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Contrasted genetic patterns in two egg-parasitoids associated with the complex species of the processionary moth *Thaumetopoea pityocampa/wilkinsoni* around the Mediterranean basin

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Abstract: The winter pine processionary moth is a major pest that causes heavy pine defoliation around the Mediterranean basin. It is also a major public health concern because the late instar larvae bear strongly urticating hairs and cause allergic reactions both for human beings and domestic animals. This well-known forest Lepidoptera has been proved to belong to a species complex, comprising *Thaumetopoea pityocampa* and *T. wilkinsoni* which are respectively distributed in the Western part of the Mediterranean Basin and in the Middle-East. Previous mitochondrial data showed that each species exhibited a strong geographical structure over most of its geographical range. A highly differentiated clade was further identified in Eastern North Africa. Due to the contemporary climate warming, this pest species is expanding northwards and towards higher elevations, and shows a reduced genetic diversity in the recently colonized habitats.

All over the Mediterranean Basin, the pine processionary moths are associated to a rich community of natural enemies that comprises both parasitoids and predators. Among these, egg parasitoids have been extensively studied because they can act as biocontrol agents against the eruptive dynamics of their host. Our goal was to study the patterns of genetic diversity of two species of egg parasitoids, the generalist species *Ooencyrtus pityocampae* (Hym., Chalcidoidea, Encyrtidae), and the specialist *Baryscapus servadeii* (Hym., Chalcidoidea, Eulophidae). Using mitochondrial markers, we analyzed the phylogeographic patterns of both parasitoids species in order to determine if their evolutionary histories were similar, and to compare the main genetic structures between the parasitoids and their hosts throughout the Mediterranean Basin. The results showed that genetic diversity was very high in the specialist parasitoid, and that differentiated clades occurred in (i) Crete, (ii) North Africa and parts of Corsica, and (iii) the rest of the range. In contrast, genetic diversity was limited in *Ooencyrtus pityocampae*, and no phylogeographical signal could be identified in this species, in which 64% of the studied individuals had the same haplotype. Still, both species showed clear geographic structures, that did not correspond to the main mitochondrial clades and sub-clades identified in the pine processionary moth. The distribution of genetic variation on both parasitoids could not be explained by a host-plant effect. We further discuss whether congruent patterns could be identified at regional scales between partners. Interestingly, both parasitoid species were proved to have a very reduced genetic diversity along the latitudinal expansion corridor of the pine processionary moth in France, which suggests that these natural enemies also recently expanded northwards.