Appendix S2. Details on fossil calibrations.

Detailed information on the three fossil calibrations and justifications following best practices *sensu* Parham *et al.* (2012). For each fossil taxon, information on specimens, justifications on phylogenetic assignment, ages of geological formations and amber deposits are reported for the molecular dating analyses. CR = criterion for best practices *sensu* Parham *et al.* (2012), MRCA = most recent common ancestor, Myrs = million years. Detailed justifications for not using several potential fossil calibrations are also provided.

Fossil taxon #1: †Roesleriana exotica Martins-Neto & Vulcano, 1989

- Node calibrated: stem of Nemopteridae.
- Node A: MRCA of Nemopteridae + Ascalaphidae + Myrmeleontidae.
- **Reference specimen (CR #1)**: Its type specimen is GP/1T-1627, an exoskeleton, and it is a compression fossil. Its type locality is Crato (IGC-USP collection), which is in an Aptian lacustrine large carbonate in the Crato Formation of Brazil.
- Paleobiology Database link:

https://paleobiodb.org/classic/checkTaxonInfo?taxon_no=326045&is_real_user=1

- Phylogenetic placement (CR #2 and CR #3): Nemopteridae are distinctive in their spoon- or filament-shaped hindwings. The earliest fossils exhibiting this condition are †*Roesleriana exotica*, and †*Cratonemopteryx robusta* Martins-Neto, both recovered from the Crato Formation (Martins-Neto, 1992a, 1997) (late Aptian; Batten, 2007). †*Roesleriana exotica* belongs to the subfamily †Roeslerianinae Martins-Neto (Lu *et al.*, 2019), whereas the three species in our dataset belong to Crocinae Navás and Nemopterinae Burmeister. We used this fossil as a stem calibration for Nemopteridae in a conservative manner due to the uncertainty surrounding the placement of the †Roeslerianinae subfamily.
- Minimum age: 113 Myrs (Walker *et al.*, 2022).
- Locality, stratigraphic and age information (CR #4 and CR #5): This fossil was found in an Aptian lacustrine large carbonate in the Crato Formation of Brazil. The Aptian stage spans the time between 113 and 125 Ma (Walker *et al.*, 2022). Therefore, we used the youngest age estimated for this stage for this calibration (113 Myrs).

- **Previous use(s) as calibration and Discussion**: This fossil was used by Michel *et al.* (2017) and Winterton *et al.* (2018) as a crown calibration for Nemopteridae.
- Best practices score: 5/5.

Fossil taxon #2: †Pristinofossor rictus Badano & Engel, 2018

- Node calibrated: stem of Myrmeleontidae.
- Node B: MRCA of Ascalaphidae + Myrmeleontidae.
- **Reference specimen (CR #1)**: The holotype specimen AMNH JCZ-Bu304 is relatively well-preserved but mostly hidden by detritus and cracks (Badano *et al.*, 2018). Body proportion and chaetotaxy suggest that this specimen is a 2nd or 3rd larval instar. Its type locality is Burmese amber (Zigras coll), which is in Cenomanian terrestrial amber in Myanmar.
- Paleobiology Database link:

https://paleobiodb.org/classic/checkTaxonInfo?taxon_no=375312&is_real_user=1

- Phylogenetic placement (CR #2 and CR #3): It is firmly established that *†Pristinofossor rictus* belongs to the Myrmeleontidae family. *Pristinofossor* lacks strong digging setae on the ventral surface of sternite 9, unlike current antlions. With the exception of those belonging to the tribe Dendroleontini Banks, Pristinofossor also differs from the majority of existing antlions in that abdominal segment 9 is longer than wide and rastra is relatively unnoticeable. This ancient species may be distinguished from living members of the Dendroleontini by the morphology of its mandible, which has a median tooth that is longer than an apical tooth. However, the similarity to Dendroleontini may suggest a shared lifestyle, even though it is not a clear indication of such a relationship. Several genera of Dendroleontini (e.g., Dendroleon Brauer, Cymothales Gerstaecker, Tricholeon Esben-Petersen) are specialized inhabitants of cave-like microhabitats, including tree holes and rock overhangs. Pristinofossor was reconstructed as sister to all the remaining antlions in all analyses, thus representing the oldest undisputed larva of this group. The absence of specialized digging setae on the apical abdominal sternite shows that Pristinofossor actually descends from a myrmeleontid stem lineage even if its general shape is similar to that of modern antlions. Therefore we used this fossil as a stem calibration for Myrmeleontidae.
- Minimum age: 93.9 Myrs (Walker *et al.*, 2022).

- Locality, stratigraphic and age information (CR #4 and CR #5): The fossil was extracted from the amber deposits located in Kachin Province, northern Myanmar, ca. 100 km west of the town of Myitkyina which is dated in the Cenomanian. The Cenomanian age spans the time between 93.9 and 100.5 Ma (Walker *et al.*, 2022). Therefore, we used the youngest age estimated for this stage for this calibration (93.9 Myrs).
- **Previous use(s) as calibration and Discussion**: Up to our knowledge this fossil has never been used before in any dating analysis.
- Best practices score: 5/5.

Fossil taxon #3: †Porrerus dominicanus Poinar & Stange, 1996

- Node calibrated: crown of Myrmeleontini Latreille.
- Node C: MRCA of *Myrmeleon carolinus* Banks, 1943 + *Hagenomyia tristis* (Walker, 1853).
- **Reference specimen (CR #1)**: The holotype specimen (adult MACT-1220, Poinar and Stange, 1996) and other specimens (adults: MACT- 1170, MACT-1414, and MACT-3496; larva: MACT-1282; Engel & Grimaldi, 2007) were all found in the Miocene amber of the Dominican Republic, which is in a Burdigalian/Langhian terrestrial amber.
- Paleobiology Database link:

https://paleobiodb.org/classic/checkTaxonInfo?taxon_no=260460&is_real_user=1

• **Phylogenetic placement (CR #2 and CR #3)**: Based on a fossil adult, the extinct species †*Porrerus dominicanus* of the subfamily Myrmeleontinae Latreille was described (Poinar & Stange, 1996). Engel & Grimaldi (2007) further tentatively assigned a fossil larva from the same fossil formation to the same species. This fossil larva could be chosen for calibration because it is unmistakably a member of the tribe Myrmeleontini based on its combination of elongate mandibles, elongate mandibular setae, sessile mesothoracic spiracle, presence of submedian teeth on S8, and absence of bladelike digging setae on S9. Myrmeleontines' immatures, however, are generally uniform, and the characteristics that distinguish the genera are currently not well characterized, making it difficult to confidently assign them to an existing genus (Engel & Grimaldi, 2007). With specimens for five genera and 22 *Myrmeleon* species from different lineages, we used this fossil as a crown calibration for Myrmeleontini.

- Minimum age: 13.82 Myrs (Walker *et al.*, 2022).
- Locality, stratigraphic and age information (CR #4 and CR #5): This fossil was found in the Miocene amber of the Dominican Republic, which ranges from the Langhian to Burdigalian ages. The Langhain and Burdigalian ages span the time between 13.82 and 20.44 Ma (Walker *et al.*, 2022). Therefore, we used the youngest age estimated for this stage for this calibration (13.82 Myrs).
- **Previous use(s) as calibration and Discussion**: This fossil was used by Michel *et al.* (2017) as a crown calibration for Myrmeleontini.
- Best practices score: 5/5.

Other potential fossil calibrations

[*†Choromyrmeleon*]

As an alternative for a stem calibration for Myrmeleontidae, fossils belonging to the genus \dagger *Choromyrmeleon* were considered. The two known species of the genus \dagger *Choromyrmeleon*, namely \dagger *Choromyrmeleon othneius* Ren & Guo and \dagger *Choromyrmeleon aspoeckorum* Ren & Engel, were recovered from the Yixian Formation (Ren & Guo, 1996; Ren & Engel, 2008) in China, which is about 125 Myrs of age (Chang *et al.*, 2009). This genus was originally placed in the Myrmeleontinae by Ren & Guo (1996), but Ren & Engel (2008) later moved it to the Myrmeleontidae. A detailed reassessment of these fossils (see Michel *et al.*, 2017) raised a number of unresolved issues regarding the placement of \dagger *Choromyrmeleon* spp. as a potential stem Myrmeleontidae lineage. Therefore, the reliance on \dagger *Pristinofossor rictus* to provide a minimum age constraint for stem Myrmeleontidae was favoured.

[†*Araripeneura*]

 \dagger *Araripeneura* is in the same formation (Crato Formation) as \dagger *Roesleriana exotica* Martins-Neto & Vulcano, which we used to calibrate node A (as a stem Nemopteridae). The most comprehensive review of araripeneurids (Makarkin *et al.*, 2018) indicates that \dagger *Araripeneura* (and other true araripeneurids) are a stem nemopterid lineage, and so using them as a stem calibration of Nemopteridae (on node A) would be redundant to using \dagger *Roesleriana exotica* to calibrate the same node.

[*†Triassopsychops superbus*]

For the root we did consider using the oldest known fossil of Psychopsidae, *†Triassopsychops* superbus Tillyard from the Late Triassic Blackstone formation of Australia (Peng et al., 2011). This species and other Mesozoic Psychopsidae (e.g., see Lambkin et al., 2014) belong to a stem psychopsid lineage, with crown-group Psychopsidae appearing in the Cenozoic (Engel et al., 2018). However, its use as a constraint on the root is problematic because it biases age estimates. Indeed, and as pointed out by Chazot et al. (2019): ["deep calibrations still tend to underestimate the mean substitution rate, especially when substitution models are unable to correctly estimate the amount of "hidden" substitutions along the deeper branches. Such underestimation can lead to an overestimation of shallow node ages, and is referred to as "tree extension"]. In our study, it is even amplified because about half of our molecular dataset is made of mitochondrial gene fragments, and mitochondrial-based dated phylogenies are more sensitive to this bias (e.g., see Phillips, 2009). If we use *†Triassopsychops superbus* to set a minimum age for the root, this dramatically inflates the age of the myrmeleontid lineages and gives much older age estimates than the results of previous studies. For example, the age of the MRCA of [Myrmeleontidae + Ascalaphidae] goes up from ~117 Ma to ~168 Ma, to be compared with a median age of ~125 Ma in Michel et al. (2017) or of ~120 Ma in Winterton et al. (2018). For shallow nodes, the impact of this root calibration is even more pronounced, resulting in species pair ages that are likely really overestimated (sometime more than 15 Ma). In the end, we decided to not implement this root calibration to avoid significant overestimation biases.

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