

Genetic structure of breeds of goats bred in Slovakia

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The genetic structure of five goat breeds bred in Slovakia was characterized using a visible genetic profile and biochemical polymorphic systems. Tree dairy goat breeds – White Shorthaired, Brown Shorthaired and Alpine goats – and two wool goat breeds – Angora and Cashmere goats – were evaluated. Calculated were the heterozygosity and the effective number of alleles for each locus based on the allele frequencies of eight genes determining type traits and biochemical polymorphic systems, as well as their average values as indicators characterizing the genetic variability of each breed. The genetic differences between breeds were also determined.

Keywords: Goats, White Shorthaired, Brown Shorthaired, Alpine, Angora Cashmere, genetics, Slovakia

1 Introduction

Goat farming in Slovakia is a specific livestock sector where most goats are concentrated in small-scale breeding. At the end of 2018 of 36.9 thous. goats were bred in Slovakia. Goat-farming is of minor importance and has features of self-subsistence. An extensive production system with one kidding per year is applied according Oravcová (2013).

2 Material and methods

Using a visible genetic profile and biochemical polymorphic systems, we characterized the genetic structure of 5 goat breeds bred in Slovakia. We evaluated three dairy goat breeds (White shorthair goat – BKK, Brown shorthair goat – HKK, Alpine goat – AK), and two wool goat breeds (Angora goat – ANK, and Cashmere goat – KK). The goats of the BKK breed came from 3 herds ($n = 53\text{--}205$ pieces depending on the analyzed polymorphic system, HKK, AK, ANK and KK from one herd ($n = 7\text{--}54$).

In all individual breeds, we found the frequency of alleles for polledness (Ho), the occurrence of wattles of the goats (Wa), occurrence of the beard (Br) and length of ears (EL). In ANK and KK we have also determined the phenotype representation for the type (shape) of horns.

In the biochemical polymorphic of transferrin (Tf), X-protein (X), plasma arylesterase (Es) and haemoglobin (Hb) were calculated allele frequencies. Based on the allele frequencies of all eight genes determining type traits and biochemical polymorphic systems, were calculated the heterozygosity and the effective number of alleles for each locus as well as their average values. The genetic difference between individual breeds was also determined.

3 Results

We found that the frequency of the dominant Ho^p allele for polledness was 0.487 for BKK and 0.209 for HKK and AK; thus, the proportion of polled goats in BKK was higher

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than for HKK and AK. All evaluated KK and ANK were horned ($Ho^P = 0$). Three types of horns were observed in wool-type goats: markhor, ibex and intermediate type. The largest part of ANO and KK were goats with the type of markhor horns.

The occurrence of wattles on the neck of goats was observed in all breeds except for ANK ($Wa^+ = 1$). The frequency of the dominant Wa^w allele for the occurrence of wattles was low in other breeds (0.051–0.136), except for AK (0.567).

The recessive allele of the Br^B beard (0.633–0.870) prevailed in the female sections of the studied populations. Only in the HKK breed (0.378 and AK (0.250)) the frequency of the Br^B allele was lower than that of the dominant Br^+ allele for the lack of beard.

The occurrence of short-haired goats with reduced ear was observed in only one BK^K herd. The recessive EL^r allele frequency was 0.017 for the whole evaluated population.

In the analysis of biochemical polymorphic systems we found that all evaluated populations resp. the breeds were monomorphic in the haemoglobin system, with the fixation on Hb^A allele. All studied subjects also reacted negatively without dark colouring of plasma when testing arylesterase activity with the so-called tube test; i.e. all evaluated breeds were monomorphic in the plasma arylesterase system.

In the Tf system, the polymorphic breeds were BKK ($Tf^A = 0.898$; $Tf^B = 0.102$) and KK ($Tf^A = 0.914$; $Tf^B = 0.086$), but these populations can be considered panmictic in terms of the Tf system.

Other breeds were monomorphic in the Tf system ($Tf^A = 1$). In the X protein polymorphic system, the X^+ phenotype was higher in all populations.

The frequency of the dominant X^+ allele ranged from 0.342 to 0.863.

The highest genetic variability assessed based on the eight analyzed systems and expressed as mean heterozygosity (H) was found in BKK and AK ($H = 0.207$) with an average effective allele count only in AK ($Ne = 1.362$). The smallest genetic difference (D) was found between KK and ANK ($D = 0.0075$) and HKK and AK ($D = 0.0323$). The largest difference was found between AK and KK ($D = 0.1209$) and AK and ANK ($D = 0.0970$). The observed genetic differences primarily reflected the phylogenetic relatedness of the evaluated breeds and focus on their produce.

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