horses, 158 founders (85 stallions and 73 mares). The value of f_e in their work was 28.15. To explain 78% genetic diversity, the joint contribution of 30 founders was needed. Therefore, the British Thoroughbred population was much less varied than the Silesian horses in the present study. In recent research on Thoroughbreds from Hungary Bokor et al. (2013), found that the total number of founders was 1,062 and the f_e reached 42, which was a lower value than for the examined Silesian horses. Noteworthy is that 232 founders (all born before 1793) were responsible for 88.58% of diversity in the reference population gene pool. The total and the effective number of ancestors were 908 and 15.32, respectively. Only six ancestors explained 50% of the genetic diversity of the Hungarian Thoroughbreds, which was slightly lower than in the Silesian horses.

For Lipizzan horses from European studs investigated by Zechner et al. (2002) the f_e was on average 48.2 and ranged from over 39 in Piber stud to almost 56 in Fagaras stud, whereas the f_a for all studs exceeded 26 with the range from 12.5 for Djakovo stud to 18.8 in Piber

and Szilvásvárads studs. Those results were lower than in this study, although they were conducted on greater number of individuals. The authors (Zechner et al. 2002) also found that over 52% of genetic variability of Lipizzan horses originated from so-called baroque horses, which in most cases were of Italian and Spanish origin. Among other founder breeds there were Arabian horses (21% of gene contribution), Lipizzan horses (10%), Frederiksborg horses (8%), Kladruby horses, Thoroughbreds and Shagya Arabians. It was quite similar to the examined Silesian horses, since their founders were also of different breeds, with, however, Thoroughbreds, Silesian and Oldenburg horses predominating. The above-mentioned authors concluded that exchanging stallions between Lipizzan studs according to relationship coefficients calculated from the joint pedigree file should be taken into consideration in mating plans.

The total number of founders for four Slovak horse breeds examined by Pjontek et al. (2012) and the effective number of founders for Hucul horses, Lippizan horses, Shagya Arabians and Slovak Sport Ponys, respectively. Those results were close to or lower than those in the presented study. The authors recommended use for mating stallions with optimal contribution for the genetic management of those Slovak horse breeds.

Recently Kania-Gierdziewicz et al. (2015), who examined pedigrees of the American Quarter horses, obtained similar values of the f_e and f_a (121 and 26, respectively). The number of ancestors explaining 50 and 90% of the genetic pool was found to be 10 and 39 ancestors, respectively, which was slightly

more than in the presented study. Duru (2017) analyzed Turkish Arab horse population and, for reference population of 14,838 animals, obtained the f_e and f_a values of 40 and 22, respectively. Those values were similar to our findings, but they were calculated for a much bigger population and indicated that Turkish Arab population had lower genetic diversity than the examined Silesian horses.

In the work of Siderits et al. (2013), for German Paint Horse population, much higher f_e and f_a values (from two to 10 times higher) were found than in Silesian horses. The authors concluded that the genetic variability of the German Paint Horse population was kept at a satisfactory high level.

Pinheiro et al. (2013) found for endangered Sorraia horse population very low values of f_e and f_a (7.46 and 4, respectively). Additionally, only 2 ancestors explaining 50% of the Sorraia breed gene pool. The authors concluded that Sorraia horse breed is still in the brink of extinction and required the introduction of an efficient conservation plan.

Bhatnagar et al. (2011), for f_e and f_a in North American Norwegian Fjord horses found the values of 96 and 30, respectively. The authors pointed out that the effective number of founders and ancestors and also the f_a/f_e were low, thus the reduction of the genetic variability is possible.

Teengen et al. (2009) examined the contribution of other breeds to the recent Trakehner horse population and found that over 22% of genes came from Thoroughbred horses and almost 12% of gene pool originated from Anglo-Arabian horses. The authors found also increasing rate of inbreeding and relationship in

the examined Trakehner population and recommended bettering of monitoring system.

Hamann and Distl (2008) calculated the effective number of founders (f_e) and ancestors (f_a) for Hanoverian horses, which were higher than in present study. They also examined the average contribution of various breeds to the genetic pool of Hanoverian horses and found that the breeds with the highest contribution (except Hanoverians with 49.1%) were Thoroughbred horses (34.8%), and then Trakehner horses (7.9%), Arabians, Holsteiner warmblood horses and Oldenburg horses. The above mentioned authors found the large random loss of founder alleles due to the fact that only 15 stallions (from famous sire lines) had about 35% of gene contribution to examined breed.

Olsen et al. (2010) examined genetic variation in two native Norwegian horse breeds and found that in Døle breed the most influenced ancestor (stallion) had the gene contribution about 22% and in Nordland/Lyngen population the top ancestor (stallion) had the contribution value over 26%. The authors suggested that in both populations the loss of genetic diversity appeared because of low number of animals and high level of relationship and inbreeding.

Toro et al. (2011) summarized the findings about the different ways to measure of genetic diversity is small livestock populations in order to conserve animal genetic resources. They concluded that the maintenance of genetic variability is the most important in all cases, but the most useful tools for measuring genetic variability could be the rate of inbreeding and coancestry or even the effective

population size, all basing on pedigree information. On the other hand the effective population size would be useful for indicating changes in longer time periods, and the effective number of founders and ancestors – for estimating recent changes in gene pool taking place as a result of current breeding decisions (Kania-Gierdziewicz 2006).

CONCLUSIONS

Summing up all the above results, genetic variability of Silesian horses from Książ National Stud is still on the satisfactory level, which was confirmed by high values of the effective number of founders and relatively small values of individual contributions of founders and ancestors in the genetic pool in comparison to the small number of examined horses. However, the relatively low value of the effective number of ancestors and the fact that 100% individuals were related to each other and 90% individuals were inbred in the Książ National Stud, which is treated as a breeding center for Silesian horses, suggest that now the downward tendency in genetic variability exists. Because the whole population of Silesian horses is very limited in size – in general less than 2,000 animals and slightly above 1,000 individuals included in the conservation programme (Tomczyk-Wrona 2017), which may be insufficient to maintain genetic diversity, artificial subdivision of this population, as it is proposed in the new breeding programme, which would result in creation of two subpopulations: old-type and new-type Silesian horses, is not recommended. We suggest one thing that certainly could be necessary – namely,

introducing different ways for breeding value estimation for the two types of Silesian horses depending on their kind of use, but without subdividing the whole population, and also more clarification of the Herdbook requirements, which should be written clearly in the newly introduced breeding programme (Wójcik et al. 2014). Specifying the old-type Silesian horse as having less Thoroughbred ancestors in the pedigree (up to two ancestors only in the third generation back) for mares and with less restrictive conditions for stallions and the new-type Silesian horse with more Thoroughbred ancestors (in some cases it could be one-half Silesian and one-half Thoroughbred) seems to be highly insufficient, because in the latter case the generations, in which those ancestors occur are also very important. In our opinion, for maintaining genetic diversity of Silesian horses, it could be also possible to introduce a well thought-out importation of semen or stallions of similar breeds, i.e. German Alt-Oldenburger horses or German Heavy Warmblood horses (last year one of the stallions of the latter breed was mated to the mares from the Książ National Stud), because these breeds have to some extent the same ancestors as the Silesian horses. The plan should include, as suggestions for the breeders, the matings recommended within the population of all available Silesian horses regardless of their type – old or new. It should be also clearly stated in the plan how large proportion of the Silesian mares population could be each year mated to Thoroughbred stallions. Division into two such types implies that some fraction of new-type Silesian horses and their progeny would not be

regarded as potential parents of individuals that would fulfill the conditions for the conservation programme. Yet such a possibility would allow some Silesian horses of the new-type, especially those with more than 75% Silesian breed contribution, to serve as a sort of the initial group in the conservation programme. Mating them to old-type Silesian horses would give, in the next one or two generations, the progeny eligible to enter the main conservation programme, broadening therefore the gene pool of the Silesian breed. The authors consider introducing such a program essential. Analogous solutions, concerning various livestock breeds for which procedures of protection have been initiated because of small population size and low genetic variability, appear frequently in literature (Olsen et al. 2010, Bhatnagar et al. 2011, Pinheiro et al. 2013). The point is not to give up protecting or improvement of the breed but to gain control of what is happening to the population as a whole and to direct breeders' efforts not only towards advantages for the breeders themselves but, primarily, towards the preservation of the breed. Such a procedure could facilitate the management of the whole Silesian horse breed and should be profitable for breeders and also beneficial for breed resources protection.

REFERENCES

- ÁLVAREZ I., ROYO L.J., PÉREZ-PARDAL L., FERNÁNDEZ I., PAYERAS L., GOYACHE F. 2010: Assessing losses of genetic variability in the endangered Mallorquí horse. *Czech J. Anim. Sci.* 55 (10): 456–462.
- BHATNAGAR A.S., EAST C.M., SPLAN R.K. 2011: Genetic variability of the Norwegian Fjord horse in North America. *Anim. Genet. Res.* 49: 43–49.
- BOICHARD D., MAIGNEL L., VERRIER E. 1996: Analyse g n alogique des races bovines laiti res fran aises. *INRA Prod. Anim.* 5: 323–335.
- BOICHARD D., MAIGNEL L., VERRIER E. 1997: The value of using probabilities of gene origin to measure genetic variability in a population. *Genet. Sel. Evol.* 29: 5–23.
- BOKOR  ., J N  S D., DUCRO B., NAGY I., BOKOR J., SZABARI M. 2013: Pedigree analysis of the Hungarian Thoroughbred population. *Livest. Sci.* 151: 1–10.
- CUNNINGHAM E.P., DOOLEY J.J., SPLAN R.K., BRADLEY D.G. 2001: Microsatellite diversity, pedigree relatedness and contributions of founder lineages to thoroughbred horses. *Anim. Genet.* 32: 360–364.
- CZEŚNIK B. 1999: Ślązaki czy Oldenburgi? *Koń Polski* 12: 12–14.
- DURU S. 2017: Pedigree analysis of the Turkish Arab horse population: structure, inbreeding and genetic variability. *Anim.* 11 (9): 1449–1456.
- GIERDZIEWICZ M., KANIA-GIERDZIEWICZ J. 2007: A study of efficiency of recursive algorithm for estimating relationship coefficients. *Acta Sci. Pol.-Zoot.* 6: 29–36.
- HAMANN H., DISTL O. 2008: Genetic variability in Hanoverian warmblood horses using pedigree analysis. *J. Anim. Sci.* 86: 1503–1513.
- HASLER H., FLURY C., MENET S., HAASE B., LEEB T., SIMIANER H., PONCET P.A., RIEDER S. 2011: Genetic diversity in an indigenous horse breed – implications for mating strategies and the control of future inbreeding. *J. Anim. Breed. Genet.* 128: 394–406.
- Instytut Zootechniki PIB 2017: Program ochrony zasobów genetycznych koni rasy śląskiej. Retrieved from <http://www.bioroznorodnosc.izoo.krakow.pl/konie/programy-ochrony> [access: 25.05.2017].
- KANIA-GIERDZIEWICZ J. 2006: Analiza struktury genetycznej – udział założycieli w puli genów populacji. *Wiad. Zoot.* 45 (2): 27–34.
- KANIA-GIERDZIEWICZ J. 2008: Metody szacowania spokrewnienia i inbrodu stosowane w analizie struktury genetycznej populacji. *Wiad. Zoot.* 46 (3): 29–41.
- KANIA-GIERDZIEWICZ J., GIERDZIEWICZ M., STANKOWSKA-ŻOŁĄDŹ E. 2015: Analiza struktury genetycznej koni rasy American Quarter. *Roczn. Nauk. PTZ* 11 (3): 9–21.

- LACY R.C. 1989: Analysis of founder representation in pedigrees: Founder Equivalents and Founder Genome Equivalents. *Zoo Biol.* 8: 111–123.
- LACY R.C. 1995: Clarification of genetic terms and their use in the management of captive populations. *Zoo Biol.* 14: 565–578.
- LAWIN J. 2004a: Konie śląskie. Part 1. Historia powstania rasy. *Koński Targ* 2: 24–25.
- LAWIN J. 2004b: Konie śląskie. Part 4. Historia powstania rasy. *Koński Targ* 5: 23–25.
- MAIGNEL L., BOICHARD D., VERRIER E. 1996: Genetic variability of French dairy breeds estimated from pedigree information. *Interbull Bull.* 14: 49–54.
- OLSEN H.F., KLEMETSDAL G., RUANE J., HELFJORD T. 2010: Pedigree structure and genetic variation in the two endangered Norwegian horse breeds: Døle and Nordland/Lyn-gen. *Acta Agric. Scand., Section A* 60: 13–22.
- PINHEIRO M., KJÖLLERSTRÖM H.J., OOM M.M. 2013: Genetic diversity and demographic structure of the endangered Sorraia horse breed assessed through pedigree analysis. *Livest. Sci.* 152: 1–10.
- PJONTEK J., KADLEČÍK O., KASARDA R., HORNÝ M. 2012: Pedigree analysis in four Slovak endangered horse breeds. *Czech J. Anim. Sci.* 57 (2): 54–64.
- RAJCA-PISZ I. 2005: Stado Ogierów Książ. Oficyna Wydawnicza Volumen, Warszawa.
- SEVINGA M., VRIJENHOEK T., HESSELINK J.W., BARKEMA H.W., GROEN A.F. 2004: Effect of inbreeding on the incidence of retained placenta in Friesian horses. *J. Anim. Sci.* 82: 982–986.
- SIDERITSM., BAUMUNG R., FUERST-WALTL B. 2013: Pedigree analysis in the German Paint Horse: Genetic variability and the influence of pedigree quality. *Livest. Sci.* 151: 152–157.
- TEEGEN R., EDEL C., THALLER G. 2009: Population structure of the Trakehner Horse breed. *Anim.* 3 (1): 6–15.
- TIER B. 1990: Computing inbreeding coefficients quickly. *Genet. Sel. Evol.* 22: 419–430.
- TOMCZYK-WRONA I. 2014a: Charakterystyka ogierów śląskich, dopuszczonych do krycia klaczy uczestniczących w programie ochrony zasobów genetycznych koni rasy śląskiej. *Wiad. Zoot.* 52 (1): 38–46.
- TOMCZYK-WRONA I. 2014b: Frekwencja rodów męskich ogierów śląskich dopuszczonych do krycia klaczy uczestniczących w Programie ochrony zasobów genetycznych koni rasy śląskiej. *Wiad. Zoot.* 52 (2): 25–35.
- TOMCZYK-WRONA I. 2017: Ochrona zasobów genetycznych koni ex situ. *Wiad. Zoot.* 55 (3): 120–128.
- TORO M.A., MEUWISSEN T.H.E., FERNÁNDEZ J., SHAAT I., MÄKI-TANIŁA A. 2011: Assessing the genetic diversity in small farm animal populations. *Anim.* 5 (11): 1669–1683.
- WALKOWICZ E. 2009: Ocena zimbredowania współczesnej populacji koni śląskich. *Zesz. Nauk. Uniw. Przyrod. Wrocław, Biol. i Hod. Zw.* 58 (572): 159–170.
- WÓJCIK K., HELON P., KAPICA B., LAWIN J., MÜLLER D., PECKIEL P., WYSZOMIRSKI M. 2014: Program hodowli koni rasy śląskiej. Wydawnictwo Polskiego Związku Hodowców Koni, Warszawa. Retrieved from http://pzhk.pl/wp-content/uploads/pr_hodow_slas-2015_03_27.pdf.
- ZECHNER P., SÖLKNER J., BODO 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. *Livest. Prod. Sci.* 77: 137–146.

Streszczenie: *Analiza struktury genetycznej populacji koni śląskich ze Stada Ogierów Książ.* Celem pracy była analiza struktury genetycznej koni rasy śląskiej hodowanych w Stadzie Ogierów Książ na podstawie danych rodowodowych oraz wypracowanie odpowiedzi na pytanie, czy słuszny jest założony w programie hodowlanym koni rasy śląskiej podział na stary i nowy typ konia śląskiego z osobnymi wymogami dotyczącymi wpisu do ksiąg. Materiałem badawczym była grupa 72 koni rodowodowych, zakwalifikowanych jako hodowlane (populacja aktywna). Populację referencyjną do analiz stanowiły 72 konie należące do populacji aktywnej urodzone w latach 1991–2009. Udział osobników zimbredowanych w populacji aktywnej wynosił 93,1%, przy czym więcej było zimbredowanych ogierów niż klaczy. Średnie zimbredowanie dla wszystkich koni wynosiło 2,3%, a w grupie koni zimbredowanych było równe 2,5%. Bardziej zimbredowane były klacze

niż ogiery. Wszystkie badane 72 konie śląskie były ze sobą spokrewnione, a średni współczynnik spokrewnienia dla nich wyniósł 8,5%. Ogólna liczba założycieli wyniosła 458, zaś przodków – 64. Efektywna liczba założycieli wynosiła 163, a przodków – 22. Wśród ras założycielskich przeważała pełna krew angielska, a następnie konie oldenburskie i śląskie. Wśród przodków występowały przeważnie konie śląskie, a udział koni pełnej krwi był niewielki. Ogólnie można stwierdzić, że zmienność genetyczna wśród koni śląskich ze Stada Ogiarów Książ pozostaje jeszcze na zadowalająco dobrym poziomie, ale wymaga monitorowania ze względu na tendencję do wzrostu inbrodu przy jednoczesnym spokrewnieniu wszystkich osobników. Ze względu na małą liczebność populacji koni śląskich (poniżej 2000 osobników, w tym nieco ponad 1000 osobników w programie ochrony zasobów genetycznych rasy) wprowadzenie bardziej restrykcyjnego podziału na 2 subpopulacje koni starego i nowego typu będzie dla rasy bardzo niekorzystne. Aby utrzymać zmienność genetyczną koni śląskich na zadowalającym poziomie, korzystne byłoby również posłużenie się reproduktorami ras mających te same korzenie co rasa śląska, np. Oldenburgami w starym typie czy końmi rasy ciężkiej gorącokrwistej niemieckiej. Wprowadzenie indywidualnego planu kojarzeń w obrębie całej populacji koni śląskich jest, według autorów niezbędne. Plan taki powinien jasno określić, jaka część populacji klaczy śląskich corocznie mogłaby być ewentualnie krzyżowana z ogierami pełnej krwi angielskiej. Powinien on

uwzględniać, jako sugestie dla hodowców, możliwości kojarzeń w obrębie całej dostępnej populacji koni śląskich bez podziałów na stary i nowy typ. Podział taki powoduje, że pewna część koni śląskich nowego typu i ich potomstwo nie jest brana pod uwagę jako ewentualni rodzice koni, które będą spełniały warunki programu ochrony. Na przykład pozwoliłoby to wykorzystać konie śląskie nowego typu, u których udział genów rasy śląskiej jest większy niż 75%, i które stworzyłyby „grupę wstępną programu ochrony”. Ich kojarzenie z końmi starego typu mogłyby dać potomstwo (dzieci, wnuki), które spełniałyby w przyszłości warunki programu ochrony, powiększając tym samym dostępną pulę genów.

Słowa kluczowe: inbred, pokrewieństwo, założyciel, przodek, konie śląskie

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