



further sub-structuring reflects the main post-domestication migration routes. The reconstruction of past migration events highlighted several exchanges mainly between African populations, which often involve admixed and cosmopolitan breeds. In addition, extensive gene flow was revealed within specific areas (e.g., southern Europe, Morocco and Mali-Burkina Faso-Nigeria), while isolation due to geographical causes (e.g. insularity) or human management has brought a decrease in local gene flow. Taken together, these results confirm that after domestication in the Fertile Crescent in the early Neolithic era (approx. 15,000 BP), domestic goats spread to Europe, Africa and Asia through divergent migration routes, which determined the major genomic background of the continental populations. During the following centuries, due to geographical and reproductive isolation, further sub-structuring of diversity occurred at the local level. This has been accompanied by additional migrations and/or importations, the traces of which are still detectable, such as the clear African signatures in the goat populations of the Canary Islands and Southern America.

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## O075

### Italian Goat Consortium: a collaborative project to study the Italian caprine biodiversity

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The Italian Goat Consortium (IGC), joined the effort of many Universities and Research Institutes, in a comprehensive study of the Italian goat population genetic makeup using a medium density (54K) SNPs chip. Currently IGC has genotyped more than 1,000 animals from more than 30 goat breeds and populations from all Italian geographical and agro-ecological areas of goat rearing.

The aim of this work is to obtain a clear picture of the Italian caprine biodiversity, to reconstruct the ancestry, to disentangle the genetic background and to assess the relationships among and within the investigated breeds. To date, the IGC dataset includes about 50 million genotypes. The data were quality checked by excluding markers and individuals on the basis of missing genotypes, minor allele frequency and close individual relatedness. Genetic relationships among and within breeds was investigated by Multi-Dimensional Scaling and Principal Component Analysis. Population structure, ancestry models and admixture were estimated by ADMIXTURE and fastSTRUCTURE software. Finally, phylogenetic trees were reconstructed with PHYLIP software suite starting from shared-allele identity by state, and Reynolds distance matrices, while past migration events were modeled with TreeMix software.

The results confirmed high levels of genetic polymorphism and confirmed the North-South geographical pattern of diversity, previously reported on a smaller sample of Italian goat breeds. The analysis also revealed a pivotal role of Central Italy in connecting the genetic resources of the northern and southern areas of the country, and confirms the genetic isolation of insular breeds. Moreover, some breeds show clearly distinctive and homogeneous gene pools, whereas other breeds present complex and, in some cases, dishomogeneous genetic background.



Even if “A breed is a group of domestic animals, termed such by common consent of the breeders” (Lush J.L., 1994), genomic tools are useful in understanding the genetic background of populations and in defining their relationships or uniqueness. These tools can complement the traditional ones in providing farmers and their associations a powerful aid for a more conscious management of goat populations and their biodiversity.

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