

Monophyly of the genera *Pyla* and *Delplanqueia* (Lepidoptera: Pyralidae)

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Pyla fusca is the only European species in an otherwise Nearctic genus. For this reason, it is sometimes placed in a separate genus, *Matilella*. However, the phylogenetic analysis of the available sequence fragments of the *Mt-CO1* gene (this gene codes for subunit I of the cytochrome c oxidase) provides no support for this notion (Fig. 1). In this analysis, sp. *fusca* is grouped amongst its American relatives; classifying it in a separate genus *Matilella* would render the "remaining" genus *Pyla* paraphyletic. I therefore follow here the notion that *Matilella* as a synonym of *Pyla*.

However, the separation of the genus *Delplanqueia* is well supported in the phylogenetic analysis of the available sequence fragments of the *Mt-CO1* gene. It forms a monophyletic group that is clearly distinct from the closely related genera *Pyla* and *Pempeliella*.

Fig. 1 (on next page): Phylogenetic tree of the selected taxa of the tribus Phycitini. The analysis is based on the available sequence fragments of the mitochondrial gene *Mt-CO1*. The information content of the sequence fragment (usually less than 700 bp, known as '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-CO1* 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 *Cryptoblabes bistriga*. The letter-number combinations shown in the phylogenetic tree are the accession numbers of the respective sequences in GenBank (Sayers et al. 2022) and the BOLDsystems database (Ratnasingham & Hebert 2007), respectively.

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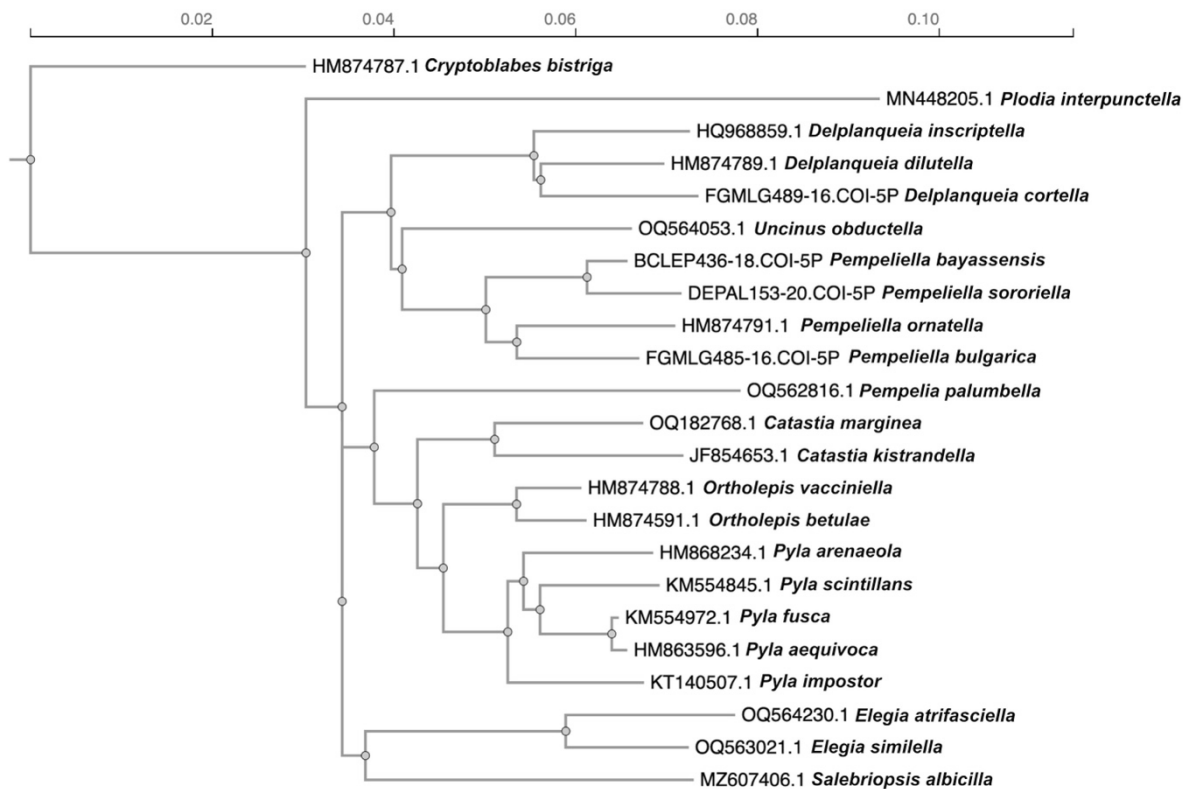


Fig. 1 (legend on previous page)

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