

Abstract

Twisted-winged parasites (Strepsiptera: Xenidae) are an excellent group for studying the specialisation of parasites on hosts. Their parasitic lifestyle led to the evolution of numerous morphological, behavioural, physiological, and reproductive adaptations. Moreover, many complex adaptive traits of Strepsiptera have no parallel in other organisms. In contrast, little attention has been paid to the study of strepsipteran molecular phylogeny, phylogeography, species delimitation, and their implications for taxonomic classification.

Using the methods of molecular phylogeny, we created the first dated phylogenetic study of the family Xenidae. By investigating historical biogeography and ancestral host groups, we indicate that multiple lineages were exchanged between the New World and the Old World + Australia until Antarctica became completely frozen over. During the late Paleogene and Neogene periods, several lineages spread from the Afrotropics to other Old World regions and Australia. The original hosts of Xenidae were most likely social wasps, and the subsequent host switch from social to solitary wasps was secondary and probably occurred only once. The parallel host switch from solitary wasps to digger wasps (Sphecidae) occurred independently in the New and Old World. The biogeography and macroevolutionary history of Xenidae can be explained by a combination of dispersal, lineage extinction, and climatic changes during the Cenozoic era. A habitable Antarctica and the presence of now-submerged islands and plateaus that connected the New World and Old World + Australia facilitated the possibility of biotic exchange of Strepsiptera along with their hymenopteran hosts.

To analyse strepsipteran cryptic species diversity, we used three quantitative methods of species delimitation from molecular phylogenetic data – one distance-based (ABGD) and two tree-based (GMYC, bPTP). We found 77–96 putative species in our data and suggested the number of Xenidae species to be more diverse than expected. We identified 67 hosts to species level. Almost half of them were not previously known as hosts of Xenidae. The rate in net diversification is constant, which can be explained by the flexibility of this parasitic group, represented by their ability to colonise new host lineages combined with passive long-range dispersal by hosts.

Based on the results of molecular phylogenetic studies, we provide a taxonomic revision of Xenidae worldwide using morphological characters of female cephalothorax and male cephalotheca. We delimited 13 genera including 3 newly established. Furthermore, we devised a consistent approach of detailed species description, and we demonstrated it on the example of two new species of *Xenos* Rossi and one new species of *Paraxenos* Saunders.