PINE MARTEN AND STONE MARTEN: MORPHOLOGICAL AND GENETIC DIFFERENCES IN COMPARISON

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The *status* of these two “twin” species in Italy is extremely different; stone marten is widely spread throughout the entire peninsula, while absent in the islands, pine marten is spread in Sardegna, Sicilia and Isola d'Elba, but its distribution in the peninsula is very fragmented. Such a situation allows presuming a competition between the two species, where the beech marten comes out as the “winner”. This information points out the possibility of conservation programs to preserve the pine marten and to contain the stone marten. Thus it is of primary the necessity of an unmistakable differential taxonomical diagnosis between the two species.

Objective difficulties in the identification and recognition of these Mustelids are already known. Thus a program of genetic characterization of pine and stone marten is being performed, also to prove the existence of effectively discriminating morphological characters.

Up to now, 24 individuals were been analyzed from Toscana, Umbria, Marche, Lazio and Basilicata. Taxonomical ascription was been performed according to several morphological and metrical characters such as the coat-color and markings pattern and the length of the *baculum*. The reliability of this diagnosis has been verified through the genetic analysis performed on tissues sampled from each one individual.

Genetic analysis was arranged both with direct sequencing and specific PCR-RFLP processing DNA by specific restriction enzymes (AluI and HaeIII) which cut a diagnostic mtDNA fragment in the beech but not in the pine marten.

Morphological characters ascribed 10 individuals to *Martes martes* and 14 to *Martes foina*; genetic results confirm the 10 pine martens, but only 12 out of the 14 stone martens. Therefore 2 individuals morphologically diagnosed as “stone marten” resulted genetically “pine marten”.

Furthermore, for 6 individuals it was possible to analyze the DNA extracted from the faeces, thus giving the chance to perform a genetic identification through those indices of presence.