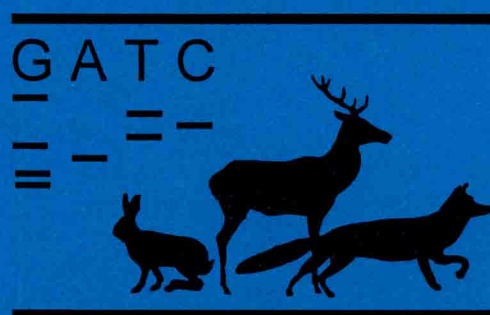


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Partitioning of genetic variability among mountain hares (*Lepus timidus*) from Europe

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Mountain hares (*Lepus timidus*) show a disjunct distribution in Europe, with major ranges in the subarctic/arctic regions of Russia and Fennoscandia, the Alps, Scotland and Ireland. Mountain hares in these regions are considered as separate subspecies (*L.t.timidus*, *L.t.sylvaticus*, *L.t.varronis*, *L.t.scoticus*, *L.t.hibernicus*), mainly due to morphometric differences and pelage coloration. Based on late pleistocene and early holocene ecology, geography and according to fossil records, however, this hare species was likely continuously distributed over large parts of Europe by the end of the last ice age. Provided the late pleistocene population of European mountain hares exhibited a panmictic gene pool, rather than an already substructured one, and no severe or long lasting demographic bottlenecks (founder effects etc.) have occurred during postglacial colonisation of the present ranges, we expect a very shallow overall gene pool differentiation among the present subspecies in Europe. This can be expected particularly because of the short time in terms of evolution since the last glaciation (some 10-12 ka). Multilocus allozyme electrophoresis of 209 specimens from Scandinavia, the Ural mountain range in Russia, the Alps, Scotland and Ireland revealed a level of cross nuclear gene pool differentiation similar to the one found among local populations of European brown hares *L. europaeus*. Also, partitioning of relative genetic variability of mountain hares (Wright's hierarchical F-statistics) due to nominal subspecies amounted to less than 1% whereas almost 13% of partitioning of relative genetic variability was due to local populations. These results agree with the hypothesis of a rather panmictic gene pool by the late pleistocene and quite reasonable population sizes of colonizing postglacial populations.