

Population and geographical distribution analysis of the Rhodope Tsigai sheep

Zhivko Duche¹ and Tsonka Odjakova²

¹ *Agricultural Academy, Institute of Animal Science, 2232 Kostinbrod, Bulgaria*

² *Agricultural Academy, Research center for Stockbreeding and Agriculture – Smolyan, 4700, Smolyan, Bulgaria*

*Corresponding author: zhivko.duchev@agriacad.bg

Abstract

Duchev, Zh. & Odjakova, Ts. (2023). Population and geographical distribution analysis of the Rhodope Tsigai sheep. *Bulg. J. Agric. Sci.*, 29(5), 932–937

The aim of this study was to analyse the available in 2021 pedigree and geographic distribution data of the Rhodope Tsigai sheep. Some of the important population parameters, including generation interval and effective population size were calculated. The potential threats related to the concentration of the breed in the region of the Rhodope Mountains were estimated via the number of animals kept in farms in a circle with 25 and 50 km radius.

Keywords: effective population size; risk; concentration

Introduction

The Tsigai breed is one of the oldest sheep breeds. In 1950, two teams of scientists were appointed to develop semifine-wool breeds of Tsigai type for the mountainous regions of Northern, Southwestern and Southern Bulgaria (Bonchevska and Ivanova, 2022). The development of these breeds was based on assimilative and reproductive cross-breeding between the local sheep bred in each area and the introduced Tsigai rams of Azov type (Odjakova, 2022). In 1990, the Rhodope Tsigai (RTs) was one of the two newly recognized breeds. It was developed in the mountainous regions of the Rhodope, Rila, Pirin, Central Balkan and Strandzha-Sakar. The animals are hardy and able to cope with the harsh conditions in the mountains. The first studies of this breed are published by Balevska et al., (1970); Balevska and Petrov, (1972); Tyankov (1988), and others.

The changes in the economy system after 1989 led to 60% decline in the sheep population by year 2000 and consequently the share of the Tsigai breeds went down to 14.7% (Stancheva et al., 2014). The breeding activities were transitioned from the state to non-governmental organizations

– breed societies. Nowadays, there is only one approved breed society for the RTs– „Association for breeding Central Rhodope sheep, Karakachan sheep and Rhodope Cigay sheep“, located in Smolyan. The breeding process was revived in 2014 by choosing animals, phenotypically conforming to the breed description and in 2015 the association in Smolyan has established the herdbook of the breed.

Although the breed is not considered at risk by Food and Agriculture organization of the United Nations (FAO, 2023), in Bulgaria it falls under the endangered category by the national criteria, which is based on several parameters, inter alia, the geographic concentration of the breed (Nikolov and Duchev, 2022). The geographic distribution of the farms has its impact on the management and conservation activities. The close distance between farms benefits the farmers' collaboration and exchange of animals, whereas in the case of dispersed flocks, the germplasm exchange is more difficult, resulting in complications in avoidance of inbreeding, as noticed in a study in Brazil of McManus et al., (2014). The concentration of large part of the population in a given area, presents a risk for increased loss in case of disease outbreak (Carson et al., 2009). To account for the risk due to geo-

graphical isolation, Alderson, (2009) proposed to use the radius of the circle containing 75% of the population. Sturaro et al., (2013), also utilized this approach, using the radius of the circle, centred at the mean centre of the geographical distribution of the farms, weighted by the number of animals in each farm, and containing 75% of the population, defining three thresholds – 12.5 km for critical, 25 km for endangered, and 50 km for vulnerable class. In a study of the Bulgarian Screw-Horn Longhair Goat, Ducheve et al., (2022) presented an approach to investigate the concentration on sub-population level and the associated risk of reduction of the population size and diversity.

The purpose of this study was to assess the existing pedigree, determine the current population structure and important parameters including generation interval and effective population size, in order to evaluate the work of the breeding society. The geographic distribution of the breed was investigated for clusters of animals and to estimate their potential threat to the breed diversity.

Material and Methods

Data for this study was provided by the Association for breeding Central Rhodope sheep, Karakachan sheep and Rhodope Cigay sheep in 2021. The dataset represents the available in October 2021 population of 7666 animals, born during 2014-2021, and their parents and grandparents. Quality of the pedigree was assessed by the pedigree completeness index (PCI) following the algorithm described in MacCluer et al. (1983):

$$I_d = \frac{4I_{d_{pat}}I_{d_{mat}}}{I_{d_{pat}} + I_{d_{mat}}}, \quad I_{d_k} = \frac{1}{d} \sum_{i=1}^d a_i \quad k = pat, mat,$$

where k is the paternal or maternal line of an individual, a_i is proportion of known ancestors in generation i and d is the number of generations.

The generation interval (GI) was computed by the definition of Falconer and Mackay (1996) as the average age of the parents at the time their selected offspring was born. The computations were done for the four selection pathways: sire->son; sire->daughter; dam->son; dam->daughter, and for the whole population.

The effective population size (N_e) was estimated by year through the rate of inbreeding (ΔF), based on the classical equations (Falconer and Mackay, 1996):

$$N_e = \frac{1}{2\Delta F}, \quad \Delta F = \frac{F_t - F_{t-1}}{1 - F_{t-1}},$$

where F_t and F_{t-1} are the average inbreeding coefficients of the offspring and their parents.

All the above calculations were done with the software PopReport (Groeneveld et al., 2009).

For the analysis of the geographical distribution of the breed in year 2021, the locations of the 44 farms were set to the villages where the respective farms are recorded. The farms belonging to the same village were treated as one, resulting in 42 analysed farms. Their positions were geocoded, based on the village name, with the Nominatim Geocoder service of the OpenStreetMap project. The groups of farms containing at least 25% of the population and concentrated in a circle with radius up to 50 km were generated in a GIS software – QGIS (QGIS Development Team, 2023). The data about each group, and the radius of its minimum enclosing circle were loaded in PostgreSQL database for estimation of potential threats to the breed diversity. This was done in two ways; by estimating the number of animals which would be lost in case several farms needs to be eliminated, e.g. due to disease outbreak; and by the effective size of the population outside these farms. For each combination of farms, the number of the breeding males and females in the population outside these flocks were calculated. The effective population size – N_e was calculated for the whole breed as potential parents, and for the population outside each group of farms. The calculations were done using the classic formula (Wright, 1931), corrected by a 0.7 to account for the mass selection applied to RTs, as proposed by Santiago and Caballero (1995): $N_e = \frac{4N_mN_f}{N_m+N_f} \cdot 0,7$, where N_m is the number of males and N_f – the number of females, respectively.

Results and Discussion

Population structure

The completeness of the pedigree has gradually improved with the time, starting with year 2017 and reaching 100% known parents in years 2019-2021 (Figure.1). The only exception from this trend is the cohort born in year 2018, where the average pedigree completeness in the first generation is almost 3% lower than that of the animals born in the previous year. This is a result of the herdbook being still open and before 2019 inclusion of animals of unknown pedigree, phenotypically conforming to the RTs breed characteristics, was allowed.

The population in October 2021 consists mostly of animals of 1-5 years age (Figure 2.). The average age of the dams is increasing with the time, meaning the female animals are kept in reproduction and not quickly replaced. The average age of the sires, which is around 3.5 years in 2018-

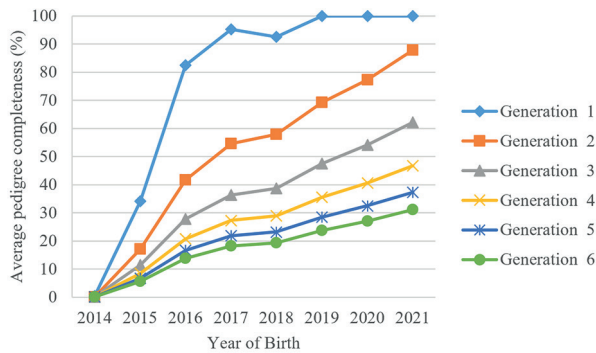


Fig. 1. Average pedigree completeness of Rhodope Tsigai sheep

2020, goes down in year 2021, evidence of the efforts of the breeding society to replace the old males with younger ones. The average age of the parents is not shown for year 2014, as there are only few sires and dams with known birthdates.

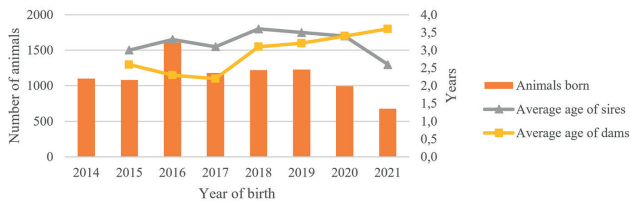


Fig. 2. Distribution of the animals born per year and the average age of their parents

The GI was calculated as 3.3 years for the population, 3.7 – for the males and 2.9 for the females. The GI for the generation born in 2019 (animals born in year 2019 that later become parents) – 4.3 years (Figure 3) is close to the reported by Odjakova (2022) 4.223 years in year 2022. The GI for the sire pathways is higher than the dam pathways,

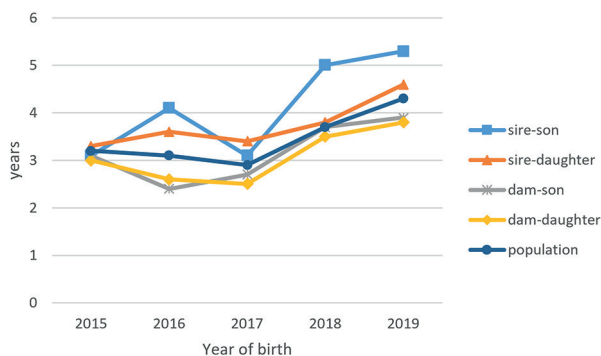


Fig. 3. Generation interval per year of birth for the four gametic pathways and for the population

and this is probably due to the use of older males in the previous years.

From the 4411 dams, 61.2% have only 1 progeny in the population, 26.3% – 2, and only four dams have 6 progeny (Table 1). Of these, 76.7% have 1 progeny, and 19.2% – 2 progeny, which has offspring in the current population. By the sires, there are 2 animals, which have 250 and 240 progeny respectively. These sires have offspring in 3 herds, and account for almost 100% of the offspring in one of these herds. From their offspring, 79 and 72 animals also became parents of animals in the current population. The sire with most “selected” progeny has 128 daughters, all in one herd, of which 83 also became parents.

Table 1. Number of progeny and number of progeny, which became parents per sire and dam

	Min	Max	Avg	Std
Number of progeny per dam	1	6	2	0.8
Number of “selected” progeny per dam	1	5	1	0.6
Number of progeny per sire	1	250	30	32.5
Number of “selected” progeny per sire	1	83	16	17.9

The effective population size (Table 2) is shown only for animals in the generations in last 3 years, as there were no enough data to calculate the inbreeding coefficients of the parents of the previous generations. For the generation of animals born in one generation interval of 3.3 years ending in 2021, the effective population size is 10. However, the pedigrees are shallow, and more years of data recording are needed to capture the common ancestors.

Table 2. Effective population size by year via rate of inbreeding

Year	Average F					Ne
	Animals	Sire	Dam	Parents	ΔF	
2019	0.0346	0.0003	0.0020	0.0012	0.0334	15
2020	0.0454	0.0027	0.0041	0.0034	0.0422	12
2021	0.0543	0.0060	0.0080	0.0070	0.0476	10

Geographic distribution

In October 2021, the RTS breed was present with 7666 animals in 44 farms in 6 provinces (Figure 4). They were located in 42 villages within 16 municipalities. In comparison to the situation in 2019 (Duchevev, 2021), the number of animals has been increased by 31%, keeping almost the same number of farms – 44 in 2021 vs 45 in 2019. Although the farms are located in the same number of villages – 42, only 37 of these coincide. Two farms in 2021 are extending the

presence of the breed to two more provinces – Haskovo and Bourgas. A comparison with the distribution of the breed in 2022 reported by Odjakova (2022), shows further increase in the population in the Haskovo region.



Fig. 4. Location of RTs farms in 2021

Most of the farms are keeping less than 250 animals, and there is a single farm per village. Two exceptions are Smolyan and Bagryanka village, with two farms each, and these two villages are the ones with most animals (Figure 5). The largest farm of the breed is also in Bagryanka keeping 499 animals.

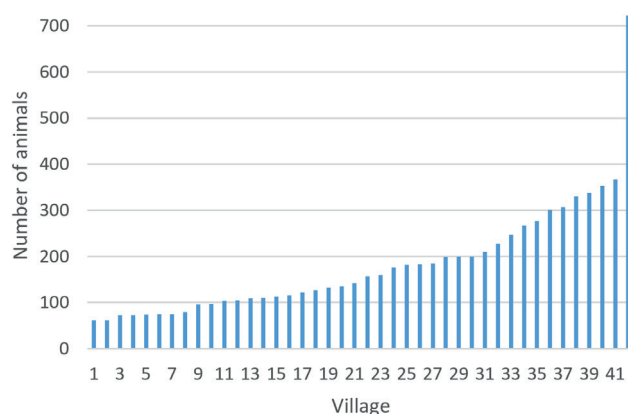


Fig. 5. Number of animals per village

The changes in the breed distribution can be also observed in the concentration around its WMC. In 2019 the most distant farm was 149 km to WMC_2019 and 14.96% of the population was within 25 km distance from the WMC_2019 (Duchev, 2021). In 2021, the farthest farm is 229 km away from WMC_2021, and only 8.94% of the population is within 25 km to WMC_2021. The concentration

of the 75% of the population, an indicator used to estimate the risk due to endemism has also went down – from a circle with 50 km radius in 2019 to 55 km in 2021.

Table 3. Number of farms combinations, concentrated in a circle with a radius of 25 (50) km, and keeping at least 25% (50%) of the population

Minimum percentage of the population included	Number of combinations in a circle with radius 25 km	Number of combinations in a circle with radius 50 km
25%	769 358	50 422 675
50%	264	281 342

However, in 2021, the breed distribution is still dense in the region of Rhodope region in 2021, an evidence being the presence of 264 combinations of farms (Table 3) concentrated in a circle with radius of up to 25km and keeping more than 50% of the population (“50% in 25 km” category). The number of combinations of farms in “25% in 25 km” category – almost 770000 also speaks about concentration. Although some of the scientists considered such concentration also positive for the breed management and conservation (Verrier et al., 2015), which we agree with, we think that the risk of animals loss in case of disease outbreak is a significant threat. For example, the recent outbreak of African Swine Fever in Bulgaria reduced the population size of the East Balkan Swine to less than 200 animals in 2021 (DAD-IS,2021).

The potential loss of population size in RTS is between 1917 and 4874 animals (Table 4). In the “25% in 25 km” category ranges from 25% of the population size (1917 animals) to 55% (4212 animals), and in the “50% in 50 km” category– from 50% to 64%. These 4212 animals in the “25% in 25 km” category are located in 20 farms, nineteen in Kardzhali and one in Haskovo region, depicted in the inner circle in Figure 6. The maximum value of 4874 animals is reached by adding to the previous 20 farms, the remaining three farms in Kardzhali region and the 2 closest farms in Smolyan region (enclosed by the outer circle in Figure 6).

Regarding the genetic diversity, the effective population size of the breed might be reduced from 638 to 232 for the “25% in 25 km” and to 191 for the “50% in 50 km”. The same combinations of farms (Figure 6) are resulting in these extreme values. This cluster in Figure 6 contains also the two subsets of two most concentrated farms groups in each category. In the “25% in 25 km” category, there is a group of ten farms – 4 in Momchilgrad municipality and 6 in Krumovgrad municipality, containing 26.48% of the population within a circle with radius 9 km (Figure 7). In the “50% in 50 km” category, a group of 18 farms, containing 50.5% of the

Table 4. Lower and upper limit of the number of potentially lost animals, and the effective population size of the remaining population per category

Farms groups category	Minimum number of potentially lost animals	Maximum number of potentially lost animals	Minimum Ne of the remaining population	Maximum Ne of the remaining population	Minimum radius (km)	Maximum radius (km)
25% in 25 km	1917	4212	232	551	9	25
50% in 25 km	3833	4212	232	331	17	25
50% in 50 km	3833	4874	191	391	17	50

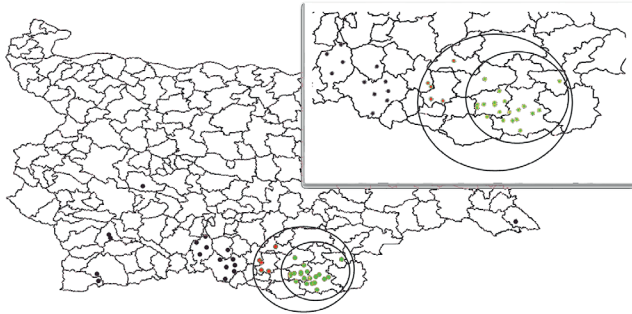


Fig. 6. Groups of RTs farms, which loss will reduce maximally the population size and the effective population size in “25% in 25 km” and “50% in 50 km” categories

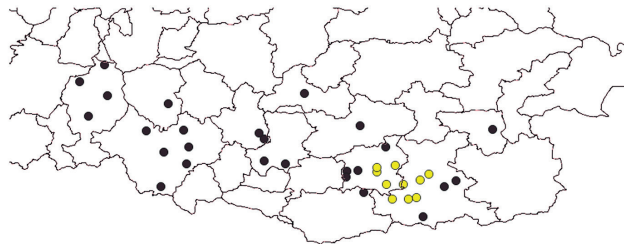


Fig. 7. Group of 10 RTs farms keeping 26% of the population, located in a circle with radius 9 km

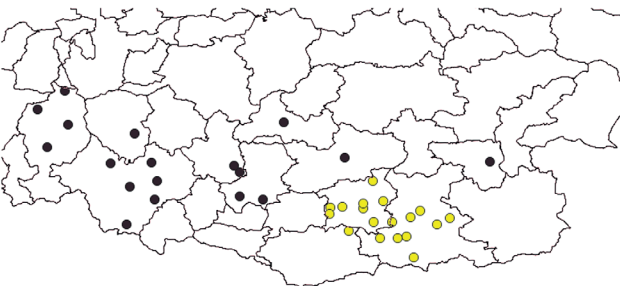


Fig. 8. Group of 18 RTs farms keeping 50% of the population, located in a circle with radius 17.2 km

population, is located in a circle with radius 17.2 km (Figure 8). These are all the farms in the municipalities of Momchilgrad, Kirkovo and Krumovgrad.

Conclusion

The pedigree data is getting improved with the time, an evidence for the strive of the breeding society to keep proper documentation. However, there are still gaps in the data, e.g. unknown birthdates of known parents, and an effort to complete them might prove beneficial.

There are overrepresented sires in some of the herds, which should be replaced.

Although there are few herds away from Rhodope Mountains, half of the population is concentrated in only 3 municipalities of Kardzhali region – Momchilgrad, Krumovo and Kirkovo. This presents a moderate risk to the loss of population size in case of disaster.

References

- Alderson, L. (2009). Breeds at risk: Definition and measurement of the factors which determine endangerment. *Livestock Science*, 123(1), 23-27.
- Balevska, R., Ralchev, G., Mirkov, V. & Marinov, I. (1970). Methods and results in the creation of a semi-thin-type Tsigai type for the mountainous regions of Southern Bulgaria. In: Symposium on Sheep Breeding in the Balkan Countries, BAS, Sofia, 419-423 (Bg).
- Balevska, R. & Petrov, A. (1972). The Zackel sheep in Bulgaria and Southeastern Europe, BAS, Sofia (Bg).
- Bonchevska, S., & Ivanova, T. (2022). Current state and dynamics of Staroplaninski Tsigai Breed in Bulgaria. *Journal of Mountain Agriculture on the Balkans*, 25(1), 145-155 (Bg).
- Carson, A., Elliott, M. Groom, J., Winter, A. & Bowles, D. (2009). Geographical isolation of native sheep breeds in the UK-Evidence of endemism as a risk factor to genetic resources. *Livestock Science*, 123, 288-299.
- Duchevev, Z. I. (2021). Assessment of the risk status of four local Bulgarian breeds based on their geographic distribution. In: *Proceedings of the 13th International Symposium Modern Trends in Livestock Production October 6-8, 2021, Belgrade, Serbia*, 468-476.
- Duchevev, Zh., Sedefchev, A. & Vuchkov, A. (2022). Geographic

- distribution of the Bulgarian Screw-Horn Longhair Goat – potential threats to the population diversity. *Bulg. J. Agric. Sci.*, 28(6), 1110–1115.
- Falconer, D. S. & Mackay, T. F. C.** (1996). Introduction to Quantitative Genetics (4th ed.), Longman Group, LTD., Harlow, Essex, UK.
- FAO** (2023). Domestic animal information system *Rodopski tsigay / Bulgaria (Sheep)*, <https://dadis-breed-datasheet-ext ws.firebaseio.com/?country=BGR&specie=Sheep&breed=Rodopski%20tsigay&lang=en>, last accessed 21.02.2023.
- Groeneveld, E., Westhuizen, B. V. D., Maiwashe, A., Voordewind, F. & Ferraz, J. B. S.** (2009). POPREP: a generic report for population management. *Genet. Mol. Res.*, 8(3), 1158–1178.
- McManus, C., Hermuche, P., Paiva, S. R., Moraes, J. C. F., Barros de Melo, C. & Mendes, C.** (2014). Geographical distribution of sheep breeds in Brazil and their relationship with climatic and environmental factors as risk classification for conservation. *Brazilian Journal of Science and Technology*, 1, 3.
- Nikolov, V. & Ducheve, Zh.** (2022). A methodology for assessment of the risk status of the breeds in Republic of Bulgaria. *Bulg. J. Agric. Sci.*, 28(Supplement 1), 5–13.
- Odjakova, T.** (2022). Monitoring and trends for development of Rodope Tsigai sheep. *Zhivotnovadni Nauki*, 59(6), 13–19 (Bg).
- QGIS Development Team** (2023). QGIS Geographic Information System. *Open Source Geospatial Foundation Project*. <http://qgis.osgeo.org>.
- Santiago, E. & Caballero, A.** (1995). Effective size of populations under selection. *Genetics*, 139, 1013–1030.
- Stancheva, N., Raicheva, E., Laleva, S., Ivanova, T., Iliev, M. & Kalaydzhev, G.** (2014). Present status, problems and development of the Synthetic Population Bulgarian Milk sheep from the herds of Agricultural Accademy, *Journal of Animal Science*, 6, 3–11 (Bg).
- Sturaro, E., Kompan, D., Alderson, L. & Ligda, Ch.** (2013). Assessment of breeds risk status by investigating their geographic distribution. *Agricultural Sciences*, 5(13), 147–150 (Bg).
- Tyankov, Sv.** (1988). Improvement of the Tsigai breed of sheep for Southern Bulgaria, Dissertation, Sofia
- Verrier, E., Audiot, A., Bertrand, C., Chapuis, H., Charvolin, E., Danchin-Burge, C., Danv, S., Gourdine, J. L., Gaultier, P., Guémené, D., Laloë, D., Lenoir, H., Leroy, G., Naves, M., Patin, S. & Sabbagh, M.** (2015). Assessing the risk status of livestock breeds: a multi-indicator method applied to 178 French local breeds belonging to ten species. *Anim. Genet. Resour.*, 57, 105–118.
- Wright, S.** (1931). Evolution in Mendelian populations. *Genetics*, 16, 97–159.

Received: May, 05, 2023; Approved: June, 23, 2023; Published: October, 2023