

Bravia Goat Breed Population Sample Structure Analysis Evidences of ecotypes existence

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ABSTRACT

There is a tacit recognition that the bravia goat breed has different subpopulations that result in two ecotypes (Alvão and Gerês). Microsatellite markers were used to analyze the genetic structure of a sample (n=2127) of the population of the bravia goat breed assuming a possible different number of subpopulations (K), from 2 to 5. The clustering supports information about the genetic connections between the animals from different regions. Animals from Alvão cluster together, supporting the idea that there is in fact a Alvão subpopulation, and within Gerês it is possible to cluster two different subpopulations, the first one with animals with genetic connections with the Alvão subpopulation and a second one with almost none genetic connections with the Alvão subpopulation.

INTRODUCTION

With less than 12500 animals, the bravia goat breed is one of the six, at risk of extinction, goat breeds native from Portugal. This particular breed is reared in the north of Portugal in mountain areas and breeders use traditional systems applying free-range grazing paths. With two main geographic areas, in Alvão and in Gerês, where the frequency of occurrence of breeders is higher, and with the support of previous studies (Hugo and Chaves, 2016), the idea that this breed has two ecotypes, seem to be indisputable. The animals from Alvão ecotype (figure 1) are bigger and heavier than the animals from the Gerês ecotype (figure 2), they are also mainly brown and red-haired whilst the Gerês animals are mainly black, dark brown and bicolored. The ANCABRA (Associação Nacional de Criadores de Cabra Bravia) is the entity responsible for the elaboration and execution of the several genetic selection and conservation programs for this breed. The main objective of this study was to find, using records based on genotypes, if there is a genetic support to claim that this breed has indeed two subpopulations.



Figure 1 – Bravia goats from Alvão.



Figure 2 – Bravia goats from Gerês.

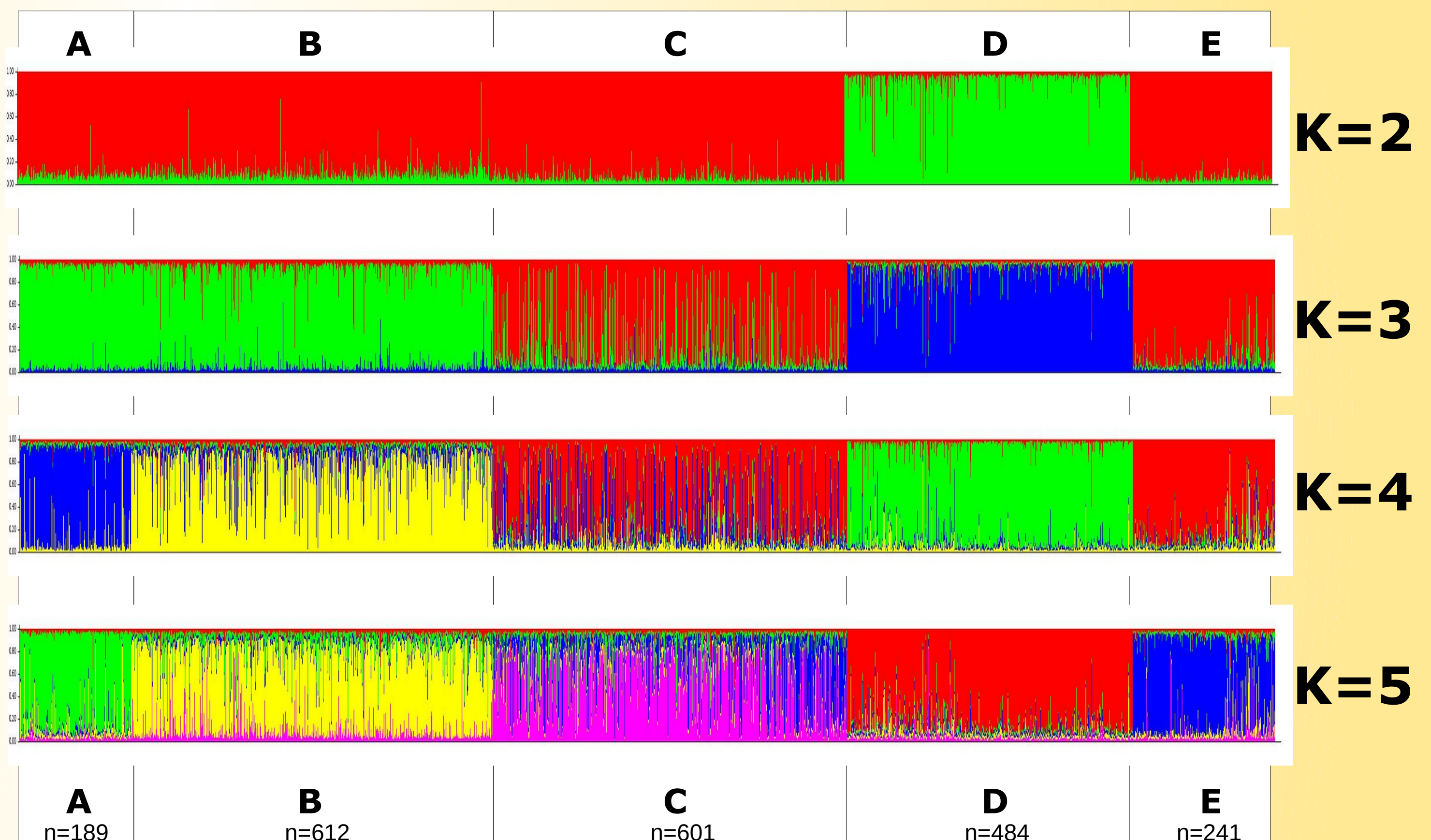


Figure 3 – Clustering analysis by structure for the full-loci dataset assuming K = 2 to 5. Animals from breeders A, B, C, D and E are labeled on top and below the structure result. Breeders A and B are from Alvão region and breeders C, D and E are from Gerês region.

METHODS

In this study, 19 polymorphic microsatellite markers (BM1258, BM1329, CSR247, ETH10, FCB20, HSC, ILSTS11, ILSTS19, ILSTS30, ILSTS87, INR005, INR006, INR023, INR063, INR172, MF65, SRCRSP5, SRCRSP8, TGL53) were used to analyze the genetic structure of a sample (n=2127) of the population of the bravia goat breed. The genetic data collected by ANCABRA in the past 5 years with the objective for use in filiation tests were used. Animals from 5 breeders were selected, 2 breeders from the Alvão region (A and B) and 3 breeders from the Gerês region (C, D and E). The population structure was analyzed using the Structure software (Pritchard et al., 2003) assuming a possible different number of populations (K), from 2 to 5.

RESULTS AND DISCUSSION

Before discussion, it is important to state the following information provided by ANCABRA: (i) Breeder A used (in the past 10 years) to sale males for reproduction purposes to breeder C and E. (ii) Breeder D is the most isolated breeder from Gerês region (geografically and regarding the genetic connections with other breeders).

Figure 3 shows when K (number of populations) was assumed to be equal to 2 (K=2), the animals from breeders A, B, C and E where clustered in the same group. But when K=3 animals from breeders A and B cluster in the same group, and animals from breeders C and E also cluster in the same group, although it is noticeable some "noise" from the cluster of animals from breeders A and B in this cluster. Regarding K=4 it is noticeable that the animals from breeders C and E cluster together, with a high level of mixture from the animals from breeder A in the animals from breeder C. When K=5 it is obvious that the animals from each breeder cluster together. The several conclusions of this study are: (i) The clustering supports ANCABRA information about the genetic connections between the animals from breeders A, C and E. (ii) When K=3 the animals from Alvão cluster together supporting the idea that there is in fact a Alvão subpopulation, and with some influence from the Alvão cluster, the animals from breeders C and E also cluster together. The animals from breeder D cluster alone. Because animals from breeders C and E and the animals from breeder D cluster separately from the cluster of animals from Alvão, there is a support to the idea that there is in fact, although with genetic connections from Alvão, a diferente subpopulation of bravia goat breed in Gerês. In deed, in Gerês it is possible to cluster two different subpopulations, the first one with animals with genetic connections with the Alvão subpopulation and a second one with almost none genetic connections with the Alvão subpopulation.

REFERENCES

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Pritchard, J., Wen, X., & Falush, D. (2003). Documentation for STRUCTURE software: version 2.3

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To bravia goat breeders. Because they really understand and can define, with a simple word, the essence of this goat. That word is "bravia".