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Genetics of Italian small mammals: differentiation in both the south and north

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Over the past 35 years, I have studied genetic variation in small mammals in Italy in collaboration with many colleagues. In this synthesis, I will particularly focus on our published work for which the listed collaborators were principal authors. Populations of small mammals are readily isolated from each other by geographic barriers, reflecting limited dispersal capability. This can be seen in the genetic structure of several species of small mammals in Italy, and the differentiation is most notable in the extreme south and north of the country. Calabria is currently part of the southern Italian mainland, but in the Middle Pleistocene and earlier there were periods when it was a group of islands and the very distinctive Calabrian genetic lineages of bank vole (*Clethrionomys glareolus*) and pygmy shrew (*Sorex minutus*) likely reflect island evolution, with later expansion within southern Italy. For the pygmy shrew, mitochondrial and Y-chromosome sequence data were analysed while for the bank vole genomic data are available. In the north of Italy, the genetic differentiation can be related to geographic subdivision created by the alpine massif, with highland and lowland areas either at the macro- or micro-geographical scale. The genetic differentiation that I will describe is more recent than that described for southern Italy. For the Valais shrew (*Sorex antinorii*), the mitochondrial sequence variation described likely relates to geographic subdivision determining the location of refugia at the Last Glacial Maximum. For the house mouse (*Mus musculus*), the chromosomal variation is even more recent – likely originating within the last 4000 years, with this anthrodependent taxon being brought in by humans. All-in-all, the geographic features of Italy make it a fascinating area for the study of genetic variation in small mammals.