Host-parasite associations: no simple answers in *Gallotia* lizards

Fátima Jorge [1*], Vicente Roca [2], Ana Perera [1] , D. James Harris [1,3], Miguel A. Carretero [1]

[1] CIBIO-UP, Centro de Investigação em Biodiversidade e Recursos Genéticos, Campus Agrario de Vairão, 4485-661 Vairão, Portugal
e-mail: fatima.esperanca@mail.icav.up.pt
[2] Dpto Zoología, Facultat de Ciències Biològiques, Universitat de Valencia, Dr. Moliner, 50, 46100
Burjassot, València, Spain
[3] Departamento de Zoologia e Antropologia, Faculdade de Ciências da Universidade do Porto, 4099-002 Porto, Portugal

Abstract: Parasites are still playing a small role in the analysis of evolutionary events of their hosts, even so there are already some examples where parasites have been successfully used as an additional marker, highlighting undetected phylogenetic patters within their hosts. However, parasite taxonomy still mostly relies on morphoanatomic characteristics and differences in life cycles to distinguish between different species, which can hide more complex phylogenetic relationships between similar parasites. Also, genetic analyses frequently reveal cryptic species. In this study, we analysed the phylogenetic variation within the nematode *Spauligodon atlanticus*, parasite of the Canarian lizards genus *Gallotia* inferring about its phylogeographic pattern. We also attempt to determine its relationships to other *Spauligodon* species parasitising others lacertids. We use the mitochondrial *Cytochrome oxidase subunit 1* to estimate the genetic variation within these nematodes. Even though *S. atlanticus* presents a direct life cycle, with its dispersion completely dependent on the host, and has been described as specific to *Gallotia*, results suggest that its phylogeography does not completely parallel that of the lacertid host. Namely, the shallow phylogeny of *S. atlanticus* mostly track the process of island colonization by the host. However, the apparent similarity of the deep phylogeny separating Eastern from Western lineages disappeared when others *Spauligodon* species are included in the analysis; the phylogeographic pattern becomes more complicated. Parasites, hence, may provide an additional element for inferring the phylogenetic and phylogeographic patterns of the hosts but can no longer be seen as mere spectators of their hosts' life.