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Geographic distribution of the Bulgarian Screw-Horn Longhair Goat – potential threats to the population diversity

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Abstract

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The geographic distribution of the breeds has its role in the management and conservation of the animal genetic resources. Geographically concentrated populations are more vulnerable, due to increased risk of loss of animals in case of disaster or disease outbreak. Many systems for estimation of the risk include components to account for the concentration, usually via the minimum enclosing circle centred in the centroid of the farm locations and containing 75% of the breed. In this study, we present an approach to investigate the concentration on sub-population level and its impact on the population size and diversity. For each subset of farms, concentrated in a circle with radius 25 km and 50 km, we have calculated the potential loss of animals and estimated the effective population size of the remaining population. Although this method is applicable to breeds present in a small number of farms, it provides insight of potential loss of groups of closely located farms The Bulgarian Screw-Horn Longhair Goat, one of the few local goat breeds, is an example of such breed. In year 2020, 20 flocks with 3107 animals were kept, mainly in two distant regions in North-West and South-West Bulgaria, estimated effective population size of the Bulgarian Screw-Horn Longhair Goat showed that although the breed is not geographically concentrated on country and regional level, there are some clusters of farms in the two main regions. The distribution of the farms and the animals within the farms present a threat of potential loss of 25% to 58% of the population size and effective population size of the remaining population 40% to 88% of the current one.

Keywords: autochthonous goat breeds; risk; concentration

Introduction

The local goats in Bulgaria were always integral part of the autochthonous breeds (Hinkovski et al., 1984), however they were usually treated as one breed. The name Bulgarian Screw-Horn Longhair Goat was mentioned already in the early 60's, when ex situ in vivo conservation measures were taken by Dr. Altman, exporting, in year 1968, 22 animals to the Erfurt Zoo (Schumann, 2001) and organizing their breeding there. In the recent times, Sedefchev et al. (2011) reported significant differences in the exterior traits between the Bulgarian Screw-Horn Longhair Goat (BSLG) and Kalofer Longhair Goat (KLG). This and other studies resulted in several breeds and sub-breed populations of local goats being distinguished (Nikolov, 2015) The BSLG was included in the catalogue of livestock breeds in Bulgaria (Yordanov, 2017) and is considered endangered due to its numerical scarcity (FAO, 2022). Nowadays, the breed is present in two main habitats – the mountainous regions of Southwest Bulgaria and West Stara Planina (Vuchkov, 2020).

The geographic distribution of the breeds is relevant to various aspects of the characterization management and con-

servation of animal genetic resources. The concentration of the animals in a given area presents a risk even to numerically rich populations, e.g. by increased loss in case of disease outbreak due to their geographical isolation (Carson et al., 2009). An example in this regard is the Foot and Mouth Disease outbreak in 2001 in the UK when some 44% of the farms completely terminated were in the Cumbrian region of the North-West of England (Carson et al., 2009). On the other hand, the dispersion of the herds on a large territory might present a problem for the management of the breed, especially for vast countries. In a study of the geographical distribution of the sheep breeds in Brazil, McManus et al. (2014) concluded that "Flocks in the center west and northeast tend to further away from the midpoint for the breed, making germplasm exchange, and therefore avoidance of inbreeding and their conservation, more difficult". The current distribution of the breeds can be also mapped to the geographic distribution of the existing samples in gene bank collections, to identify new sampling regions and enrich the collections by sampling based upon environment adaptability (McManus et al., 2021).

To account for the threats presented by the geographical isolation, Alderson, (2009) proposed model system for identification of endangered breeds, based on numerical, genetic and geographical criteria. In this system the geographical concentration is estimated by the radius of the circle containing 75% of the population. The criteria defines five classes, the thresholds for the radius ranging from 12.5 to 25 km. Following on this, Sturaro et al. (2013) analysed the geographic distribution of 8 local breeds from 4 countries utilizing a spatial approach. The breeds included in the study represented some of the typical cases in terms of combinations of population size and concentration, e.g. very concentrated large population breed, widely distributed small population breed, very concentrated small population breed with only few flocks, and widely distributed large population breeds with numerous flocks. In this study, the concentration of the breed was also expressed via 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. The thresholds for the radius in the proposed by Sturaro et al., 2013 criteria are 12.5 for critical, 25 for endangered, and 50 km for vulnerable class. The GENMON WebGIS platform, which provides a multi-criteria approach for monitoring endangered breeds based on subjective thresholds of a government agency. (Duruz et al., 2017) also takes into account the geographical concentration, computing the smallest circle containing at least 75% of the animals.

In Bulgaria, the methodology for assessment of the risk status of the breeds present in the country (Nikolov & Duchev,

2022) also accounts for the concentration as one of the indicators increasing the risk. By this methodology, the BSLG is also considered endangered mainly due to its population size.

The BSLG is a breed with geographic concentration in more than one area, and the 3 regions where the breed is present are so distant, that there are no animals within 25km distance from the centroid of the farms locations (Duchev, 2021). This is an example of the non-conventional cases mentioned by Sturaro et al. (2013) and requires further research at sub-breed level. The current study is focused on the geographic concentration of the BSLG on the sub-population level and presents a method for estimation of the threat to the population diversity in the perspective of potential loss of groups of closely located farms. Such information can be used for taking decisions for conservation activities.

Material and Methods

Data for the distribution of the Bulgarian Screw-Horn Longhair Goat breed in year 2020, representing 20 flocks with 3107 animals (129 males and 2978 females) in 6 regions were collected from the Association for Autochthonous Goat Breeds in Bulgaria. The location of each herd was mapped to the village, where the respective farm is registered. In case of multiple farms in the same village, they were merged in a single virtual farm. Thus, the two farms in Zgorigrad with 133 and 141 animals respectively, were analysed as a single farm with 274 animals. The resulted 19 farms were geocoded by the village coordinates, using the Nominatim Geocoder service provided by the OpenStreetMap project. The distances between the farms were calculated in a GIS software - QGIS (QGIS Development Team, 2021). All combinations of farms keeping more than 25% (50%) of the population and potentially concentrated in a circle with radius 25 km (50 km) were generated. The radius of the minimum enclosing circle for each combination was calculated in QGIS.

To estimate the potential loss of genetic diversity if all animals in a group of farms are eliminated, e.g. due to disease outbreak, the effective size of the remaining population was used. For each combination of farms, the number of the breeding males and females in the population outside these flocks were calculated. Then the effective population size – Ne was calculated:

$$N_e = \frac{4N_m N_f}{N_m + N_f} \times 0.7,$$

where N_m and N_f are the number of breeding males and females in the population outside the chosen farms. For this calculation we have used the (Wright, 1931) formula, with 30% correction following the model proposed by Santiago and Caballero (1995) to account for the mass selection applied to BSLG. The effective population size of the whole breed was also estimated by the same formula as 346.

Results and Discussion

The distribution of the animals within the flocks before and after merging the farms are depicted in Figure 1 and Figure 2 respectively. As can be seen from these figures, most of the farms keep up to 150 animals. There are only two larger farms with more than 400 animals, and these are located in different distant regions.







Fig. 2. Number of animals per village (virtual farm)

Table 1. Number of subsets of farms, concentrated in a circle with a given radius, and keeping more than a given proportion of the population

Minimum percent-	Number of subsets	Number of subsets
age of the popula-	in a circle with	in a circle with
tion included	radius 25 km	radius 50 km
25%	409	4049
50%	0	119

From all possible 524287 combinations of the 19 (virtual) farms, there are only 409 combinations (Table 1), where the farms are keeping together more than 25% of the population, and are concentrated in a circle with radius of up to 25 km ("25% in 25 km"). Although 62% of the animals are located in South-West Bulgaria, there are no combinations of farms concentrated in a circle with radius of up to 25km and keeping more than 50% of the population ("50% in 25 km"). Thus, not only the breed as a whole is not geographically concentrated, but also the separate populations in the three regions are not very dense.

In 280 cases in the "25% in 25 km" category, the population size might be potentially reduced by up to 33% (Figure 3), which is a threat to BSLG due to its numerical scarcity. In the "50% in 50 km", from 119 possible combinations, 89 might reduce the population size by 50% to 53%. This loss is large in absolute animal numbers; however, such event is less likely to occur.



Fig. 3. Frequency of number of potentially lost animals in "25% in 25km" category.



Fig. 4. Frequency of number of potentially lost animals in "50% in 50km" category.

In both categories, there are only few combinations resulting in maximum population size reduction. The situation with the effective population size of the remaining population is different. Due to the used formula, which is heavily influenced by the scarcer gender (usually the males), and the distribution of the male animals across the BSLG flocks, most of the combinations reduce the Ne of the breed to 63%-81% (Figure 5) and 43%-53% of its original value in the "25% in 25 km" and "50% in 50 km" categories, respectively.



Fig. 5. Frequency of *Ne* in the remaining population in "25% in 25km" category



Fig. 6. Frequency of *Ne* in the remaining population in **"50% in 50 km" category.**

Table 2 illustrates the extreme cases of loss of population size and diversity expressed via the effective population size of the remaining animals. These boundary values for the each category are reached for different combinations of farms. The potential population loss in the "25% in 25 km" category ranges from 25% of the population size (777 animals) to 47% (1430 animals). In the "50% in 50 km" category, the potential loss is even greater - from 50% to 58%. In terms of genetic diversity, the effective population size of the whole breed is estimated as 346. In the worst case scenario, it will be reduced to 197 for the "25% in 25 km" (the set of farms depicted in Figure 7) and 137 for the "50% in 50 km" (Figure 8). There is another subset in the "50% in 50 km", which also results in Ne = 137. This is a subset of the set of farms shown in Figure.8; spare the farm in Novo Delchevo, which keeps only female animals. This result is also due to the formula used for estimation of the effective population size. Because of the way it estimates the Ne, although the two subsets result in different population loss, the resulting Ne is identical.



Fig. 7. The group of BSLG farms from "25% in 25 km" category, which loss will reduce maximally the effective population size

Table 2. Lower and u	pper limit of the numbe	er of potentially lost	animals, and the effect	tive population siz	e of the re-
maining population pe	er category				

Minimum percentage of the population in a circle with a given radius	Minimum number of potentially lost animals	Maximum number of potentially lost animals	Minimum <i>Ne</i> of the remaining population	Maximum <i>Ne</i> of the remaining population
25% in 25 km	777	1430	197	304
25% in 50 km	777	1796	137	304
50% in 50 km	1554	1796	137	195



Fig. 8. The group of BSLG farms from "50% in 50 km" category, which loss will reduce maximally the effective population size

Two subsets of farms are two most concentrated ones in each category. In the "25% in 25 km" category, there is a cluster of three farms in North-West Bulgaria (in fact four, since the two farms in Zgorigrad are merged in one virtual farm), containing 26.42% of the population within a circle with radius 4.5 km (Figure 9). In the "50% in 50 km" category, a cluster of 10 farms in South-West Bulgaria, containing 50% of the population, is located in a circle with radius 30 km (Figure 10).

Vuchkov (2020) has reported variation in the morphological variation in the body composition, horns shape and coat color between the animals from the two distribution areas in North-West and South- West Bulgaria. This makes the conservation of the populations in both areas equally important. Although these populations are not very concentrated and



Fig. 9. Group of BSLG farms keeping 26% of the population, located in a circle with radius 4.5 km



Fig. 10. Group of BSLG farms keeping 50% of the population, located in a circle with radius 30 km

isolated in their areas, the risk for loss of diversity, associated with their geographic distribution has to be accounted for by the respective breeding organization.

In calculating the effective population size we have used the (Wright, 1931) formula, corrected for selection as no long enough pedigrees were available, thus following the recommendation of Verrier et al. (2015). If such information is available, a more precise methods for estimation of Ne should be used.

We have not used the coordinates of the farms, but the coordinates of the villages where the respective farms are registered as in the case of BSLG this shifts the real location by only few kilometres and allows to merge some of the farms to reduce the complexity of the computation.

The number of distinct farms is the major limitation of the proposed method. The number of all subsets of a set of N farms is 2^N-1, which is an exponential function. Iterating over all possible subsets is feasible only for a small number N; hence, the method is applicable for breeds kept in small number of farms regardless of their population size or distribution.

Conclusion

The proposed method has a limited scope of application to breeds kept in a few farms. However, it provides valuable information on the geographic distribution and concentration at sub-population level and the associated risk of reduction in the number of animals and effective population size.

In the case of BSLG clusters of concentration are present in both main areas inhabited by the breed, the one in North-West Bulgaria being dense. Although the population is not concentrated as a breed, there is a risk on sub-population level, and even a 25% loss in numbers will reduce its relatively small population size.

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