

PRELIMINARY ASSESSMENT OF TRENDS IN INBREEDING AND AVERAGE RELATEDNESS OF THE FORMER VALACHIAN SHEEP

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ABSTRACT

The objective of this study was to analyse the trends in inbreeding and in average relatedness of the former Valachian sheep. Investigation was based on pedigree data of a single flock, population of which consisted of 27 animals born during the period 2007-2010 (reference population). A whole pedigree population (individuals with genetic ties to reference population) consisted of 137 animals. A total of 8 generations of ancestors were identified. Proportions of known parents decreased with an increasing number of generations (100% to 0.07% in the reference population vs. 63% to 0.01% in the whole pedigree population). Inbreeding (F%) and average relatedness (AR%) were investigated separately for each sex. Zero inbreeding coefficients were found in males. In females, average values of inbreeding ranged from 0% to 14% (across the years of birth). Inbreeding was of zero values in females born before 2003; the exceptions were females born in 1995 (average value of inbreeding about 3%). Inbreeding was of non-zero values since 2003; the exceptions were females born in 2010. Average relatedness was similar in males and in females; average values ranged from 2% to 12% across the years of birth. The analysis provided an insight to management practice and it may also be useful for mating policy. Regular monitoring of breed genetic structure is recommended.

Key words: Valachian breed; genealogical data; trends; inbreeding; average relatedness; pedigree completeness

INTRODUCTION

The Convention on Biological Diversity (1992) represents the commitment of the world community to focus on conservation of biological diversity, sustainable use of its components, and fair and equitable sharing of benefits arising from the use of genetic resources. Awareness to preserve livestock breeds and species has increased during the last two decades (Simon and Buchenauer, 1993; FAO, 1999, 2007a,b). Within the European Union, measures to prevent breeds from extinction are in place (Council Decisions No. 1257/99, 817/2004). Small populations can be lost because of increase in inbreeding and decrease in genetic variability (Danchin-Burge *et al.*, 2010). Management methods

based on pedigree analysis (Goyache *et al.*, 2003; Gutiérrez and Goyache, 2005; Gutiérrez *et al.*, 2005, 2008, 2009) can act as a tool for preventing the breeds from extinction. Danchin-Burge *et al.* (2010), however, underlined the fact that managers of small populations are usually not aware of such research and they generally do not wish to incorporate its results. Setting up these methods at a farm level seems to be either too complicated or too constraining.

Research aimed at pedigree analysis of small populations is currently ongoing in Slovakia (see Oravcová and Krupa, 2011 for a review). Pedigree analysis was used to calculate the population means of inbreeding and average relatedness for the former Valachian sheep (Oravcová and Krupa, 2011). Inbreeding

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and average relatedness can vary across the years of birth and sex of the animals; also they can show various trends and evolution. Therefore, the objective of the study was to investigate these parameters in detail.

MATERIAL AND METHODS

Pedigree data of the former Valachian sheep were analysed to assess the amount of genetic diversity in a population. A single flock (opened nucleus; males born out of flock including imported individuals are allowed for mating) of 27 animals born during the period 2007-2010 was investigated (reference population, considered to be an actual breeding population). A four-year period was preferred, because this length of the average generation interval was found in the breed (Oravcová and Krupa, 2011). A total of 137 animals with genetic ties were identified (whole pedigree population). An individual pedigree record consisted of animal, father and mother unique identification, animal sex and birth date.

Coefficients of inbreeding and of average relatedness of each animal with pedigree information were computed using the ENDOG v.4.8 programme (Gutiérrez and Goyache, 2005). Pedigree completeness was analysed as proportion of known parents across individual generations of ancestors. Equivalent complete generations were defined as the sum of generations separating each animal from its ancestors (Maignel *et al.*, 1996). Coefficient of inbreeding (F%) was defined as the probability of having two identical alleles by descent and is computed following Meuwissen and Luo (1992). Coefficient of average relatedness (AR%) was defined as the probability that an allele randomly chosen

from the whole population in the pedigree belongs to a given animal. It is computed as the average of the coefficients in the row corresponding to the animal in the numerator relationship matrix and can be interpreted as the representation of the animal in the whole pedigree. In founder individuals, average relatedness can be obtained assigning to each individual a value of 1 for its belonging to the population; 1/2 for each offspring; 1/4 for each grandson and so on; and weighting by the size of population (Dunner *et al.*, 1998). See studies of Dunner *et al.* (1998), Goyache *et al.* (2003), Gutiérrez *et al.* (2005) and Royo *et al.* (2007) for details.

Trends in inbreeding and in average relatedness were expressed as average values across the years of birth of the animals, separately for each sex. Variation in equivalent complete generations was investigated across the years of birth.

Calculations were done using SAS/STAT v.9.2 (2002-2008).

RESULTS

Coefficients of inbreeding are highly sensitive to the quality of available pedigree and are affected by the fact that actual populations do not remain closed for considerable period of time (Goyache *et al.*, 2003). The larger number of known generations is available, the more precise coefficients of inbreeding can be computed. For this reason, pedigree completeness was analysed in detail.

A total of 8 generations of ancestors were identified. Proportions of known parents across each generation are given in Figure 1. These decreased

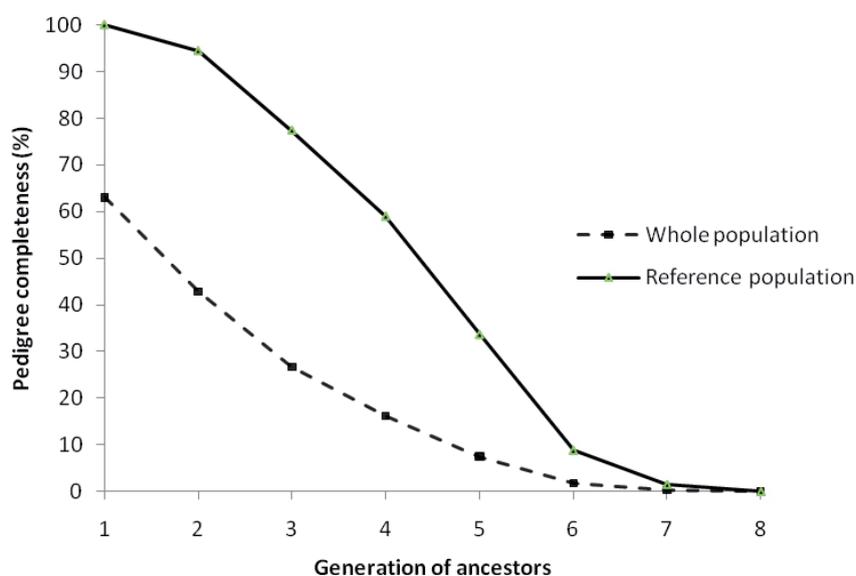


Fig. 1: Pedigree completeness by generation of ancestors (%)

continually from 100% to 34% in the first to fifth generation of the reference population and from 63% to 16% in the first to fourth generation of the whole pedigree population, respectively. Proportions of known parents less than 10% were found in the sixth to eighth generation of the reference population (9% to almost 0%) and in the fifth to eighth generation of the whole pedigree population (8% to almost 0%).

Up to the fifth generation of ancestors, proportions of known fathers and mothers (separately for the reference population and for the whole pedigree population) are given in Tables 1 and 2 (upper halves of tables indicating sire ancestors and lower halves of tables indicating dam ancestors, respectively). Higher proportions of known fathers and mothers were found in the reference population (differences by 30% to 40%).

Table 1: Pedigree completeness up to the 5th generation of ancestors - reference population (%)

	1 st generation	2 nd generation	3 rd generation	4 th generation	5 th generation	
27 animals	100%	96.2%	96.2%		22.2%	
				77.8%	77.8%	
				74.1%		
			96.2%	77.8%		
			96.2%	77.8%		
				96.3%		
			0%			
		96.2%	22.2%			
		96.2%	70.4%	70.4%		51.9%
						51.9%
				0%		
			70.4%	29.6%		
	51.9%		18.5%	18.5%		18.5%
						18.5%
		18.5%				
	51.9%	18.5%				
	100%	92.6%	92.6%	92.6%		3.7%
					74.1%	62.9%
				62.9%		
			88.9%	62.9%		
			92.6%	59.3%		
				74.1%		
			0%			
		88.9%	14.8%			
92.6%		70.4%	55.6%		11.1%	
					22.2%	
			11.1%			
		70.4%	22.2%			
	40.7%	3.7%	3.7%		3.7%	
					3.7%	
40.7%	3.7%					
40.7%	3.7%					

An upper half - sire ancestors, a lower half - dam ancestors; males precede females in each parent pair

In the first generation of ancestors of the reference population, all fathers and mothers were known. In the second generation, proportion of known parents was 3.6 percentage points higher in father ancestors. In the first generation of ancestors of the whole pedigree population, a difference in proportion of known parents was 6.5 percentage points (fathers vs. mothers). In the

second generation of ancestors of the whole pedigree population, a higher proportion of father ancestors were found (1/2 vs. 1/3). Similar patterns were found across the remaining generations.

Table 2: Pedigree completeness up to the 5th generation of ancestors - whole population (%)

	1 st generation	2 nd generation	3 rd generation	4 th generation	5 th generation
137 animals	59.2%	46.7%	31.4%	16.8%	4.4%
				29.2%	16.8%
			39.4%	16.1%	
				28.5%	16.1%
				34.3%	16.1%
		54.7%	29.2%	21.9%	15.3%
				28.5%	27.7%
			20.4%	3.6%	0%
				17.5%	12.4%
				17.5%	10.2%
	65.7%	33.6%	27.7%	16.0%	10.9%
				21.9%	0%
			32.8%	16.0%	5.8%
				24.8%	3.6%
				24.8%	3.6%
		32.8%	15.3%	11.7%	3.6%
				15.3%	0.7%
			11.7%	1.6%	12.4%
				11.7%	12.4%
				11.7%	13.1%

An upper half - sire ancestors, a lower half - dam ancestors; males precede females in each parent pair

In females, trends in inbreeding and in average relatedness across the years of birth are given in Figure 2. Variation in number of equivalent complete generations is also shown. Zero coefficients of inbreeding were computed across the years before 2003. The exceptions were females born in 1995 (average value of inbreeding about 3%). In females born between 2003 and 2009, coefficients of inbreeding were non-zero (average values from 6% to 14%; about 2% in 2007). In 2010, no inbred females were born. A total of 21 inbred females (71% of them belonged to the reference population) were found. In males, zero coefficients of inbreeding were computed (no figure given).

In spite of slightly fluctuating patterns, average relatedness showed increasing trends in females (Figure 2) and also in males (no figure given). In the oldest females (born before 1992), low coefficients of average relatedness (average values from 2% to 3%) were found. Between 1994 and 2009, average relatedness in females increased (to 12%). It was slightly lower in the youngest individuals born in 2010 (9%). Similarly, in the oldest males (born before 1993), low average relatedness (2% to 3%) was found. Between 1994 and 2001, average relatedness in males ranged to a greater extent (3% to 10%). It was the highest in males born during the period 2006-2007 (11% to 12%). The youngest males were of lower average relatedness (6% to 8%).

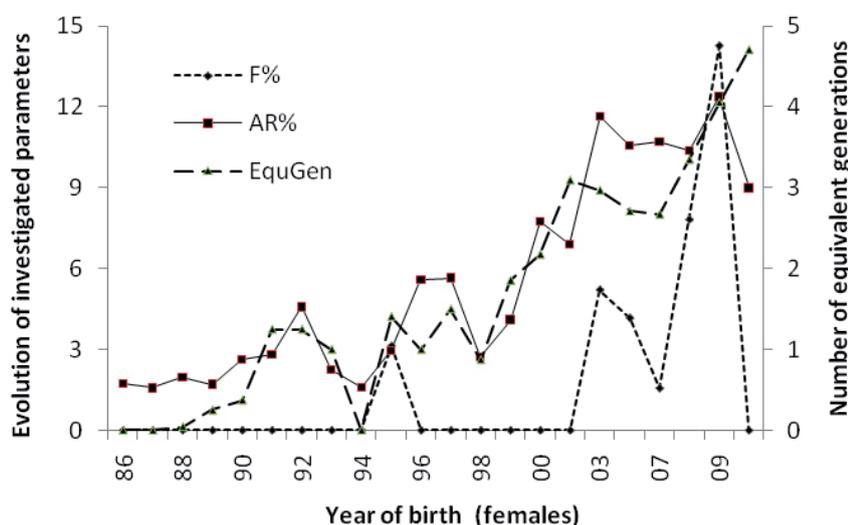


Fig. 2: Mean values of inbreeding (F %), average relatedness (AR %) and number of equivalent generations (EquGen) in females (according to years)

In inbred females, coefficients of inbreeding and of average relatedness were higher (both about 11% ranging from 6.25% to 15.65% and from 3.62% to 13.65%, respectively) than average values of the whole population (1.69% and 5.36%, according to Oravcová and Krupa, 2011).

DISCUSSION

Papers dealing with pedigree analysis of sheep also assess pedigree completeness as the quality of pedigree has an impact on estimates of coefficients of inbreeding. Because of different circumstances affecting evolution of

breeds and availability of pedigrees, all comparisons of the former Valachian sheep with other breeds should be considered as informative. Azor *et al.* (2008) carried out analyses of pedigree completeness in the Spanish Merino sheep separately across each sex and various strains. Higher pedigree completeness was found in males than in females: in the first four generations of ancestors, proportions of known parents decreased from 100% to 80% in males and from 75% to 55% in females. Opposite tendencies were found when the reference population of the former Valachian sheep was split in dependence on sex. Up to the fourth generation, pedigree completeness was higher in females (differences ranged from 10% to 15%). Regardless of sex, proportions of known parents

found for individual strains of the Spanish Merino breed and proportions of known parents found for the former Valachian sheep were similar up to the fifth generation. In the sixth to eighth generation, the quality of pedigree was higher in the Spanish Merino sheep. Also, less shallow pedigree was found in the Spanish breed (13 vs. 8 generations). The quality of pedigree was the highest in the youngest individuals of the former Valachian sheep (4.7 equivalent complete generations; population mean 1.16). In contrast, the lower quality of pedigree was found by Goyache *et al.* (2010) in the Mallorquina breed (1.4 equivalent complete generations in the youngest individuals, population mean 0.43).

Trends in inbreeding and in average relatedness enable to check how breeding management influences genetic similarity between animals (Goyache *et al.*, 2003). Average relatedness investigated across the years of birth was higher in the former Valachian (up to 12%) than in the Mallorquina (up to 1% according to Goyache *et al.*, 2010) and Xalda sheep (up to 2.5% according to Goyache *et al.*, 2003). Average values of coefficients of inbreeding ranged to a greater extent in the former Valachian (0% to 14%) than in Xalda sheep (0% to 5%). Lower inbreeding also was found by Goyache *et al.* (2010) in the Mallorquina breed (maximum 3% across the years of the analysed period).

Because of a relatively high number of founders with unknown ancestors registered till 1998, zero coefficients of inbreeding in the former Valachian sheep were mostly found till 2002. With exception of females born in 2010, non-zero coefficients of inbreeding were found in the youngest females born since 2003. Higher values of average relatedness and of equivalent complete generations preceded/overlapped inbreeding accumulated across the latest years of the analysed period. This indicates that mating between individuals showing a certain degree of relatedness was impossible to avoid. According to Gutiérrez *et al.* (2003), average relatedness tends to be high when all animals are highly related and there is no chance of mating unrelated or slightly related individuals. Zero inbreeding coefficients in females born in 2010 contrasted with findings of Goyache *et al.* (2003), who reported both inbreeding and average relatedness being the highest at the end of the analysed period (Xalda sheep). Zero coefficients of inbreeding in males were also in contrast to findings of Goyache *et al.* (2003), who reported higher coefficients of inbreeding in males than in females. Probably because of missing/insufficiently deep pedigrees (as a matter of fact, the investigated flock is opened for imported rams of the same breed from Czechia), zero coefficients of inbreeding were found in males. Increasing coefficients of inbreeding in females during the period 2003-2009 were due to the fact that female lambs originated from mating between parents sharing common ancestors in both genealogical paths.

When such mating were eliminated (here it was an unrelated ram of the Improved Valachian origin used for breeding season 2009-2010), zero inbreeding coefficients in females born in 2010 occurred. Nevertheless, both the youngest females and the youngest males were of almost as high coefficients of average relatedness as individuals born few years earlier. This indicates that underlying inbreeding exists and could be demonstrated in the future.

Average relatedness acts as an indicator of the long-term inbreeding of population (Goyache *et al.*, 2003). To maintain inbreeding at low levels, Dunner *et al.* (1998) recommended that individuals with the lowest coefficients of average relatedness should be preferred as parents of the next generation. It is not easy to apply this recommendation for the investigated flock as limited number of live animals can be mated. In this respect, the variant analyses that considered also animals belonging to multiplier and commercial flocks (4 flocks together) might be useful. First, all animals of multiplier and commercial flocks born during the period 2007-2010 were included in the analysis (almost fourfold increase in size of the reference population); second, animals with known parents were included in the analysis (almost twofold increase in size of the reference population). Calculations showed (variant results not given) that lower coefficients of average relatedness in individuals of the initially formed reference population (difference by 30% and 21%, respectively) were computed. This is probably a consequence of the fact that changing population size changes the average percentage of genes these animals share with the remaining population. According to available pedigrees, we can suppose that mutual relations between animals within the initially formed reference population are closer than relations they share with animals outside the flock (parallel trend lines estimated when plotting the respective variant values of coefficients of average relatedness on the same graph). Generally, coefficients of average relatedness were lower in animals of multiplier and commercial flocks. Therefore, it may be useful an investigated flock will be opened for these individuals (and their descendants) in the future. However, this is a preliminary study and more research is needed.

CONCLUSION

The analysis extends the knowledge summarized in our previous study (Oravcová and Krupa, 2011). It indicates limitations in both genetic diversity and available pedigree information of the investigated population. It is not easy to provide suggestions for practice purposes, however, regular monitoring of breed genetic structure and mating of genetically less represented animals

(with genes less spread within population) may be recommended to be carried out on regular basis. Also, pedigrees need to be known to a greater extent (mainly in multiplier and commercial flocks).

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REFERENCES

- AZOR, P.J. - CERVANTES, I. - VALERA, M. - ARRANZ, J.J. - MEDINA, L. - GUTIÉRREZ, J.P. - GOYACHE, F. - MUNOZ, A. - MOLINA, A. 2008. Análisis preliminar de la estructura genética del Merino: situación de las estirpes tradicionales mediante análisis genealógico y molecular. [Preliminary assessment of population structure of Spanish Merino breed: traditional strains situation using genealogical and molecular analysis]. ITEA, 2008, vol. 104, (2), p. 295-302.
- DANCHIN-BURGE, C. - PALHIÉRE, I. - FRANCOIS, D. - BIBÉ, B. - LEROY, G. - VERRIER, E. 2010. Pedigree analysis of seven small French sheep populations and implications for the management of rare breeds. *J. Anim. Sci.*, 2010, vol. 88, p. 505-516.
- DUNNER, S. - CHECA, M. L. - GUTIERREZ, J. P. - MARTIN, J. P. - CANON, J. 1998. Genetic analysis and management in small populations: the Asturcon pony as an example. *Genet. Sel. Evol.*, 1998, vol. 30, p. 397-405.
- FAO. 1999. The Global Strategy for the Management of Farm Animal Genetic Resources. Executive brief. Rome: FAO Rome. 1999, 46 p.
- FAO. 2007a. The State of the World's Animal Genetic Resources for Food and Agriculture. Eds. D. Pilling, B. Ritchovskyy. Rome: FAO Rome, 2007a, 511 p.
- FAO. 2007b. Global Plan of Action for Animal Genetic Resources. Rome: FAO Rome, 2007b, 37 p.
- GOYACHE, F. - GUTIÉRREZ, J.P. - GÓMEZ, E. - ÁLVAREZ, I. - DIEZ, J. - TOYO, L. J. 2003. Using pedigree information to monitor genetic variability of endangered populations: the Xalda sheep breed of Asturias as an example. *J. Anim. Breeding and Genetics*, 2003, vol. 120, p. 95-105.
- GOYACHE, F. - FERNÁNDEZ, I. - ESPINOZA, M. A. - PAYERAS, L. - PÉREZ-PARDAL, L. - GUTIÉRREZ, J. P. - ROYO, L. J. - ÁLVAREZ, I. 2010. Análisis demográfico y genético de la raza ovina Mallorquina. [Demographic and genetic analysis of the Mallorquina sheep flockbook]. ITEA, 2010, vol. 106, (1), p. 3-14.
- GUTIÉRREZ, J. P. - ALTARRIBA, J. - DÍAZ, C. - QUINTANILLA, R. - CANÓN, J. - PIEDRAFITA, J. 2003. Pedigree analysis of eight Spanish cattle breeds. *Genet. Sel. Evol.*, 2003, vol. 35, p. 43-63.
- GUTIÉRREZ, J. P. - GOYACHE, F. 2005. A note on ENDOG: a computer program for analysing pedigree information. *J. Anim. Breeding and Genetics*, 2005, vol. 120, p. 357-360.
- GUTIÉRREZ, J. P. - MARMI, J. - GOYACHE, F. - JORDANA, J. 2005. Pedigree information reveals moderate to high levels of inbreeding and a population genetic structure in the Catalanian donkey breed. *J. Anim. Breeding and Genetics*, 2005, vol. 122, p. 378-386.
- GUTIÉRREZ, J. P. - CERVANTES, I. - MOLINA, A. - VALERA, M. - GOYACHE, F. 2008. Individual increase in inbreeding allows estimating effective sizes from pedigree. *Genet. Sel. Evol.*, 2008, vol. 40, p. 359-378.
- GUTIÉRREZ, J. P. - CERVANTES, I. - GOYACHE, F. 2009. Improving the estimation of realised effective population sizes in farm animals. *J. Anim. Breeding and Genetics*, 2009, vol. 126, p. 327-332.
- MAIGNEL, L. - BOICHARD, D. - VERRIER, E. 1996. Genetic variability of French dairy breeds estimated from pedigree information. *Interbull Bulletin*, 1996, no. 14, p. 49-54.
- MEUWISSEN, T. I. - LUO, Z. 1992. Computing inbreeding coefficients in large populations. *Genet. Sel. Evol.*, 1992, vol. 24, p. 305-313.
- ORAVCOVÁ, M. - KRUPA, E. 2011. Pedigree analysis of the former Valachian sheep. *Slovak J. Anim. Sci.*, 2011, vol. 44, p. 6-12.
- ROYO, L. J. - ÁLVAREZ, I. - GUTIÉRREZ, J. P. - FERNÁNDEZ, I. - GOYACHE, F. 2007. Genetic variability in the endangered Asturcon pony assessed using genealogical and molecular information. *Livestock Sci.*, 2007, vol. 107, p. 162-169.
- SAS/STAT (2002-2008) v.9.2. SAS Institute Inc., Cary, NC, USA.
- SIMON, D. L. - BUCHENAUER, D. 1993. Genetic diversity of European livestock breeds. EAAP Publication No. 66. Wageningen: Wageningen Pers., 1993, 581 p.