A new molecular phylogeny of Noctuoidea reveals robust family-level relationships

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Introduction

Owlet moths (Noctuoidea) include seven families and 42,000 described species[1]. The classification of the superfamily is still very unstable, mainly due to the lack of morphological apomorphies and analyses based solely on genetic data, resulting in different taxonomic hypotheses supported by multiple different authors[2,3].

Given the complexity of this mega-diverse superfamily, we undertook the first and most comprehensive phylogenomic analysis of the Noctuidae family (Noctuidae *sensu stricto* and Noctuidae *sensu lato*). Additionally, we performed one of the most rigorous morphological examinations in the past two decades to describe or redescribe these family-group clades and identify their apomorphies[4].
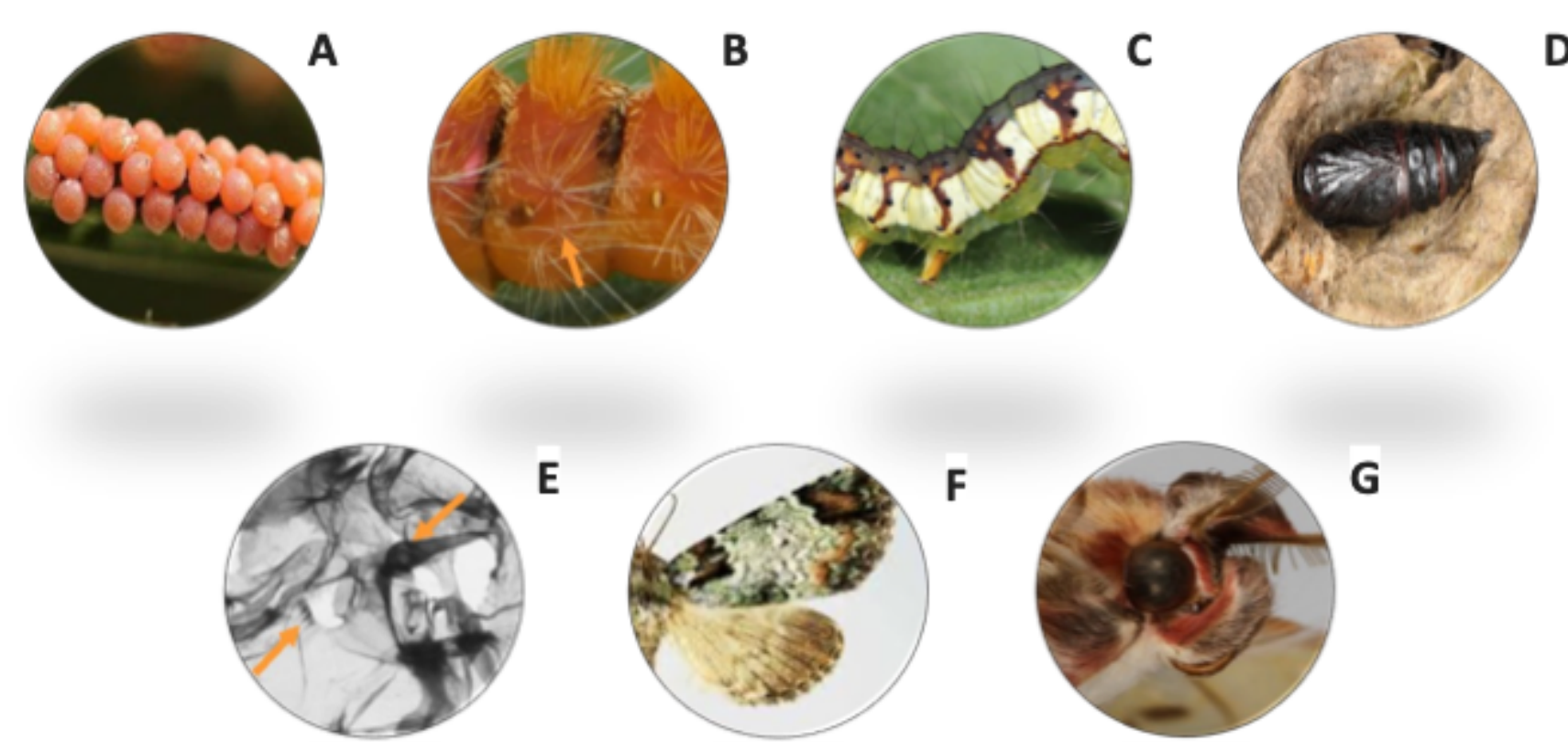

Figure 1 (A-G). Important morphological characters for classification. A. Eggs; B. Chaetotaxy; C. Legs; D. Pupa; E. Tympanal organs; F. Wing patterns; G. Palps.
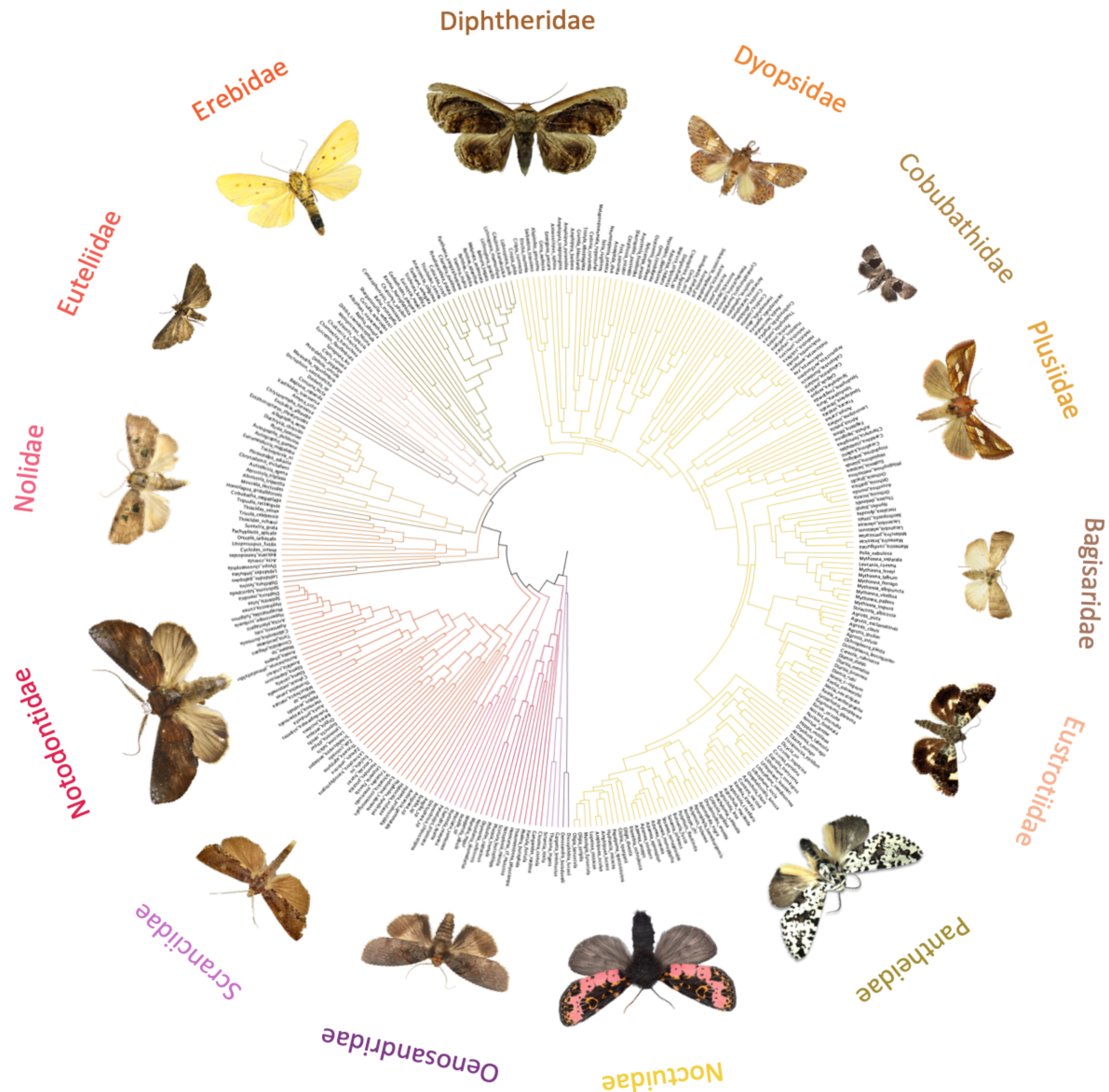

Figure 2 . Maximum likelihood tree constructed using 792 loci from 247 putative noctuid and 75 other noctuoid specimens. Node support values were calculated using the Shimodaira–Hasegawa-like approximate likelihood ratio test (SH-aLRT) and ultrafast bootstrap approximation (UFBoot).

Methods

In order to unravel the deep-level evolutionary relationships among Noctuidae clades, we employed two complementary approaches. First, we conducted an extensive phylogenetic analysis using multiple genomic datasets (including anchored hybrid enrichment, transcriptomes, and genomes) from 322 noctuoids (247 putative noctuids and 75 non-noctuids) and 27 outgroup taxa, utilizing our LEP1 probe kit5. Also, we examined morphological characters of 284 genera and 454 species.

We conducted the phylogenetic analyses using Maximum Likelihood with IQ-TREE2 and multi-species coalescent analyses through ASTRAL6,7. Additionally, we performed an Ancestral State Reconstruction using the R package Phytools8. Finally, we employed the TNT software for parsimony analyses9.

Results & Discussion

Utilizing both genomic and morphological data, we successfully differentiated Noctuidae sensu stricto from Noctuidae sensu lato. We recommend elevating seven subfamilies (Bagisaridae, Cobubathidae, Diphtheridae, Dyopsidae, Eustrotiidae, Pantheidae, and Plusiidae) to full family status. Furthermore, 40 putative apomorphic characters were identified.

This study serves more as a complement to previous works rather than a disagreement with them. While earlier studies on Noctuoidea systematics understandably simplified the classification, they also conflicted with evolutionary history research that lacked comparative morphological data[10,11]. Ultimately, the entire superfamily Noctuoidea requires further study, as this work only begins to uncover how this group evolved.

Acknowledgements

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