

## SNP-based characterization of Montecristo feral goats in a Mediterranean perspective

Elisa Somenzi(1), Ettore Randi(2), Gwenola Tosser-Klopp(3), and Licia Colli(1)

(1) DIANA Dipartimento di Scienze Animali, della Nutrizione e degli Alimenti, Università Cattolica del S. Cuore, Piacenza, Italy

(2) Laboratory of Genetics, Istituto Superiore per la Protezione e la Ricerca Ambientale (ISPRA), Ozzano Emilia, BO, I-40064 Italy

(3) GenPhySE, Université de Toulouse, INRAE, ENVT, F-31326 Castanet-Tolosan, France

The Montecristo wild goat is an endangered free-ranging goat population inhabiting the homonymous island in the Tuscan Archipelago. The origin of this feral population is still debated: some authors suggest that goats were introduced during Neolithic times while others date their first occurrence between the 6<sup>th</sup> and 13<sup>th</sup> century of the Common Era, when Montecristo island was occupied by a monk community. In this study we assessed genetic diversity and population structure of two different nuclei of Montecristo goats, one sampled on the island, the other from an *ex situ* conservation project on the Italian mainland. Furthermore, to investigate the origin and evolutionary relationships of Montecristo goats we assembled a 50K SNPs dataset including 44 breeds from the Mediterranean basin. Observed ( $H_o$ ) and expected ( $H_e$ ) heterozygosity were calculated to estimate diversity levels, while gene flow, population structure and relationships were assessed through multiple approaches, i.e. runs of homozygosity (ROHs), Principal Component Analysis (PCA), Neighbour-network reconstruction, Treemix software analysis.

$H_o$  and  $H_e$  values for the insular Montecristo population were the lowest recorded in the dataset, highlighting reduced genetic diversity, while the nucleus from the mainland displayed a less severe reduction. Results from PCA, Neighbour-network and population structure analysis clearly separated the insular population from all other breeds, and further highlighted a remarkable distance between the two Montecristo nuclei. Also, Treemix software analysis pinpointed possible genetic contributions received by the two Montecristo goat populations from different sources. Lastly, ROHs indicated the occurrence of an ancient bottleneck or founder effect in the insular population, and of recent inbreeding in the continental nucleus.

Taken together, our results indicate that Montecristo goats faced several demographic fluctuations combined with admixture events over time, and also emphasized the marked genetic differentiation between the goats sampled on the island and those from the *ex situ* nucleus. This evidence can represent a starting point for the implementation of a marker-assisted monitoring and conservation plans for the autochthonous feral goat of Montecristo.

### Acknowledgments

The authors wish to thank the Italian Goat Consortium.