

Pedigree-based analysis of genetic variability in the Chinese Crested dog population in Poland

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SUMMARY

The aim of the study was to analyse the level of genetic diversity within the small population of Chinese Crested dogs bred in Poland, considering the common occurrence of hereditary diseases, which is probably linked to the high level of inbreeding. Pedigree data provided by the Polish Kennel Club were used to estimate various genealogical parameters in the ancestral (1860 animals) and active population (1313 animals). The mean equivalent number of complete generations known per animal was 5.97 and 6.75 in the ancestral and active population, respectively. The mean inbreeding levels were 0.083 and 0.049 in the ancestral and active population, respectively. The effective number of founders (f_e) and ancestors (f_a) and the f_a/f_e ratio were 38, 20, 0.54 and 79, 34, 0.43 in the ancestral and active population, respectively. It can be concluded that the level of genetic variability in Chinese Crested dogs in Poland is currently satisfactory. However, the high proportion of related male–female pairs may cause future mating problems. The population should be monitored for inbreeding and genetic variation, and breeders should choose males for breeding in such a way as not to create large groups of paternal half-siblings in the offspring.

KEY WORDS: dog, relatedness, inbreeding, founders, ancestors



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INTRODUCTION

Through many centuries of animal breeding, planned in varying degrees, breeders have created animal breeds that met their conformation and performance requirements. This also applies to dog breeding. Due to the many different uses of dogs, dog breeds are much more differentiated than most livestock breeds and species. In most cases, however, the genetic variability of dog breeds is burdened with its origin (few initial founders), and is currently also strongly linked to the popularity of a given breed. The most popular dog breeds, such as German Shepherds, have populations reaching thousands of animals in many countries worldwide. Less popular or native dog breeds usually have a very limited number of animals, so in most cases they are related or even inbred. In these breeds, it is often difficult to maintain genetic diversity (Nicolas and Wade 2011).

Dog breeding is generally carried out by many breeders and associations of breeders, which makes it difficult to coordinate efforts (Nicolas and Wade 2011; Shariflou et al. 2011). Dog breeders prefer to decide for themselves how to manage their breeding, i.e. whether to allow mating between their own animals (sometimes closely related) or to attempt to find a male dog outside the kennel. The high inbreeding level in dog breeding may also be the result of the breeding policy in some breeds, which has imposed closed registries and line breeding. Mating between close relatives increases homozygosity in the progeny, which may reduce variability and lead to numerous hereditary diseases. Dog breeders exacerbate the inbreeding problem through the intensive use of a small number of popular sires. Moreover, in some dog breeds, popular sires may be carriers of genetic diseases, and their intensive use could contribute to rapid dissemination of those diseases in the population (Leroy and Baumung 2010; Leroy 2011; Leroy and Rognon 2012; Lewis et al. 2015). The health problems of pedigree dogs have recently been discussed extensively among dog owners and breeders. Recent regulations by the International Cynological Federation (Fédération Cynologique Internationale – FCI) concern maintaining genetic diversity and preventing the spread of genetic diseases in pedigree dog breeding, in order to achieving the overriding goal of enhancing canine genetic health (Hedhammar and Indrebo 2011).

Inbreeding and relatedness have been the key parameters for genetic variability analysis. They have been used for many years to analyse the genetic diversity of populations and study the impact of high or excessive homozygosity on the occurrence of genetic diseases, especially in small populations (Melka et al. 2013; Howard et al. 2017). The problem of hereditary diseases and reduced genetic diversity is very common in dog breeding. Now breeders have two important problems to solve: controlling the dissemination of inherited disorders and preventing the loss of genetic diversity. To promote the breeding of healthy dogs, the FCI has developed rules and regulations that should be followed by breeders in order to maintain the health and welfare of their animals (Hedhammar and Indrebo 2011; Nicolas and Wade 2011; Farrell et al. 2015; Donner et al. 2018).

The level of inbreeding has been investigated in working dog breeds used as guide dogs (Cole et al. 2004), in some hunting dog breeds (Voges and Distl 2009; Michels and Distl 2022), and in shepherd dog breeds (Acs et al. 2019; Michels and Distl 2020), as well as in Czech Spotted dogs (Machova et al. 2020). Mortlock et al. (2016) conducted a joint pedigree and molecular analysis of genetic diversity in Bullmastiff dogs from Australian kennels. Jansson and Laikre (2018) examined the genetic variability of Swedish native dog breeds. Other analyses have concerned the genetic variability of many different dog breeds in one or more countries. Genetic diversity has been examined for native French dog breeds (Leroy et al. 2006) and many other popular dog breeds in

France (Leroy et al. 2009). Genetic variability has also been repeatedly investigated for various dog breeds bred in the UK (Mellanby et al. 2013; Lewis et al. 2015), as well as for dog breeds in Australia (Shariflou et al. 2011) and Sweden (Jansson and Laikre 2014). Most of the authors cited above found that the small populations of the native or less popular dog breeds had high levels of inbreeding combined with the high occurrence of various hereditary diseases. This is also true of the Chinese Crested dog breed, which is less popular and thus less numerous. There are currently over 100 Chinese Crested dog kennels in Poland, and their number is gradually growing as the popularity of the breed is increasing. According to the Polish Kennel Club (<http://www.zkwp.pl/main.polish/index.php/ct-menu-item-28.html>), between 200 and 300 breeding animals and about 200 puppies on average were registered annually in the years 2009–2019. Farrell et al. (2015) reported that Chinese Crested dogs are ranked only 64th in the British Kennel Club's registration ranking, with 390 to 638 dogs per year in 2004–2013.



Figure 1. Chinese Crested dogs: A) fully-coated homozygous recessive bitch, CHILI Modern Family ('Powderpuff' variety), B) heterozygous hairless dog, DIAMENT MOLKA Modern Family (phot. A. Pietuszyńska, K. Zienkiewicz)

This breed is burdened with a genetic lethal trait (dominant hairlessness), which is entered into the breed standard (Fig. 1). It also suffers from many other genetic diseases, such as eye diseases (Farrell et al. 2015).

The common occurrence of hereditary diseases in Chinese Crested dogs is probably linked to the small size of the population and high level of inbreeding, due to mating of related animals and probably to the overuse of popular stud dogs. However, the genetic diversity and level of inbreeding of the Polish population of Chinese Crested dogs have not been analysed, so the aim of this study was to analyse the level of genetic diversity of the small population of Chinese Crested dogs in Poland.

MATERIAL AND METHODS

The pedigree data of 3173 Chinese Crested dogs, born in 1989–2019, obtained from the Polish Kennel Club (PKC), were used to determine the degree of genetic diversity of the population. The

analysis was conducted in two reference populations: 1860 animals from the ancestral population (Ancestral) and 1313 animals born in 2009–2019, referred to as the active population (Active).

Individual inbreeding coefficients (F_X) were estimated for dogs and bitches from each of the reference populations. Relatedness coefficients (R_{XY}) for both reference populations were estimated as follows: between dogs (for all pairs and for pairs with $R_{XY} > 0$); between bitches (for all pairs and for pairs with $R_{XY} > 0$); and between dogs and bitches (for all pairs and for pairs with $R_{XY} > 0$). The pedigree analysis was performed with the PEDIG software package (Boichard 2002).

Pedigree completeness was estimated according to Boichard et al. (1997) as the mean equivalent of complete generations (EqG) known per animal, by applying the following equation:

$$EqG = \frac{1}{N} \sum_{j=1}^N \sum_{i=1}^{n_i} \frac{1}{2^{g_{ij}}}$$

where:

EqG – mean equivalent of complete generations

N – number of examined animals

n_i – total number of ancestors of the j^{th} animal in the population

g_{ij} – number of generations between the j^{th} animal and its i^{th} ancestor

Ancestral and Active groups were treated as the reference populations in the founder and ancestor analysis. The total number of founders (f) and the effective numbers of founders and ancestors were estimated, and the founders and ancestors with the highest gene contribution to each reference population were identified.

The effective number of founders (f_e), which were animals of unknown pedigree, was estimated according to Lacy's formula (Lacy 1989):

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

where:

f_e – effective number of founders

f – number of founders

q_k – probability of gene origin from the k^{th} founder

The f_e/f ratio indicates how balanced the founders' contributions were, with higher values indicating more equal contributions of the founders to the reference population.

The effective number of ancestors (f_a), which were the most influential animals for the examined population (not necessary the founders), was estimated according to the formula below (Boichard et al. 1997):

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

where:

f_a – effective number of ancestors

f – number of ancestors

p_k – marginal contribution of the k^{th} ancestor

The effective number of ancestors (f_a), which accounts for the ‘bottleneck effect’, is always lower than the effective number of founders (f_e), which includes all founders, whether their genes are still present in the reference population or have been lost through the generations. Therefore, the f_a/f_e ratio shows the amount of losses in the genetic pool of the reference population due to the ‘bottleneck effect’. This parameter is between 0 and 1, while the border values are virtual (0 – all genes lost, 1 – no loss of genes).

The effective number of founder genomes (f_g) was calculated according to the following formula (Boichard et al. 1997):

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

where:

f – number of founders

q_k – probability of gene origin from the k^{th} founder

r_k – expected proportion of founder alleles in the reference population

The value of f_g describes the random losses of founder genes in descendant generations and the balance of founder contributions. Therefore, the f_g/f_e ratio accounts for random genetic losses caused by ‘genetic drift’.

The amount of genetic variability (GD) due to losses from genetic drift and unequal contributions of founder genes (Melka et al. 2013) was estimated as follows:

$$GD = 1 - \frac{1}{2f_g}$$

The genetic diversity (GD*) due to losses from unequal gene contributions by founders (Melka et al. 2013) was calculated using following formula:

$$GD^* = 1 - \frac{1}{2f_e}$$

Therefore, the genetic variability lost due to genetic drift can be estimated as the difference between GD* and GD.

RESULTS AND DISCUSSION

Inbreeding and relatedness coefficients

Our study concerns the genetic variability of the Polish Chinese Crested dog population. The inbreeding and relatedness coefficient values calculated from pedigree information strongly depend on the quality of those pedigrees. The mean equivalent of complete generations known per animal (EqG) is one of the parameters commonly used to measure pedigree completeness. In the Ancestral

population (1860 animals), the value of the *EqG* was about 6 generations, with a maximum of 8.18 generations traced back. The corresponding average *EqG* value for the Active population (1313 animals) was 6.75, with a maximum of 9.16 generations. Figure 2 shows the distribution of the mean *EqG* and the number of animals over time. The decrease in *EqG* in litters born in 2000 and 2001 could probably be linked to the fact that some of them may have been imported and their pedigrees had no ‘connection’ to those of the rest of the population.

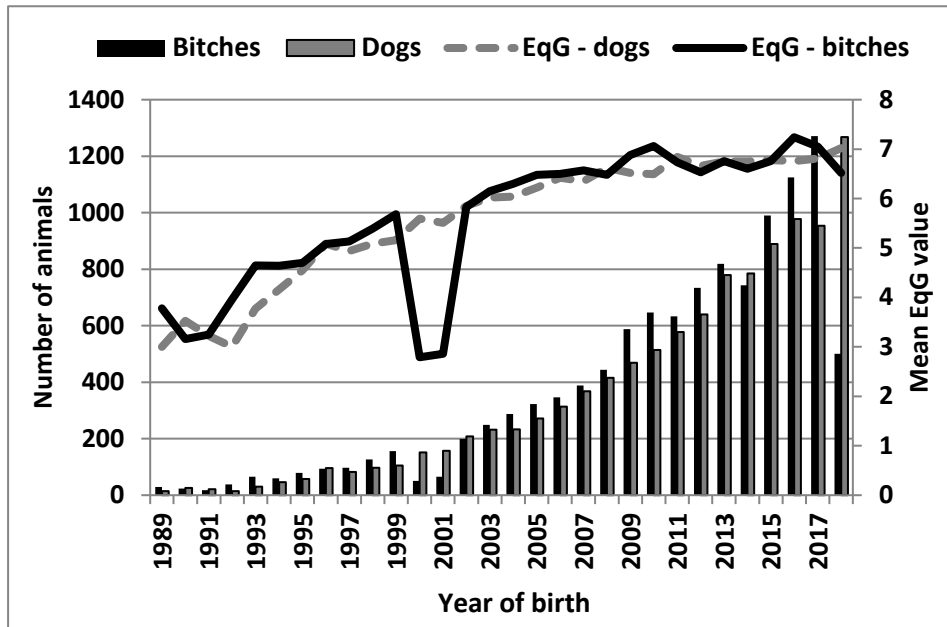


Figure 2. Mean equivalent of complete generations known per animal (*EqG*) and number of animals in consecutive birth years

Inbreeding and relatedness, obtained from pedigree analysis, are basic parameters for analysing genetic structure, especially in small populations. In our study the mean inbreeding coefficients in the Ancestral population were 0.063 and 0.083 for all animals and for inbred animals, respectively. The average F_x values in the Active population were 0.034 and 0.049 for all and for inbred dogs, respectively. In the Ancestral population, about 75.6% of the animals were inbred, while in the Active population only about 70.0% of the dogs had an F_x value above zero.

Table 1 presents the mean *EqG*, generation interval, and inbreeding values for male and female dogs in both populations (Ancestral and Active).

Table 1.

Inbreeding coefficients, generation intervals, and mean equivalent of complete generations in both populations

	Ancestral population		Active population	
	Males	Females	Males	Females
Number of animals	780	1080	552	761
Number of animals in pedigrees	1898	2454	1898	2454
Average generation interval [years]	4.19	4.11	4.25	4.39
Mean <i>EqG</i>	5.91	6.01	6.70	6.78
Maximum of <i>EqG</i>	8.18	8.18	8.67	9.16
Number of inbred animals	579	827	390	529
Mean <i>EqG</i> for inbred animals	6.21	6.24	7.18	7.29
Mean F_X– all animals	0.063	0.062	0.036	0.033
Mean F_X– inbred animals	0.085	0.081	0.051	0.048
Maximum F_X level	0.325	0.337	0.270	0.270

F_X – inbreeding coefficient; *EqG* – mean equivalent of complete generations

The generation interval in the Ancestral population was slightly lower than in the Active population, but exceeded 4 years in both. The mean *EqG* values were higher than 6 full generations known per animal in both populations, but were higher in the Active population. In general, the mean *EqG* values for inbred animals were higher than for all animals. In the Active population they exceeded 7 full generations known per animal, in both males and in females, indicating that the pedigree information used in our study was of good quality. About 74.2% of males and about 76.6% of females in the Ancestral population were found to be inbred. There were slightly fewer inbred animals in the Active population: about 70.7% of males and 69.5% of females. The maximum F_X values for both populations were high, which indicates that mating had occurred between full siblings (Table 1).

The vast majority of animals in both populations, i.e. over 56% in the Ancestral population and over 81% in the Active population, were not inbred or had F_X up to 0.063. Thus, inbreeding values above 0.25 were found in only 0.86% of animals from the Ancestral population (16 animals) and in only 0.53% of animals from the Active population (7 animals). The distribution of the F_X values can be regarded as not very advantageous for the populations, as about 44% of the individuals in the Ancestral population and about 19% of animals in the Active population had F_X levels above 0.063, which Falconer (1996) suggested as a safe inbreeding value. This could confirm our assumption that higher incidence of at least some genetic diseases may be associated with high levels of inbreeding in Chinese Crested dogs.

Figure 3 shows the inbreeding trend for males and females from the Ancestral population. Figure 4 shows the inbreeding trend for the dogs and bitches from Active population.

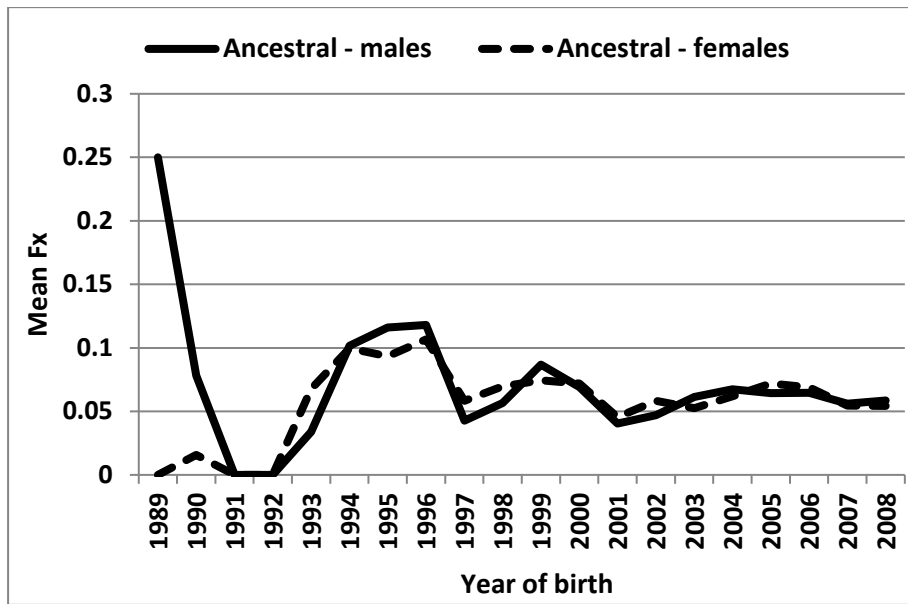


Figure 3. Inbreeding (F_x) trend for males and females from the Ancestral population

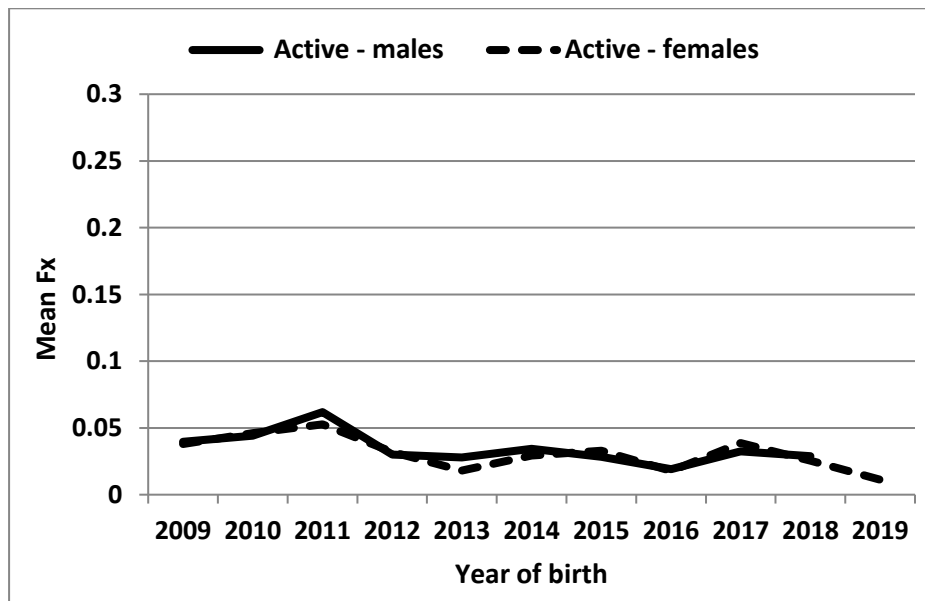


Figure 4. Inbreeding (F_x) trend for males and females from the Active population

A downward trend in inbreeding was found in the Ancestral population of Chinese Crested dogs (Fig. 3). The mean inbreeding levels in the years before 2000 were high, with maximum values over 0.10 for all animals and about 0.16 for animals with $F_x > 0$, irrespective of sex. In some cases (animals born in 1989) the F_x reached 0.25. This was probably because these were the early years of breeding of Chinese Crested dogs in Poland, when a limited number of animals were imported for breeding, and thus most of the progeny were related. At the end of 20th century, Chinese Crested dogs were not very popular in Poland because of the relatively high purchase prices of animals imported from abroad. Therefore only a few Polish kennels bred this breed of dogs. Since the year 2000, however, the popularity of this dog breed in Poland has been increasing slowly but steadily, and the level of inbreeding began to decrease and has fallen to well below 0.1. This may be due to the importation of breeding animals from abroad and the possibility of using foreign dogs to inseminate breeding females, which is currently easier and much more common than in the past. For the last 10 years the number of Chinese Crested kennels in Poland has been increasing steadily. Breeders have more and new opportunities to exchange breeding animals. This is a way to increase their income, as there is more interest in unique mating than in using animals simply because they are more accessible. Breeders now have greater knowledge of genetic diseases commonly occurring in Chinese Crested dogs. They also know which hereditary disorders tend to appear more frequently in specific bloodlines of Chinese Crested dogs. This allows most breeders to plan pairings so as to avoid mating close relatives and prevent the appearance of pups burdened with those diseases. Thus, in the last 10 years some signs of stabilization have become visible in the Active population; inbreeding remains at a relatively low level, between 0.02 and 0.06 in the years 2012–2019 (Fig. 4).

The average relatedness coefficients for the Ancestral population were 0.106 and 0.122 for all and related pairs of animals, respectively. In this population about 86.7% of pairs of animals were related to each other. For the Active population, the corresponding mean R_{XY} levels were found to be slightly lower: 0.061 and 0.064 for all and for related pairs of animals, respectively. In the Active population, however, the percentage of related pairs of animals was higher, reaching 95.5%. Table 2 presents the R_{XY} values for the Ancestral and Active populations.

Table 2.
Relatedness coefficients for the Ancestral and Active populations

	Ancestral population – pairs			Active population – pairs		
	Male	Female	Male x Female	Male	Female	Male x Female
Number of all pairs	303810	582660	842400	152076	289180	420072
Number of related pairs	257673	512756	727804	143273	278788	400500
Mean R_{XY} – all pairs	0.104	0.107	0.105	0.062	0.061	0.061
Mean R_{XY} – related pairs	0.122	0.122	0.122	0.066	0.063	0.064
Maximum R_{XY} value	0.727	0.737	0.727	0.685	0.686	0.686

R_{XY} – relatedness coefficient

As shown in Table 2, in the Ancestral population about 85%, 88% and about 86.4% of male pairs, female pairs and male x female pairs, respectively, were related. The relatedness levels were higher in the Ancestral population than in the Active population. However, the Active population had a higher proportion of related pairs: about 94% of male pairs, 96.4% of female pairs, and about 95.3% of male x female pairs. The maximum relatedness values in both populations indicate that in some cases even double full-sib mating had probably been used, which in male x female pairs could lead to highly inbred progeny. However, the average F_x coefficients in both populations were low (Table 1), indicating that many breeders try to avoid mating close relatives.

Many authors (Shariflou et al. 2011; Leroy and Rognon 2012; Lewis et al. 2015; Jansson and Laikre 2018; Machova et al. 2020; Michels and Distl 2020) have agreed that if the number of animals in the population is low, the problems of increased inbreeding and the occurrence of hereditary diseases will be unavoidable. For 26 dog breeds in Sweden, Jansson and Laikre (2014) found that a loss of genetic variation and an increase in inbreeding levels had taken place in all examined dog breeds. According to their research, the inbreeding increase was not the main cause of genetic diseases in pedigree dogs. The same authors (Jansson and Laikre 2018) later examined genetic diversity in 12 native Swedish dog populations, and the results showed that the average inbreeding coefficients had doubled from 0.03 to 0.07. They also found extensive loss of within-breed variation. Most of these breeds numbered thousands of individuals, so this rapid increase in inbreeding coefficient values should have been avoidable. In other research, on four French dog breeds, Leroy and Rognon (2012) investigated two types of breeding strategies (elimination of an inherited recessive disease through various mating limitations and various initial frequencies of the allele, and limiting the number of offspring per reproducer) and their influence on the level of genetic diversity and the frequency of a deleterious allele. The authors found that limiting the number of offspring per reproducer might have a positive impact on genetic diversity. Another important conclusion was that the elimination of all carriers from breeding might affect the genetic diversity of a population in many ways, depending on the frequency of the deleterious allele and the number of animals in the breed.

The high percentage of related male x female pairs in the Active population found in our study – over 96% – may make it difficult to find unrelated animals for mating. Furthermore, the Chinese Crested dog breed has a dominant lethal hairlessness trait, so that breeders will not mate two hairless animals. It also has many genetic diseases more or less related to nakedness, which could additionally complicate planning of mating and make it difficult to apply the mating rules proposed in the aforementioned studies. Similar limitations on breeding programmes for dog breeds with hereditary diseases entered in the breed standard were mentioned by Broeckx (2020).

Founder and ancestor contributions

The genetic variability in a population, analysed using probabilities of gene origin obtained from pedigrees, is currently a tool frequently used for genetic conservation purposes, because these values indicate the state of genetic diversity. In our study, we also calculated the contributions of founders and ancestors as the probability of gene origin. Table 3 shows the parameters of gene origin in Chinese Crested dogs from the Ancestral and Active populations in Poland.

Table 3.

Parameters of gene origin in Chinese Crested dog populations in Poland

	Reference population			
	Ancestral		Active	
	Dogs	Bitches	Dogs	Bitches
Number of animals	780	1080	552	761
Total number of animals in pedigrees	4352	4352	4352	4352
f	291	255	533	513
f_e	38	37	78	79
Total number of ancestors	79	70	130	131
f_a	20	20	33	36
f_g (SD)	9.32(1.94)	9.55(1.98)	15.82(3.30)	16.24(3.35)
f_e/f ratio	0.131	0.145	0.146	0.154
f_a/f_e ratio	0.53	0.54	0.42	0.46
f_g/f_e ratio	0.25	0.26	0.20	0.21
Founders explaining:				
50% of variability	16	15	23	42
90% of variability	88	85	195	264
Ancestors explaining:				
50% of variability	7	7	13	13
90% of variability	29	28	64	65

f – total number of founders (animals without pedigrees); f_e – effective number of founders;

f_a – effective number of ancestors; f_g – effective number of founder genomes; SD – standard deviation

The f_e and the f_a values in the Ancestral population of Chinese Crested dogs were lower than in the Active population, which may best demonstrate that the genetic condition of the Active population is better than that of the Ancestral population. The number of founders explaining 50% or 90% of the genetic diversity was also higher in the Active population, which indicated higher variability, probably due to importation of animals. The f_e/f ratio was slightly lower in the Ancestral population than in the Active population and indicated that the contribution of founders in the latter was more balanced. However, the f_a/f_e ratio was lower for the Active population than for the Ancestral population. This could be explained by the higher number of related animals in this population and may indicate decreasing genetic variability and the possible occurrence of the ‘bottleneck effect’. The f_g/f_e ratio was also lower in the Active population than in the Ancestral population, indicating minor random genetic losses caused by ‘genetic drift’. The number of ancestors explaining 50% and 90% of the genetic diversity was low. These values were lower for the Ancestral population than for the Active population, indicating that the smaller number of ancestors in the Ancestral population had a higher contribution of genes (Table 3).

The genetic variability lost in the Ancestral population due to bottlenecks and genetic drift ($1 - GD$) was 0.054 for male dogs and 0.052 for female dogs. The corresponding values for the Active population were 0.032 and 0.031 for male dogs and female dogs, respectively. The losses due to genetic drift ($GD^* - GD$) in the Ancestral population amounted to 0.041 for dogs and 0.039 for bitches. However, losses in the Active population were lower, at about 0.025 both for dogs and bitches. The losses caused by the unequal gene contribution of founders ($1 - GD^*$) were 0.013 and 0.014 for dogs and bitches from the Ancestral population. The corresponding values for male and female dogs from the Active population were roughly halved, amounting to about 0.006. The relative shares of the genetic drift effect in variability were 75.5%, 74.2%, 79.7% and 79.4% in dogs and bitches from the Ancestral and Active populations, respectively. These values were higher than the effects of unequal proportions of founders' genes: 24.5% for dogs and 25.8% for bitches from the Ancestral population and 20.3% for dogs and 20.6% for bitches from the Active population. It can be concluded that the influence of random losses of genes due to genetic drift was greater in the Active population than in the Ancestral population, while the relative influence of the unequal founder contributions was smaller.

These values can be compared with the results of other studies. Mäki (2010) found much lower f_e and f_a ratios but similar or higher f_{a/f_e} ratios for Nova Scotia Duck Tolling Retrievers and Lancashire Heelers compared to the present study. In a broad study involving 32 dog breeds bred in Australia, Shariflou et al. (2011) obtained f_e values ranging between 8 and 258 animals, f_a values between 4 and 113 animals, and f_{a/f_e} ratios from 0.27 to 0.78. Our results were also in this range (Shariflou et al. 2011), but closer to the lower limit, which reflects the level of genetic variability in dog breeds with a small population size. However, Mortlock et al. (2016), in a study of the genetic diversity of Bullmastiff dogs, found higher f_e and f_a values as well as a higher f_{a/f_e} ratio than in our results: 79, 62 and 0.79, respectively. For the Hungarian Border Collie population, Acs et al. (2019) recently reported an f_e value of 117, which was higher than in our results, while the f_a value was 20 and the f_{a/f_e} ratio was 0.17 – lower than in the present study. For the Czech Spotted Dog, a breed originating from 10 animals and initially developed for laboratory purposes, Machova et al. (2020) obtained much lower f_e and f_a values of 4 and 3, respectively, but a much higher f_{a/f_e} ratio (0.75) than in our study. Michels and Distl (2020), for Polish Lowland Sheepdogs bred in Germany, also reported much lower f_e and f_a values, amounting to 10 and 6 animals, respectively, compared to those obtained in our study. Michels and Distl (2022), who recently investigated the genetic diversity of the Deutsch Drahthaar dog population, obtained a slightly higher f_{a/f_e} ratio of 0.58 and a similar f_{g/f_e} ratio of 0.25, while the f_e/f ratio was nearly the same as for our Ancestral population and just over half that obtained for our Active population. Our study showed the same pattern of relative losses due to genetic drift and unequal use of founders as in the study by Michels and Distl (2022).

The number of ancestors explaining 50% of the gene variability of the reference population in this study was lower than that obtained by Mortlock et al. (2016) for Bullmastiff dogs. More recently, Machova et al. (2020) found a much lower number of ancestors needed to explain 50% or 90% of the gene contribution to the reference population of Czech Spotted Dogs. They reported only 2 ancestors explaining 50% of the gene pool of this breed, and 5 explaining 90%. Michels and Distl (2020), who studied Polish Lowland Sheepdogs from Germany, also reported only 2 and 5 ancestors explaining 55% and 75% of genetic diversity, respectively. However, more recently Michels and

Distl (2022) obtained higher numbers of ancestors explaining 50% and 90% of the gene pool (13 and 110, respectively) for Deutsch Drahthaar dogs.

In the present study most of the founders had low gene contributions in both reference populations of Chinese Crested dogs. The vast majority of founders in both reference populations had trace contributions of genes of under 0.1%, i.e. 53% of founders among Ancestral bitches, 57% of founders among Ancestral dogs, 60% of founders among Active bitches, and over 71% of founders among Active dogs. More founders had gene contributions up to 1% in the Active population (200 animals) than in the Ancestral population (112 animals), whereas in both reference populations nearly the same number of founders had a gene contribution between 1% and 4%: 9 animals in the Ancestral population, and 7 in the Active population. The highest gene contribution was found in 7 founders (4 dogs and 3 bitches) in the Ancestral population, and in only 3 male founders and one female founder from the Active population.

Figure 5 shows the main founders of both populations, with gene contributions higher than 1%. In both populations there were 9 such founders (4 dogs and 5 bitches). They were the same animals in the Ancestral and Active population, but with lower contributions to the latter. The same male founder had the highest gene contribution in both populations, with a gene contribution of over 9% to the males and females of the Ancestral population and a slightly smaller contribution to the Active population, amounting to over 8% for dogs and over 6% for bitches. The rest of the main founders had lower gene contributions that did not exceed 6% (Fig. 5).

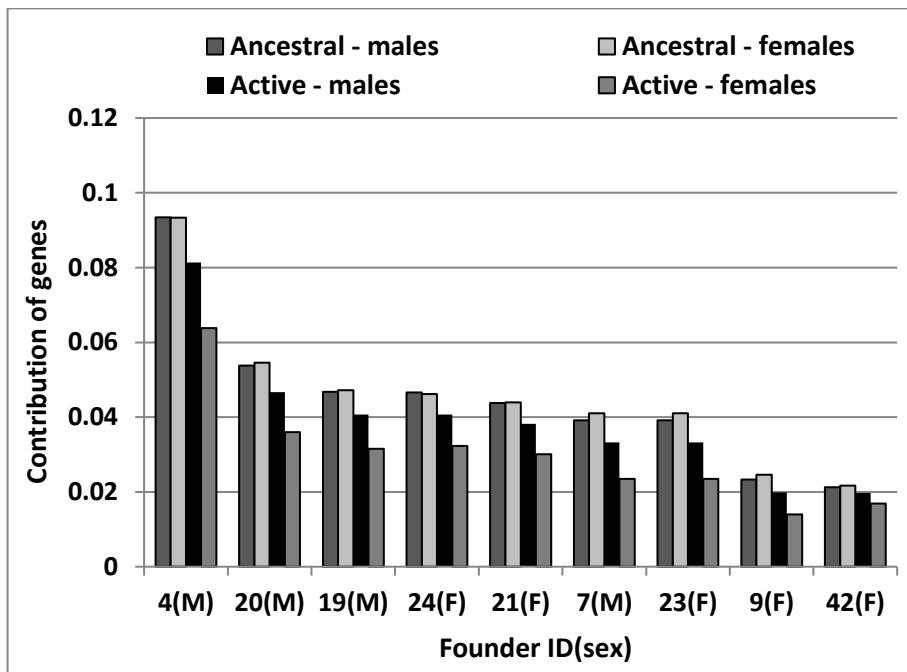


Figure 5. The main founders in males and females of both analysed populations

In the Ancestral population there were 149 ancestors (79 dogs and 70 bitches). The number of ancestors was slightly higher in the Active population, amounting to 261 animals (130 male and 131 female ancestors). In most cases the gene contribution of ancestors in both reference populations was below 0.5%. This was the case for 50% of ancestors of bitches and 58% of ancestors of dogs in the Ancestral population, and 61% of ancestors of bitches and over 65% of ancestors of dogs in the Active population. However, slightly more ancestors had gene contribution values up to 1% in the Active population than in the Ancestral population. The same pattern was established for the number of ancestors whose gene contributions were between 1% and 4%, i.e. there were 20 and 16 such ancestors for males and females from the Ancestral population and 21 and 32 for males and females from the Active population. The number of ancestors with a gene contribution of over 4% was nearly the same for both reference populations: 5 and 8 animals for the Ancestral population and 4 and 5 for the Active population.

Figure 5 shows the main ancestors with a gene contribution of over 1% to both populations. The ancestors in the Ancestral population were quite different from those in the Active population. There were 15 main ancestors (8 dogs and 7 females) in the Ancestral population, while the number was higher in the Active population, at 22 (10 dogs and 12 bitches). Only 12 ancestors (5 dogs and 7 bitches) were common to both populations, which indicates substantial changes in the gene pool of the breed, probably through the importation of new animals (ancestors). Among the top six ancestors with the highest gene contribution, the first three were the same in the both reference populations. The first main male ancestor in both populations contributed over 10% of genes to the Ancestral population, and slightly under 6% to only the females from the Active population, which means that this ancestor has lost some of its importance in the Active population. The second major male ancestor made almost equal contributions of genes to both reference populations. The third main female ancestor was of greater importance in the Ancestral population; its contribution in the Active population was only half of that noted in the Ancestral population (Fig. 6).

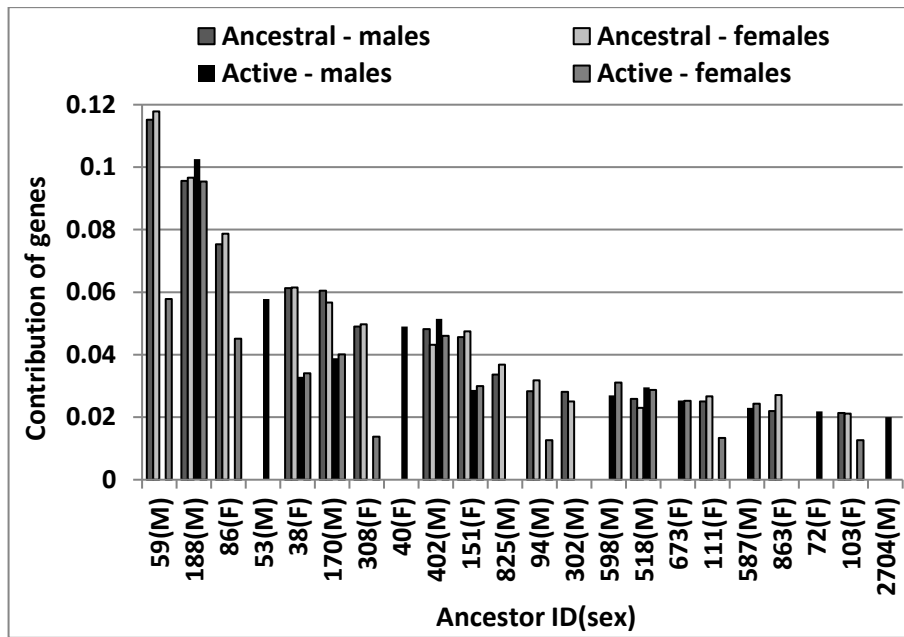


Figure 6. The main ancestors of both analysed populations

Although the parameters of gene origin in our study were generally similar to those obtained by the other authors cited above, some differences between the two Chinese Crested dog groups can be attributed to changes in genetic variability caused by the relatively recent import of dogs for breeding as well as by the increase in the popularity of the breed and the gradual increase in the number of kennels, leading to changes in the number and composition of ancestors.

The final problem studied here was the potential overuse of some stud dogs. A total of 844 stud dogs were used in the Chinese Crested dog population, of which 34 had between 20 and 40 progeny, and 58 had from 10 to 20 progeny. There were 742 stud dogs with up to 10 offspring. Table 4 lists the 10 stud dogs with highest number of progeny in the pedigrees and shows that the 10 most popular stud dogs had 560 offspring in total. Four of them (in bold in Table 4) were also listed as main ancestors with high gene contributions (Figure 5). Only 3 of 10 stud dogs were not inbred.

Table 4.

Ten most popular stud dogs in the Chinese Crested dog population

Dog ID	Sex	Year of birth	F_x	Number of progeny in the pedigrees
188	M	1994	0.041	104
402	M	1998	0.043	74
663	M	2006	0.065	50
265	M	2000	0.050	49
295	M	2000	0.088	49
170	M	1994	0.125	48
825	M	1999	0	48
480	M	2001	0.045	47
826	M	2003	0	46
629	M	2001	0	45

F_x – inbreeding coefficient; Dog ID – identification number of the dog

Table 5 shows the relatedness of the 10 most popular stud dogs. Sixty per cent of pairs of stud dogs were related. There were three sire lines created by some of the 10 main stud dogs. Dog no. 188 and his sons nos. 265 and 480 sired 200 offspring in total. The next dog, no. 402, and his grandson no. 663 both had 124 progeny in total, and dog no. 825 and his son no. 826 had 94 offspring in total. This additionally contributed to the reduction in the genetic variability of the population.

Table 5.

Kinship coefficients for the 10 most popular stud dogs

Dog ID	188	265	295	402	480	629	663	825	826
170	0	0.259	0.254	0.036	0	0.015	0.016	0	0
188		0.546	0.129	0.069	0.542	0.044	0.204	0	0
265			0.210	0.076	0.328	0.061	0.143	0	0
295				0.098	0.165	0.107	0.113	0	0
402					0.060	0.026	0.292	0	0
480						0.288	0.152	0	0
629							0.173	0	0
663								0	0
825									0.500

Dog ID – identification number of the dog

Leroy and Baumung (2010), using simulations and genealogical data, investigated the popular sire effect, the effect of line inbreeding, and the close mating effects (mating between half- or full sibs) on the genetic variability of a dog population. Their research showed that these three popular mating practices materially affect the dissemination of genetic disorders. The effective number of dog sires was found to range from 33% to 70% of all sires, and after two generations the percentage of inbred dogs ranged from 1% to 8%. The simulation confirmed that the popular sire effect led to problems, because the risk of dissemination of hereditary disorders was 4.4 times the risk under random mating conditions. However, line breeding and close mating practices caused a decrease in this dissemination risk (Leroy and Baumung 2010). Calboli et al. (2008) found that one selected top sire was used many times for mating and had more than 2,500 offspring over his lifetime. Thus the use of popular stud dogs in pedigree dog breeding may contribute to the loss of genetic variability, in proportion to inequality in the use of breeding dogs, and to the high incidence of recessive genetic disorders. Leroy (2011) emphasized that breeders must improve the management of existing dog breeds in terms of preventing the loss of diversity and the considerable increase in inbreeding. According to Leroy (2011), restrictions on the number of offspring per breeding dog should be introduced, which would require breeders to select more breeding animals available for mating. The FCI recently recommended, for all dog breeds, that one dog should not sire more than 5% of all registered puppies over a 5-year period. This could help to control the popular sire effect, which contributes to the loss of genetic variation in dog breeds. The problem of the overuse of some stud

dogs has recently been pointed out by many other authors (Farrell et al. 2015; Donner et al. 2018; Broeckx 2020).

CONCLUSIONS

To sum up the results of our research, the population of Chinese Crested dogs bred in Poland is not in poor condition in terms of the level of genetic variation. New opportunities for the exchange of genetic material between Polish and foreign breeders has resulted in significant and generally positive changes in the genetic diversity of the breed. These were mainly a reduction in the mean inbreeding level of the youngest animals in the Active population, and a partial change in the composition of ancestors and their contributions. However, over 70% of animals in the Active population had inbreeding values above zero, and about 19% dogs had F_x levels exceeding the safe mark of 0.063. We believe this may be linked to the increased incidence of at least some genetic diseases in the population of Chinese Crested dogs in Poland. In addition, random losses, i.e. genetic drift, have a stronger impact of variability in the Active population. This may indicate a decrease in genetic variability in the population, despite the gradual increase in its actual size. Therefore, it can be concluded that the effect of unfavourable phenomena reducing genetic diversity, such as drift or the bottleneck effect, was also revealed in this population. The high percentage of related male x female pairs in the Active population (over 95%) could cause problems with mating in the future, given the limitations imposed by hairlessness and other hereditary diseases found in Chinese Crested dogs. For this reason, Chinese Crested breeders should pay close attention to the selection of animals for mating, taking into account the FCI regulations regarding the equal use of reproducers. Breeders can import dogs for mating or plan mating so that the animals are as unrelated as possible. Unfortunately, this will not be an easy task, as there is still a trend among some Chinese Crested breeders to overuse popular stud dogs. However, there is also a noticeable recent tendency to use imported dogs and not to repeat the same pairings. If the maximum number of litters per dog were limited in the Chinese Crested dog breeding, as recommended by the FCI, the problem could be reduced. However, it would be helpful to encourage breeders to pay more attention to the inbreeding coefficient value of planned puppies. Due to the relatively large number of hereditary diseases, we recommend that the Chinese Crested dog breed should be continually monitored in order to maintain genetic variability and prevent the spread of hereditary diseases.

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