

Status of the Genera *Aphomia* and *Lamoria* (Lepidoptera: Pyralidae)

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The boundaries between genera within the subfamily Galleriinae are often unclear, and the monophyly of some genera is not well supported. As a result, the assignment of some species to one of the genera is also uncertain and controversial. For example, the systematics of the taxa associated with the genus *Aphomia* is currently not satisfactorily resolved. Some authors recognise two separate genera, *Aphomia* and *Lamoria*, whilst others treat *Lamoria* as a synonym and include it in the genus *Aphomia*.

The phylogenetic distance analysis of the publicly available sequence fragments of the mitochondrial gene *Mt-COI* (this gene encodes subunit I of cytochrome c oxidase) provides a clear result in this case (Fig. 1). The analysis does not support the monophyly of the genus *Lamoria*. Moreover, if the species are divided into two genera, *Aphomia* (sensu stricto) and *Lamoria*, neither genus is monophyletic. I therefore place the species within a single genus, for which the older name, *Aphomia*, has nomenclatural priority, and regard *Lamoria* as a synonym of *Aphomia*.

Fig. 1 (on next page): Phylogenetic tree of the taxa *Aphomia* (sensu stricto) and *Lamoria*. The taxon names used in the figure follow the conventions of those authors who recognise both taxa as genera. The analysis is based on the available sequence fragments of the mitochondrial gene *Mt-COI*. The information content of the sequence fragment (usually less than 700 bp, known as a ‘DNA barcode’) is severely limited due to its short length. However, in closely related species (as in this case), a phylogenetic signal can often still be recovered. For the phylogenetic tree, the genetic distance between the sequence fragments was calculated (the scale indicates the extent of genetic change). Distance-based methods are only meaningful for DNA sequences that evolve according to the molecular clock, which applies to only a few genes, but is approximately the case for the *Mt-COI* gene. The distance calculations shown are based on a sequence alignment performed using Clustal Omega (Sievers & Higgins 2021; Madeira et al. 2024). The phylogenetic tree was rooted using the species *Galleria mellonella*. The letter-number combinations shown in the phylogenetic tree are the accession numbers of the respective sequences in GenBank (Sayers et al. 2022).

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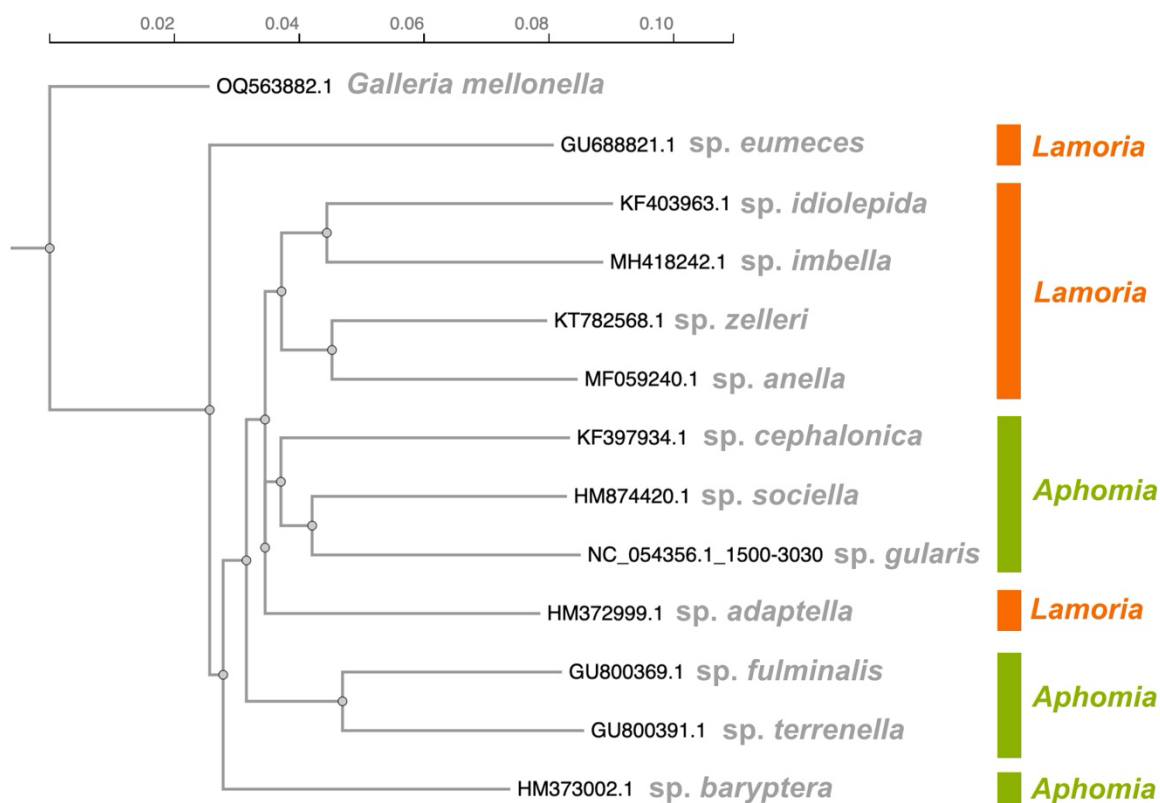


Fig. 1 (legend on previous page)

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