

PEDIGREE ANALYSIS OF MANGALICA PIG BREEDS

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Abstract

An effective gene conservation programme requires the knowledge of genetic variability of the population. The genetic structure of Mangalica pig breeds (Blonde, Red and Swallow-bellied) was studied from pedigree records. Herdbook data available up to 2011 of registered Mangalica pig breeds (Blonde, Red and Swallow-bellied) were analysed. The number of complete generations was 6 for Blonde and 5 for Red and Swallow-bellied Mangalica whereas the average complete generation equivalent was between 3.51 and 6.01. The average level of inbreeding of the reference population was low (4.07–5.87%). The investigated breeds could be considered as small populations based on the probability of gene origin. The most important ancestor contributed between 9 and 16% of the gene pool of the reference populations. The longest generation interval was found for the sire-to-son pathways whereas the shortest for dam-to-daughter pathways for each breed.

Key words: genetic variability, pedigree analysis, Mangalica

An effective gene conservation programme requires the knowledge of genetic diversity of the population. The Mangalica pig breeds were most popular in the late 1800s (Kovács, 2006). The gene conservation started in 1973, only with 39 sows (Bodó, 2002). According to Zsolnai et al. (2006), the different colour varieties of the breed are genetically different, which is why there are three different breeds called Mangalica. The Mangalica pig is a representative example for the success of preserving endangered breeds. Its population is stable and continuously increasing in all colour types although the number of Swallow Belly and Red Mangalica is still critical (Egerszegi et al., 2003). The breeds have numerous populations in Austria (Prevost, 2010) and Romania (Zăhan et al., 2009) as well. Prevost (2010) reported insufficient data quality of the Austrian Mangalica pigs born between 2004 and 2007 based on the low pedigree completeness (2.54). The number of founders and effective number of founders were 156 and 70.6 in the Austrian population, based on their research work. Zăhan et al. (2009) reported high heterogeneity and low inbreeding in

the Romanian Red Mangalica stock. Baumung and Prevost (2010) studied the pedigree structure of Austrian Turopolje pig. They reported loss of genetic variability of the population and the successful conservation breeding programme. Many research groups (Baumung et al., 2002; Janssens et al., 2005; Krupa et al., 2015) found low level of inbreeding in the most important breeds (Large White, Landrace, Pietrain). The quality of the pedigree was shown through pedigree completeness for the Belgian and Czech populations (Janssens et al., 2005; Krupa et al., 2015). There are a lot of studies concerning the evaluation of genetic structure for various domestic species (e.g. pig, horse, cattle and sheep). Pedigree analysis was carried out both for the French (Moureaux et al., 1996) and the Hungarian (Bokor et al., 2013) English Thoroughbred population. Arabian Thoroughbred (Cervantes et al., 2008; Glazewska and Jezierski, 2004; Moureaux et al., 1996), the Lipizzaner Horse (Zechner et al., 2002) as well as other local breeds (Royo et al., 2007) were also described based on pedigree data. Research results for dairy and beef cattle breeds are also available in various studies (Mc Parland et al., 2007; Sorensen et al., 2005; Baumung et al., 2002; Gutiérrez et al., 2003; Maignel et al., 1996). The aim of the study was to analyse pedigree information of the registered Hungarian Mangalica population.

Material and methods

Breeds and data

Herdbook data available up to 2011 of registered Mangalica pig breeds (Blonde, Red and Swallow-bellied) were analysed. Earliest pigs were born in 1980. Data used for the analysis were obtained from the Hungarian National Association of Mangalica Breeders. The Blonde Mangalica had the largest population size (19,156) whereas the Red (5,519) and Swallow-bellied (3,468) breeds had only fewer records in the pedigrees. Animals born between 2009 and 2011 were chosen as reference population for each breed to evaluate the genetic structure.

Analysis of pedigree structure and inbreeding

Pedigree completeness expresses how much generation information we have on average in any individual's pedigree. The average complete generation equivalent (CGE) describes the number of traceable generations in a comparable complete pedigree. The number of complete generations shows the furthest generation where all ancestors of the individual are known. The maximum number of generations gives the number of generations separating the individual from its furthest ancestor. The homozygosity of the population was described by using the inbreeding coefficient (Wright, 1922). The average relatedness coefficient (AR) (Goyache et al., 2003; Gutiérrez et al., 2003) of each individual is defined as the probability that an allele randomly chosen from the whole population in the pedigree belongs to a given animal. Generation interval was defined as the average age of the parents, when their offsprings, which were used in breeding, are born. This parameter was estimated for the whole pedigree, and also for the reference population, on 4 different pathways: sire-daughter, sire-son, dam-daughter and dam-son. The different generation intervals were compared with t-test. Founders are defined as animals with unknown parents in the pedigree. Effective number of founders (fe) describes the number of founders that are expected to generate the same genetic variability as that observed in the population under study, given that all founders equally contribute to the genetic diversity of the reference population (Lacy, 1989). Number of ancestors is the minimum number of individuals in the pedigree, which explains the total genetic variability in the reference population. Effective number of ancestors (fa) is defined as the least number of ancestors that would create the same genetic diversity in the population, given that all ancestors would contribute equally to the gene pool of the population. The ratio of the two indexes (fa/fe) described above indicates if the bottleneck effect characterizes the population under study, or not. Bottleneck effect occurs when the number of breeding animals (and therefore the genetic variability of the population) narrowed in one, or more generations. The bottleneck effect occurs when the effective number of ancestors is much lower than the effective number of founders (equivalently, if the ratio of fa/fe is much lower than one). The genetic variability of the population was also described with effective population size. Effective population size is the number of animals that would lead to the same increase in inbreeding, as observed in the population under study, if they would contribute equally to the next generation. Effective population size is derived from the rate of inbreeding using the formula $N_e = 1/(2\Delta F)$, where ΔF is the annual increase of inbreeding caused by unbalancing of founders contribution. The above mentioned parameters were computed using the ENDOG software package (Gutiérrez and Goyache, 2005). The formulas and methods are explained more detailed in the instructions of the used software

Results

Table 1 gives an overview of all available pedigree records for the three investigated breeds. Animals of the reference population and their ancestors, but also animals with no link to the reference population, were included. The number of complete generations were 6 for Blonde and 5 for Red and Swallow-bellied Mangalica. The average complete generation equivalent (CGE) varied between 3.51 and 6.01 for the three breeds. The inbreeding of the total population (Table 1) is similar to the reference (Table 2) for the Red Mangalica while slightly lower for the Blonde and Swallow-bellied Mangalica breeds. The lowest number of inbred animals was found for the Swallow-bellied Mangalica population.

Table 2 presents the various measures for genetic variability. In our study the average level of inbreeding of the reference population was low (4.07–5.87%). The total number of founders was the highest for Blonde Mangalica (159) and the lowest for Red Mangalica (84) for the reference population. The effective number of founders and ancestors ranged from 27 to 50 and from 15 to 24, respectively. The lowest numbers were estimated for the Red Mangalica.

	Blonde Mangalica	Red Mangalica	Swallow-bellied Mangalica
Animals in the pedigree file	19.156	5.519	3.468
Animals in the reference population	2292	1142	752
Complete generation equivalent	6.01	5.02	3.51
Number of complete generations	6	5	5
Maximum no. of generations traced	17	14	14
Effective population size	58	27.8	51.8
Average inbreeding (%) in the whole pedigree	3.86	5.02	3.29
Average relatedness (%)	6.76	9.81	4.68
Inbred animals (%)	80.83	79.05	53.32
Average inbreeding (%) of inbred animals	4.77	6.34	6.17
% known ancestors at generation			
1	97	97	93
2	93	92	81
3	87	84	60
4	77	74	44
5	66	60	30
6	54	44	19
7	45	28	12
8	35	14	7
9	25	6	3
10	14	2	1

Table 1. Pedigree information about the three pig breeds

Table 2. Results of the pedigree analysis for the reference pig populations

	Blonde Mangalica	Red Mangalica	Swallow-bellied Mangalica
Average inbreeding coefficient (%)	5.67	5.87	4.07
Total number of founders	159	84	97
Effective number of founders (fe)	50	27	35
Effective number of ancestors (fa)	22	15	24

Table 3 gives the proportions of genes contributed to the reference population by the most important ancestors. The Blonde Mangalica breed had the largest size of the founder population and, consequently, the number of ancestors that accounts for the population diversity increased very quickly at the beginning, but slower than in the other breeds later; in other words, several ancestors explained a high percentage of the population, but the rest of the population was explained by many others. The most important ancestor contributed between 9 and 16% of the gene pool of the reference populations. Only 6 ancestors were sufficient to explain 50% of the genes of the Red Mangalica population.

	Blonde Mangalica	Red Mangalica	Swallow-bellied Mangalica
Proportion of genes contributed by	/:		
first ancestor	0.0945	0.1568	0.13040.0947
second ancestor	0.0898	0.1051	0.12500.0897
third ancestor	0.0842	0.0810	0.09100.0596
first 10 ancestors	0.6021	0.6718	0.5505
No. of ancestors contributing:			
50% of the gene pool	8	6	9
80% of the gene pool	21	15	23
100% of the gene pool	126	62	77

Table 3. Description of the most important ancestors for the reference pig population

Generation intervals for the three breeds are presented in Table 4. The longest generation intervals were found for the sire-to-son pathways whereas the shortest were found for dam-to-daughter pathways for each breed.

	Blonde Mangalica	Red Mangalica	Swallow-bellied Mangalica
Sire/Son	2.99	2.91	2.75
Sire/Daughter	2.57	2.47	2.97
Dam/Son	2.47	2.57	2.48
Dam/Daughter	2.32	2.31	2.38
Average	2.43	2.47	2.49

Table 4. Generation intervals (years) of the Mangalica pig breeds for the different pathways

In order to distinguish between recent and cumulated inbreeding, the evolution of this parameter per year of birth was also computed taking into account only the last three generations (Figure 1). All three breeds exhibited a similar pattern showing that inbreeding was mainly due to the recent generations, in most of the cases because a historical knowledge of the pedigree is lacking. Almost all animals born in the end of the research period were inbred. The Swallow-bellied Mangalica had the lowest inbreeding level.



Figure 1. Evolution of inbreeding in the whole population and in inbred animals only, in Mangalica pig breeds (per breed)

Discussion

Maignel and Labroue (2001) found deep and complete pedigrees for several pig breeds in France (CGE of 6.9-10). The CGE was high for Blonde and Red Mangalica (Table 1) and near to Baumung et al. (2002) results (7.85, 6.2 and 5.74 for Large White, Landrace and Pietrain, respectively) whereas it was lower for Swallowbellied Mangalica. Prevost (2010) found lower CGE values (2.54) for the Austrian Mangalica population and Tang et al. (2013) also reported lower values (1.82–2.65) compared to our results of the Hungarian Mangalica breeds. Such information determines how accurately the inbreeding coefficient can be estimated, therefore it has a high effect on the validity of the estimated values. The poor pedigree information (lowest CGE) for the Swallow-bellied Mangalica leads to a low average inbreeding coefficient, and allows no meaningful statement about the true level of inbreeding in the reference population. The inbreeding of the breeds is higher than what was found for Landrace and Large White breeds (Baumung et al., 2002; Janssens et al., 2005; Krupa et al., 2015). Lowest percentage of inbred animals and average relatedness was found for the Swallow-bellied Mangalica. The reason could be the low pedigree information of the breed (shown by the low CGE value). Though the Red Mangalica is not with the lowest number of animals it seems to be the most endangered based on the average inbreeding and average relatedness of the whole population. The effective population sizes based on increase of the inbreeding coefficients for the Blonde, Red, and Swallow-bellied Mangalica were 58, 27.8 and 51.8, respectively. The effective population size of the Red Mangalica population is below the desired size (Ne=50) suggested by the FAO (1998) guidelines and close to be critically low for the fitness of the breed (Meuwissen and Woolliams, 1994). However, these results for the effective population size are difficult to interpret, because of the high sensitivity to completeness of pedigree information (Boichard et al., 1997).

Several populations in France (Maignel and Labroue, 2001) showed similar level of inbreeding (2.2–4.6%) as in our study (Table 2). From a genetic point of view the three investigated breeds could be considered as small populations based on the probability of gene origin (fe, fa). When the effective number of founders was compared to the effective population size, the Blonde Mangalica had the higher effective population size and effective number of founders. Despite the largest population, the bottleneck effect was also the highest for the Blonde Mangalica, as the ratio of fa/fe was the lowest (0.44). Based on this parameter, the gene loss was the lowest for the Swallow-bellied Mangalica (fa/fe=0.69).

There were significant differences (P<0.05) between sire-to-son and sire-todaughter pathways based on independent samples t-test for each breed (Table 4). Also significant differences were found between dam-to-daughter and dam-to-son pathways for the Blonde and Red Mangalica breeds. The generation interval of Belgian Pietrain pigs (3.15) (Janssens et al., 2005) was higher than our values while the estimated values for sires exceeded their results for Belgian Landrace (2.15).

There were differences among the annual changing of average inbreeding (ΔF) for the three breeds (Figure 1). The average inbreeding of the whole population increased only for the Blonde Mangalica breed, though almost all piglets were inbred

at the end of the analysed time interval. This tendency could cause problems in the near future, so minimization of inbreeding level of the future generations has to be taken into account in the breeding plans of all breeds.

Conclusions

The main conclusion of our study is that the status of genetic variability in relation to gene conservation differs among Mangalica breeds, so a single practical recommendation could not be drawn. The causes of these differences could be related to various population sizes among them. The effective number of founders is considerably higher than the effective number of ancestors for each breed showing bottleneck effect during the history of all breeds. It was shown that the status of Red Mangalica is the most dangerous among the Mangalica breeds.

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