



Molecular characterization of the Montecristo feral goats in the Mediterranean context

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The Montecristo wild goat is an endangered feral population occurring on the homonymous island in the Tuscan Archipelago since a long time. The origins of Montecristo goats are still debated, with authors dating their introduction either back to Neolithic times or between the 6th and 13th century of the Common Era. To investigate the evolutionary history and relationships of this population we assembled a 50K SNP dataset including 55 Mediterranean breeds and two nuclei of Montecristo goats sampled on the island and from an *ex situ* conservation project on the Italian mainland, respectively. Diversity levels, gene flow, population structure and relationships were assessed through multiple approaches. The insular population scored the lowest values of both observed and expected heterozygosity, highlighting reduced genetic variation, while the *ex situ* nucleus highlighted a less severe reduction. Multivariate statistics, Neighbour-network and population structure analyses clearly separated the insular nucleus from all other breeds, but also the two Montecristo populations from each other. Treemix software analysis pinpointed possible genetic inputs received by the two Montecristo goat nuclei from different sources, while Runs Of Homozygosity (ROHs) indicated an ancient bottleneck/founder effect in the insular population and recent inbreeding in the *ex situ* one. Overall, our results suggest that Montecristo goats experienced several demographic fluctuations combined with admixture events over time, and highlighted a noticeable differentiation between the two *nuclei*. This evidence can serve as a starting point to implement marker-assisted conservation plans for the endangered Montecristo feral goat.

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