
A parasite reveals cryptic phylogeographic history of its host

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This study compares the continental phylogeographic patterns of two wild European species biologically linked by a « host-parasite » association : the field mouse *Apodemus sylvaticus* (Muridae) and one of its direct and specific endoparasites, the Nematode *Heligmosomoides polygyrus* (Heligmosomoidea). 687 bp of the mitochondrial cytochrome b gene were sequenced in 122 specimens of *H. polygyrus* and compared to 94 cytochrome b gene sequences (974 bp) previously obtained for *A. sylvaticus*.

The results reveal partial spatial and temporal congruences in the differentiation of the lineages of both species: the parasite and its host are split into two major genetic lineages, i.e. western European and Italo-Balkan, that differentiated simultaneously in the past; moreover, the Sicilian populations of both species form a distinct and ancient lineage inside the Italo-Balkan clade. Both species survived during the cold stages of the Pleistocene in the Iberian, Italian, and Balkan refuges and recolonised north-western Europe at the end of the Pleistocene from the Iberian refuge.

However, *H. polygyrus* presents more diverse genetic and geographic structures than its host. Indeed, in comparison with the phylogeographic pattern of *A. sylvaticus*, the parasite is characterized by three ancient duplication events, the first one between the Italian and the Balkan populations, the second one between the northern and southern parts of Italy, the third one occurring in the western European group. Moreover, *H. polygyrus* populations from northern Europe (Ireland, Denmark) are markedly differentiated, suggesting the existence of a northern refuge in the southern British Isles for *H. polygyrus* during the Quaternary.

The partial temporal and spatial congruences of the phylogeographic patterns of both species allowed us to estimate the relative rate of molecular evolution of the cytochrome b gene of both species, which appeared to be about 1.5 times higher for the parasite than for its host. The more diverse phylogeographic structure of *H. polygyrus* may be partially explained by its higher rate of molecular evolution of the cytochrome b gene, in comparison with *A. sylvaticus*. Therefore, *H. polygyrus* can be used as a biological magnifying glass as it highlights previously undetected historical events of its host. The results show how incorporating phylogeographic information of an obligate associate, i.e. a parasite, may help to better understand the phylogeographic pattern of its host.

(1) Michaux J.R., Magnanou E. Paradis, E., Nieberding, C. and Libois R.M. (2003) Mitochondrial phylogeography of the Woodmouse (*Apodemus sylvaticus*) in the Western Palearctic region. *Molecular Ecology* ;12(3):685-97.