ANALYSIS OF THE GENETIC HISTORY OF THE PALAS MEAT BREED

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Abstract

The creation of a high-performance meat sheep breed was necessary in the context of the growing national and global consumer demands. To increase meat production in sheep, the Palas Meat Breed was created at Research and Development Institute for Sheep and Goat Breeding Palas - Constanta, approved in 2012, based on a complex program of crosses between the Palas Merino breed, Île-de-France and a low percentage of sheep from the Suffolk, Romanov and Ost Friesian breeds, aiming at high growth speed, slaughter yield and obtaining high-quality carcasses in the selection. The analysis of the genetic history of the breed was made based on the pedigrees of four random lines, extracted from the Genealogical Register of the Meat Line - Palas and has in the genome more than 93% genes from the Palas Merino and Île-de-France breeds and less than 7% genes from other breeds. The average interval between generations was 3.65 years and the average inbreeding per generation recorded a value, in recent years, of 2.38%.

Key words: sheep, genetic analysis, Palas Meat Breed

INTRODUCTION

In the conditions where the demand on the national and international market for products and by-products from small ruminants is constantly increasing, it was resorted to the creation of a new performing meat Romanian breed, well adapted to the environmental conditions of the lowland areas of Romania.

Approved in 2012, the Palas Meat Breed was created at the Research and Development Institute for Sheep and Goat Breeding - Palas, Constanta in order to obtain a population of sheep with skills for meat production, high growth rate, body conformation similar to specialized breeds for this production, high slaughter yield and increased carcass quality, placed in the upper classes of the European classification grid [1].

Currently, at the Research and Development Institute for Sheep and Goat Breeding - Palas, Constanta, there is a total flock of 515 sheep, of which 361 ewes, 41 rams and 113 lambs. Approximately 150 rams are delivered annually, contributing to the creation of daughter herds in lowland areas.

An important aspect regarding the increase of meat production in sheep is that this breed can be used in crosses with other native breeds, improving growth speed, feed conversion to growth gain, slaughter yield and carcass quality indices [2,3,4].

The genetic history analysis of the new sheep breed is of great importance for both researchers and breeders for the improvement of native sheep breeds for meat production. Moreover, this study was essential to create valuable documentation for the approval of the Palas Meat Breed and to establish a foundation for future molecular genomic analyses.

MATERIAL AND METHOD

The Palas Meat Breed was formed between 1973 and 1989, by crossing the Palas Merino breed with Île-de-France rams, obtaining products F, F_2, F_3, F_4 (Île-de-France x Palas Merino), in parallel backcrosses were carried out, as a result of which R_1 crossbreeds were obtained (75% Île-de-France x 25% Palas Merino), aiming to improve the weight gain up to 6 months of age, live weight at 6 months and body conformation. At the same time, a small number of complex crossbreeds (especially ewes) with genes from the Romanov, East Friesian, Finnish Landrace and Suffolk breeds participated at the creation of the breed, to increase prolificacy. After 1989, the population was reproductively closed, when specimens with conformation close to the Île-de-France breed, high growth speed, good slaughter yield and high quality carcasses were obtained, which had 56.25% genes from Île-de-France breed, 37.5% genes from Palas Merino and 6.25% genes from other breeds, mainly Romanov, East Friesian and Suffolk [1].

The research was conducted on the current number of sheep (140 heads) consisting of 100 females and 40 males, reproductive isolate since 1989.

The analysis of the genetic history of the breed was made based on the pedigrees of four random lines, extracted from the Genealogical Register of the Palas Meat Line. For the studied populations with pedigrees, 50 pedigree samples of the ewes that have been involved in reproduction and all the pedigree samples of the rams that have been involved in reproduction are extracted from the genealogical records. Using Wright and Robertson's method, as synthesized by Draganescu in 1970, a pedigree is established for four random lines by rolling a dice. The registration number and birth year of each sheep or ram, whose pedigree has been extracted from the genealogical registry of the respective population, are listed on a sheet of paper. Beneath the registration number, to the right, the registration number and birth year of the father are listed and to the left, the registration number and birth year of the mother are listed. The paternal grandparents' data are listed beneath the father's registration number, and the maternal grandparents' data are listed beneath the mother's registration number. This establishes the founders of the four random lines. Subsequently, a dice is rolled to determine whether the male or female ancestors are to be listed for the even or odd numbers, respectively. This process is repeated for each of the four random lines, tracing back to the last common ancestor.

A population (even a large one) can disappear if it is highly reproductively isolated. The coefficient of reproductive isolation is the fundamental criterion for considering a population of sheep as a breed, and is determined according to the formula:

$$R.I.C. = \frac{AA - (AI + II)}{AA + AI + II}$$, where:

AA - the number of individuals admitted for reproduction with both parents from their own flock;

AI - the number of individuals with one immigrant parent acquired through purchases or acquisitions outside of their own flock;

II - the number of individuals with both parents being immigrants [5].

Calculation of genetic similarity, coefficients of inbreeding and kinship was carried out according to the method of Wright, Lush and Robertson, synthesized by Draganescu [5,6,7].

To establish the genetic similarity with each of the founding races, the following formula was used:

Similarity to breed X = (Number of occurences in the pedigree of X breed) / (Number of pedigrees analyzed x 4).

Self-relatedness of a population is the average relatedness among all individuals and is due to reproductive isolation, its limited size and selection. The individuals of a population (breed) are at all times related to each other, that is for they come from a series

of previously existing common ancestors (in descent).

The kinship is calculated in the analyzed years on the pedigree of 4 random lines, according to the formula:

$$R = \frac{N}{N_p} \times 100, \text{ where:}$$

N – the number of couples – maternal pedigrees in which a common ancestor was found (this assumes that in each pedigree the father's side is compared with all the mothers' parts in the other pedigrees, less the mother's side in the pedigree in question);

N_p – the possible number of pedigree couples of 4 random lines;

N_p = 4 x pedigree number x (pedigree number – 1).

To determine whether a sheep population is vulnerable or endangered, it is necessary to determine its level of inbreeding. This is done using the coefficient of inbreeding, denoted by F, which is calculated based on the pedigree data of each one.

The value of F is calculated according to the formula:

$$F(x) = \sum \left(\frac{1}{2}\right)^{n1+n2} (1+F_A),$$

where:

F(x) is the coefficient of inbreeding of individual X;

n_1 = the number of generational changes from individual X to the common ancestor;

n_2 = the number of generational changes from individual Y to the common ancestor;

F_A is the coefficient of inbreeding of the common ancestor A.

Fractional summation occurs when parents have multiple common ancestors or when the same ancestor is repeated.

At the population level, ΔF is calculated, which measures the average increase in homozygosity from one generation to another and the decrease in heterozygosity. To calculate ΔF, the total realized inbreeding must be calculated from the analysis of four random pedigrees using the formula:

Total inbreeding = (Total number of appearances of the common ancestor) / (Number of pedigrees analyzed x 4).

Total realized inbreeding can be broken down into current inbreeding and non-current inbreeding (which can be moderate and distant). The calculation formulas are:

Current inbreeding = (Total number of appearances of common ancestors up to the grandpaparent generation) / (Number of pedigrees x 4).

Non-current inbreeding = (Total number of appearances of common ancestors beyond the grandparent generation) / (Number of pedigrees x 4).

The average inbreeding per generation ΔF is calculated according to the formula:

ΔF = (Total inbreeding) / (Average number of generations).

Inbreeding occurs in small populations formed by one male and several females, where ΔF values are between 12-25%. These populations undergo genetic drift and can disappear after a few generations. Close inbreeding (ΔF = 6-12%) also occurs in small populations formed by one to two males and up to 50 females. It has the same effect as inbreeding and can lead to the disappearance of the population in a few generations. Moderate inbreeding (ΔF = 1-6%) is used in the implementation of genetic conservation programs to maintain genetic similarity with certain valuable breeders or as a result of intense family selection.

Distant inbreeding (ΔF ≤ 1.0%) allows selection to control the evolution of the population and has the role of preserving the integrity of reproductively isolated populations.

From the analysis of four random pedigrees, possible inbreeding, strain inbreeding and the subdivision index of a population can also be calculated (which highlights the degree of subdivision of a population; the smaller the value of the ratio, the less subdivided the population is).

To highlight the degree of subdivision of a population, the subdivision index was calculated (the lower it is, the less subdivided the population is), according to the formula:

Subdivision index = (Current inbreeding)/ (Possible inbreeding).

The genetic size (Ne) is given by the formula:

$$Ne = \frac{4Nm \times Nf}{Nm+Nf}, \text{ where:}$$

N_e – effective (genetic) size;
N_m – the number of reproductively active males;
N_f – the number of females.

RESULTS AND DISCUSSIONS

In the period 1973-1981 the value of the Reproductive Isolation Coefficient was evolving from the value -1.0 to the value + 0.81 (only certain individuals had one immigrant parent each) and from 1989 the value of the reproductive isolation coefficient of was +1.0 or close (among the analysed pedigrees there were also pedigrees that belonged to ewes whose father was an Île-de-France ram from their own dam). The evolution of the coefficient of reproductive isolation is presented in table 1.

Table 1 Evolution of the reproductive isolation coefficient in the Palas Meat Breed

Year	1973	1976	1981	1989	1999	2003	2009
Reproductive Isolation Coefficient	-1.0	+0.54	+0.81	+1.0	+0.98	+1.0	+1.0

In the evolution of the breed, the genetic similarity with the founding breeds oscillated until 2009, after which the population stabilized genetically, remaining reproductively isolated. The genetic similarity with the Île-de-France breed started at 55.67% in 1989, oscillating in the following years, in 2009 stabilizing around 57%. The genetic similarity with the Palas Merino breed has decreased progressively over the years, stabilizing around 36%, and the similarity with other breeds was in 2009 as follows: with the Suffolk breed at 3.66%, with the Romanov breed in the proportion of 2.36%, and with the East Friesian breed in the proportion of 0.88%; the evolution being detailed in table 2.

Table 2 Evolution of the genetic similarity of the Palas Meat Breed with the founder breeds

Breed	Rxy (%)				
	1989	1994	1999	2003	2009
Île-de-France	55.67	58.45	53.29	56,67	56.78
Palas Merino	41.25	40.15	39.71	34.10	36.28
Other breeds (Romanov, East Friesian, Suffolk)	3.03	1.39	6.98	9.19	6.9

From the analysis of the data on the evolution of the breed between 1898-2009 it was observed that an important contribution to the gene pool of the Palas Meat Breed was made by 20 breeding rams, of which 7 Île-de-France rams, 1 Suffolk ram and 11 hybrids, all of them coming from own litter. It is considered that an important breeder is that ram with which the population is genetically similar in proportion to at least 5%, the most representative ones being presented in table 3.

Table 3 Genetic similarity of the Palas Meat Breed with important breeders

Breeder (registration number, breed, year of birth)	Rxy (%) of population born in the year:				
	1989	1994	1999	2003	2009
7012 – Île-de-France, 1974	7.36	10.61	4.27	13.51	12.50
1318 – Île-de-France, 1978	8.74	13.63	16.46	22.30	10.89
438 – Suffolk, 1997	0.00	0.00	0.00	5.41	2.02
31307 – Hybrid, 1983	5.21	2.27	1.83	5.40	7.66
10111 – Hybrid, 2001	0.00	0.00	0.00	0.00	6.05

Analysing the evolution of the interval between generations in the period 1989-2009, it was observed that the average interval for father-son and father-daughter filiations was 3.24 years, respectively 3.12 years, lower than for mother-son and mother-daughter filiations, where it resulted 4.15 years and 4.38 years. For the total analysed period and total offspring, the average interval between generations at the Palas Meat Breed was 3.65 years, highlighted in table 4.

Table 4 Evolution of the interval between generations in the period 1989-2009

Year	The range in years				
	Father-son	Father-daughter	Mother-son	Mother- daughter	Average
1989	3.31	3.19	4.51	4.30	3.77
1994	4.10	4.01	3.75	3.46	3.83
1999	2.60	2.49	4.65	4.83	3.33
2003	2.85	2.81	4.40	4.70	3.53
2009	3.32	3.12	3.44	4.63	3.78
Average	3.24	3.12	4.15	4.38	3.65

Thus, a detailed analysis, presented in table 5, showed that the kinship increased progressively from the year 1989, when it had the value of 5.57%, to the value of 18.62% in the year 2003, after which it decreased to the value of 13.41% in 2009. The total inbreeding of the breed in 2009 was registered at the value of 10.0%, incest at 0%, and the possible one registered a value of 7.19%.

Strain inbreeding is caused by the subdivision of the population into several reproductively isolated herds and is calculated by subtracting the possible inbreeding from the moderate inbreeding [8], registering a value in 2009 of 2.81% and a maximum in 1994 of 11.66%.

From the analysis of the subdivision index, it was demonstrated that the Palas Meat Breed tended to subdivision throughout the observed period.

The average inbreeding per generation (ΔF) is obtained by dividing the total inbreeding by the average number of generations, registering relatively high values in the period 1989-2003, the reason being to maintain genetic similarity with some valuable breeders [8], subsequently decreasing to the value of 1.04%.

Table 5 Evolution of inbreeding of the Palas Meat Breed

Specification	The years analysed				
	1989	1994	1999	2003	2009
Pedigree number	163	33	41	37	62
Average number of generations	4.77	5.28	6.18	5.97	9.61
Relatedness itself – R (%)	5.57	10.89	12,14	18.62	13.41
Total inbreeding – F (%)	5.06	17.42	9.15	14,19	10.0
Current inbreeding – incest (%)	0.92	0.0	0.0	0.0	0.0
Non-current inbreeding moderate (%)	4.14	17.42	9.15	14,19	10.0
Possible inbreeding (%)	2.86	5.76	6.46	10.27	7.19
Line inbreeding (%)	1.28	11.66	2.69	3.92	2.81
Subdivision index	1.45	3.02	1.42	1.38	1.39
Average inbreeding per generation - ΔF (%)	1.06	3.30	1.48	2.38	1.04

Thus, $Ne = \frac{4 \times 25 \times 338}{25+338} = 93.11$

individuals (in terms of 338 females) giving the new breed security in future evolution.

Body conformation is specific to sheep of meat breeds. The head is suitably long and wide, with a straight or slightly convex face profile (rams), suitably large ears,

carried horizontally and the neck is short, well joined to the trunk. The trunk is long and wide, cylindrical in shape. The chest is broad, the ribs are slightly arched, the back and shoulders are long and well-muscled. The croup is wide, appropriately long, horizontal or slightly oblique and the legs have a convex profile. Limbs are suitably long with fine bone and correct poise. The udder is globular, symmetrical and of appropriate size.

Body sizes are characteristic of breeds specialized for meat. The height at the withers and rump are 69-71 cm in males and 67-69 cm in females, the length of the trunk is 73-75 cm in males and 68-70 cm in females and that of the rump is 26-28 cm in males and 25-27 cm in females. The width at the shoulders is 27-28 cm in males and 24-26 cm in females and that of the chest is 31-33 cm in males and 29-31 cm in females [1].

The weight of the rams wool is 5-6 kg and 4-4.5 kg for ewes, the fineness of the fibres is 24-26 microns and the washing yield is 52-54%. The reproductive indices present advantages: fecundity of 96-98% and prolificacy of 125-132%, the breeding season being throughout the year, with a peak of calving in the months of December and January [9].

Regarding the growth dynamics of male lambs during the nursing period and in fattening conditions, it was found that they had an average weight at birth of 3.90 kg, at weaning (80 days) they had a weight of 22.03 kg achieving average daily growths of 229.50

g and 233.10 g respectively from birth to 5 months of age, where they recorded an average weight of 38.86 kg, demonstrating high weight gain performance.

One of the main characteristics of the Palas Meat Breed is the increased yield at slaughter. The values of this indicator were calculated in comparison with 3 native sheep breeds (Palas Merino from the Research and Development Institute for Sheep and Goat Breeding Palas Constanța flock; Tigaie breed from the Reghin Experimental Base flock and Țurcana breed from the Bilciuresti Experimental Base flock), on batches of 20 males subjected to fattening intensive from each breed, at the age of 5 months, calculating 2 values:

$$Yield\ 1 = \frac{Cooled\ weight\ carcass(kg)}{Living\ weight(kg)}\ x\ 100$$

$$Yield\ 2 = \frac{Cooled\ weight\ carcass\ (kg)}{Empty\ living\ weight\ (kg)}\ x\ 100,$$

where empty living weight is the living weight from which the contents of the digestive tract (prestomach, glandular stomach and intestines) were subtracted.

According to the data presented in table 6, it was found that the Palas Meat Breed differs from the other breeds. It had a yield 1 at slaughter of 48.35%, higher by 3.75 percentage points compared to the Palas Merino breed, by 3.65 percentage points compared to the Tigaie breed and by 5.15 percentage points compared to the Turcana breed.

Table 6 Slaughter yields compared by breed

Specification	MU	Palas Meat Breed	Palas Merino	Tigaie breed	Turcana breed
		X ± sx	X ± sx	X ± sx	X ± sx
Living weight before slaughter	kg	39.26±0.96	39.56±1.40	38.93±0.93	35.33±2.20
Empty living weight	kg	33.34±0.97	34.71±1.38	32.93±1.18	31.50±1.89
Weight of cooled carcass	kg	18.98±0.97	17.64±0.80	17.40±0.69	15.28±1.27
Yield 1	%	48.35	44.60	44.70	43.20
Yield 2	%	56.94	50.83	52.80	48.50

At the same time, following the research carried out, the dimensions and carcass indices were calculated, these being important to demonstrate the superior qualities of the Palas Meat Breed compared to local breeds. Although the carcasses of the Palas Meat Breed lambs were approximately equal in length to those of the other breeds, the width at the coxofemoral joints and that at the scapulohumeral joints were higher. At the same time, according to table 7, it can be observed the superiority of the compactness index of the gigot in the Palas Meat Breed by approximately 23-46% compared to Palas Merino, Tigaie breed and Turcana breed, but also the amount of muscle in the carcass, which was 3.88 points percentage higher than Palas Merino, 9.74 percentage points higher than Tigaie and 4.30 percentage points higher than Turcana [1,4].

The compactness index of the gigot (C.I.G.) was calculated according to the formula [1]:

$$\text{C.I.G.} = \frac{\text{Width of the coxofemoral joints}}{\text{Length of the gigot}}$$

Table 7 Dimensions of the carcass and its tissue structure in male lambs from the Palas Meat Breed compared to other breeds

Size (cm)	Palas Meat Breed	Palas Merino	Tigaie	Turcana
	X ± sx	X ± sx	X ± sx	X ± sx
Width of the coxofemoral joints	23.83 ± 0.44	20.50 ±0.28	20.13 ± 0.31	18.83 ± 0.60
Chest width	27.67 ± 0.44	23.44 ±0.57	25.50 ± 0.61	23.00 ± 0.28
Width of the scapulohumeral joints	22.67 ± 0.60	20.06 ±0.33	19.50 ± 0.20	18.80 ± 0.33
Chest depth	29.83 ± 0.60	28.22 ±0.75	27.38 ± 0.31	30.17 ± 0.66
Carcass length	64.50 ± 0.50	63.56 ± 0.47	63.13 ± 1.19	63.00 ± 0.50
Gigot length	24.83 ± 0.44	26.67 ± 0.62	25.88 ± 0.42	28.33 ± 1.01
The perimeter of the gigot	47.83 ± 0.44	41.33 ± 0.64	43.63 ± 0.89	41.67 ± 0.83
Compactness Index of the gigot	0.96	0.77	0.78	0.66
Total half-carcass, of which:	100	100	100	100
Muscle	61.30	57.42	51.56	57.00
Fat	17.49	19.25	24.22	17.42
Bones	20.96	23.14	24.06	25.37
Muscle/bone ratio	2.92/1	2.48/1	2.14/1	2.25/1

CONCLUSIONS

The Palas Meat Breed is the most performing Romanian breed of sheep specialized for meat production. With a remarkable adaptability to the arid environmental conditions in the south-eastern part of Romania, this breed retains its characteristics, recording growth increases and high slaughter yields, but also a placement of the carcasses in the European classification grid (EUROP) in classes E (excellent carcasses) and U (very good carcasses).Another advantage worth considering for this breed is that of increasing meat production on commercial farms by improving growth rate, feed conversion to growth and carcass quality indices.

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