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## Exploring the genetic diversity and relationships between Spanish and Moroccan goats using microsatellite markers

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## ABSTRACT

Nineteen microsatellite markers were used to tag 668 goats from Spanish breeds from the Iberian Peninsula and Canary Islands and a population from north Morocco. The mean value of the allelic number per locus for the whole population studied was 12.7. The Moroccan population showed the highest values in allelic richness (8.043), with a mean number of alleles per locus of 10.7 and 17 private alleles. The levels of breed differentiation were relatively low ( $F_{ST} = 0.05$ ). The AMOVA analysis revealed a significant genetic differentiation among populations, but only 4.96% of the variance could be explained by differences between the 13 populations. Most of the variation (93.42%) was due to variation within individuals. The dispersion of the breeds, according to the Correspondence Analysis, was consistent with the geographical locations of the different populations studied. We used microsatellite markers to carry out the first genetic study, which included a population from northern Morocco and 12 Spanish goat breeds which were mainly bred in southern Spain and the Canary Islands. All the approaches used showed that the Spanish and, in particular, the Moroccan population, presented an important level of genetic diversity. We reported that the Agrupacion de las Mesetas, Payoya and Malagueña breeds differ little and have a closer relationship with the Moroccan population. As for the Payoya and Malagueña breeds, this indicated that geographical proximity favoured the gene flow between them.

Our results showed that the population studied had a robust structure, with a clear differentiation between the Moroccan population and the Spanish goat breed. The cluster of three Canary Island breeds was completely separate. Coincidences in geographical location and the genetic structures suggested that common ancestries and/or genetic flow between the Iberian Peninsula and North Africa may have occurred over a long period of time or more recently.

### 1. Introduction

The origin of the world's current livestock breeds is a complex history that includes human-driven migration, dispersion, crossbreeding and trading (FAO, 2007). Local genetic resources are endangered by a number of factors, including indiscriminate and uncontrolled crossbreeding with cosmopolitan breeds (Ajmone-Marsan et al., 2014). Robustness, adaptability and relative ease in the transport of goats may have played an important role in the history of human populations and commerce. Compared with cattle, goats appear to have experienced a more extensive intercontinental flow and the world goat population is less genetically structured (Luikart et al., 2001).

The geographical proximity of the Iberian Peninsula to Africa makes the Straits of Gibraltar a possible area of interaction between the two

continents (Curat et al., 2010). Early human communities and cultures (including the Phoenicians, Carthaginians and Romans) are known to have existed simultaneously on both sides of the Straits, and interactions between these communities must have occurred with the exchange of populations, ideas, goods and livestock (Anderung et al., 2005). Previous studies have highlighted the importance of the Mediterranean Sea as a route for the movement of livestock and humans in a continuous network of trade and commercial exchange, including contact between the Maghreb and the Iberian Peninsula. Human migration and the Islamization of eastern and northern Africa further favoured livestock dispersion, and European influences added a layer of genetic diversity to that of northern Africa (Cañón et al., 2006). A phylogeographic interpretation of the data reveals numerous traces of African–Iberian contacts (Pereira et al., 2009). Indigenous goat breeds

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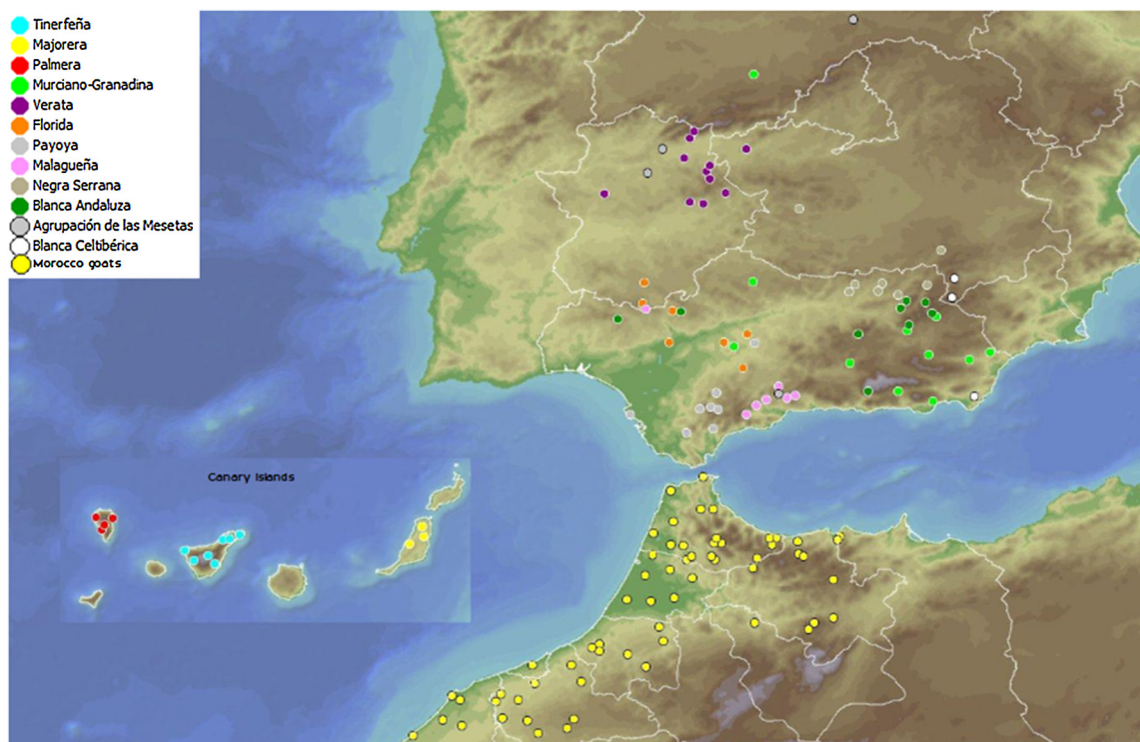


Fig. 1. Dispersion of goats sampled. Each point represents one herd and different colours correspond to the main breed.

in Morocco reared under extensive production systems, similar to those of other Mediterranean countries, play an important role as food at social gatherings and in limiting the growth of vegetation in marginal areas where fire can be a danger (Rancourt et al., 2006; Chentouf and Boulanour, 2011). The lack of any pressure from artificial selection or breeding plans has favoured the gene flow between goat populations and this makes it difficult to determine well differentiated breeds (Benjelloun et al., 2015). Nevertheless, some phenotypic groups showing specific morphological and adaptive characteristics have been identified, which are classified as "breeds". The three major local goat groups in Morocco are: (i) Black goats with three sub-populations recently recognized (Atlas, Barcha and Ghazalia) (Boujenane et al., 2016), (ii) the Draa population, (iii) and the Northern population (Benjelloun et al., 2015) with 785,000 heads, representing 12.6% of the total goat census in Morocco and 43% of the small ruminants in the region (Chentouf, 2014). This latter population includes a small well-organized and well-maintained subpopulation, the Beni Arouss, recently defined as a breed (Official bulletin 6430). Goat populations in the Northern regions show some phenotypic resemblance to Spanish breeds such as the Murciana-Granadina, the Malagueña or Andalusia breeds (Benlekhal and Tazi, 1996). The use of neutral genomic diversity to compare the genetic structure of the northern Morocco goats with the other local goat breeds, e.g. the Draa and Black Rahalli populations, was considered in the studies of Ouragh et al. (2012) and Benjelloun et al. (2011, 2015). Genetic relations between Moroccan and European goat breeds were studied by Tadlaoui Ouafi et al. (2002), who compared Black Rahali and Draa with goat breeds reared in France (Alpine, Saanen, Poitevine and Pyrenean). The Pyrenean breed was the French goat breed most closely related to the Moroccan breeds. Despite the intense exchange of farm animals between southern Spain and northern Morocco, the relationship between Morocco and Spanish breeds has not been previously analysed.

Spanish goat breeds are mostly defined by their geographical locations, morphological characteristics and production performance. They have been inventoried according to their danger of extinction and have also been classified based on their production status: milk, meat and

dual type (Rodero et al., 2015). However, there is still a lack of information on the genetic relationship and differences amongst the Spanish breeds. Studies with microsatellite markers in Spanish goat breeds (Magdalena et al., 2009; Parejo et al., 2015; Martínez et al., 2011) have shown a high genetic variability within and between goat breeds. Studies of the genetic relationships between Spanish and Portuguese breeds (Martínez et al., 2015) on the one hand, and North African goats (Martínez et al., 2016) on the other, detected the existence of gene flow, high diversity levels and weak population structures. This diversity has been attributed to multiple introductions of caprines into the Iberian Peninsula, not only through maritime colonization from Italy and France, but through subsequent introductions from Africa (Zeder, 2008). Seasonal pastoralism and long-distance cyclical migrations could be the reasons for the lack of breed isolation in the Iberian Peninsula for mtDNA (Azor et al., 2005). The goal of the present study was to investigate the genetic diversity, population structure and genetic relationships between Spanish and Moroccan goats. Based on their historical influence, geographical proximity and their current relevance, or even in anticipation of their possible sensitivity to crossing, we opted to compare all the recognized Spanish breeds from the Spanish regions nearest to Morocco, with goats from northern Morocco. For this purpose, twelve Spanish goat breeds reared in central-south Iberian Peninsula and Canary Islands were selected: Blanca Andaluza (BA), Blanca Celtiberica (BC), Florida (F), Malagueña (MAL), Agrupacion de las Mesetas (AGM), Negra Serrana (NS), Payoya (P), Verata (V), Murciano-Granadina (MG), Palmera (PAL), Majorera (MAJ) and Tinerfeña (TIN). All these breeds are well-organized and maintained by their respective improvement programs.

The Moroccan goats (MOR) included animals from a large population of the northern region, previously studied phenotypically (El Moutchou et al., 2014; El Moutchou et al., 2017a) and genetically (El Moutchou et al., 2017b) to characterize and identify a possible geographical subdivision. The results showed a highly heterogeneous, unstructured population in terms of geographical area, based on their phenotypic (zoometric traits and morphology) or genotypic (Microsatellites markers) characteristics. Given that there was no obvious

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