1	FOSSIL CALIBRATIONS FOR THE ARTHROPOD TREE OF LIFE
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13	ABSTRACT
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15	Fossil age data and molecular sequences are increasingly combined to establish a timescale for the
16	Tree of Life. Arthropods, as the most species-rich and morphologically disparate animal phylum, have
17	received substantial attention, particularly with regard to questions such as the timing of habitat shifts
18	(e.g. terrestrialisation), genome evolution (e.g. gene family duplication and functional evolution),
19	origins of novel characters and behaviours (e.g. wings and flight, venom, silk), biogeography, rate of
20	diversification (e.g. Cambrian explosion, insect coevolution with angiosperms, evolution of crab body
21	plans), and the evolution of arthropod microbiomes. We present herein a series of rigorously vetted
22	calibration fossils for arthropod evolutionary history, taking into account recently published guidelines
23	for best practice in fossil calibration. These are restricted to Palaeozoic and Mesozoic fossils, no
24	deeper than ordinal taxonomic level, nonetheless resulting in 80 fossil calibrations for 102 clades. This
25	work is especially timely owing to the rapid growth of molecular sequence data and the fact that many
26	included fossils have been described within the last five years. This contribution provides a resource

- 27 for systematists and other biologists interested in deep-time questions in arthropod evolution.
- 28

# 29 **KEYWORDS**

- 30
- 31 Arthropods; Fossils; Phylogeny; Divergence times
- 32

# 33 ABBREVIATIONS

34

35 AMNH, American Museum of Natural History; AMS, Australian Museum, Sydney; AUGD, University of 36 Aberdeen; BGR, Bundesanstalt für Geowissenschaften und Rohstoffe, Berlin; BMNH, The Natural 37 History Museum, London; CNU, Key Laboratory of Insect Evolutionary & Environmental Change, 38 Capital Normal University, Beijing; DE, Ulster Museum, Belfast; ED, Ibaraki University, Mito, Japan; 39 FMNH, Field Museum of Natural History; GMCB, Geological Museum of China, Beijing; GSC, 40 Geological Survey of Canada; IRNSB, Institut Royal des Sciences Naturelles de Belgique, Brussels; 41 KSU, Kent State University; Ld, Musée Fleury, Lodève, France; LWL, Landschaftsverband Westfalen-42 Lippe-Museum für Naturkunde, Münster: MACN, Museo Argentino de Ciencias Naturales, Buenos 43 Aires; MBA, Museum für Naturkunde, Berlin; MCNA, Museo de Ciencias Naturales de Álava, Vitoria-44 Gasteiz, Alava, Spain; MCZ, Museum of Comparative Zoology, Harvard University; MGSB, Museo 45 Geologico del Seminario de Barcelona; MN, Museu Nacional, Rio de Janeiro; MNHN, Muséum 46 national d'Histoire naturelle, Paris; NHMUK, The Natural History Museum, London; NIGP, Nanjing 47 Institute of Geology and Palaeontology; NMS, National Museum of Scotland; OUM, Oxford University 48 Museum of Natural History; PBM, Palaöbotanik Münster; PIN, Paleontological Institute, Moscow; PRI, 49 Paleontological Research Institution, Ithaca; ROM, Royal Ontario Museum; SAM, South Australian 50 Museum, Adelaide; SM, Sedgwick Museum, University of Cambridge; SMNK, Staatliches Museum für 51 Naturkunde, Karlsruhe; SMNS, Staatliches Museum für Naturkunde, Stuttgart; TsGM, F.N. Chernyshev 52 Central Geologic Prospecting Research Museum, St. Petersburg; UB, University of Bonn; USNM, US

- 53 National Museum of Natural History, Smithsonian Institution; UWGM, University of Wisconsin Geology
- 54 Museum; YKLP, Yunnan Key Laboratory for Palaeobiology, Yunnan University; YPM, Yale Peabody
- 55 Museum; ZPAL, Institute of Paleobiology, Polish Academy of Sciences, Warsaw.

59 Accurate and precise systematic placement and dating of fossils underpins most efforts to infer 60 a chronology for the Tree of Life. Arthropods, as a whole or in part, have received considerable focus 61 owing to their incredible morphological disparity, species richness, and (relative to much of the Tree of 62 Life) excellent fossil record. A growing number of recent studies have constructed timetrees for 63 arthropods as a whole or for major groups therein (e.g. Bellec and Rabet, 2016; Bond et al., 2014; 64 Bracken-Grissom et al., 2014, 2013; Djernæs et al., 2015; Fernández et al., 2016, 2014; Fernández 65 and Giribet, 2015; Garrison et al., 2016; Garwood et al., 2014; Giribet and Edgecombe, 2013; Herrera 66 et al., 2015; Klopfstein et al., 2015; Legendre et al., 2015; Malm et al., 2013; McKenna et al., 2015; 67 Misof et al., 2014; Oakley et al., 2013; Rehm et al., 2011; Schwentner et al., 2013; Song et al., 2015; 68 Sun et al., 2015; Thomas et al., 2013; Tsang et al., 2014; Wahlberg et al., 2013; Wiegmann et al., 69 2011; Wood et al., 2013; Xu et al., 2015; Zhu et al., 2015). These studies vary in how well they have 70 adhered to best practices for selecting calibration fossils, as many previous calibrations assume that 71 fossil taxonomy accurately reflects phylogeny. Compounding the issue is the expansion of divergence 72 time studies for a variety of comparative questions far beyond systematics and biogeography, 73 including habitat shifts (Letsch et al., 2016; Lins et al., 2012; Rota-Stabelli et al., 2013a; Yang et al., 74 2013), genome evolution (Cao et al., 2013; Schwarz et al., 2014; Starrett et al., 2013; Wissler et al., 75 2013; Yuan et al., 2016), origins of novel characters and behaviours (Rainford et al., 2014; Sanggaard 76 et al., 2014; Wheat and Wahlberg, 2013), evolution of parasites and disease (Ibarra-Cerdeña et al., 77 2014; Palopoli et al., 2014; Rees et al., 2014; Zhou et al., 2014), rate of diversification and its 78 relationship to morphology and ecology (Lee et al., 2013; Wiens et al., 2015), coevolution (Kaltenpoth 79 et al., 2014; Shelomi et al., 2016; Wilson et al., 2013), conservation (Owen et al., 2015), and the use 80 of arthropods as a model for methodological development (O'Reilly et al., 2015; Ronquist et al., 2012; 81 Warnock et al., 2012; Zhang et al., 2016).

82

Recent consensus on best practices for selecting calibration fossils comes with several

83 requirements. There must be references to specific fossil specimen(s), phylogenetic or morphological 84 evidence justifying placement of the fossil, and stratigraphic and/or radiometric dating information for 85 the fossil (Parham et al., 2012). The importance of accurate phylogenetic knowledge of calibration 86 fossils is underscored by recent controversies in dating the evolution of insects, where arguments 87 hinge on the classification of particular 'roachoid' fossils on the stem lineage of Dictyoptera, with 88 resulting differences on the order of 100 Myr (Kjer et al., 2015; Tong et al., 2015). With the explosion of 89 taxonomic sampling in molecular phylogenies due to improvements in sequencing technology, 90 improving the coverage of fossil calibrations is equally important. Recommendations include, for 91 example, including as many as one fossil per ten extant taxa for precise ages, with a varied 92 distribution across lineages and clade depth (Bracken-Grissom et al., 2014). As a response, we have 93 compiled an atlas of 80 rigorously scrutinized calibration fossils for 102 key nodes in arthropod 94 phylogeny. These represent four basal ecdysozoan and arthropod clades, 17 chelicerates, 12 95 myriapods, 30 non-hexapod pancrustaceans, and 39 hexapod clades.

96 Where possible, we favour clade topologies resulting from a phylogenetic analysis of the 97 largest total dataset. If phylogenomic analysis of genomes or transcriptomes has been performed but 98 conflicts with morphology, a strongly supported molecular result is presented (e.g. putative clades 99 such as Oligostraca that do not yet have identified morphological autapomorphies). If, however, 100 molecular phylogenies have been constructed with few genes (e.g. clades such as Peracarida) or with 101 highly conflicting results (e.g. Arachnida), morphological results are given greater weight. Where 102 relevant, we discuss clade names with respect to NCBI's GenBank taxonomy (as recommended by 103 the Fossil Calibrations Database: Polly et al., 2015), as this review is intended to be used by molecular 104 biologists who are interested in dating the evolution of arthropod groups.

As there are >1.2 million species of arthropods, our calibrations are limited to fossils from the Palaeozoic and Mesozoic. Many extant clades have their oldest fossils in Cenozoic ambers such as the Eocene Baltic amber but are predicted to be vastly older based on fossils of allied taxa (e.g. Symphyla and Pauropoda relative to Chilopoda and Diplopoda).

109 While acknowledging the complexity of estimating an age prior for a fossil species known from 110 multiple deposits, we use the oldest (e.g. section 28.3) and/or best known (e.g. section 51.3) horizons 111 to provide minimum age constraints with the narrowest and most accurate age interval. Where there is 112 substantial variation in age estimates for a fossil species, this issue is noted in the text. To 113 accommodate the possibility of older fossils not yet discovered, we provide generous soft maxima (Ho 114 and Phillips, 2009). Accordingly, when conducting divergence time analyses, prior distributions 115 accounting for the large probability tail (e.g. gamma or lognormal) of an older undiscovered fossil may 116 be appropriate. All fossil calibrations described herein are listed with their age information in Table A.1. 117 formatted for adding age constraints in BEAST or PhyloBayes. 118 119 2. Crown Ecdysozoa 120 121 This clade comprises Euarthropoda, Onychophora (velvet worms), Tardigrada (water bears), 122 Nematoida (itself comprising Nematoda and Nematomorpha), and Scalidophora (itself comprising Kinorhyncha, Loricifera, and Priapulida), their last common ancestor and all of its descendants (Fig. 123 124 1). Monophyly has been demonstrated on the basis of coding and non-coding molecular data 125 (Campbell et al., 2011).

- 126
- 127 2.1. Fossil specimens
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*Rusophycus* trace fossils in Member 2 of the Chapel Island Formation of the southwestern
Burin Peninsula of southeastern Newfoundland, defining the base of the *R. avalonensis* Biozone.
Arbitrarily, we fix this calibration on a specimen (**Fig. 2a**) from this unit figured by Narbonne et al.
(1987: Fig. 6I; GSC 85983), as in Benton et al. (2015).

133

134 2.2. Phylogenetic justification

*Rusophycus* trace fossils are widely accepted to have been produced by arthropod-grade
 organisms, showing bilateral symmetry and evidence of segmented limbs used in their construction,
 the latter an apomorphy of Euarthropoda (Budd and Jensen, 2000).

139

140 2.3. Age justification

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142 Rusophycus occurs well below the first animal body fossils in Cambrian sections around the 143 world (Crimes, 1987; Crimes and Jiang, 1986; Goldring and Jensen, 1996; MacNaughton and 144 Narbonne, 1999; Weber and Zhu, 2003). In many of these regions, records of Rusophycus begin with 145 proximity to the base of the Cambrian. However, their ages are only well constrained in sections in 146 Newfoundland, Canada, and Yunnan, China. Of these, records of Rusophycus begin low in Member 2 147 of the Chapel Island Formation of the southwestern Burin Peninsula of southeastern Newfoundland, 148 defining the base of the *R. avalonensis* Biozone (Narbonne et al., 1987). The Biozone is itself dated 149 through correlations to a section in New Brunswick where the younger ash bed has been dated by U-150 Pb series to 530.02 Ma ± 1.2 Myr (Isachsen et al., 1994; Peng et al., 2012), thus providing for a minimum constraint of 528.82 Ma. 151

A soft maximum constraint is based on that used by Benton et al. (2015), the maximum age interpretation of the Lantian Biota (Yuan et al., 2011). This, together with the Doushantuo Biota (Yuan et al., 2002), provides a series of Konservat-Lagerstätten preserving the biota in Orsten- and Burgess Shale-like modes of fossilization. None of these Lagerstätten, least of all the Lantian, preserves anything that could possibly be interpreted as even a total group eumetazoan and on this basis we define our soft maximum constraint at 635.5 Ma  $\pm$  0.6 Myr (Condon et al., 2005) and, thus, 636.1 Ma.

159 **3. Crown Arthropoda** 

160

161	This clade comprises Euarthropoda and Onychophora (sensu Ortega-Hernández, 2016), their
162	last common ancestor and all of its descendants (Fig. 1). This clade has traditionally been called
163	Panarthropoda (Nielsen, 1995), however, this latter name is most often used to refer to a group
164	encompassing Arthropoda and Tardigrada, but we exclude tardigrades from our current grouping.
165	Monophyly of this clade has been established through phylogenetic analysis of both non-coding and
166	protein-coding gene datasets (Campbell et al., 2011), and morphological data sets (Legg et al., 2013),
167	although it has been challenged by other recent morphological analyses that endorsed a rival sister
168	group relationship between Euarthropoda and Tardigrada (e.g. Smith and Ortega-Hernández, 2014).
169	Note the name Arthropoda in GenBank refers to what we consider Euarthropoda; there is no GenBank
170	taxonomy ID for the clade comprising Euarthropoda and Onychophora.
171	
172	3.1. Fossil specimens
173	
174	As for 2.1.
175	
176	3.2. Phylogenetic justification
177	
178	As for 2.2.
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180	3.3. Age justification
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182	As for 2.3.
183	
184	4. Crown Euarthropoda
185	
186	This clade comprises Chelicerata, Myriapoda and Pancrustacea, their last common ancestor

187	and all of its descendants (Fig. 1). The monophyly of Euarthropoda, comprising the sister clades
188	Chelicerata and Mandibulata (itself comprising Myriapoda and Pancrustacea) has been established on
189	the basis of protein-coding and noncoding molecular data, as well as morphological data (Rota-Stabelli
190	et al., 2011). Note that in Benton et al. (2015) this node was named Arthropoda (likely with reference
191	to GenBank taxonomy). Here we follow the naming conventions outlined by Ortega-Hernández (2016).
192	
193	4.1. Fossil specimens
194	
195	Yicaris dianensis Zhang et al., 2007. YKLP 10840, holotype (Fig. 2b,c), consisting of an almost
196	complete articulated specimen (Zhang et al., 2007).
197	
198	4.2. Phylogenetic justification
199	
200	Several phylogenetic analyses of morphology (Edgecombe, 2010; Legg et al., 2013; Wolfe and
201	Hegna, 2014) and morphology plus molecules (Oakley et al., 2013) place Y. dianensis within the
202	crown group of Pancrustacea. Key characters include the presence of epipodites on the thoracic
203	limbs; paddle-shaped mandibular and maxillary exopods; and the protopodite of post-mandibular limbs
204	elongated as soft, setiferous endites. Any position supported within the crown group of Pancrustacea
205	is within crown Euarthropoda.
206	
207	4.3. Age justification
208	
209	Y. dianensis was recovered from the Yu'anshan Formation at Xiaotan section, Yongshan,
210	Yunnan Province, attributed to the Eoredlichia-Wutingaspis Biozone (Zhang et al., 2007). Chinese
211	Cambrian stratigraphy has been revised substantially and the Eoredlichia – Wutingaspis Biozone is no
212	longer recognized (Peng, 2009, 2003). However, Eoredlichia is known to co-occur with Hupeidiscus,

213	which is diagnostic of the Hupeidiscus-Sinodiscus Biozone, which is formally recognised as the
214	second biozone of the Nangaoan Stage of the Qiandongian Series of the Cambrian of China (Peng
215	and Babcock, 2008). The Nangaoan is the proposed third stage of the Cambrian System for the
216	International Geologic Timescale (Peng et al., 2012). Thus, a minimum constraint can be established
217	on the age of the top of the Nangaoan, which has been dated to 514 Ma (Peng et al., 2012; Peng and
218	Babcock, 2008).
219	Soft maximum as for 2.3.
220	
221	4.4. Discussion
222	
223	There are older records of euarthropods than Y. dianensis, notably trilobites, but their
224	phylogenetic position within Arthropoda is contested (it is unclear whether trilobites are stem-
225	Euarthropoda, stem-Chelicerata or stem-Mandibulata). Wujicaris muelleri Zhang et al., 2010 has an
226	equal claim to being the earliest record of Arthropoda, but it is of equal age to the holotype of Y.
227	dianensis.
228	
229	5. Crown Chelicerata
230	
231	This clade comprises Pantopoda (sea spiders) and Euchelicerata, their last common ancestor
232	and all of its descendants (Figs. 1, 3 and 4). Monophyly of this clade has been established by
233	phylogenetic analysis of nuclear protein-coding genes (Regier et al., 2010), transcriptomes
234	(Meusemann et al., 2010; Rota-Stabelli et al., 2011), and morphology (Legg et al., 2013).
235	
236	5.1. Fossil specimens
237	
238	Wisangocaris barbarahardyae Jago, García-Bellido and Gehling, 2016. SAM P45427,
	10

239 holotype, almost complete specimen (**Fig. 2d**).

240

241 5.2. Phylogenetic justification

242

243 Few recent phylogenetic studies have addressed the stem-lineage of Euchelicerata (notable 244 exceptions being Lamsdell, 2013; Legg, 2014; Legg et al., 2013). Including W. barbarahardyae in the 245 dataset of Legg (2014), this species was resolved in most shortest cladograms as sister taxon to the 246 middle Cambrian Sanctacaris and Sidnevia, and in all shortest cladograms as more closely related to 247 Euchelicerata than Pantopoda, i.e. as crown group Chelicerata (Jago et al., 2016). This relationship is 248 supported by the shared presence of pediform cephalic exites, multi-partite trunk exites, and a trunk 249 composed of a posterior limb-less abdomen in both crown euchelicerates and the Cambrian taxa. 250 251 5.3. Age justification 252 253 W. barbarhardyae was collected from the Emu Bay Shale on Kangaroo Island, South Australia. 254 Trilobite biostratigraphy correlates this unit with the upper part of the *Pararaia janeae* Zone in 255 mainland South Australia (Jell in Bengtson et al., 1990; Fig. 2 in Jago et al., 2012), equivalent to the 256 Canglangpuan Stage in South China and the late Botoman in Siberia (Gehling et al., 2011, Fig. 9). This dates the Emu Bay Shale to Cambrian Series 2, Stage 4, providing a minimum constraint of 509 257 258 Ma. 259 Soft maximum as for 2.3. 260 261 5.4. Discussion 262 263 264 Until recently the oldest evidence of chelicerates in the fossil record were thought to be

265 represented by Chasmataspis-like trace fossils from the Furongian of Texas (Dunlop et al., 2004), and 266 a putative pycnogonid larva from the Furongian of Sweden (Waloszek and Dunlop, 2002). However, in a number of recent phylogenetic analyses (e.g. Legg, 2014; Legg et al., 2013), a number of taxa from 267 268 the middle Cambrian Burgess Shale Formation, namely Sanctacaris uncata Briggs and Collins, 1988. 269 Sarotrocercus oblita Whittington, 1981, and Sidneyia inexpectans Walcott, 1911, have been resolved 270 as stem-lineage representatives of Euchelicerata. These relationships are preserved with the addition 271 of the older W. barbarahardyae to the dataset (Jago et al., 2016). Although another purported species 272 of Sidneyia (S. sinica Zhang et al., 2002) is known from the older Chengijang biota, it lacks many 273 diagnostic features of this genus, and could therefore not be reliably used for calibration purposes. It 274 should also be noted that Sidneyia only resolved as a stem representative of Euchelicerata under 275 some iterations of the analysed data set of Legg (2014), specifically only when all characters were 276 weighted equally, and therefore its exact phylogenetic position is equivocal.

277

## 278 **6. Crown Pantopoda**

279

This clade comprises Ammotheidae, Austrodecidae, Callipallenidae, Colossendeidae, Endeididae, Nymphonidae, Pallenopsidae, Phoxichilidiidae, Pycnogonidae and Rhynchothoracidae, their last common ancestor and all of its descendants (**Fig. 3**). Phylogenetic analyses of proteincoding genes (Arabi et al., 2010) or protein-coding genes combined with morphology (Arango and Wheeler, 2007) indicate monophyly.

285

286 6.1. Fossil specimens

287

Haliestes dasos Siveter et al., 2004. OUM C.29571, holotype (Fig. 5a). As the reconstruction of
Herefordshire fossils requires serial grinding and photography of 20 µm sections (Sutton et al., 2002),
the holotype figured in Siveter et al. (2004) and herein was thus destroyed in preparation.

Morphological data for Herefordshire fossils are published as 3D models of the thin sectionphotographs.

293

294 6.2. Phylogenetic justification

295

296 Arango and Wheeler (2007) resolved H. dasos as sister to part of Ammotheidae (nested within 297 clade of Ammotheidae, Callipallenidae, Nymphonidae, Pallenopsidae, Phoxichilidiidae, 298 Rhynchothoracidae), i.e. as crown-group Pantopoda. *H. dasos* was classified separately from extant 299 pycnogonids (Pantopoda) as an Order Nectopantopoda by Bamber (2007), although without explicit 300 phylogenetic justification. It should be noted that H. dasos was included in the phylogenetic analysis of 301 Legg et al. (2013), and resolved as sister-taxon to Palaeopantopus, which in turn resolved as sister-302 taxon to extant pycnogonids, however, just three extant exemplars were included in this study and as 303 this was not extensive enough to determine the exact position of these fossil taxa with respect to 304 crown-group exemplars, we continue to follow Arango and Wheeler (2007) in their placement. 305 306 6.3. Age justification 307 308 This fossil is preserved as a carbonate concretion from the volcaniclastic Herefordshire 309 Lagerstätte of Herefordshire, England, at the Sheinwoodian-Homerian stage boundary, within the 310 Early Silurian Wenlock Series (Siveter, 2008). As the Homerian begins at 430.5 Ma  $\pm$  0.7 Myr, a 311 minimum age constraint for the Herefordshire can thus be placed at 429.8 Ma. 312 Soft maximum as for 2.3. 313 314 6.4. Discussion 315 316 Although *H. dasos* is the oldest assignable crown group pycnogonid, there is an older fossil,

317	Cambropycnogon klausmuelleri Waloszek and Dunlop, 2002, from the Cambrian Orsten biota
318	(minimally 497 Ma). C. klausmuelleri, however, is known only from larval stages, and does not share
319	specific apomorphies with any extant larva. Without such characters, it is not possible to adequately
320	confirm crown group affinity. Another fossil species, Palaeomarachne granulata Rudkin et al., 2013
321	from the Late Ordovician of Manitoba, is specifically noted as a stem pantopod due to its likely
322	plesiomorphic head tagmosis.
323	
324	7. Crown Euchelicerata
325	
326	This clade comprises Xiphosurida (horseshoe crabs) and Arachnida, their last common
327	ancestor and all of its descendants (Fig. 3). Monophyly is established on the basis of phylogenetic
328	analysis of transcriptomes (Rota-Stabelli et al., 2011; Sharma et al., 2014) and morphology (Legg et
329	al., 2013). Note that monophyly of Euchelicerata is challenged by a recent morphological phylogeny, a
330	result attributed to outgroup sampling (Garwood and Dunlop, 2014). Euchelicerata is not recognized in
331	GenBank taxonomy.
332	
333	7.1. Fossil specimens
334	
335	Chasmataspis-like resting trace fossils (MBA 1084), Fig 5b. Described and illustrated in
336	Dunlop et al. (2004, Figs. 9 and 10).
337	
338	7.2. Phylogenetic justification
339	
340	The assignment of the traces to Chasmataspida is based on impressions of plate-like
341	opisthosomal opercula, one of the characters used to define Euchelicerata (Dunlop et al., 2004)
342	Furthermore, recent phylogenetic analyses of morphology place chasmataspid body fossil species
	14

within Euchelicerata, as sister group to eurypterids (Garwood and Dunlop, 2014; Legg et al., 2013) or
sister group to a clade composed of eurypterids and arachnids (Lamsdell, 2013; Lamsdell et al., 2015;
Selden et al., 2015).

**7.3.** Age justification

349	The Chasmataspis-like resting traces were found in the Cambrian Hickory Sandstone Member
350	of the Riley Formation, Texas (Dunlop et al., 2004). The top of the Hickory Sandstone preserves
351	trilobite representatives of the Bolaspidella Zone and the Cedarina Zone (Miller et al., 2012; Palmer,
352	1954). These trilobite biozones are assigned to the lowermost Marjumiid Biomere in the Marjuman
353	Stage of the Lincolnian Series (Miller et al., 2012). The early Marjuman itself is correlated to the
354	Drumian Stage of Cambrian Series 3 (Taylor et al., 2012). The end of the Drumian is dated to 500.5
355	Ma, providing a minimum age for Chasmataspis-like trace fossils.
356	Soft maximum as for 2.3.
357	
358	8. Crown Xiphosurida
359	
360	This clade comprises four extant species, all members of the family Limulidae: Carcinoscorpius
361	rotundicauda, Limulus polyphemus, Tachypleus gigas and Tachypleus tridentatus, their last common
362	ancestor and all of its descendants (Fig. 3). Monophyly is established by phylogenetic analyses of
363	housekeeping genes (Obst et al., 2012) and morphology (Lamsdell and McKenzie, 2015).
364	
365	8.1. Fossil specimens
366	
367	Tachypleus gadeai Vía Boada and de Villalta, 1966. MGSB 19195, holotype.
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- 369 8.2. Phylogenetic justification
- 370

371 *Heterolimulus gadeai* Vía Boada and de Villalta, 1966 was reassigned to the extant genus 372 *Tachypleus* by Diedrich (2011), who cited the presence of lateral immobile opisthosomal spines as 373 evidence. This was validated by the phylogenetic analysis of Lamsdell and McKenzie (2015), who 374 resolved *T. gadeai* as sister-taxon to a clade composed of all other members of *Tachypleus*. This more 375 inclusive clade in turn resolved as sister-taxon to the extant genus *Carcinoscorpius*.

376

377 8.3. Age justification

378

379 T. gadeai was discovered in the Alcover unit of the Montral site, Tarragona province, Catalonia, 380 Spain (Vía Boada and de Villalta, 1966). Based on sequence stratigraphy, the Alcover dolomite unit is 381 dated to the late Muschelkalk, a European regional stage of the Triassic (Calvet and Tucker, 1995; Vía 382 Boada and de Villalta, 1966). The middle and late Muschelkalk correspond to the global Ladinian 383 stage (Calvet and Tucker, 1995). The upper boundary of the Ladinian is  $237.0 \text{ Ma} \pm 1 \text{ Myr}$  (Ogg, 384 2012), thus, a minimum age of 236.0 Ma. 385 Soft maximum as for 2.3. 386 387 8.4. Discussion

388

We note that morphological phylogenetic analysis has suggested paraphyly of Xiphosura (crown Xiphosurida plus several fossil genera), and resolved synziphosurines as basal euchelicerates (Lamsdell, 2013). A subsequent morphological phylogeny resolved synziphosurines as polyphyletic (Garwood and Dunlop, 2014). Some other morphological phylogenies resolve the traditional

393 monophyletic Xiphosura (Briggs et al., 2012; Legg et al., 2013).

394 Crown xiphosurid affinities of older fossils cannot be confirmed. For example, an undescribed

Early Ordovician fossil from Morocco (Van Roy et al., 2010) exhibits fused opisthosomal tergites, a synapomorphy of Xiphosurida *sensu* Lamsdell (2013), but its position with respect to the crown has not been tested in a phylogeny. The Late Ordovician *Lunataspis aurora* Rudkin et al., 2008 and the Pennsylvanian genus *Euproops* are resolved on the stem group of Xiphosurida in a morphological phylogeny (Lamsdell, 2013).

400 Morphological conservatism in the evolution of Xiphosura (as illustrated by a Jurassic member 401 assigned to a living genus) has led to use of the misnomer 'living fossil' for the clade, despite 402 continued molecular evolution throughout its history (Avise et al., 1994; Obst et al., 2012). The more 403 appropriate term of 'stabilomorph' was proposed with the discovery of Limulus darwini (Kin and 404 Blażejowski, 2014); it refers to morphological stability over evolutionary history, at the genus level. 405 However, long branches unbroken by unsampled extinct species may have significantly 406 underestimated divergence times among crown Xiphosurida (Lamsdell and McKenzie, 2015), though 407 this assertion has not yet been tested with a divergence time analysis.

408

#### 409 **9. Crown Arachnida**

410

411 This clade comprises Acariformes (acariform mites), Opiliones (harvestmen), Palpigradi 412 (microwhip scorpions), Parasitiformes (parasitiform mites, ticks), Pseudoscorpiones, Ricinulei (hooded 413 tickspiders), Schizomida, Scorpiones, Solifugae (camel spiders), and Tetrapulmonata, their last 414 common ancestor and all of its descendants (Fig. 4). Monophyly is established on the basis of 415 phylogenetic analysis of transcriptomes (Rota-Stabelli et al., 2013a), nuclear protein-coding genes 416 (Regier et al., 2010), strong support from morphology (Garwood and Dunlop, 2014; Legg et al., 2013; 417 Rota-Stabelli et al., 2011; Shultz, 2007), and combined morphological and molecular data (Giribet et 418 al., 2002; Lee et al., 2013). Some recent phylogenetic analyses of transcriptomes have failed to 419 resolve a monophyletic Arachnida; instead Xiphosurida is variably placed within the traditional 420 arachnids (Sharma et al., 2014; von Reumont et al., 2012).

# 422 9.1. Fossil specimens

423

424 Palaeophonus loudonensis Laurie, 1899. NMS 1897.122.196 (holotype), a dorsally preserved
425 specimen lacking walking legs and telson (Fig. 5h). For additional anatomical detail, we refer to
426 Eramoscorpius brucensis Waddington et al., 2015. ROM 53247, holotype (Fig. 5g).

427

# 428 9.2. Phylogenetic justification

429

430 The genus Dolichophonus Petrunkevitch, 1949, was erected for P. loudonensis, based on the 431 increased length of the prosoma compared to other palaeophonids, namely *P. nuncius* Thorell and 432 Lindström, 1885, and P. caledonicus Hunter, 1886. An examination (by D.A.L.) of the single known 433 specimen of *P. loudonensis* could not confirm this character because the specimen is very poorly 434 preserved, and the junction between the prosoma and mesosoma is not easily distinguished. We 435 retain the holotype within Palaeophonus. It is even possible that this specimen may belong to one of 436 the other currently recognised species of *Palaeophonus*, although more material would be required. P. 437 loudonensis was included in a phylogenetic analysis by Legg et al. (2013), in which it resolved 438 amongst total-group Scorpiones. Other Siluro-Devonian fossil scorpions such as Proscorpius osborni 439 Whitfield, 1885 and Palaeoscorpius devonicus Lehmann, 1944 have been placed in the stem group of 440 Orthosterni (crown-group Scorpiones) (e.g. Legg et al., 2013; Garwood and Dunlop, 2014), which are 441 therefore crown group members of Arachnida.

442

443 9.3. Age justification

444

*P. loudonenesis* was recovered from the Gutterford Burn section of the "Eurypterid Bed"
(Reservoir Formation) in the Pentland Hills, Midlothian, Scotland (Kjellesvig-Waering, 1986), which

447	has been dated as Late Llandovery. The associated graptolite fauna suggests a late Llandovery
448	(Telychian) age for this formation, within the Oktavites spiralis Biozone (Bull and Loydell, 1995). A
449	spline-fit age for the upper boundary of the O. spiralis Biozone provides a minimum age constraint of
450	435.15 Ma (Melchin et al., 2012).
451	Soft maximum as for 2.3.
452	
453	10. Crown Opiliones
454	
455	This clade comprises Cyphophthalmi and Phalangida (itself comprising Laniatores, Dyspnoi
456	and Eupnoi), their last common ancestor and all of its descendants (Fig. 4). Monophyly has been
457	demonstrated by phylogenetic analysis of transcriptomes (Sharma et al., 2014), morphology (Garwood
458	et al., 2011), and combined morphology and molecules (Garwood et al., 2014; Giribet et al., 2002).
459	
460	10.1. Fossil specimens
461	
462	Eophalangium sheari Dunlop et al., 2003. PBM slide no. 3503, holotype (Fig. 5d), consisting of
463	a lateral thin section outlining nearly the entire female body (Dunlop et al., 2003).
464	
465	10.2. Phylogenetic justification
466	
467	In a phylogenetic analysis of morphology, E. sheari was placed in a polytomy with members of
468	Phalangida, to the exclusion of Cyphophthalmi (Garwood and Dunlop, 2014). In combined analysis of
469	molecules and morphology, E. sheari was resolved as a stem group Cyphophthalmi (Garwood et al.,
470	2014). Both positions, however, fall within the crown group of Opiliones.
471	
472	10.3. Age justification

474 This fossil is known from the Early Devonian (Pragian) Rhynie Chert of Aberdeenshire, 475 Scotland. Spore assemblages of the Windyfield and stratigraphically underlying Rhynie Chert are 476 dated to the early but not earliest Pragian to early (earliest?) Emsian (polygonalis-emsiensis Spore 477 Assemblage Biozone) (Parry et al., 2011). Radiometric dating of the underlying Milton of Noth 478 Andesite at ca. 411 Ma (Parry et al., 2013, 2011) has been subject to a dispute over its temporal 479 relationship to hot spring activity associated with the cherts (Mark et al., 2013, 2011) and predates the 480 biostratigraphic dating of the Rhynie Chert relative to the global dating of the base of the Pragian 481 Stage. Therefore, a minimum age constraint may be defined at 405.0 Ma for the Rhynie Chert, using 482 the Pragian-Emsian boundary (407.6 Ma  $\pm$  2.6 Myr) as a reference. 483 A soft maximum constraint comes from the oldest chelicerate W. barbarbardyae from the Emu

Bay Shale on Kangaroo Island, South Australia, which has been correlated based on trilobite
biostratigraphy to the upper part of the *Pararaia janeae* Zone in mainland South Australia (Jell in
Bengtson et al., 1990; Fig. 2 in Jago et al., 2012). As this is equivalent to the Canglangpuan Stage in
South China and the late Botoman in Siberia (Gehling et al., 2011, Fig. 9), the Emu Bay Shale can be
dated to Cambrian Series 2, Stage 4, providing a maximum age of ~514 Ma.

489

#### 490 **11. Crown Acariformes**

491

This clade comprises Sarcoptiformes, Trombidiformes and 'Endeostigmata', their last common ancestor and all of its descendants (**Fig. 4**). Monophyly is established by phylogenetic analysis of nuclear ribosomal genes (Pepato and Klimov, 2015), morphology (Garwood and Dunlop, 2014), and combined molecular and morphological data (Pepato et al., 2010).

496

497 11.1. Fossil specimens

498

20

499	Protacarus crani Hirst, 1923. BMNH In. 24665, holotype, preserving a nearly complete
500	individual in chert ( <b>Fig. 5k</b> ).
501	
502	11.2. Phylogenetic justification
503	
504	Originally described as a single species (Hirst, 1923), P. crani from the Rhynie Chert was
505	subsequently treated as five species belonging to five different genera (Dubinin, 1962). P. crani itself,
506	as exemplified by the holotype, was described as a member of Eupodidae, within Trombidiformes
507	(Hirst, 1923), or potentially more basal within the Acariformes (Bernini, 1986). While the specifics of its
508	classification may be debatable due to the lack of preserved diagnostic characters, the fan-like setae
509	observed dorsally in P. crani support a relationship with endeostigmatids within crown group
510	Acariformes (Bernini, 1986; Dunlop and Selden, 2009).
511	
512	11.3. Age justification
513	
514	As for 10.3.
515	
516	11.4. Discussion
517	
518	Bernini et al. (2002) figured a putative oribatid mite from terrestrial sediments dated to the Early
519	Ordovician of Sweden. However, its age and systematic placement were queried by Dunlop (2010, p.
520	134) and this species is not used for calibration herein.
521	Arguments that P. crani is a Recent contaminant (Crowson, 1985) have been countered by
522	Kühne and Schlüter (1985) and Greenslade (1988). Other species of fossil Acariformes have also
523	been described from the Rhynie Chert (all originally P. crani), including Protospeleorchestes
524	pseudoprotacarus, Pseudoprotacarus scoticus, Palaeotydeus devonicus, and Paraprotocarus hirsti (all

525 Dubinin, 1962). 526 527 **12. Crown Parasitiformes** 528 529 This clade comprises Opilioacariformes, Ixodida (hard and soft ticks), Holothyrida and 530 Mesostigmata, their last common ancestor and all of its descendants (Fig. 4). Monophyly is 531 established by phylogenetic analysis of nuclear ribosomal genes (Pepato and Klimov, 2015) and 532 morphology (Garwood and Dunlop, 2014). 533 534 12.1. Fossil specimens 535 536 Cornupalpatum burmanicum Poinar and Brown, 2003. Holotype larva (accession number A-10-537 260; Fig. 5i) and paratype (accession number A-10-261; Fig. 5j) deposited in the Poinar amber 538 collection maintained at Oregon State University, later to be deposited at the California Academy of 539 Sciences (Poinar, 2015; Poinar and Brown, 2003). 540 541 12.2. Phylogenetic justification 542 543 Morphological characters such as the subcircular body with a marginal groove, free coxae, 544 ventral anal opening, the presence of a capitulum and Haller's organ, absence of an anal groove, and 545 elongate four-segmented palpi are all suggestive of Parasitiformes affinity for C. burmanicum (Poinar 546 and Brown, 2003). A particularly diagnostic character, suggesting placement within at least total-group 547 Ixodida (and thus crown Parasitiformes), is the presence of claws on palpal segment 3 in the larva 548 (Poinar and Brown, 2003). Putative morphologies similar to bacterial pathogens exclusive to modern Ixodida were recently described from the paratype (Poinar, 2015). 549 550

553 This fossil is sourced from amber mines in the Hukawng Valley of Kachin State, northern 554 Myanmar (formerly Burma). The depositional age of Burmese amber was estimated from U-Pb dating 555 of zircons from the volcaniclastic matrix surrounding the amber (Shi et al., 2012). Shi et al. (2012) 556 argue the amber is not older than its associated sediments, as burial and preservation would have to 557 be rapid for survival of organic material, so the amber was probably formed at, but not earlier than the 558 U-Pb date: at 98.79 Ma ± 0.62 Myr. Therefore, a minimum age for any fossil from Burmese amber 559 deposits is 98.17 Ma. 560 Soft maximum as for 10.3. 561 562 13. Crown Pseudoscorpiones 563 564 This clade comprises Feaelloidea, Chthonioidea, Neobisiodea, Garypoidea, Sternophoroidea 565 and Cheliferoidea, their last common ancestor and all of its descendants (Fig. 4). While relationships 566 between superfamilies remain unclear, monophyly of Pseudoscorpiones was demonstrated with wide 567 taxon sampling and three genes (Murienne et al., 2008). More limited taxon sampling supports 568 monophyly with morphology (Garwood and Dunlop, 2014) and morphology combined with ribosomal 569 genes (Pepato et al., 2010). 570 571 13.1. Fossil specimens 572

573 *Protofeaella peetersae* Henderickx in Henderickx and Boone, 2016. NHM II 3115, holotype, 574 near complete specimen preserved in amber (**Fig. 5c**).

575

576 13.2. Phylogenetic justification

578 Although P. peetersae has not been included in a formal phylogenetic analysis, it was assigned 579 to the extant family Feaellidae by Henderickx and Boone (2016:8), based on its narrow cephalothorax, 580 granulated abdomen, and presence of small pedipalps with narrow coxa and small hands. Whilst 581 these features are certainly found in both P. peetersae and feaellids, other features, such as slender 582 pedipalp fingers, and the overall shape of the cephalic shield are more like those of pseudogarypids 583 (Harvey, 1992). Both the feaellid and pseudogarypids belong to the superfamily Feaelloidea (sensu 584 Harvey, 1992), and thus it is still likely *P. peetersae* belongs within the pseudoscorpion crown-group. 585 586 13.3. Age justification 587 588 As for 12.3. 589 590 591 13.4. Discussion 592 593 Dracochela deprehendor Schawaller et al., 1991 from the Middle Devonian of Gilboa, New

York State, was originally interpreted as a crown-group pseudoscorpion but was reassigned to the pseudoscorpion stem group (Judson, 2012). Preliminary morphological phylogenetic analyses by one of us (D.A.L.), however, suggest that *D. deprehendor* may be within the crown group. If so, this would drastically extend the range of crown Pseudoscorpiones by over 280 Myr (to a minimum age of 382.7 Ma; Richardson et al., 1993).

599 Note that other Cretaceous pseudoscorpions have been preserved in amber (older from 600 Lebanon and Spain; younger from France, New Jersey and Alberta), but these have yet to be fully 601 described or examined for their systematic positions (Judson, 2009). If the Lebanese or Spanish 602 fossils were found to be members of the crown group, they could extend the range of

24

603	Pseudoscorpiones by up to 27 Myr.
604	
605	14. Crown Palpigradi
606	
607	This clade comprises the families Eukoeneniidae and Prokoeneniidae, their last common
608	ancestor and all of its descendants (Fig. 4). Monophyly has been supported by a phylogenetic
609	analysis of two nuclear ribosomal and one mitochondrial gene (Giribet et al., 2014).
610	
611	14.1. Fossil specimens
612	
613	<i>Electrokoenenia yaksha</i> Engel et al., 2016b. NIGP 163253, holotype in amber ( <b>Fig. 5e</b> ).
614	
615	14.2. Phylogenetic justification
616	
617	<i>E. yaksha</i> was classified within the extant family Eukoeneniidae (Engel et al., 2016b). This was
618	justified with morphological characters, in particular the rounded lateral "arms" to the frontal organ of
619	the propeltidium, as seen in the extant genus Leptokoenenia (Engel et al., 2016b). Thus E. yaksha is
620	within the crown group of Palpigradi.
621	
622	14.3. Age justification
623	
624	As for 12.3.
625	
626	15. Crown Solifugae
627	
628	This clade comprises Ammotrechidae, Ceromidae, Daesiidae, Eremobatidae, Galeodidae,
	25

629 Gylippidae, Hexisopodidae, Karschiidae, Melanoblossidae, Mummuciidae, Rhagodidae and 630 Solpugidae, their last common ancestor and all of its descendants (Fig. 4). No phylogenetic analysis has yet included all families, but limited taxon sampling has shown monophyly with morphology 631 632 (Garwood and Dunlop, 2014; Shultz, 2007) and morphology combined with nuclear genes (Giribet et 633 al., 2002; Pepato et al., 2010). Extensive morphological work on the homology of cheliceral characters 634 was recently published by Bird et al. (2015). 635 636 15.1. Fossil specimens 637 638 Cratosolpuga wunderlichi Selden and Shear, 1996 (Sol. 1 in the private Wunderlich collection, 639 Straubenhardt, Germany), holotype. An additional specimen (SMNK 1268 PAL; Fig. 5f), not a 640 paratype, is also deposited. 641 642 15.2. Phylogenetic justification 643 644 C. wunderlichi was assigned to the extant family Ceromidae on the basis of shape of the 645 cheliceral flagellum, shape of the propeltidium, eye tubercle, and leg spination (Selden and Shear, 646 1996). Only a single tarsal segment is present on the legs (Selden and Shear, 1996). A position in 647 total-group Ceromidae would therefore be within crown-group Solifugae. 648 649 15.3. Age justification 650 651 This fossil was recovered from the Nova Olinda Member of the Crato Formation in the Araripe 652 Basin, northeastern Brazil. This unit is generally agreed to be around the Aptian/Albian border (Martill 653 et al., 2007). Batten (2007) suggests that if assemblages in the upper layers are consistent across the 654 lower layers, a late Aptian date should be considered. The Crato formation has been dated using 26

655	palynomorphs (Pons et al., 1990) to the Aptian, though an accurate date for the Nova Olinda Member
656	is not available. The upper boundary of the Aptian, at 113.0 Ma $\pm$ 0.4 Myr, gives a minimum date of
657	112.6 Ma.
658	Soft maximum as for 10.3.
659	
660	15.4. Discussion
661	
662	The Pennsylvanian Protosolpuga carbonaria Petrunkevitch, 1913, the only older possible fossil
663	solifuge, was discounted from the crown group of Solifugae in the same paper as described C.
664	wunderlichi (Selden and Shear, 1996). It is too poorly preserved to assign to the crown group without
665	additional phylogenetic justification.
666	
667	16. Crown Scorpiones
668	
669	This clade comprises Buthida and Iurida, their last common ancestor and all of its descendants
670	(Fig. 4). The composition of Buthida and Iurida are as detailed in Sharma et al. (2015). Monophyly has
671	been supported by phylogenetic analysis of transcriptomes (Sharma et al., 2015, 2014), morphology
672	(Garwood and Dunlop, 2014; Shultz, 2007), and combined ribosomal sequences and morphology
673	(Pepato et al., 2010).
674	
675	16.1. Fossil specimens
676	
677	Protoischnurus axelrodurum Carvalho and Lourenço, 2001. MN-7601-I, holotype, a male. We
678	also refer to the specimen SMNS 65534, which preserves phylogenetically relevant details of the
679	pedipalps (Fig. 3c in Menon, 2007).
680	
	27

- 681 16.2. Phylogenetic justification
- 682

683 Menon (2007) placed P. axelrodurum in the extant family Hemiscorpiidae, based on, amongst 684 other things, an inverse Y-shape on sulcus on the cephalic shield, the placement of Est trichobothria 685 on the pedipalp chela, and the placement of carinae V2 and V3 in the pedipalp chela, all of which are 686 diagnostic of the hemiscorpidid subfamily Hormurinae (Soleglad et al., 2005). Hemiscorpidae is 687 classified within lurida (Sharma et al., 2015), and is thus crown group Scorpiones. 688 689 16.3. Age justification 690 691 As for 15.3. 692 693 16.4. Discussion 694 695 A number of fossil taxa have been placed within crown group scorpion families, including 696 Protobuthus elegans Lourenco and Gall, 2004, from the Early Triassic Buntsanstein of France. It was 697 assigned to the superfamily Buthoidea, however, a subsequent study (Baptista et al., 2006), 698 considered this taxon and Archaeobuthus from the Early Cretaceous of Lebanon, outside the crown-699 group based on trichobothrial arrangement. 700 Araripescorpius ligabuei Campos, 1986 is coeval to P. axelrodurum, and from the same locality. 701 Menon (2007) placed A. ligabuei in the extant family Chactidae based on general habitus and 702 trichobothrial pattern. Therefore it is also a member of the crown group of Scorpiones, albeit a less 703 well-preserved species. 704 705 17. Crown Tetrapulmonata 706

707	This clade comprises Pedipalpi and Araneae (spiders), their last common ancestor and all of its
708	descendants (Fig. 6). Monophyly is supported by phylogenetic analysis of transcriptomes (Sharma et
709	al., 2014), nuclear protein-coding genes (Regier et al., 2010), and morphology (Garwood and Dunlop,
710	2014; Legg et al., 2013; Shultz, 2007). This clade is not recognized in GenBank taxonomy.
711	
712	17.1. Fossil specimens
713	
714	Parageralinura naufraga (Tetlie and Dunlop, 2008), LWL Ar.K.1 (Fig. 7a). Counterpart in the
715	private collection of W. Elze, Ennepetal, Germany.
716	
717	17.2. Phylogenetic justification
718	
719	Tetlie and Dunlop (2008) interpreted Coal Measures uropygids to comprise a plesion on the
720	stem of the extant Thelyphonidae, the sole extant family of Thelyphonida. A subchelate pedipalp is
721	considered apomorphic of the crown group but is lacking in Geralinura and P. naufraga. This identifies
722	them as crown Uropygi, and thus, Tetrapulmonata.
723	
724	17.3. Age justification
725	
726	Of the uropygid fossils, the oldest are P. naufraga (formerly Prothelyphonus naufragus) from
727	deposits of "Ziegelei-Grube," Hagen-Vorhalle, Nordrhein-Westphalia, Germany (Brauckmann and
728	Koch, 1983; Tetlie and Dunlop, 2008). The fossil-bearing deposits are assigned to the Namurian B
729	(Marsdenian) based on the Bilinguites metabilinguis R2c1 subzone of ammonoid stratigraphy
730	(Brauckmann et al., 1994; Tetlie and Dunlop, 2008). The (late) Namurian-(early) Westphalian
731	boundary is defined by the earliest occurrence of the goniatite Gastrioceras subcrenatum (Waters and
732	Davies, 2006), but lacks a precise isotopic date. Pointon et al. (2012) estimated an age of c. 319.9 Ma

733	for the base of the Westphalian (top of the Namurian, only slightly younger than the Marsdenian)
734	based on Milankovitch cycles of sedimentation, giving a minimum age for <i>P. naufraga</i> .
735	Soft maximum as for 10.3.
736	
737	18. Crown Pedipalpi
738	
739	This clade comprises Amblypygi (tailless whip scorpions) and Uropygi, their last common
740	ancestor and all of its descendants (Fig. 6). Monophyly is supported by phylogenetic analysis of
741	transcriptomes (Sharma et al., 2014), nuclear protein-coding genes (Regier et al., 2010), and
742	morphology (Garwood and Dunlop, 2014; Legg et al., 2013; Shultz, 2007). This clade is not
743	recognized in GenBank taxonomy.
744	
745	18.1. Fossil specimens
746	
747	As for 17.1.
748	
749	18.2. Phylogenetic justification
750	
751	As for 17.2.
752	
753	18.3. Age justification
754	
755	As for 17.3.
756	
757	19. Crown Uropygi
758	
	30

759	This clade comprises Thelyphonida (whip scorpions) and Schizomida, their last common
760	ancestor and all of its descendants (Fig. 6). Monophyly is supported by phylogenetic analysis of
761	nuclear protein-coding genes (Regier et al., 2010), and morphology (Garwood and Dunlop, 2014;
762	Legg et al., 2013; Shultz, 2007).
763	
764	19.1. Fossil specimens
765	
766	As for 17.1.
767	
768	19.2. Phylogenetic justification
769	
770	As for 17.2.
771	
772	19.3. Age justification
773	
774	As for 17.3.
775	
776	20. Crown Amblypygi
777	
778	This clade comprises Paracharontidae, Charinidae, Charontidae, Phrynichidae and Phrynidae,
779	their last common ancestor and all of its descendants (Fig. 6). Monophyly of Amblypygi has not been
780	fully investigated with phylogenetic analysis; however, monophyly has been shown for at least some
781	families with morphological data (Garwood and Dunlop, 2014; Shultz, 2007) and morphology
782	combined with nuclear genes (Pepato et al., 2010).
783	
784	20.1. Fossil specimens

786 Graeophonus anglicus Pocock, 2011. BMNH In. 31233, holotype (Fig. 7b). Figured in Dunlop 787 et al. (2007: Fig. 1 a,b). 788 789 20.2. Phylogenetic justification 790 791 G. anglicus was redescribed by Dunlop et al. (2007) as a member of the Amblypygi crown 792 group. This was based on several morphological character comparisons to living members, such as 793 the pedipalp femur with dorsal spination similar to Paracharon (the monotypic extant species of the 794 family Paracharontidae). G. anglicus, unlike Paracharon, has a pear-shaped ocular tubercle, 795 suggesting it was not blind. G. anglicus is inferred to be on the stem lineage of Paracharontidae, and 796 thus, crown group Amblypygi (Dunlop et al., 2007). 797 798 20.3. Age justification 799 800 The genus *Graeophonus* was originally described from the Sydney Basin, Cape Breton 801 Carboniferous Coal Measures, Nova Scotia, Canada, which corresponds to Westphalian in age 802 (Dunlop et al., 2007; Giles et al., 2002; Scudder, 1890a). Further studies are needed on the Canadian 803 material, so the minimum age was taken from the oldest European specimen (which is roughly the 804 same age as the Cape Breton specimen) from the British Middle Coal Measures (Coseley,

805 Stafffordshire), which is Westphalian B (or Duckmantian) at the youngest (Waters et al., 1994; Waters

and Davies, 2006). U-Pb dating of zircons constrains the upper boundary of the Duckmantian to

 $313.78 \text{ Ma} \pm 0.08 \text{ Myr}$  (Pointon et al., 2012), so a minimum age for *G. anglicus* is 313.70 Ma.

808 Soft maximum as for 10.3.

809

810 **21. Crown Araneae** 

811	
812	This clade comprises Mesothelae, Mygalomorphae (tarantulas, funnel-web spiders) and
813	Araneomorphae (most spiders), their last common ancestor and all of its descendants (Fig. 6).
814	Monophyly is established by phylogenetic analysis of transcriptomes (Fernández et al., 2014a;
815	Garrison et al., 2016) and morphology (Garwood and Dunlop, 2014; Legg et al., 2013; Shultz, 2007).
816	
817	21.1. Fossil specimens
818	
819	Palaeothele montceauensis Selden, 2000. Muséum d'Histoire naturelle, Autun: 51961
820	(holotype; Fig. 7c), and BMNH 62050, second specimen (not a paratype, Fig. 7d; Selden, 1996). We
821	also compare to Arthrolycosa sp. B Selden et al. 2014. PIN 5431/9 (Fig. 7e).
822	
823	21.2. Phylogenetic justification
824	
825	The deep, narrow sternum of P. montceauensis (formerly Eothele montceauensis Selden,
826	1996) is shared by extant members of Mesothelae (Selden, 1996). Several other characters that are
827	symplesiomorphic within Araneae, such as spinnerets, suggest a position within crown Araneae, and
828	perhaps on the stem lineage of Mesothelae (Selden, 1996).
829	
830	21.3. Age justification
831	
832	P. montceauensis was found in the Montceau Lagerstätte, Montceau-les-Mines, Massif
833	Central, France. The nodule-rich layer is just above the first seam in the Great Seams Formation (late
834	Stephanian) (Perrier and Charbonnier, 2014). The age within the Stephanian has been assigned to
835	Stephanian B, with some biostratigraphic evidence for Stephanian C (Racheboeuf et al., 2002). The
836	Stephanian B/C is a European stage of the Pennsylvanian, straddling the boundary of the globally

	837	used Kasimovian and Gzhelia	n (Richards	, 2013). Th	ne upper boundar	y of the	Gzhelian	is 298.9 Ma :
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838 0.15 Myr, hence the minimum age of the Montceau Lagerstätte is 298.75 Ma.

839 Soft maximum as for 10.3.

- 840
- 841 21.4 Discussion
- 842

843	A possible older spider, Arthrolycosa sp. B Selden et al., 2014, is known from the
844	Krasnodonsky Horizon of Rostov Province, Russia (Duckmantian, ~313 Ma). It shares characters with
845	extant Mesothelae, such as the position and morphology of the eye tubercles, but lacks spinnerets, so
846	the inference is largely based on better-known Arthrolycosa from other localities (Selden et al., 2014).
847	Because phylogenetic evidence for crown group membership is largely indirect, we maintain P.
848	montceauensis as the oldest well-supported Araneae.
849	
850	22. Crown Mandibulata
851	
852	This clade comprises Myriapoda and Pancrustacea, their last common ancestor and all of its
853	descendants (Fig. 1). Monophyly has been independently demonstrated based on protein-coding
854	genes and microRNAs, as well as morphological data (Rota-Stabelli et al., 2011).
855	
856	22.1. Fossil specimens
857	
858	As for 4.1.
859	
860	22.2. Phylogenetic justification
861	
862	As for 4.2.
	34

863	
864	22.3. Age justification
865	
866	As for 4.3.
867	
868	22.4. Discussion
869	
870	Wujicaris muelleri Zhang et al., 2010 has an equal claim to being the earliest record of
871	Mandibulata, but it is of equal age to the holotype of Y. dianensis.
872	
873	23. Crown Myriapoda
874	
875	This is the clade comprising Chilopoda (centipedes) and Progoneata, their last common
876	ancestor and all of its descendants (Fig. 1). Monophyly has been demonstrated by morphology
877	(Edgecombe, 2004; Legg et al., 2013; Rota-Stabelli et al., 2011), nuclear protein-coding genes (Regier
878	et al., 2010; Zwick et al., 2012), transcriptomes (Rehm et al., 2014), and combined analysis of
879	molecules and morphology (Lee et al., 2013).
880	
881	23.1. Fossil specimens
882	
883	Cowiedesmus eroticopodus Wilson and Anderson, 2004. AMS F.64845, holotype (Fig. 2e).
884	
885	23.2. Phylogenetic justification
886	
887	Membership of <i>C. eroticopodus</i> in Diplopoda is indicated by its strict diplosegmentation,
888	whereas its cuticular mineralization supports membership in the subgroup Chilognatha, and its
	35

889 modified legs on trunk segment 8 support membership in Helminthomorpha. C. eroticopodus is

890 resolved as total-group Helminthomorpha in the morphological cladistic analysis of Fernández et al.

891 (2016) and is accordingly a member of the crown-groups of Chilognatha, Diplopoda, Progoneata and892 Myriapoda.

893

894 23.3. Age justification

895

896 The earliest myriapods in the body fossil record are three species of Diplopoda from the 897 Dictyocaris Member of the Cowie Formation at Cowie Harbour, near Stonehaven, Aberdeenshire, 898 Scotland, one of which is C. eroticopodus (Wilson and Anderson, 2004). Based on associated spores, 899 the Cowie Formation taxa are late Wenlock to early Ludlow in age (Marshall, 1991; Wellman, 1993) 900 and the Early Ludlow upper boundary (Gorstian-Ludfordian boundary) is 425.6 Ma ± 0.9 Myr, so the 901 minimum age for Myriapoda is 424.7 Ma. 902 Soft maximum as for 2.3. 903 904 23.4. Discussion 905 906 Albadesmus almondi and Pneumodesmus newmani (both described by Wilson and Anderson, 907 2004) have an equal claim to being the oldest myriapod, sourced from the same locality and unit as C. 908 eroticopodus. The latter was selected because it has been explicitly coded in a morphological cladistic 909 analysis (Fernández et al., 2016). We have not used trace fossil evidence suggestive of Ordovician 910 diplopods (Wilson, 2006) for dating.

911

913

914 This clade comprises Diplopoda (millipedes), Pauropoda and Symphyla, their last common
915	ancestor and all of its descendants (Fig. 8). Monophyly is supported by phylogenetic analysis of
916	nuclear protein-coding genes (Regier et al., 2010; Zwick et al., 2012), whole mitochondrial genomes
917	(Brewer et al., 2013), and morphology (Edgecombe, 2004; Legg et al., 2013). Two recent molecular
918	phylogenies reject monophyly of Progoneata in favour of a putative clade of Chilopoda and Diplopoda:
919	one based on three protein-coding genes (Miyazawa et al., 2014) and one on transcriptomes (Rehm
920	et al., 2014). This clade is not recognized in GenBank taxonomy.
921	
922	24.1. Fossil specimens
923	
924	As for 23.1.
925	
926	24.2. Phylogenetic justification
927	
928	As for 23.2.
929	
930	24.3. Age justification
931	
932	As for 23.3.
933	
934	24.4. Discussion
935	
936	As for 23.4.
937	
938	25. Crown Diplopoda
939	
940	This clade comprises Penicillata (bristly millipedes) and Chilognatha, their last common

941	ancestor and all of its descendants (Fig. 8). Monophyly is supported by morphological analyses
942	(Blanke and Wesener, 2014), nuclear protein-encoding genes (Regier et al., 2010), and
943	transcriptomes (Fernández et al., 2016; Rehm et al., 2014).
944	
945	25.1. Fossil specimens
946	
947	As for 23.1.
948	
949	25.2. Phylogenetic justification
950	
951	As for 23.2.
952	
953	25.3. Age justification
954	
955	As for 23.3.
956	
957	25.4. Discussion
958	
959	As for 23.4.
960	
961	26. Crown Penicillata
962	
963	This clade comprises Polyxenoidea and Synxenoidea, their last common ancestor and all of it
964	descendants (Fig. 8). Monophyly has been defended based on the shared presence of serrate setae
965	arranged in lateral and caudal tufts (Enghoff, 1984).
966	

its

967	26.1.	Fossil	specimens
	-		

*Electroxenus jezzinensis* Nguyen Duy-Jacquemin and Azar, 2004 (Acra collection, provisionally
 deposited at MNHN: JS 231/1), holotype (Fig. 9a,b), adult in amber (Nguyen Duy-Jacquemin and
 Azar, 2004, Fig. 1A, B).

972

973 26.2. Phylogenetic justification

974

975 Cretaceous amber penicillates are readily assigned to two of the three extant families,
976 Polyxenidae and Synxenidae (Nguyen Duy-Jacquemin and Azar, 2004; classification of Penicillata
977 following Short in Enghoff et al., 2015). *E. jezzinensis* preserves diagnostic characters of Polyxenidae
978 such as lateral extensions of the gnathochilarial palps. Membership in an extant family indicates status
979 as crown Penicillata.

980

981 26.3. Age justification

982

983 *E. jezzinensis* was discovered in amber from the Jouar Ess-Souss locality, in the Jezzine area, 984 South Lebanon (Azar et al., 2010). Previous work suggested a Neocomian (Valanginian-Hauterivian) 985 age for the Jezzine area (Azar et al., 2010). However, Lebanese stratigraphy has recently been 986 revised; the Jouar Ess-Souss locality is now recognized as part of the lowermost interval of the Grès 987 du Liban (Maksoud et al., 2016). The lower interval lies below a shale layer bearing the echinoid fossil 988 Heteraster oblongus, and below a pisolitic interval bearing charyophyte fossils (Maksoud et al., 2016). 989 The charyophyte layer is associated to the Cruciata-Paucibracteatus Zone of Martín-Closas et al. 990 (2009) in the late Barremian-early Aptian, but this layer is also older than the Banc de Mrejatt subunit 991 within Lebanon, thus Jezzine amber is older than the Ba2 layer in Fig. 6 of Maksoud et al. (2016). 992 Jezzine amber is therefore no younger than early Barremian. The upper boundary of the early

Barremian is proposed to be the first appearance of the ammonite *Ancyloceras vandenheckii* (Ogg et al., 2012). Cyclostratigraphy dates the *A. vandenheckii* Zone beginning at 129.41 Ma (Ogg et al., 2012), providing a minimum age for Jezzine Lebanese amber fossils.

996 A soft maximum age is obtained from the oldest mandibulate, Y. dianensis, which was 997 recovered from the Yu'anshan Formation at Xiaotan section, Yongshan, Yunnan Province, attributed to 998 the Eoredlichia–Wutingaspis Biozone (Zhang et al., 2007). Chinese Cambrian stratigraphy has been 999 revised substantially and the *Eoredlichia – Wutingaspis* Biozone is no longer recognized (Peng, 2009, 1000 2003). However, *Eoredlichia* is known to co-occur with *Hupeidiscus*, which is diagnostic of the 1001 Hupeidiscus-Sinodiscus Biozone, which is formally recognised as the second biozone of the 1002 Nangaoan Stage of the Qiandongian Series of the Cambrian of China (Peng and Babcock, 2008). The 1003 Nangaoan is the proposed third stage of the Cambrian System for the International Geologic 1004 Timescale (Peng et al., 2012). Thus, a soft maximum constraint can be established on the age of the 1005 lower boundary of the Nangaoan, which has been dated to 521 Ma (Peng et al., 2012; Peng and 1006 Babcock, 2008).

1007

1008 26.4. Discussion

1009

1010 Another species of Polyxenidae from Lebanese amber, *Libanoxenus hammanaensis* Nguyen 1011 Duy-Jacquemin and Azar, 2004, is likewise known from a single specimen, from the Mdeiriji/Hammana 1012 locality in Central Lebanon. Its age data are similar to those of the more completely known *E.* 1013 *jezzinensis*, so the latter is used for calibration.

1014

## 1015 **27. Crown Chilognatha**

1016

1017 This clade comprises Pentazonia (pill millipedes) and Helminthomorpha (long-bodied

1018 millipedes), their last common ancestor and all of its descendants (**Fig. 8**). Monophyly is supported by

1019	morphological analyses (Blanke and Wesener, 2014), nuclear coding genes (Miyazawa et al., 2014),
1020	and transcriptomes (Fernández et al., 2016). Chilognthan monophyly has rarely been opposed: some
1021	analyses of nuclear protein coding genes by Regier et al. (2005) found weak support for an
1022	unconventional grouping of Penicillata with Pentazonia, but others retrieved Chilognatha.
1023	
1024	27.1. Fossil specimens
1025	
1026	As for 23.1.
1027	
1028	27.2. Phylogenetic justification
1029	
1030	As for 23.2.
1031	
1032	27.3. Age justification
1033	
1034	Minimum as for 23.3. Soft maximum as for 26.3.
1035	
1036	27.4. Discussion
1037	
1038	As for 23.4.
1039	
1040	28. Crown Chilopoda
1041	
1042	This clade comprises Scutigeromorpha (house centipedes) and Pleurostigmophora, their last
1043	common ancestor and all of its descendants (Fig. 8). Monophyly is robustly supported by
1044	morphological analyses (Edgecombe and Giribet, 2004; Murienne et al., 2010), nuclear protein-coding

1045 genes (Miyazawa et al., 2014; Regier et al., 2010; Zwick et al., 2012), and transcriptomics (Fernández 1046 et al., 2016; Rehm et al., 2014). 1047 1048 28.1. Fossil specimens 1049 1050 Crussolum sp. Jeram et al., 1990. DE 1.3.2/50 (Fig. 1N) and DE 3.1.1/88 (Fig. 1P; Jeram et al., 1051 1990). As mentioned below, we also refer to material from the Windyfield Chert (AUGD 12307-12308; 1052 Anderson and Trewin, 2003) for morphological details (Fig. 9c-e). 1053 1054 28.2. Phylogenetic justification 1055 1056 Crussolum was resolved as stem-group Scutigeromorpha in the morphological cladistic 1057 analysis of Fernández et al. (2016). Codings were a composite of material described as *Crussolum* sp. 1058 from the Windyfield Chert (Pragian) of the Dryden Flags Formation, Aberdeenshire, Scotland (figured by Anderson and Trewin, 2003), and the one formally named species of the genus, C. crusseratum 1059 1060 (Shear et al., 1998), known from isolated and fragmentary legs from the Middle Devonian Gilboa 1061 locality, Schoharie County, New York State (Givetian). 1062 1063 28.3. Age justification 1064 1065 The oldest examples of Crussolum are isolated legs from Ludford Lane in England (Shear et 1066 al., 1998), which come from a horizon 0.15-0.20 m above the base of the Ludlow Bone Bed Member, 1067 in the Downtown Castle Sandstone Formation. The Ludlow Bone Bed Member is early Pridoli in age 1068 (Jeram et al., 1990), that stage having an upper boundary of 419.2 Ma ± 3.2 Myr, providing a minimum 1069 age of 416.0 Ma. Crussolum as currently delimited crosses the Silurian-Devonian boundary.

1070 Soft maximum as for 2.3.

1071	
1072	29. Crown Scutigeromorpha
1073	
1074	This clade comprises Scutigeridae, Scutigerinidae and Psellioididae, their last common
1075	ancestor and all of its descendants (Fig. 8). Monophyly is robustly supported by morphological
1076	analyses (Edgecombe and Giribet, 2004), targeted gene sequencing (Murienne et al., 2010), and
1077	transcriptomics (Fernández et al., 2016).
1078	
1079	29.1. Fossil specimens
1080	
1081	Fulmenocursor tenax Wilson, 2001. SMNS 64275, holotype (Fig. 9f), nearly complete
1082	specimen (Wilson, 2001, Pl. 1, Fig. 2).
1083	
1084	29.2. Phylogenetic justification
1085	
1086	Wilson (2001) assigned F. tenax to the extant family Scutigeridae based on the proportions of
1087	its antennal articles and its styliform male gonopods. Paired spine-bristles on the tibia of the second
1088	maxilla (synapomorphy of Pselliodidae + Scutigeridae) are consistent with this interpretation
1089	(Edgecombe, 2011). These affinities place the genus in crown-group Scutigeromorpha.
1090	
1091	29.3. Age justification
1092	
1093	Minimum as for 15.3. Soft maximum as for 26.3.
1094	
1095	29.5 Discussion
1096	

1097	A total-group scutigeromorph from the Carboniferous Mazon Creek deposits, Latzelia
1098	primordialis Scudder, 1890b, cannot be reliably assigned to the scutigeromorph crown group
1099	(Edgecombe, 2011; J. T. Haug et al., 2014) and is accordingly not used for dating that clade.
1100	
1101	30. Crown Pleurostigmophora
1102	
1103	This clade comprises Craterostigmomorpha and Amalpighiata, their last common ancestor and
1104	all of its descendants (Fig. 8); membership is identical if the internal relationships of the clade are
1105	resolved as Lithobiomorpha + Phylactometria. Monophyly is supported by morphological analyses
1106	(Edgecombe and Giribet, 2004), nuclear ribosomal and mitochondrial genes, and their combination
1107	with morphology (Giribet and Edgecombe, 2006; Murienne et al., 2010), nuclear protein coding genes
1108	(Regier et al., 2010), and transcriptomics (Fernández et al., 2016, 2014b).
1109	
1110	30.1. Fossil specimens
1111	
1112	Devonobius delta Shear and Bonamo, 1988. AMNH slide 411-15-AR18, holotype (Fig. 9g),
1113	complete head with 15 or 16 trunk segments. We also refer to AMNH slide 4329-AR4 (Fig. 9h).
1114	
1115	30.2. Phylogenetic justification
1116	
1117	D. delta was resolved in a trichotomy with Craterostigmus and Epimorpha in the morphological
1118	cladistic analysis of (Edgecombe and Giribet, 2004, Fig. 9), and as sister group to extant
1119	Phylactometria when those data were combined with sequence data from four genes (Edgecombe
1120	and Giribet, 2004, Fig. 14). Published analyses agree on it being more closely related to Epimorpha
1121	than to Lithobiomorpha (Shear and Bonamo, 1988, Fig. 1; Murienne et al., 2010, Fig. 2; Fernández et
1122	al., 2016) and it is accordingly crown Pleurostigmophora.

1123
------

1124 30.3. Age justification

1125

1126	D. delta occurs in the Middle Devonian Gilboa locality, Schoharie County, New York State,
1127	USA. Fossils come from the upper part of the Panther Mountain Formation, dated to the Tioughniogan
1128	regional Stage, Givetian in the global time scale. Palynomorphs are consistent with a Givetian age
1129	(Richardson et al., 1993). Accordingly, minimum date for the end of the Givetian/base of the Frasnian
1130	is applied (382.7 Ma).
1131	Soft maximum as for 26.3.
1132	
1133	31. Crown Amalpighiata
1134	
1135	This clade comprises Lithobiomorpha (stone centipedes) and Epimorpha, their last common
1136	ancestor and all of its descendants (Fig. 8). Monophyly is supported by targeted gene sequencing
1137	(Regier et al., 2010) and transcriptomics (Fernández et al., 2016, 2014b).
1138	
1139	31.1. Fossil specimens
1140	
1141	Mazoscolopendra richardsoni Mundel, 1979. FMNH PE 22936, holotype, nearly complete
1142	specimen in siderite concretion (J. T. Haug et al., 2014; Mundel, 1979). We also refer to FMNH PE
1143	29002 ( <b>Fig. 9i</b> ).
1144	
1145	31.2. Phylogenetic justification
1146	
1147	M. richardsoni was coded by Fernández et al. (2016) for its morphological data based on
1148	descriptions and figures of Mundel (1979) and Haug et al. (J. T. Haug et al., 2014), and personal

1149	observation by G.D.E. of type and other material in the Field Museum. It was resolved as total-group
1150	Scolopendromorpha based on possession of autapomorphies of that order (e.g. single tergite on the
1151	forcipular/first leg-bearing segments, 21 pairs of trunk legs) but cannot be placed more precisely with
1152	regards to whether it is a stem- or crown-group scolopendromorph. Nonetheless, its membership in
1153	Scolopendromorpha assigns it to crown Amalpighiata. The same calibration would apply were the
1154	putative clade Phylactometria endorsed in lieu of Amalpighiata.
1155	
1156	31.3. Age justification
1157	
1158	Specimens are derived from the Francis Creek Shale Member of the Carbondale Formation,
1159	Mazon Creek, Illinois, of Westphalian D age (Baird et al., 1985; Shabica and Hay, 1997). The
1160	Westphalian D is equivalent to the latest Moscovian stage of the Pennsylvanian (Richards, 2013). As
1161	the upper boundary of the Moscovian is 307.0 Ma $\pm$ 0.1 Myr, this provides a minimum age of 306.9
1162	Ma.
1163	Soft maximum as for 26.3.
1164	
1165	32. Crown Epimorpha
1166	
1167	This clade comprises Scolopendromorpha and Geophilomorpha, their last common ancestor
1168	and all of its descendants (Fig. 8). Monophyly is supported by morphological analyses (Fernández et
1169	al., 2016; Murienne et al., 2010) and transcriptomics (Fernández et al., 2016, 2014b).
1170	
1171	32.1. Fossil specimens
1172	
1173	As for 31.1.
1174	

1175	32.2. Phylogenetic justification
1176	
1177	As for 31.2.
1178	
1179	32.3. Age justification
1180	
1181	As for 31.3.
1182	
1183	33. Crown Geophilomorpha
1184	
1185	This clade comprises Placodesmata and Adesmata, their last common ancestor and all of its
1186	descendants (Fig. 8). Monophyly is supported by morphological analyses, targetted sequencing, and
1187	combination of molecular and morphological data (Bonato et al., 2014a; Fernández et al., 2014b;
1188	Murienne et al., 2010) and transcriptomics (Fernández et al., 2016).
1189	
1190	33.1. Fossil specimens
1191	
1192	Kachinophilus pereirai Bonato et al., 2014b. AMNH Bu-Ba41a, holotype ( <b>Fig. 9j,k</b> ), complete
1193	adult male in amber (Bonato et al., 2014b, Fig. 1A-B, 2).
1194	
1195	33.2. Phylogenetic justification
1196	
1197	K. pereirai was originally assigned to the extant family Geophilidae based on a combination of
1198	characters that is unique to that family. More precisely it compares most closely to a subgroup within
1199	Geophilidae that has been classified as subfamilies Chilenophilinae or Pachymeriinae. K. pereirai was
1200	coded by Fernández et al. (2016) for its morphological data based on original observations on the type
	47

1201 material. It was resolved as more closely related to extant Geophilidae (sensu Bonato et al., 2014a) 1202 than to members of any of the other sampled geophilomorph family, as predicted by its original 1203 classification. Thus it is unambiguously a member of crown Adesmata and accordingly crown 1204 Geophilomorpha. 1205 1206 33.3. Age justification 1207 1208 Minimum as for 12.3. Soft maximum as for 26.3. 1209 1210 33.4. Discussion 1211 1212 A total-group geophilomorph from the Late Jurassic of Germany, *Eogeophilus jurassicus* 1213 Schweigert and Dietl, 1997 (refigured by J. T. Haug et al., 2014), is too inadequately known to 1214 establish whether or not it is a member of the geophilomorph crown-group. 1215 1216 34. Crown Pancrustacea 1217 1218 This clade comprises Oligostraca, Multicrustacea, and Allotriocarida, their last common 1219 ancestor and all of its descendants (Fig. 1). The inclusion of Hexapoda in a paraphyletic 'Crustacea' 1220 (and hence, erection of the clade Pancrustacea; Zrzavý and Štys, 1997) has been supported by 1221 numerous phylogenetic analyses, including those based on nuclear protein-coding genes (Regier et 1222 al., 2010, 2005), transcriptomes (Andrew, 2011; Meusemann et al., 2010; Rota-Stabelli et al., 2011; 1223 von Reumont et al., 2012), morphology (Legg et al., 2013; Schram and Koenemann, 2004; Strausfeld 1224 and Andrew, 2011) and combined morphological and molecular data (Oakley et al., 2013). 1225 This clade has also been named Tetraconata (Dohle, 2001) referring to the shared apomorphy 1226 of four cone cells within the compound eye; however this character is absent in many members of the 48

1227	clade, with multiple possible reconstructions of homology (Oakley, 2003; T. Oakley, pers. comm.).
1228	Terminology that does not rely on the homology of cone cell arrangement is thus preferred. More
1229	recently, an amended version of 'Crustacea' has been proposed (Haug and Haug, 2015) to avoid a
1230	different application of the 'Pan-' prefix (Lauterbach, 1989). While this concept of Crustacea is in our
1231	view valid, for this purpose we favour the original use of Pancrustacea referring to the crown group
1232	members only (Zrzavỳ and Štys, 1997). Haug and Haug (2015) argue that fossils such as
1233	Phosphatocopina would need to be included within Pancrustacea, however recent phylogenetic
1234	analyses show the sister group to crown Pancrustacea is in fact crown Myriapoda, with all other fossils
1235	outside (Legg et al., 2013). Pancrustacea is the clade name implemented in GenBank, and is the most
1236	commonly used name among molecular workers.
1237	
1238	34.1. Fossil specimens
1239	
1240	As for 4.1.
1241	
1242	34.2. Phylogenetic justification
1243	
1244	As for 4.2.
1245	
1246	34.3. Age justification
1247	
1248	As for 4.3.
1249	
1250	34.4. Discussion
1251	
1252	As for 22.4.
	49

# **35. Crown Oligostraca**

1256	This clade comprises Ostracoda (seed shrimp), Branchiura (fish lice), Pentastomida (tongue
1257	worms), and Mystacocarida, their last common ancestor and all of its descendants (Fig. 10).
1258	Monophyly of this clade has been demonstrated with nuclear protein-coding genes (Regier et al.,
1259	2010; Zwick et al., 2012) and combined phylogenetic analysis of molecules and morphology (Lee et
1260	al., 2013; Oakley et al., 2013; Zrzavỳ et al., 1998). GenBank taxonomy does not recognize this clade.
1261	Instead GenBank prefers the Maxillopoda hypothesis (Branchiura, Pentastomida, Mystacocarida,
1262	Thecostraca and Copepoda), which has not been recovered in molecular analyses (Abele et al., 1992;
1263	Regier et al., 2005) despite support from morphology (Legg et al., 2013).
1264	
1265	35.1. Fossil specimens
1266	
1267	Boeckelericambria pelturae Walossek and Müller, 1994. UB W116, holotype, consisting of a
1268	complete larva (Fig. 11a).
1269	
1270	35.2. Phylogenetic justification
1271	
1272	B. pelturae is likely a stem group pentastomid, based especially on the diagnostic
1273	synapomorphy of a head with two pairs of grasping hooks (similar to the extant Reighardia larva;
1274	Walossek and Müller, 1994, Fig. 25a). This species is a member of the round headed (as opposed to
1275	hammer headed) morphotype (Walossek and Müller, 1994). It was resolved in the pentastomid stem-
1276	group in a cladistic analysis that sampled the extant genera by Almeida and Christoffersen (Almeida
1277	and Christoffersen, 1999). Its pentastomid identity is not dependent on whether pentastomids are
1278	interpreted as Ichthyostraca (Møller et al., 2008; Regier et al., 2010; Sanders and Lee, 2010) or early

1279	diverging euarthropods (e.g. Castellani et al., 2011). Because we accept crown pentastomids as sister
1280	group to crown branchiurans on the basis of strong support from molecular data, B. pelturae must
1281	therefore be within crown Oligostraca.
1282	
1283	35.3. Age justification
1284	
1285	The Orsten fossils come from the lowest zone of the late Cambrian Alum Shale, formally called
1286	the Agnostus pisiformis Zone or Zone 1, previously corresponding to the Uppermost Zone of the
1287	Middle Cambrian (Babcock et al., 2005). The Agnostus pisiformis Zone was recently redefined as the
1288	uppermost zone of the Guzhangian, at the upper boundary of Cambrian Series 3 (Nielsen et al.,
1289	2014). This age of the uppermost stage of the Cambrian Series 3 is 499 Ma $\pm$ 2 Myr. Thus the
1290	minimum age applied to Oligostraca is 497 Ma.
1291	Soft maximum as for 2.3.
1292	
1292 1293	36. Crown Ichthyostraca
1292 1293 1294	36. Crown Ichthyostraca
1292 1293 1294 1295	36. Crown Ichthyostraca This clade comprises Branchiura and Pentastomida, their last common ancestor and all of its
<ol> <li>1292</li> <li>1293</li> <li>1294</li> <li>1295</li> <li>1296</li> </ol>	36. Crown Ichthyostraca This clade comprises Branchiura and Pentastomida, their last common ancestor and all of its descendants (Fig. 10). It was first proposed based on sperm ultrastructure (Wingstrand, 1972).
<ol> <li>1292</li> <li>1293</li> <li>1294</li> <li>1295</li> <li>1296</li> <li>1297</li> </ol>	36. Crown Ichthyostraca This clade comprises Branchiura and Pentastomida, their last common ancestor and all of its descendants (Fig. 10). It was first proposed based on sperm ultrastructure (Wingstrand, 1972). Subsequent analyses of morphology combined with protein-coding genes (Zrzavỳ et al., 1998) or with
1292 1293 1294 1295 1296 1297 1298	36. Crown Ichthyostraca This clade comprises Branchiura and Pentastomida, their last common ancestor and all of its descendants (Fig. 10). It was first proposed based on sperm ultrastructure (Wingstrand, 1972). Subsequent analyses of morphology combined with protein-coding genes (Zrzavỳ et al., 1998) or with transcriptomes (Oakley et al., 2013), as well as molecular data on their own (Møller et al., 2008;
<ol> <li>1292</li> <li>1293</li> <li>1294</li> <li>1295</li> <li>1296</li> <li>1297</li> <li>1298</li> <li>1299</li> </ol>	36. Crown lchthyostraca This clade comprises Branchiura and Pentastomida, their last common ancestor and all of its descendants (Fig. 10). It was first proposed based on sperm ultrastructure (Wingstrand, 1972). Subsequent analyses of morphology combined with protein-coding genes (Zrzavỳ et al., 1998) or with transcriptomes (Oakley et al., 2013), as well as molecular data on their own (Møller et al., 2008; Regier et al., 2010) have supported monophyly of this clade.
1292 1293 1294 1295 1296 1297 1298 1299 1300	36. Crown Ichthyostraca This clade comprises Branchiura and Pentastomida, their last common ancestor and all of its descendants (Fig. 10). It was first proposed based on sperm ultrastructure (Wingstrand, 1972). Subsequent analyses of morphology combined with protein-coding genes (Zrzavỳ et al., 1998) or with transcriptomes (Oakley et al., 2013), as well as molecular data on their own (Møller et al., 2008; Regier et al., 2010) have supported monophyly of this clade.
<ol> <li>1292</li> <li>1293</li> <li>1294</li> <li>1295</li> <li>1296</li> <li>1297</li> <li>1298</li> <li>1299</li> <li>1300</li> <li>1301</li> </ol>	36. Crown Ichthyostraca This clade comprises Branchiura and Pentastomida, their last common ancestor and all of its descendants (Fig. 10). It was first proposed based on sperm ultrastructure (Wingstrand, 1972). Subsequent analyses of morphology combined with protein-coding genes (Zrzavý et al., 1998) or with transcriptomes (Oakley et al., 2013), as well as molecular data on their own (Møller et al., 2008; Regier et al., 2010) have supported monophyly of this clade. 36.1. Fossil specimens
1292 1293 1294 1295 1296 1297 1298 1299 1300 1301 1302	36. Crown Ichthyostraca This clade comprises Branchiura and Pentastomida, their last common ancestor and all of its descendants (Fig. 10). It was first proposed based on sperm ultrastructure (Wingstrand, 1972). Subsequent analyses of morphology combined with protein-coding genes (Zrzavý et al., 1998) or with transcriptomes (Oakley et al., 2013), as well as molecular data on their own (Møller et al., 2008; Regier et al., 2010) have supported monophyly of this clade. 36.1. Fossil specimens
<ol> <li>1292</li> <li>1293</li> <li>1294</li> <li>1295</li> <li>1296</li> <li>1297</li> <li>1298</li> <li>1299</li> <li>1300</li> <li>1301</li> <li>1302</li> <li>1303</li> </ol>	36. Crown lchthyostraca This clade comprises Branchiura and Pentastomida, their last common ancestor and all of its descendants (Fig. 10). It was first proposed based on sperm ultrastructure (Wingstrand, 1972). Subsequent analyses of morphology combined with protein-coding genes (Zrzavỳ et al., 1998) or with transcriptomes (Oakley et al., 2013), as well as molecular data on their own (Møller et al., 2008; Regier et al., 2010) have supported monophyly of this clade. 36.1. Fossil specimens As for 35.1.
1292 1293 1294 1295 1296 1297 1298 1299 1300 1301 1302 1303 1304	36. Crown Ichthyostraca This clade comprises Branchiura and Pentastomida, their last common ancestor and all of its descendants (Fig. 10). It was first proposed based on sperm ultrastructure (Wingstrand, 1972). Subsequent analyses of morphology combined with protein-coding genes (Zrzavý et al., 1998) or with transcriptomes (Oakley et al., 2013), as well as molecular data on their own (Møller et al., 2008; Regier et al., 2010) have supported monophyly of this clade. 36.1. Fossil specimens As for 35.1.

1305	36.2. Phylogenetic justification
1306	
1307	As for 35.2.
1308	
1309	36.3. Age justification
1310	
1311	As for 35.3.
1312	
1313	37. Crown Ostracoda
1314	
1315	This clade comprises Myodocopa, Podocopa (including Palaeocopida), their last common
1316	ancestor and all its descendants (Fig. 10). Monophyly of this clade has been demonstrated by
1317	phylogenetic analysis of a dataset including nuclear protein-coding genes, transcriptomes, and
1318	morphology (Oakley et al., 2013). Additional phylogenetic analyses of morphology alone (Legg et al.,
1319	2013; Wolfe and Hegna, 2014) also support monophyly.
1320	
1321	37.1. Fossil specimens
1322	
1323	Luprisca incuba Siveter et al., 2014. YPM IP 307300, holotype, consisting of a complete
1324	pyritized specimen in ventral aspect (Fig. 11b).
1325	
1326	37.2. Phylogenetic justification
1327	
1328	To date, <i>L. incuba</i> is yet to be included in an extensive phylogenetic analysis, but a number of
1329	features confirm both its placement within Myodocopida, and therefore Myodocopa. Specifically, the
1330	arrangement of setae on the antenula of L. incuba is currently only observed amongst extant
	52

1331 myodocopid ostracods (Kornicker, 1981).

1332

1333 37.3. Age justification

1334

1335 The holotype of L. incuba was collected from siltstone of the Original Trilobite Bed, Walcott 1336 Quarry of Beecher's Trilobite Bed, in the Frankfort Shale of upstate New York (Siveter et al., 2014). 1337 Beecher's site within the Frankfort Shale is within the Lorraine Group, part of the regional Maysvillian 1338 Stage of the Cincinnatian Series (Farrell et al., 2011, 2009). Globally, the Maysvillian (Amplexograptus 1339 manitoulinensis Graptolite Zone) corresponds to the early Katian Stage, from the base of the 1340 Diplacanthograptus caudatus Graptolite Zone to the base of the Pleurograptus linearis Graptolite Zone 1341 (Bergström et al., 2009). The upper boundary of the Katian is  $445.2 \text{ Ma} \pm 1.4 \text{ Myr}$ , providing a 1342 minimum age of 443.8 Ma.

1343 As in Oakley et al. (2013), we suggest the maximum age of ostracods must be 509 Ma, the 1344 age of the Burgess Shale. Myodocope ostracods possess bivalved, calcified carapaces, which are 1345 preserved from many other Burgess Shale arthropods. There is no taphonomic reason why they would 1346 not have been preserved from ostracods. The Burgess Shale type locality is from Unit 3 of the Collins 1347 Quarry on Mount Stephen in the Canadian Rocky Mountains, British Columbia, which falls within the 1348 Kicking Horse Shale Member of the "thick" Stephen Formation (Aitkin, 1997; Caron et al., 2010; 1349 Stewart, 1991), also referred to as the Burgess Shale Formation (Fletcher and Collins, 2003, 1998). 1350 This unit yields trilobites from the Polypleuraspis insignis Subzone of the Glossopleura Zone (Fletcher 1351 and Collins, 1998), and is the oldest soft-bodied fossil excavation of the Burgess Shale sites. The age 1352 of the Glossopleura Zone corresponds to the Cambrian Series 3 Stage 5, giving a maximum constraint 1353 of 509 Ma.

1354

1355 37.4. Discussion

1356

1357 Older fossils, from the Tremadocian (~40 Myr older) have been reported from numerous 1358 localities across the current and Ordovician world: Argentina, Australia, China, Iran, Norway, Sweden, 1359 and the UK (Williams et al., 2008). However, all of these fossils are known solely from carapaces, 1360 which are known to be highly homoplastic (Siveter et al., 2013). The affinities of Tremadocian 1361 ostracods are therefore ambiguous. Other bivalved crustacean-like taxa from the Cambrian, such as 1362 bradoriids and phosphatocopines, are demonstrably not closely related to ostracods, or even Oligostraca, based on phylogenetic analyses (Hou et al., 2010; Legg et al., 2013; Oakley et al., 2013; 1363 1364 Wolfe and Hegna, 2014).

1365

## **1366 38. Crown Podocopa**

1367

This clade comprises Palaeocopida, Podocopida and Platycopida, their last common ancestor and all of its descendants (**Fig. 10**). Monophyly has been demonstrated by phylogenetic analysis of morphology (Horne et al., 2005), and morphology combined with nuclear protein-coding genes and transcriptomes (Oakley et al., 2013). Although the sole living representative of Palaeocopida, *Manawa staceyi*, has to date only been represented by a single ribosomal sequence and morphology, bootstrap support for its position as a sister to the remaining Podocopa is strong (Oakley et al., 2013).

1374

1375 38.1. Fossil specimens

1376

1377 *Cytherellina submagna* Krandijevsky, 1963. For phylogenetically relevant details, we refer to 1378 ZPAL O.60/001 (**Fig. 11c-e**), preserving soft anatomy, and ZPAL O.60/002, preserving adductor 1379 muscle scars (Olempska et al., 2012).

1380

1381 38.2. Phylogenetic justification

1382

1383 C. submagna is very similar to modern podocopes, particularly sigilloideans and

1384 darwinuloideans, with which it shares a particular adductor muscle scar pattern, long terminal seta on

1385 the seventh limb pair, and a furca with large distal setae (Olempska et al., 2012).

1386

1387 38.3. Age justification

1388

1389 Specimens of *C. submagna* were recovered from two localities in Podolia, Ukraine: Kasperovcy 1390 village, left border of the river Seret (type locality), and from the right escarpment of the River Dniester 1391 near the village Ivanye Zlote (Olempska et al., 2012). The type locality, part of the Chortkov/Chortkiv 1392 Horizon, underlies the second locality, which is part of the Ivanye Horizon (Filipiak et al., 2012; 1393 Olempska et al., 2012). Thus we must use the Chortkiv age as a minimum constraint on the age of C. 1394 submagna, to provide the narrowest interval of clade divergence. The Chortkiv Horizon comfortably 1395 lies within the middle Lochkovian stage of the Early Devonian (Filipiak et al., 2012; Małkowski et al., 1396 2009; Plotnick, 1999). Conodont biostratigraphy places the upper boundary of the Chortkiv Horizon at 1397 the end of the Caudicriodus postwoschmidti Biozone, the oldest conodont Biozone within the 1398 Devonian (Drygant and Szaniawski, 2012). Spline fits on radiometric ages for the Devonian place the 1399 C. postwoschmidti Biozone at 417.27 Ma with a duration of 1.89 Myr (Becker et al., 2012). Thus the 1400 end of the C. postwoschmidti Biozone, and a minimum age for the first appearance of C. submagna, is 1401 415.38 Ma.

1402 Soft maximum as for 37.3.

1403

1404 *38.4. Discussion* 

1405

Although isolated ostracod carapace valves are incredibly abundant in the fossil record, the morphology of carapaces has been shown to have little systematic value (Siveter et al., 2013). For this reason we have selected a taxon with soft-tissue preservation, of which *C. submagna* is the oldest

1409	recognized example, although other species of Cytherellina are known from older deposits including
1410	the later Silurian of Ludlow, England, with only the carapaces preserved (Olempska et al., 2012).
1411	These older species cannot be ruled out as myodocopes or stem members of any of Podocopa,
1412	Myodocopa, or even Ostracoda, as they lack diagnostic soft parts.
1413	
1414	39. Crown Myodocopa
1415	
1416	This clade comprises Myodocopida and Halocyprida, their last common ancestor and all of its
1417	descendants (Fig. 10). Monophyly has been demonstrated by phylogenetic analysis of morphology
1418	(Horne et al., 2005), and morphology combined with nuclear protein-coding genes and transcriptomes
1419	(Oakley et al., 2013).
1420	
1421	39.1. Fossil specimens
1422	
1423	As for 37.1.
1424	
1425	39.2. Phylogenetic justification
1426	
1427	As for 37.2.
1428	
1429	39.3. Age justification
1430	
1431	As for 37.3.
1432	
1433	40. Crown Myodocopida
1434	
	56

1435	This clade comprises Cylindroleberidoidea, Cypridinoidea and Sarsielloidea, their last common
1436	ancestor and all of its descendants (Fig. 10). Monophyly has been demonstrated by phylogenetic
1437	analysis of morphology (Horne et al., 2005), and morphology combined with nuclear protein-coding
1438	genes and transcriptomes (Oakley et al., 2013).
1439	
1440	40.1. Fossil specimens
1441	
1442	As for 37.1.
1443	
1444	40.2. Phylogenetic justification
1445	
1446	As for 37.2.
1447	
1448	40.3. Age justification
1449	
1450	As for 37.3.
1451	
1452	41. Crown Altocrustacea
1453	
1454	This clade comprises Multicrustacea and Allotriocarida, their last common ancestor and all of
1455	its descendants (Fig. 1). Monophyly has been supported by phylogenetic analysis of nuclear protein-
1456	coding genes (Regier et al., 2010; Zwick et al., 2012), transcriptomes (von Reumont et al., 2012), and
1457	combined analysis of morphology and nuclear protein-coding genes (Lee et al., 2013) or morphology
1458	and transcriptomes (Oakley et al., 2013). However, this clade has been challenged as paraphyletic
1459	(containing Oligostraca) by Rota-Stabelli et al. (2013b), and has not been supported by morphological
1460	data alone. It is not recognized in GenBank taxonomy.

1461 1462 41.1. Fossil specimens 1463 1464 As for 4.1. 1465 1466 41.2. Phylogenetic justification 1467 1468 As for 4.2. 1469 1470 41.3. Age justification 1471 1472 As for 4.3. 1473 1474 41.4. Discussion 1475

A series of disarticulated Small Carbonaceous Fossils (Harvey and Butterfield, 2008) from the 1476 1477 early Cambrian Mount Cap Formation, Northwest Territories, Canada, have been cited as calibration 1478 fossils within Altocrustacea or even Allotriocarida (e.g. Rehm et al., 2011; Sun et al., 2015). These 1479 fossils were argued by Harvey (2008) to comprise part of the feeding apparatus of a single crustacean 1480 taxon. The Mount Cap arthropod fossils would have represented structures each specialized for 1481 precise feeding functions. The fossil species may have initially scraped food with saw-toothed and 1482 hooked setae, further processed particles with filter plates and other delicate setal associations, then 1483 macerated with mandibular molar surfaces and passed to the mouth with long fringing setae (Harvey 1484 and Butterfield, 2008). Estimates of the body size of the animal, based on regression of body length 1485 versus molar surface length (from extant crustaceans) suggest the Mount Cap arthropod was, in total, 1486 about the same size as an adult cladoceran or anostracan (Harvey and Butterfield, 2008). While direct synapomorphies linking the Mount Cap arthropod to crown group branchiopods are lacking, the
evidence together suggests affinity along the stem lineage of Altocrustacea (Harvey, 2008, Fig. 5.6).

#### 1490 **42. Crown Multicrustacea**

1491

1492 This clade comprises Copepoda, Thecostraca (barnacles) and Malacostraca, their last 1493 common ancestor and all of its descendants (Figs. 12 and 13). Monophyly was first demonstrated by 1494 nuclear protein-coding genes (Regier et al., 2010) and supported by transcriptomes (von Reumont et 1495 al., 2012) and combined analysis of molecular and morphological data (Lee et al., 2013; Oakley et al., 1496 2013). This clade has, however, not been recovered in any morphology-only phylogenetic analyses, 1497 presumably owing to widespread support for Malacostraca as sister to much of the rest of 1498 Pancrustacea (the Entomostraca hypothesis, e.g. Walossek and Müller, 1998). See Wolfe and Hegna 1499 (2014) for a morphological deconstruction of Entomostraca. Neither Multicrustacea nor Entomostraca 1500 is recognized in GenBank taxonomy. 1501 1502 42.1. Fossil specimens 1503 1504 Arenosicaris inflata Collette and Hagadorn, 2010a. PRI 10130), holotype from the Elk Mound 1505 Group (Fig. 14a), which is difficult to date (see 42.3). Therefore, we refer to a second specimen, 1506 UWGM 745.

1507

1508 42.2. Phylogenetic justification

1509

1510 A. inflata was identified within the Archaeostraca, the likely fossil sister group to extant

1511 Leptostraca (together comprising 'Phyllocarida') and included in the morphological cladistic analysis of

1512 Collette and Hagadorn (2010b). In that analysis, the exceptionally preserved fossils *Nahecaris stuertzi* 

1513 Jaeckel, 1921 and Cinerocaris magnifica Briggs et al., 2004 were also included within Archaeostraca 1514 (Collette and Hagadorn, 2010b). A separate extensive combined molecular and morphological 1515 analysis placed C. magnifica within crown Malacostraca (as is traditionally assumed for members of 1516 Archaeostraca), while N. stuertzi was equivocally stem Leptostraca or stem Malacostraca (Oakley et 1517 al., 2013), suggesting non-monophyly of Archaeostraca. C. magnifica was also crown Malacostraca in 1518 another morphological analysis that omitted N. stuertzi (Legg et al., 2013). A. inflata is within the same 1519 archaeostracan clade as N. stuertzi (Pephricaridina + Rhinocaridina) while C. magnifica is in a 1520 separate archaeostracan group (Echinocaridina; Collette and Hagadorn, 2010b). Given the uncertainty 1521 of crown affinities and potential monophyly of Archaeostraca, we conservatively assign A. inflata to 1522 crown-group Multicrustacea, but not Malacostraca.

1523

## 1524 42.3. Age justification

1525

1526 A. inflata is found in the Elk Mound Group (holotype) and in the Lodi Member of the St. 1527 Lawrence Formation, both in Wisconsin (Collette and Hagadorn, 2010a). Although the Elk Mound 1528 Group is the older of these, no biostratigraphically useful fossils co-occur with A. inflata, limiting the 1529 ability to determine the formation to which they belong (Collette and Hagadorn, 2010a). The St. 1530 Lawrence Formation is younger, containing Saukia Zone trilobites, which mark it as late Sunwaptan 1531 within the Furongian (Collette and Hagadorn, 2010a; Raasch, 1951). The Sunwaptan is the second 1532 latest stage of the Furongian, postdated by the Skullrockian (which extends into the Early Ordovician; 1533 Peng et al., 2012). The Sunwaptan-Skullrockian boundary is determined by the appearance of 1534 conodonts in the Hirsutodontus hirsutus Subzone of the Cordylodus proavus Zone (Peng et al., 2012). Based on the correlation diagram of Peng et al. (2012), the Sunwaptan-Skullrockian boundary is 1535 1536 approximately 487 Ma, providing a minimum age estimate. 1537 Soft maximum as for 2.3.

1538

- **43. Crown Copepoda**

1541	This clade comprises Calanoida, Cyclopoida, Gelyelloida, Harpacticoida (benthic copepods),
1542	Misophrioida, Mormonilloida, Platycopioida and Siphonostomatoida (fish parasites), their last common
1543	ancestor and all of its descendants (Fig. 12). Members of Calanoida, Cyclopoida, and
1544	Siphonostomatoida were included in a large combined analysis of transcriptomes and morphology,
1545	forming a monophyletic group (Oakley et al., 2013). Phylogenetic analysis of morphology (Huys and
1546	Boxshall, 1991; Ho, 1994), mitochondrial genes (Minxiao et al., 2011), and ribosomal genes combined
1547	with morphology (Huys et al., 2007) suggest this sampling covers distant lineages of Copepoda,
1548	although omitting Platycopioida, the presumed most basal order (Huys and Boxshall, 1991). Molecular
1549	data remain unavailable from Platycopioida, although comparative morphological investigations
1550	support copepod monophyly (Dahms, 2004).
1551	
1552	43.1. Fossil specimens
1553	
1554	Kabatarina pattersoni Cressey and Boxshall, 1989. BMNH IN. 63466, holotype, preserving the
1555	cephalothorax, mouthparts, oral cone, and first and second thoracic limbs (Fig. 14b). This specimen
1556	likely represents an adult female, recovered from the gills of a fossil teleost fish (Cressey and
1557	Boxshall, 1989).
1558	
1559	43.2. Phylogenetic justification

*K. pattersoni* has not been included in a formal phylogenetic analysis. Cressey and Boxshall
(1989) detail one apomorphy shared by the fossil and recent members of the family Dichelesthiidae,
which is a medial groove delimiting the distal part of the maxillary claw. A number of other characters
are shared more generally with copepods, such as the shape of the oral cone (typical for fish parasitic

copepods), and biramous thoracic limbs with a 2-segmented protopod, joined by the intercoxal plate
(Cressey and Boxshall, 1989). Dichelesthiidae is a family belonging to the Siphonostomatoida. Even a
position for *K. pattersoni* on the stem of Dichelesthiidae or stem Siphonostomatoida would be within
crown group Copepoda.

1569

1570 43.3. Age justification

1571

*K. pattersoni* was found in the Cretaceous Santana Formation, Serra do Araripe, Ceará, Brazil (Cressey and Boxshall, 1989), which is mainly famous for concretions enclosing fossil fishes. The age of the Santana Formation is poorly constrained (as it lacks biostratigraphic index fossils and igneous rocks for radiometric dating); dates have been suggested that range from the Aptian to the Albian or Cenomanian (Martill, 2007). In order to ensure a minimum date, the upper boundary of the Cenomanian, which is 93.7 Ma (from 93.9 Ma  $\pm$  0.2 Myr; Ogg et al., 2012), is used. Soft maximum as for 26.3.

1579

1580 *43.4. Discussion* 

1581

1582 Despite their overwhelming abundance in modern aquatic ecosystems, copepods have a poor 1583 fossil record, likely due to their small size, unsclerotized cuticle, and planktonic ecology. Apart from K. 1584 pattersoni, putative copepod appendages have been reported from much older sediments in the 1585 Pennsylvanian (Selden et al., 2010) and even the Cambrian (Harvey et al., 2012; Harvey and Pedder, 1586 2013; These fossils each bear one to four characters found in crown copepods, from partial maxillae 1587 (Selden et al., 2010) and partial or complete mandibular gnathal edges (Harvey et al., 2012; Harvey 1588 and Pedder, 2013). Relationships between feeding habits and mandibular morphology have been 1589 observed in extant copepods (Michels and Schnack-Schiel, 2005), and variation may occur among 1590 closely related species (Sano et al., 2015). It is therefore extremely unlikely that mandibular characters

1591 have not experienced any homoplasy since the Cambrian.

1592 Nevertheless, divergence time analyses suggest Devonian-Carboniferous (calibrated with *K*. 1593 *pattersoni*; (Rota-Stabelli et al., 2013a), Carboniferous (calibrated with external fossils from other 1594 pancrustacean clades; Oakley et al., 2013), or Permian (external fossils; Wheat and Wahlberg, 2013) 1595 origins for crown Copepoda. These analyses do not conflict stratigraphically with a crown assignment 1596 for the Pennsylvanian fossils (Selden et al., 2010). Therefore we must caution that a Cretaceous age 1597 is likely a severe underestimate of crown copepod antiquity.

1598

# 1599 44. Crown Thecostraca

1600

1601 This clade comprises Facetotecta (y-larvae), Ascothoracida, and Cirripedia, their last common 1602 ancestor and all of its descendants (**Fig. 12**). Monophyly of Thecostraca has been demonstrated by 1603 separate analysis of nuclear housekeeping genes and morphology (Pérez-Losada et al., 2009a). All 1604 included clades have complex (sometimes only partially known) life histories, but particularly strong 1605 morphological support comes from a shared larval stage, the cyprid.

More recently, the enigmatic parasitic Tantulocarida were added within Thecostraca based on analysis of a single ribosomal gene (Petrunina et al., 2014), however, other relationships within Pancrustacea differed significantly from those outlined herein. In light of the paucity of data other than ribosomal genes, we remain ambivalent about including Tantulocarida. As tantulocarids have no known fossil record, if further evidence supports their position within Thecostraca, this calibration may be modified to include them as well.

1612

1613 44.1. Fossil specimens

1614

1615 Rhamphoverritor reduncus Briggs et al., 2005. OUM C.29587, holotype (Fig. 14c,d),

1616 preserving a cyprid larva in a volcaniclastic concretion. As the reconstruction of Herefordshire fossils

requires serial grinding and photography of 20 µm sections (Sutton et al., 2002), the holotype (figured
in Briggs et al., 2005: Fig. 1) was thus destroyed in preparation. Morphological data for Herefordshire
fossils are published as 3D models of the thin section photographs.

1620

1621 44.2. Phylogenetic justification

1622

1623 In a phylogenetic analysis of morphology, R. reduncus is the sister group of two species of 1624 Thoracica (both are members of Balanomorpha) (Legg et al., 2013). This is a position likely within the 1625 crown group of Thecostraca, however, no other thecostracans (such as Facetotecta and 1626 Ascothoracida) were included. Generally, the cyprid larval morphotype (with an elongated head shield, 1627 six swimming thoracopods, and robust modified antennules) is considered a synapomorphy of 1628 Thecostraca (Høeg et al., 2004). R. reduncus differs from cirripede cyprids as it lacks attachment 1629 discs, and its abdomen extends past the head shield; a differentiated abdomen is a condition of 1630 Ascothoracida (Briggs et al., 2005; Høeg et al., 2009a). Based on the presence of five shell plates in a 1631 juvenile specimen, Høeg et al. (2009b) suggested that *R. reduncus* may be placed on the cirripede 1632 stem lineage. In combination with the phylogenetic analysis of Legg et al. (2013), these apomorphies 1633 indicate that *R. reduncus* is very likely a member of crown group Thecostraca, and likely on the stem 1634 of Cirripedia. 1635 1636 44.3. Age justification 1637

1638 Minimum as for 6.3. Soft maximum as for 26.3.

1639

1640 **45. Crown Cirripedia** 

1641

1642 This clade comprises Acrothoracica, Rhizocephala and Thoracica (barnacles), their last

1643	common ancestor and all of its descendants (Fig. 12). Monophyly has been demonstrated by separate
1644	phylogenetic analysis of nuclear housekeeping genes and morphology (Pérez-Losada et al., 2009a).
1645	
1646	45.1. Fossil specimens
1647	
1648	Illilepas damrowi Schram, 1986. FMNH P32055, holotype (Fig. 14e).
1649	
1650	45.2. Phylogenetic justification
1651	
1652	Schram (1975) described this fossil as Praelepas damrowi, a congener of P. jaworskii
1653	Chernyshev, 1930. Restudy led to the transfer of this fossil to the new genus Illilepas under the
1654	combination I. damrowi, as the original description of a carina more closely resembled a tergum, and
1655	the original tergum was more likely an enlarged spine along the margin of the aperture, similar to that
1656	seen in Ibliformes (Thoracica) (Buckeridge and Newman, 2006; Schram, 1986). However, both
1657	molecular and morphological data place Ibla as the most basal clade of Thoracica (Pérez-Losada et
1658	al., 2009a, 2008), which, if I. damrowi is on the Ibliformes stem lineage, would still situate the fossil
1659	within the crown group of Cirripedia.
1660	
1661	45.3. Age justification
1662	
1663	As for 31.3.
1664	
1665	45.4. Discussion
1666	
1667	A possible Early Ordovician stalked barnacle (Pedunculata: Lepadomorpha?) was illustrated in
1668	Fig. 2c and S3h of Van Roy et al. (2010). It has not been formally described and its affinities are
	65

1669 unclear.

1670 P. jaworskii is in some ways a more appropriate fossil calibration than I. damrowi. It is 1671 approximately coeval to *I. damrowi*, and was coded in a morphological phylogenetic analysis (Glenner 1672 et al., 1995), where it was placed within Thoracica (sister to all other Thoracica except Ibla). P. 1673 jaworskii has been used as a calibration fossil for Thoracica and Cirripedia (Pérez-Losada et al., 1674 2009b, 2008; Rees et al., 2014). However, no specimen information was available in the original 1675 publication, nor was any significant stratigraphic data beyond Carboniferous of the Kusnetzk Basin, 1676 Russia (Chernyshev, 1930). As the papers using P. jaworskii for calibration estimate its age at 306.5-1677 311.7 Ma (e.g. Rees et al., 2014), substitution of the slightly younger *I. damrowi* will not significantly 1678 violate the minimum age.

1679

#### 1680 **46. Crown Thoracica**

1681

1682 This clade comprises Ibliformes, 'Pedunculata' (goose barnacles) and Sessilia (acorn 1683 barnacles), their last common ancestor and all of its descendants (Fig. 12). Pedunculata is no longer 1684 supported as monophyletic (Buckeridge and Newman, 2006; Pérez-Losada et al., 2009a; Rees et al., 1685 2014). Ibliformes is identified as the sister group of all other Thoracica (Pérez-Losada et al., 2009a). 1686 Monophyly has been established by phylogenetic analysis of nuclear housekeeping genes (Pérez-1687 Losada et al., 2009a), although a morphological phylogenetic analysis in the same paper resolves all 1688 studied members of Rhizocephala and Thoracica together in a polytomy. This is because only larval 1689 characters can be scored for Rhizocephala, with missing data for all adult characters due to their 1690 parasitic lifestyle.

1691

1692 46.1. Fossil specimens

1693

1694 As for 45.1.

1695	
1696	46.2. Phylogenetic justification
1697	
1698	As for 45.2.
1699	
1700	46.3. Age justification
1701	
1702	As for 31.3.
1703	
1704	46.4. Discussion
1705	
1706	As for 45.4.
1707	
1708	47. Crown Sessilia
1709	
1710	This clade comprises Verrucomorpha and Balanomorpha, their last common ancestor and all
1711	of its descendants (Fig. 12). Monophyly is supported by phylogenetic analysis of nuclear protein-
1712	coding and ribosomal genes (Pérez-Losada et al., 2008; Rees et al., 2014).
1713	
1714	47.1. Fossil specimens
1715	
1716	Brachylepas fallax Withers, 1935. For calibration, we refer to the stratigraphically oldest
1717	specimen (SM 704275), which is undescribed (A. Gale, pers. comm.).
1718	
1719	47.2. Phylogenetic justification
1720	
	67

1721 This species was originally described from disarticulated material by Darwin (1851) as 1722 Pollicipes fallax. Withers (1935, 1914) recognized it was a sessile, rather than pedunculate barnacle, 1723 and that it had similarities to the basal sessilian genus Pycnolepas in overall form and plate 1724 development. Synapomorphies shared by *B. fallax* and all crown Sessilia include: the absence of a 1725 peduncle, presence of an operculum, and absence of all lateral plates (Gale and Sørensen, 2015). B. fallax shares with crown Balanomorpha a low, hemiconical carina and rostrum (Gale and Sørensen, 1726 1727 2015). On the basis of these characters, a recent cladogram depicts *B. fallax* as one of the most 1728 distant stem lineages of Balanomorpha, which is therefore a position within the crown group of 1729 Sessilia (Gale and Sørensen, 2015).

1730

1731 47.3. Age justification

1732

1733 The oldest known locality from which *B. fallax* has been recovered is Pit No. 125 (Brydone, 1734 1912), close to junction of Barnet Side Lande and King's Lane, Froxfield, Hampshire, England (A. Gale, pers. comm.). This locality bears fossils of Holaster (Sternotaxis) planus, and is thus part of the 1735 1736 S. planus echinoid zone, which is the uppermost zone of the Turonian in English Chalk (Gale, 1996; 1737 Mortimore, 2011). The GSSP defining the global upper boundary of the Turonian remains debated (due to difficulty in identifying its index ammonite fossil, Forresteria (Harleites) petrocoriensis (Ogg et 1738 1739 al., 2012). Currently, the upper boundary of the Turonian is dated to 89.8 Ma  $\pm$  0.3 Myr, providing a 1740 minimum age of 89.5 Ma.

- 1741 Soft maximum as for 26.3.
- 1742
- 1743 **47.4**. Discussion
- 1744

1745 The Albian-Cenomanian *Verruca withersi* Schram and Newman, 1980 has been shown not to 1746 be a cirripede (Jagt and Buckeridge, 2005) and cannot be used as a minimum. *Proverruca* (coded at

1747 the genus level) was included in a morphological phylogenetic analysis, where it was placed in a 1748 polytomy with the fossil *Eoverruca* and the crown family Verrucidae (Glenner et al., 1995), and 1749 subsequently used as a calibration fossil for divergence time analysis (Pérez-Losada et al., 2014, 1750 2008). However, the placement of *Proverruca* was based on similarities to the extant genus 1751 Neoverruca, which was shown in molecular analyses to fall outside Sessilia entirely, instead within the 1752 Scalpelliformes (Pérez-Losada et al., 2008; Rees et al., 2014). More recent morphological 1753 phylogenetic analyses confirm the convergence between Neoverruca + Proverruca and crown 1754 Verrucomorpha (Gale, 2015; Gale and Sørensen, 2015).

The Albian *Pycnolepas rigida* Sowerby, 1836 was included in a morphological phylogenetic analysis, where it was placed on the stem lineage of Verrucomorpha (Gale, 2015). However, that analysis did not include members of Balanomorpha, so the topology did not explicitly exclude a position on the stem lineage of Sessilia. In fact, this species was referred to stem Sessilia (Gale, 2015, p. 770). Unlike crown group Sessilia, it retains the pedunculate character of a lateral plate, the tall upper latus (Gale, 2015).

*Verruca tasmanica tasmanica* (Buckeridge, 1983), a previously used calibration fossil at the
base of Verrucomorpha (Herrera et al., 2015; Linse et al., 2013; Pérez-Losada et al., 2014, 2008;
Rees et al., 2014), is known from the Santonian Gingin Chalk Formation of Dandaragan, Western
Australia (as well as type material from younger Oligocene strata of Oamaru, New Zealand;
Buckeridge, 1979). As it is both younger than *B. fallax* and has not been studied in a phylogenetic

1766 context, it is not used herein.

1767

# 1768 **48. Crown Malacostraca**

1769

1770 This clade comprises Leptostraca and Eumalacostraca, their last common ancestor and all of 1771 its descendants (**Fig. 13**). Its monophyly is one of the least contested matters in arthropod phylogeny; 1772 it has been demonstrated by phylogenetic analysis of morphology (Legg et al., 2013; Wills et al.,

1773	1998), nuclear ribosomal and protein-coding genes (Giribet et al., 2001; Regier et al., 2010, 2005),
1774	transcriptomes (von Reumont et al., 2012), and combined analysis of molecular and morphological
1775	data (Lee et al., 2013; Oakley et al., 2013).
1776	
1777	48.1. Fossil specimens
1778	
1779	Cinerocaris magnifica Briggs et al., 2004. OUM C.29565 (holotype; Fig. 14g), and OUM
1780	C.29566 (serially ground and reconstructed specimen; Fig. 14f). Morphological data for Herefordshire
1781	fossils are published as 3D models of thin section photographs.
1782	
1783	48.2. Phylogenetic justification
1784	
1785	C. magnifica was found to be a member of the stem group of Leptostraca (therefore crown
1786	group Malacostraca) in analyses of morphology (Legg et al., 2013) and morphology combined with
1787	molecules (Oakley et al., 2013).
1788	
1789	48.3. Age justification
1790	
1791	As for 44.3.
1792	
1793	48.4. Discussion
1794	
1795	The position of other fossil phyllocarids with respect to extant malacostracans (and the
1796	monophyly of phyllocarids themselves) have not been significantly investigated. The position of the
1797	Devonian phyllocarid Nahecaris stuertzi in a phylogenetic analysis (Oakley et al., 2013) was
1798	equivocally stem Leptostraca or stem Malacostraca, casting doubt on the position of at least rhinocarid

1799 phyllocarids within crown Malacostraca. As N. stuertzi has the same relationship to crown 1800 Malacostraca as A. inflata (at least in the analysis of Collette and Hagadorn, 2010b), neither fossil can 1801 be confidently placed within crown-group Malacostraca. Recent reinvestigation of Ceratiocaris cf. 1802 macroura (related to A. inflata and N. stuertzi in the analysis of Collette and Hagadorn, 2010b) 1803 suggests this Silurian 'phyllocarid' may be a stem eumalacostracan due to possession of an antennal 1804 scale, casting further doubt on the monophyly of fossil phyllocarids (Jones et al., 2015). The C. 1805 macroura study, however, assumes malacostracan identity of phyllocarids (partly defined by biramous 1806 antennules), which, as discussed above (section 42.2), may not be robust to phylogenetic analysis. If, 1807 however, Ceratiocaris is within crown Malacostraca (either alone or with other archaeostracans), the 1808 oldest Malacostraca would be amended to Ceratiocaris winneshiekensis Briggs et al., 2015 from the Darriwilian Winneshiek Lagerstätte of Iowa (~14 Myr older than C. magnifica). 1809 1810 Thylacocephalans are an enigmatic fossil arthropod clade ranging from the Silurian to the 1811 Cretaceous (C. Haug et al., 2014; Schram, 2014). Some Cambrian fossils have been proposed as 1812 thylacocephalans, but their membership is generally discounted (Schram, 2014; Vannier et al., 2006).

1813 Thylacocephalans have been compared to several extant arthropod clades, including the

1814 malacostracan stomatopods and decapods (Schram, 2014; Schram et al., 1999; Secrétan and Riou,

1815 1983; Vannier et al., 2016), which would extend the minimum age of Malacostraca slightly older within

1816 the Silurian (~433 Ma). The Jurassic thylacocephalan *Dollocaris ingens* Van Straelen, 1923 was coded

1817 in a morphological matrix, and found to be a stem eumalacostracan (therefore crown malacostracan)

1818 by phylogenetic analysis (Legg et al., 2013). However, their malacostracan affinities have been

1819 questioned, especially by C. Haug et al. (2014) studying a Silurian species, noting divergent trunk

1820 tagmosis and similarities to remipedes. Continued uncertainty over thylacocephalan affinites make

1821 them poor calibration fossils.

1822

**1823 49. Crown Eumalacostraca** 

1824

1825 This clade comprises Verunipeltata (mantis shrimp, partial total group called Stomatopoda), 1826 Peracarida, 'Syncarida' (itself comprising Anaspidacea and Bathynellacea) and Eucarida, their last 1827 common ancestor and all of its descendants (Fig. 13). Monophyly is demonstrated by phylogenetic 1828 analysis of morphology (Legg et al., 2013; Richter and Scholtz, 2001), nuclear ribosomal and protein-1829 coding genes (Regier et al., 2010), transcriptomes (von Reumont et al., 2012), and combined analysis 1830 of molecular and morphological data (Lee et al., 2013; Oakley et al., 2013; Wills et al., 2009). Although 1831 stomatopods and/or syncarids were not sampled in some of the above analyses, the best taxon 1832 sampling still resulted in eumalacostracan monophyly (Legg et al., 2013; Wills et al., 2009). 1833 1834 49.1. Fossil specimens 1835 1836 Palaeopalaemon newberryi Whitfield, 1880. The holotype at the AMNH, figured by Schram et 1837 al. (1978: Plate 3 #1-3), has been lost (B. Hussaini, pers. comm.), thus we refer to specimen KSU 1838 3484 (Fig. 14h,i). 1839 1840 49.2. Phylogenetic justification 1841 Schram and Dixon (2004) coded P. newberryi into the morphological matrix of Dixon et al. 1842 1843 (2003), finding it sister to a clade including Anomura, Brachyura, and Achelata to the exclusion of 1844 Astacidea, Axiidea, Gebiidea and Glypheidea. This position is within the crown group of Reptantia, 1845 hence within the crown groups of Decapoda and Eumalacostraca. 1846 1847 49.3. Age justification 1848 1849 The specimen of *P. newberryi* was found in gray shale near "Paine's Creek," LeRoy, Lake 1850 County, Chagrin (Erie) Shale, northeastern Ohio, USA (Feldmann et al., 1978; Schram et al., 1978). 72
1851	The Chagrin Shale is dated to the late Fammenian based on presence of the index alga Foerstia
1852	(Murphy, 1973), which in Ohio lies 40-70 m below surface outcrops (Feldmann et al., 1978). The upper
1853	boundary of the Fammenian is 358.9 Ma $\pm$ 0.4 Myr, giving a minimum of 358.5 Ma.
1854	Soft maximum as for 26.3.
1855	
1856	50. Crown Anaspidacea
1857	
1858	This clade comprises the families Anaspididae, Koonungidae, Psammaspididae and
1859	Stygocarididae, their last common ancestor and all of its descendants (Fig. 13). Phylogenetic studies
1860	including Anaspidacea are extremely rare, but morphology (Schram, 1984) and mitochondrial 16S
1861	sequences (Camacho et al., 2002) indicated monophyly of the clade.
1862	
1863	50.1. Fossil specimens
1864	
1865	Anaspidites antiquus Chilton, 1929. AMS F64765, holotype, complete specimen (Fig. 14k).
1866	
1867	50.2. Phylogenetic justification
1868	
1869	Although not included in a formal phylogenetic analysis, Schram (1984) justified the
1870	membership of A. antiquus as essentially indistinguishable from living Anaspididacea. Fusion of the
1871	first thoracomere into the cephalon, uniramous pleopods, and absence of an antennal scale are noted
1872	as diagnostic characters (Schram, 1984). As the fossil lacks preservation of diagnostic mouthparts,
1873	exact family affinities within total-group Anaspidacea are uncertain.
1874	
1875	50.3. Age justification
1876	

1877A. antiquus was found in the Hawkesbury Sandstone at the former Brookvale Brick Quarry,1878New South Wales, Australia (Schram, 1984). The Hawkesbury Sandstone overlies the Narrabeen1879Group and underlies the Wianamatta Group (Herbert, 1997). Sequence stratigraphy places the1880Hawkesbury in Sequence F, including the appearance of Aratrisporites parvispinosus spores (Helby,18811973; Herbert, 1997). The A. parvispinosus spore zone indicates an age during the Anisian (middle1882Triassic) (Herbert, 1997). The upper boundary of the Anisian is estimated at 241.5  $\pm$  1 Ma (Ogg,18832012), providing a minimum age at 240.5 Ma.

1884Soft maximum as for 26.3.

1885

1886 *50.4. Discussion* 

1887

1888 'Syncarida', the traditional taxon containing Anaspidacea, is purposely excluded from this 1889 review, as its monophyly has been substantially challenged. In phylogenetic analyses, syncarid 1890 monophyly was only supported by the morphological dataset of Richter and Scholtz (2001). 1891 emphasizing the absence of a dorsal carapace in Anaspidacea and Bathynellacea ('Syncarida'). Each 1892 of a partial mitochondrial gene (Camacho et al., 2002), two mitochondrial genes and morphology 1893 (Jenner et al., 2009) and morphology including putative syncarid fossils (Schram and Hof, 1998; Wills 1894 et al., 2009) failed to recover a sister group relationship bewteen Anaspidacea and Bathynellacea. 1895 Wills et al. (2009) suggested that a paraphyletic grade of 'Syncarida', including fossils (Acanthotelson, 1896 Palaeocaris) represented the first divergences of Eumalacostraca.

1897

## 1898 **51. Crown Verunipeltata**

1899

1900 This is the clade comprising Bathysquilloidea, Erythrosquilloidea, Eurysquilloidea,

1901 Parasquilloidea, Gonodactyloidea, Lysiosquilloidea and Squilloidea, their last common ancestor and

all of its descendants (Fig. 13). Although the extant members are often referred to Stomatopoda, that

1903 clade includes a number of extinct members forming a paraphyletic grade (Fig. 1 of Haug et al., 2010).

1904 As membership of fossil species within a crown group is only possible if they branch along the stem

1905 lineage of a living clade that is part of the crown itself, we agree with the assertion that crown

1906 'Stomatopoda' is equivalent to the clade Verunipeltata sensu Haug et al. (2010). The stomatopod

1907 clade as a whole may be defined by several apomorphies, such as five pairs of maxillipeds, and

1908 modification of the first two pleopods as gonopods (Richter and Scholtz, 2001).

All living members form a clade in analyses of morphology including both fossil and extant taxa (Ahyong, 1997; Ahyong and Harling, 2000). Analysis of combined molecular and morphological data, with limited sampling of verunipeltatan clades, strongly supports monophyly of those members (Jenner et al., 2009). As well, representatives of Gonodactyloidea, Lysiosquilloidea and Squilloidea were sequenced for six housekeeping genes; these were monophyletic in a diverse sample of

1914 Pancrustacea (Bybee et al., 2011).

1915

1916 51.1. Fossil specimens

1917

Ursquilla yehoachi Remy and Avnimelech, 1955. For calibration, we refer to two specimens.
Based on new phylogenetically relevant details, we use a new specimen (SMNS 67703) from Fig. 1
and 2 of Haug et al. (2013). The SMNS specimen, however, lacks locality and stratigraphic information
beyond "Late Cretaceous Negev Desert, Israel" as it was privately donated (Haug et al., 2013). We
also therefore refer to the holotype (MNHN R. 62691).

1923

1924 51.2. Phylogenetic justification

1925

1926 The uropod morphology of *U. yehoachi* indicates its membership in the crown group of

1927 Verunipeltata. The uropodal exopod of *U. yehoachi* specimen SMNS 67703 is bipartite, a

synapomorphy of Verunipeltata (Haug et al., 2013). Furthermore, *U. yehoachi* shares several

characters with Squillidae (Squilloidea), such as prelateral lobes, submedian teeth with fixed apices
and a subquadrate telson (Haug et al., 2013). As *U. yehoachi* has not been included in a phylogenetic
analysis, it is uncertain whether it falls within crown Squilloidea (Haug et al., 2013) or on its stem;
either position would remain within the crown group of Verunipeltata.

1933

1934 51.3. Age justification

1935

1936The holotype of *U. yehoachi* was collected from a chert bank in the Chert Member of the1937Mishash Formation, near the city of Arad, Israel (Hof, 1998). The chert banks are within the1938*Hoplitoplacenticeras marroti* ammonite biiozone (Reiss et al., 1986). *H. marroti* co-occurs with1939*Baculites* sp. (smooth) (Lehmann and Murphy, 2001), which is dated to the uppermost early1940Campanian. Based on a spline-fit of interbedded bentonites, the base of the Tethyan *Baculites* sp.1941(smooth) Zone is dated to 79.64 Ma, with a duration of 0.63 Myr (Ogg et al., 2012), thus the minimum1942age of *U. yehoachi* is 79.01 Ma.

1943 Soft maximum as for 26.3.

1944

#### 1945 **52. Crown Peracarida**

1946

1947 This clade comprises Amphipoda (scuds/beach fleas), Isopoda (wood lice/pill bugs), Cumacea, 1948 Lophogastrida, Bochusacea, Mictacea, Mysida (opossum shrimp), Stygiomysida, Spelaeogriphacea, 1949 Tanaidacea and Thermosbaenacea, their last common ancestor and all of its descendants (Fig. 13). 1950 Monophyly has been demonstrated by phylogenetic analysis of morphology (Jones et al., 2016; 1951 Poore, 2005; Richter and Scholtz, 2001; Wills et al., 2009; Wirkner and Richter, 2010), and combined 1952 morphology and molecular data (Jenner et al., 2009). Molecular phylogenies based on ribosomal 1953 genes reject the inclusion of Mysida within Peracarida (Jenner et al., 2009; Meland and Willassen, 1954 2007; Spears et al., 2005), while Lophogastrida and Stygiomysida are removed from Mysidacea and

1955	found comfortably within Peracarida (Meland and Willassen, 2007; Meland et al., 2015). Note
1956	ribosomal genes alone are insufficient markers for deep divergences (Giribet and Ribera, 2000), so we
1957	cautiously include Mysida within Peracarida pending multilocus investigations.
1958	
1959	52.1. Fossil specimens
1960	
1961	Hesslerella shermani Schram, 1970. FMNH PE 16527, holotype, lateral view (illustrated in
1962	Wilson, 2012 and <b>Fig. 14j</b> ).
1963	
1964	52.2. Phylogenetic justification
1965	
1966	H. shermani was included in a morphological cladistic analysis by Wilson (2012). It occurred at
1967	the base of Phreatoicidea (Wilson, 2012), a position within the crown group of Isopoda and thus,
1968	crown Peracarida. Note that the assignment of our calibration fossil to crown Isopoda means that
1969	exclusion of Mysida from Peracarida (Jenner et al., 2009; Meland and Willassen, 2007; Spears et al.,
1970	2005) will not change the date assessed for Peracarida.
1971	
1972	52.3. Age justification
1973	
1974	As for 31.3.
1975	
1976	52.4. Discussion
1977	
1978	Pygocephalomorpha is a eumalacostracan fossil clade with a number of symplesiomorphic
1979	characters. Pygocephalomorpha were proposed as members of Peracarida; however, a recent
1980	phylogeny depicted them in a polytomy in any of three positions: sister to Mysidacea (Mysida +
	77

Lophogastrida), sister to all non-Mysidacea peracarids, or on the peracarid stem lineage (Jones et al.,
2016). Note also the molecular analyses discussed above that exclude Mysida from Peracarida (e.g.
Jenner et al., 2009), which would mean two of three equally parsimonious positions for
Pygocephalomorpha may be outside the peracarid crown group. If Pygocephalomorpha were shown
to be more likely within the crown group of Peracarida (e.g. as sister to non-mysid peracarids), one
species in this clade, *Tealliocaris walloniensis* Gueriau et al., 2014, would become the oldest peracarid
(from the Fammenian stage of the Devonian ~50 Myr older; Gueriau et al., 2014).

1988 Within Peracarida, several orders have putative Mesozoic calibration fossils that do not fully 1989 meet our requirements. Putative Lophogastrida fossils were described from the middle Triassic Falang 1990 Formation of China (Taylor et al., 2001) and Grès à Voltzia, France (Bill, 1914). These were attributed 1991 to the extant family Eucopiidae (Taylor et al., 2001), although they resolved outside crown 1992 Lophogastrida in an older phylogeny including only the French species (Taylor et al., 1998). Putative 1993 Mysida were described from the Late Jurassic Solnhofen Plattenkalk of Germany, but are poorly 1994 preserved (Schram, 1986). Fossils separately attributed to each of Lophogastrida and Mysida have 1995 also been described from the Middle Jurassic La Voulte-sur-Rhône of France (Secrétan and Riou, 1996 1986). Other fossils noted as "mysidaceans" have been mentioned, but not yet described, from the 1997 middle Triassic Luoping Biota of China (Feldmann et al., 2015; Hu et al., 2010). None of these fossils 1998 have been evaluated in the context of molecular discoveries, i.e. they assume a sister relationship 1999 between Mysida and Lophogastrida. Therefore, none can be used as calibrations until their 2000 relationships with respect to potential polyphyletic Mysidacea have been assessed.

Example 2001 Fossils allied to Spelaeogriphacea have been described from the Cretaceous Yixian Formation 2002 of China (Shen et al., 1998; section 60.3 for revised stratigraphy) and Las Hoyas of Spain (Jaume et 2003 al., 2013). However, poor preservation of diagnostic characters indicates these are stem

2004 spelaeogriphaceans (Jaume et al., 2013).

Although several Mesozoic fossils have been assigned to Amphipoda, none have sufficient or accurate morphological placement (Starr et al., 2016; Vonk and Schram, 2007). Thus no known

2007 Mesozoic fossil qualifies as a crown group amphipod.

53. Crown Isopoda This clade comprises Asellota, Phoratopodidea, Cymothoida, Microcereberidea, Limnoridea, Sphaeromatidea, Valvifera, Oniscidea (wood lice/pill bugs), Phreatoicidea, Calabozoidea and Tainisopidea, their last common ancestor and all of its descendants (Fig. 13). The list of isopod suborders is derived from Boyko et al. (2008). Isopod monophyly was recovered in phylogenetic analysis of four housekeeping genes (Lins et al., 2012) and of combined ribosomal genes and morphology (Wilson, 2009). 53.1. Fossil specimens As for 52.1. 53.2. Phylogenetic justification As for 52.2. 53.3. Age justification As for 31.3. 54. Crown Tanaidacea This clade comprises Apseudomorpha, Neotanaidomorpha and Tanaidomorpha, their last

2033	common ancestor and all of its descendants (Fig. 13). Phylogenetic analysis of three molecular loci
2034	demonstrated monophyly of Apseudomorpha and Tanaidomorpha; Neotanaidomorpha could not be
2035	included (Drumm, 2010). More expansive outgroup sampling (without Neotanaidomorpha) did not
2036	recover monophyletic Tanaidacea with ribosomal and morphological data (Wilson, 2009). However, a
2037	nuclear ribosomal analysis including Neotanaidomorpha supported monophyly (Kakui et al., 2011).
2038	
2039	54.1. Fossil specimens
2040	
2041	Alavatanais carabe Vonk and Schram, 2007. MCNA 9537, holotype in amber, male (Fig. 14I).
2042	For additional morphological details, we also refer to MCNA 9846a and MCNA 13888 (Fig. 14m), both
2043	males.
2044	
2045	54.2. Phylogenetic justification
2046	
2047	Spanish amber tanaids were originally misidentified as amphipods (Alonso et al., 2000). The
2048	fossils were placed in a new family, Alavatanaidae, part of the superfamily Paratanaoidea within
2049	Tanaidomorpha (Sánchez-García et al., 2015; Vonk and Schram, 2007). Characters supporting affinity
2050	within Tanaidomorpha include the presence of an articulated ischium, articulation of the last two
2051	pleopods (may be reduced in males), and seven or fewer antennal articles (Sánchez-García et al.,
2052	2015).
2053	
2054	54.3. Age justification
2055	
2056	Amber inclusions bearing arthropod fossils were discovered from the Peñacerrada I outcrop,
2057	Basque-Cantabrian Basin, Álava, Spain (Alonso et al., 2000; Peñalver and Delclòs, 2010). The
2058	Peñacerrada I outcrop itself is divided into three intervals, with the lowest bearing the amber (Barrón

et al., 2015). Earlier palynological study assigned Peñacerrada I to the Escucha Formation, in the late Aptian (Barrón et al., 2001). Recent restudy, however, amended this outcrop to the Utrillas Group (Barrón et al., 2015). The presence of marine palynomorphs characterized by *Chichaouadinium vestitum* and *Palaeohystrichophora infusorioides*, and the terrestrial *Distaltriangulisporites mutabilis* and *Senectotetradites varireticulatus* together constrain a late Albian age for the Peñacerrada I (Barrón et al., 2015). The upper boundary of the Albian stage is 100.5 Ma  $\pm$  0.4 Myr (Ogg et al., 2012), providing a minimum estimate for Álava amber fossils at 100.1 Ma.

- 2066 Soft maximum as for 26.3.
- 2067

## 2068 **55. Crown Eucarida**

2069

2070 This clade comprises Euphausiacea (krill) and Decapoda (crabs, shrimp, lobsters), their last 2071 common ancestor and all of its descendants (Fig. 13). Monophyly of Euphausiacea and Decapoda is 2072 supported by phylogenetic analysis of transcriptomes (von Reumont et al., 2012), ribosomal genes 2073 (Spears et al., 2005), and combined molecular and morphological data (Jenner et al., 2009; Wills et 2074 al., 2009). Amphionidacea was represented as its own order within Eucarida based on morphology 2075 (Jenner et al., 2009; Wills et al., 2009), but recently the first molecular sequence data have become 2076 available, indicating that Amphionidacea are larval stages of Caridea (i.e. within Decapoda) (De Grave 2077 et al., 2015).

- 2078
- 2079 55.1. Fossil specimens
- 2080
- 2081 As for 49.1.
- 2082
- 2083 55.2. Phylogenetic justification
- 2084
- 81

2085 As for 49.2.
2086
2087 55.3. Age justification
2088
2089 As for 49.3.
2090
2091 56. Crown Decapoda
2092

2093 This clade comprises Dendrobranchiata (shrimp/prawns) and Pleocyemata (caridean shrimp, mud shrimp, true crabs, hermit and king crabs, lobsters, spiny lobsters, etc.), their last common 2094 2095 ancestor and all of its descendants (Fig. 13). Decapod monophyly is established by phylogenetic 2096 analysis of protein-coding genes (Bracken et al., 2009; Bybee et al., 2011; Timm and Bracken-2097 Grissom, 2015), morphology (Legg et al., 2013; Richter and Scholtz, 2001), and combined 2098 morphology and molecular data (Jenner et al., 2009). Analyses of whole mitochondrial genomes place 2099 Euphausiacea (krill) within Decapoda (Shen et al., 2015), a result congruent with acquisition of a 2100 nauplius larval stage (though this is accepted as convergent: (Jirikowski et al., 2013; Scholtz, 2000). 2101 We apply caution in interpreting deep splits inferred from mitochondrial DNA (Simon and Hadrys, 2102 2013); hence, we accept decapod monophyly to the exclusion of krill. 2103 2104 56.1. Fossil specimens 2105 2106 As for 49.1. 2107 2108 56.2. Phylogenetic justification 2109 2110 As for 49.2.

2111	
2112	56.3. Age justification
2113	
2114	As for 49.3.
2115	
2116	57. Crown Allotriocarida
2117	
2118	This clade comprises Branchiopoda, Cephalocarida, Remipedia, and Hexapoda, their last
2119	common ancestor and all of its descendants (Fig. 15). Monophyly of this clade was proposed by a
2120	combined phylogenetic analysis of transcriptomes, nuclear protein-coding genes, and morphology
2121	(Oakley et al., 2013). As of this writing, a transcriptome remains to be sequenced for Cephalocarida.
2122	This clade is not recognized in GenBank taxonomy.
2123	
2124	57.1. Fossil specimens
2125	
2126	Rehbachiella kinnekullensis Müller, 1983. UB 644, holotype, consisting of a complete larva
2127	(Fig. 16a). This species has been extensively documented by Walossek (1993).
2128	
2129	57.2. Phylogenetic justification
2130	
2131	Recent phylogenetic analyses including R. kinnekullensis have strongly indicated a position on
2132	the branchiopod stem lineage (morphology: Legg et al., 2013; combined morphology and molecular:
2133	Oakley et al., 2013) or the cephalocarid stem lineage (morphology: Wolfe and Hegna, 2014). Either
2134	relationship (or a strict consensus position on the stem of Branchiopoda + Cephalocarida) would still
2135	be within the crown group of Allotriocarida.
2136	

2137	57.3. Age justification
2138	
2139	As for 35.3.
2140	
2141	58. Crown Branchiopoda
2142	
2143	This clade comprises Anostraca (fairy/brine shrimp), Notostraca (tadpole shrimp) and
2144	Diplostraca, their last common ancestor and all of its descendants (Fig. 15). Monophyly of this clade is
2145	established by phylogenetic analysis of protein-coding genes (Regier et al., 2010; Spears and Abele,
2146	2000), transcriptomes (von Reumont et al., 2012), morphology (Legg et al., 2013), and combined
2147	molecular and morphological data (Oakley et al., 2013).
2148	
2149	58.1. Fossil specimens
2150	
2151	Lepidocaris rhyniensis Scourfield, 1926. BMNH IN. 24493, holotype (Fig. 16b).
2152	
2153	58.2. Phylogenetic justification
2154	
2155	L. rhyniensis has been included in several phylogenetic analyses, coded from a composite of
2156	holotype and paratype material (Scourfield, 1926). With morphology only, L. rhyniensis is sister to
2157	extant Anostraca (Hegna, 2012; Legg et al., 2013); with morphology and molecular data, it is within
2158	Anostraca (Oakley et al., 2013). Therefore, it is unequivocally a crown group member of
2159	Branchiopoda.
2160	
2161	58.3. Age justification
2162	

2163 Minimum as for 10.3. Soft maximum as for 26.3.

2164

2165 **58.4**. Discussion

2166

2167 R. kinnekullensis has been frequently used to polarize the evolution of Branchiopoda. Its fossils 2168 are known only from larval stages, which may confound discussions of its morphology (Wolfe and 2169 Hegna, 2014). Recent phylogenetic analyses have indicated a position on the branchiopod stem 2170 lineage (Legg et al., 2013; Oakley et al., 2013) or the cephalocarid stem lineage (Wolfe and Hegna, 2171 2014), excluded from the branchiopod crown. Nevertheless, divergence time analyses suggest 2172 Cambrian origins for crown Branchiopoda (Oakley et al., 2013), such that molecular clock estimates 2173 do not conflict with branchiopod affinities for Cambrian filter plate fossils (Harvey and Butterfield, 2008) 2174 or *R. kinnekullensis*. 2175 2176 **59. Crown Anostraca** 2177 2178 This clade comprises Artemiidae, Branchinectidae, Branchipodidae, Chirocephalidae, 2179 Parartemiidae, Streptocephalidae, Tanymastigidae and Thamnocephalidae, their last common 2180 ancestor and all of its descendants (Fig. 15). Monophyly of five sampled families is established by 2181 phylogenetic analysis of six housekeeping genes and morphology (Richter et al., 2007). Full sampling 2182 of families produced monophyletic Anostraca in an analysis of one ribosomal gene (Weekers et al., 2183 2002). 2184 2185 59.1. Fossil specimens 2186 2187 Palaeochirocephalus rasnitsyni Trussova, 1975. TsGM 7a/10303 and 9/10303, preserving male 2188 antennae, and TsGM 2/10303, preserving a female body. The holotype does not preserve any

2189 diagnostic characters for the Anostraca crown group.

2190

2191 59.2. Phylogenetic justification

2192

*P. rasnitsyni* (formerly *Chirocephalus rasnitsyni* Trussova, 1971) has not been included in a phylogenetic analysis. Taxonomic placement of its family, Palaeochirocephalidae, implicitly relates them to the extant family Chirocephalidae, though this family is considered *incertae sedis* by Rogers (2013). Morphological characters (shared with Chirocephalidae) supporting this relationship include 11 thoracic appendages bearing two pre-epipodites, the nine-segmented abdomen, and the basally separated two-segmented antennae in males (Trussova, 1971). A possible position on the stem lineage of Chirocephalidae would therefore place *P. rasnitsyni* within the crown group of Anostraca.

2200

### 2201 59.3. Age justification

2202

2203 The type locality of *P. rasnitsyni*, briefly described by Trussova (1971), is the left bank of Daya 2204 River, upstream from Shiviya Falls, in eastern Transbaikal, Russia. This locality, within the Unda-Daya 2205 Basin, has been assigned to the Glushkovo Formation (Sinitshenkova, 2005). The age of the 2206 Glushkovo Formation is poorly constrained, suggested as Late Jurassic (Sinitsa and Starukhina, 2207 1986), Early Cretaceous (Sinitshenkova, 2005; Zherikhin et al., 1998), or perhaps at the 2208 Jurassic/Cretaceous boundary (Rasnitsyn and Quicke, 2002). However, P. rasnitsyni itself (along with 2209 palaeopteran insects such as Proameletus caudatus and Equisetum undense) correlates the 2210 Glushkovo Formation to the Baigul locality, also in Transbaikalia (Ignatov et al., 2011). The Baigul 2211 locality preserves fossil Bryokhutuliinia jurassica, one of only five known genera of Jurassic mosses 2212 (Ignatov et al., 2011). Thus Baigul can be correlated to the Ulugey Formation of Mongolia, which also 2213 preserves Bryokhutuliinia fossils (Ignatov, 1992). The Ulugey Formation, in turn, is correlated to the La 2214 Cabrúa (Sierra del Montsec, Pyrenees, Spain) locality based on the shared presence of the

2215 coleopteran genus Gobicar (Gratshev and Zherikhin, 2000; Legalov, 2010; Soriano et al., 2006). Fossil 2216 charophyte algae (Atopochara trivolvis triguetra) indicate an age of late Hauterivian-early Barremian 2217 for the freshwater deposits of La Cabrúa (Gomez et al., 2002; Martín-Closas and López-Morón, 1995). 2218 Although it has been proposed that a minimum age of the Montsec limestone may be as young as the 2219 end Maastrichtian (O'Reilly et al., 2015), recent biostratigraphic work proposes the last appearance of 2220 A. trivolvis triguetra is correlated to the Deshayesites weissi ammonite Zone at its youngest (Martín-2221 Closas et al., 2009). Revision of Tethyan ammonite dates indicates the D. weissi Zone, now the D. 2222 forbesi Zone, had an upper boundary of 125.71 Ma (Ogg et al., 2012a). This age is early Aptian, and 2223 provides a minimum for the correlated Glushkovo Formation. 2224 Soft maximum as for 26.3.

2225

### 2226 **59.4**. Discussion

2227

2228 Oakley et al. (2013) placed the Early Devonian *L. rhyniensis* in the crown group of Anostraca, 2229 having sampled extant members of Artemiidae and Streptocephalidae. Earlier descriptions (Sanders, 2230 1963; Scourfield, 1940a, 1926; Walossek, 1993) support this position. However, the most extensively 2231 sampled morphological analyses of Hegna (2012) consistently place *L. rhyniensis* as sister to all 2232 extant Anostraca. The Late Devonian *Haltinnaias serrata* Gueriau et al., 2016, described from both 2233 sexes, likely also belongs to the total group of Anostraca.

Other fossils from the Late Jurassic Daohugou Beds of China (Huang et al., 2006; Shen and Huang, 2008) and Early Cretaceous Koonwarra Formation of Australia are likely to belong to the crown group of Anostraca, as they have been included in a morphological phylogenetic analysis (Hegna, 2012), but these have not been described in detail.

2238

#### 2239 **60. Crown Notostraca**

2240

2241	This clade comprises two extant genera, <i>Triops</i> and <i>Lepidurus</i> , their last common ancestor and
2242	all of its descendants (Fig. 15). Monophyly is established by phylogenetic analysis of housekeeping
2243	genes (Mathers et al., 2013), morphology (Lagebro et al., 2015), and combined morphological and
2244	molecular data (Richter et al., 2007).
2245	
2246	60.1. Fossil specimens
2247	
2248	Chenops yixianensis Hegna and Ren, 2010. CNU-CAL-HP-2009001 (part; Fig. 16c) and CNU-
2249	CAL-HP-2009002 (counterpart), holotype.
2250	
2251	60.2. Phylogenetic justification
2252	
2253	In the morphological phylogenetic analysis of Lagebro et al. (2015), C. yixianensis was in a
2254	polytomy with other crown Notostraca, including Lepidurus batesoni. The equal size of thoracic
2255	endopods and fourth and fifth endites may exclude C. yixianensis from crown Notostraca (Hegna and
2256	Ren, 2010). However, in previous morphological phylogenies (Hegna, 2012), C. yixianensis was sister
2257	taxon to the extant L. batesoni. This is because L. batesoni lacks elongated endites on the first
2258	thoracic appendage, suggesting a synapomorphy between C. yixianensis and the extant species, and
2259	perhaps membership in an entirely different genus (Hegna, 2012; Hegna and Ren, 2010). If indeed C.
2260	yixianensis is, based on phylogenies and endite morphology, a sister group of L. batesoni, it would
2261	remain within the crown Notostraca.
2262	
2263	60.3. Age justification
2264	
2265	This fossil was discovered in the Yixian Formation of northeastern China (Hegna and Ren,
2266	2010). The Yixian Formation lies between the overlying Jiufotang Formation and underlying Tuchengzi
	88

2267 Formation; together they comprise the Jehol Group (e.g. Chang et al., 2009a; Zhou, 2006). Dating of 2268 the Jehol Group has been contentious, varying from Late Jurassic to Early Cretaceous based on 2269 biostratigraphic and radiometric techniques. Recent 40Ar/39Ar dates yielded ages of 129.7 Ma ± 0.5 2270 Myr for basaltic lava from the bottom of the Yixian Formation and 122.1 Ma  $\pm$  0.3 Myr for tuff layers at 2271 the bottom of the overlying Jiufotang Formation (Chang et al., 2009a). Other age estimates have fallen 2272 within this range (reviewed by Zhou, 2006). This debate underscores the point that reasonably precise 2273 radiometric dates may still be quite inaccurate. We conservatively use the younger of these estimates, 2274 so a minimum age for Yixian fossils is 121.8 Ma.

Soft maximum as for 26.3.

2276

2277 60.4. Discussion

2278

2279 *Strudops goldenbergi* Lagebro et al., 2015 was recently described from the Late Devonian, 2280 which would be the oldest notostracan. In a morphological phylogenetic analysis, however, it could 2281 only be identified as a member of the total group (Lagebro et al., 2015), and thus cannot assign a 2282 minimum age to crown Notostraca.

Morphological conservatism (i.e. Permian and Triassic fossils erroneously attributed to the extant species *Triops cancriformis*) has led to the misleading name 'living fossil' for Notostraca (Hegna, 2012; Mathers et al., 2013). Once touted as the 'oldest living species,' *T. cancriformis permiensis*, from the Permian of France, is more similar to the co-occurring *Lepidurus occitaniacus* than extant *Triops* (Lagebro et al., 2015). Decay experiments on living *T. cancriformis* confirm that carapace characters and elongated endites of the first thoracic limb are phylogenetically meaningful, thus rejecting a referral of any fossil to the extant species (Hegna, 2012).

2290

2291 61. Crown Diplostraca

2292

2293 This clade comprises Laevicaudata, Spinicaudata, Cyclestherida (these three collectively: 2294 'clam shrimp') and Cladocera (water fleas), their last common ancestor and all of its descendants (Fig. 2295 **15**). Monophyly is supported by phylogenetic analysis of transcriptomes (von Reumont et al., 2012) 2296 and 62 nuclear protein-coding genes (Regier et al., 2010), and combined molecules and morphology 2297 (Oakley et al., 2013) although Cyclestherida was not sampled in these analyses. Smaller molecular 2298 analyses (Richter et al., 2007 with indel costs) and morphological analyses (Hegna, 2012; Legg et al., 2299 2013; Olesen, 2009, 1998; Richter et al., 2007) including data for Cyclestherida also support 2300 monophyly of Diplostraca. 2301 2302 61.1. Fossil specimens

2303

2304 *Leaia chinensis* Shen, 1983. NIGP 51786, holotype, preserving a left valve (**Fig. 16d**).

2305

2306 61.2. Phylogenetic justification

2307

2308 L. chinensis has not been treated in a phylogenetic context. It is placed within the fossil family 2309 Leaiidae primarily based on carapace shape, including the nearly straight ventral edge (Shen, 1978; 2310 Tasch, 1987). However, congeneric fossils, L. gondwanella Tasch, 1987 and L. canadensis Shen and 2311 Schram, 2014, may have preserved soft parts (Shen and Schram, 2014). These include biramous 2312 antennae, mandibles, as well as putative shell glands and digestive tubes, and radiating carinae (Shen 2313 and Schram, 2014). The short and delicate antennal flagella and radiating carinae of L. chinensis, in 2314 particular, are similar to extant Spinicaudata and Cyclestherida; the presence of growth lines is only 2315 known from Spinicaudata (Shen and Schram, 2014). However, the head shape of L. chinensis is more 2316 similar to Laevicaudata. This suggests phylogenetic positions either on the stem of Onychocaudata 2317 (Spinicaudata, Cyclestherida, and Cladocera) or on the stem of Laevicaudata. A position as stem 2318 Diplostraca would mean growth lines are ancestral for all diplostracans, and have been lost twice (in

the ancestors of Laevicaudata and Cyclestherida + Cladocera), which is unparsimonious. Hence we
 support *L. chinensis* within crown Diplostraca.

2321

2322 61.3. Age justification

2323

2324 L. chinensis was found in sediments of the Guitou Group, near Chengma village, Hepu county, 2325 Guangxi Zhuang Autonomous Region, southern China (Shen, 1978). The upper subgroup of the 2326 Guitou Group, bearing conchostracan fossils, has purple-grey sandy shales within mudstone 2327 lamination, and is overlain by the Tungkangling Formation (Shen, 1978). The brachiopod 2328 Stringocephalus, the stromatoporoid corals Endophyllum and Sunophyllum, and the ostracods 2329 Samarella crassa and Tuberokloedenia bituberculata together indicate a Givetian age for the upper 2330 Tungkangling Formation (Liao and Ruan, 2003). The underlying Yingtang Formation (as well as the 2331 lower Tungkangling Formation) are correlated to the Eifelian Stage by the ostracods *Bairdocypris* 2332 biesenbachi and Flatiella subtrapezoidalis (Liao and Ruan, 2003), the brachiopod Bornhardtina and 2333 the conodonts Polygnathus australis, P. costatus, and P. partitus (Ma et al., 2009). As the 2334 conchostracan-bearing sediments underlie the Tungkangling Formation, they are no younger than 2335 Eifelian in age. The upper boundary of the Eifelian is  $387.7 \text{ Ma} \pm 0.8 \text{ Myr}$ , providing a minimum age of 2336 386.9 Ma.

2337 Soft maximum as for 26.3.

2338

## 2339 **62. Crown Spinicaudata**

2340

This clade comprises Leptestheriidae, Cyzicidae and Limnadiidae, their last common ancestor and all of its descendants (**Fig. 15**). Clade names are defined in Schwentner et al. (2009). Monophyly is established by phylogenetic analysis of morphology (Hegna, 2012; Olesen, 1998; Richter et al., 2007), three housekeeping genes (Schwentner et al., 2009), and six housekeeping genes plus

2345	morphology (Richter et al., 2007).
2346	
2347	62.1. Fossil specimens
2348	
2349	Dundgobiestheria mandalgobiensis Li et al., 2014. ED-A-14-1, holotype (Fig. 16e).
2350	
2351	62.2. Phylogenetic justification
2352	
2353	Phylogenetic analysis of spinicaudatan fossils is rare, owing to difficulty in character
2354	identification (Astrop and Hegna, 2015; see also 62.3). Members of Leptestheriidae appear to share
2355	emergence of dendritic reticulation and anastomizing ridge ornamentation with the fossil spinicaudatan
2356	family Loxomegaglyptidae (Astrop and Hegna, 2015; Shen, 1994). D. mandalgobiensis is perhaps the
2357	oldest definitive Loxomegaglyptidae, based on large-sized reticulate ornamentation and weakly
2358	defined growth lines, shared with other members of the family (Li et al., 2014). Due to the above
2359	ornamentation characters (Astrop and Hegna, 2015; T. Astrop, pers. comm.), it can be placed on the
2360	stem lineage of Leptestheriidae, and thus within crown Spinicaudata.
2361	
2362	62.3. Age justification
2363	
2364	D. mandalgobiensis is from the Eedemt Formation, Khootiin Khotgor coal mine region,
2365	Dundgobi Province, southeast Mongolia (Li et al., 2014). The spinicaudatan genus Triglypta (co-
2366	occurring with D. mandalgobiensis) provides a biostratigraphic constraint on the Eedemt Formation, as
2367	Triglypta species also occur in both the (older) Euestheria ziliujingensis fauna and (younger)
2368	Sinokontikia fauna in lacustrine sequences of northwestern China (Li et al., 2014; Li and Matsuoka,
2369	2012). First, the E. ziliujingensis fauna is distributed throughout east Asia, dated to a Bajocian-
2370	Bathonian (Jurassic) age by the occurrence of Euestheria trotternishensis (Chen et al., 2007). E.

2371 trotternishensis co-occurs in the Skyestheria spinicaudatan fauna of Skye, Scotland; the Bajocian-2372 Bathonian date for this locality comes from ammonite and palynological index fossils (Chen and 2373 Hudson, 1991). Although the Sinokontikia fauna was once thought stratigraphically equal to the late E. 2374 ziliujingensis fauna (Chen et al., 2007; Li and Matsuoka, 2012), Sinokontikia has been determined to 2375 be younger based on occurrence in the Qiketai Formation of the Turpan Basin, northwest China. The 2376 Qiketai Formation is constrained only to the Callovian. As Chinese Triglypta (the index genus for the 2377 Eedemt Formation) is absent from any higher strata, a minimum age comes from the upper boundary 2378 of the Sinokontikia fauna (Li et al., 2014). The upper boundary of the Callovian is 163.5 Ma ± 1.0 Myr. 2379 giving a minimum age for the Eedemt Formation of 162.5 Ma.

2380 Soft maximum as for 26.3.

2381

### 2382 62.4. Discussion

2383

2384 Preservation of the calcified spinicaudatan carapace is extremely common (some fossil species are used as biostratigraphic indices), but characters diagnostic for extant taxa (i.e. soft parts) are 2385 2386 rarely preserved (Hegna, 2012; Orr and Briggs, 1999). Uniquely among 'conchostracans' (and indeed 2387 most arthropods), Spinicaudata do not moult their carapace, instead preserving growth lines. The 2388 number of growth lines necessarily increases through ontogeny, so it is a poor character to 2389 demonstrate phylogenetic relationships. Therefore relationships among fossil taxa have been 2390 determined based on ornamentation of the carapace (e.g. Gallego, 2010); however, these characters 2391 have not yet been integrated with morphological study of extant carapaces. Ongoing work seeks to 2392 demonstrate the utility of carapace ornamentation as valid phylogenetic characters (Astrop and 2393 Hegna, 2015). Furthermore, integration of past descriptive work is hindered by language barriers 2394 between different workers (Chinese, Russian, and English; summarized by Astrop and Hegna, 2015). 2395 For example, some poorly known fossils from the Middle Devonian of Antarctica, described as 2396 members of the genus Cyzicus (Euestheria), may be assigned to Spinicaudata (Tasch, 1987), possibly

2397 on the stem lineage of 'non-Australian Cyzicidae' sensu Schwentner et al. (2009). Characters linking 2398 the Antarctic fossils to the living clade, however, are dubious. There are reports of uncertain Late 2399 Devonian stem group members for Limnadiidae (Liu and Gao, 1985), and much more likely Permian 2400 stem Limnadiidae (Novojilov, 1970), but these fossils are insufficiently described, leaving any specific 2401 crown spinicaudatan character states debatable. Therefore we must caution that Jurassic age is likely 2402 a severe underestimate of crown spinicaudatan antiquity. Finally, the Sinemurian Afrolimnadia 2403 sibiriensis Tasch, 1987 was used to calibrate crown Spinicaudata in a divergence time analysis, but 2404 with limited justification of characters for Limnadiidae (Bellec and Rabet, 2016).

2405

### 2406 **63. Crown Cladocera**

2407

This clade comprises Anomopoda, Ctenopoda, Onychopoda and Haplopoda, their last common ancestor and all of its descendants (**Fig. 15**). Monophyly of this clade is supported by phylogenetic analysis of housekeeping genes alone (Stenderup et al., 2006), morphology (Hegna, 2012; Olesen, 2009, 2007, 1998), and six housekeeping genes plus morphology (Richter et al., 2007).

2413 63.1. Fossil specimens

2414

2415 Smirnovidaphnia smirnovi Kotov, 2007, illustrated by two specimens: PIN 1873/100 (holotype,
2416 preserving the second antenna; Fig. 16f) and PIN 1873/105 (paratype, preserving both second
2417 antennae and mandibles).

2418

2419 63.2. Phylogenetic justification

2420

2421 The setal armature of the second antenna is similar to that found in extant Ctenopoda (Kotov, 2422 2007). In morphological phylogenetic analyses, *S. smirnovi* was either found in a basal polytomy with

2423	all of crown Cladocera, or it was sister to all Cladocera except Anomopoda (Hegna, 2012). The
2424	polytomy could indicate a stem cladoceran position, but the analyses in which S. smirnovi was within
2425	crown Cladocera included a lesser amount of missing data, and thus may be more robust.
2426	Furthermore, Ctenopoda itself was not recovered as monophyletic in these analyses, but S. smirnovi
2427	was related to taxa that have been previously included in Ctenopoda (Hegna, 2012).
2428	
2429	63.3. Age justification
2430	
2431	S. smirnovi was found on the right bank of the Angara River, downstream of Ust'-Baley village
2432	in the Olonkovsky District of Asian Russia (Kotov, 2007). According to the presence of
2433	Osmundacidites-type plant spores, the Ust'-Baley outcrop of the Cheremkhovo or Cheremkhovskaya
2434	Formation is correlated to the late Toarcian stage of the Early Jurassic (Akulov et al., 2015). The upper
2435	boundary of the Toarcian is 174.1 Ma $\pm$ 1.0 Myr, therefore giving a minimum age of 173.1 Ma.
2436	Soft maximum as for 26.3.
2437	
2438	63.4. Discussion
2439	
2440	Ebullitiocaris oviformis Anderson et al., 2003 from the Devonian Rhynie Chert and E. elatus
2441	Womack et al., 2012 from Carboniferous chert have both been described as Cladocera.
2442	Fragmentation patterns of both fossils are inconsistent with those observed from decay experiments,
2443	therefore casting doubt on their cladoceran membership (Hegna, 2012).
2444	Other Jurassic/Cretaceous members of the fossil family Prochydoridae are known from
2445	Mongolia and Asian Russia (Kotov, 2009). However, the Prochydoridae have been proposed as a
2446	member of the stem lineage of Anomopoda, the stem of all non-Anomopoda Cladocera, as well as the
2447	stem of Cladocera itself (Kotov, 2013, 2009). Thus crown-group affinity cannot be confirmed.
2448	

2451 This clade comprises Collembola (springtails), Protura (cone heads), Diplura (two-pronged 2452 bristletails) and Insecta (insects), their last common ancestor and all of its descendants (Fig. 17). 2453 Monophyly of Hexapoda is established by phylogenetic analysis of nuclear protein-coding genes 2454 (Regier et al., 2010, 2005; Sasaki et al., 2013), transcriptomes (Dell'Ampio et al., 2014; Misof et al., 2455 2014), and morphology (Legg et al., 2013). 2456 2457 64.1. Fossil specimens 2458 2459 Rhyniella praecursor Hirst and Maulik, 1926. NHMUK IN. 27765, lectotype (fide Ross and York, 2460 2003), head capsule with mouthparts in chert (Fig. 2f). Paralectyotypes NHMUK IN. 38225-38227. 2461 2462 64.2. Phylogenetic justification 2463 2464 The Rhynie Chert taxon *R. praecursor* Hirst and Maulik, 1926, was originally identified as an 2465 insect. Re-identification as a poduromorph collembolan was made by Tillyard (1928). Additional 2466 material was examined by Scourfield (1940a, 1940b), who considered R. praecursor to be a possible 2467 entomobryomorph rather than a poduromorph. Subsequent studies, including some additional

specimens, were made by Massoud (1967), Whalley and Jarzembowski (1981), Greenslade (1988),

2469 and Greenslade and Whalley (1986). The most recent of these investigations favour membership of at

2470 least some specimens assigned to *R. praecursor* in the extant entomobryomorph family Isotomidae

- 2471 (Greenslade and Whalley, 1986). Greenslade (1988) indicated that three species could be
- represented in the sample that is currently assigned to *R. praecursor*. Identification as an

2473 entomobryomorph underpins an assignment to the crown groups of Collembola and Hexapoda. Other

taxa from the Rhynie Chert (*Rhyniognatha* and *Leverhulmia*; Engel and Grimaldi, 2004; Fayers and

2475	Trewin, 2005) and thus as old as <i>R. praecursor</i> have also been identified as Hexapoda, and more
2476	precisely as Insecta.
2477	
2478	64.3. Age justification
2479	
2480	As for 58.3.
2481	
2482	65. Crown Collembola
2483	
2484	This clade comprises Entomobryomorpha, Neelipleona, Poduromorpha, Symphypleona and
2485	Tomoceroidea, their last common ancestor and all of its descendants (Fig. 17). Most studies with
2486	substantial outgroup sampling are based on only one or two subclades of Collembola; however,
2487	phylogenetic analysis of ribosomal genes including all subclades (Gao et al., 2008; Xiong et al., 2008)
2488	demonstrated monophyly. Additional support with limited sampling of Collembola subclades comes
2489	from transcriptomes (Dell'Ampio et al., 2014), mitochondrial genomes (Carapelli et al., 2007), and
2490	morphology (D'Haese, 2003).
2491	
2492	65.1. Fossil specimens
2493	
2494	As for 64.1.
2495	
2496	65.2. Phylogenetic justification
2497	
2498	As for 64.2.
2499	
2500	65.3. Age justification
	97

2501	
2502	As for 58.3.
2503	
2504	66. Crown Diplura
2505	
2506	This clade comprises Projapygoidea, Japygoidea and Campodeoidea, their last common
2507	ancestor and all of its descendants (Fig. 17). Monophyly of Diplura has been demonstrated by
2508	phylogenetic analysis of ribosomal genes (Gao et al., 2008), whole mitochondrial genomes (Chen et
2509	al., 2014), and morphology (Koch, 1997).
2510	
2511	66.1. Fossil specimens
2512	
2513	Ferrojapyx vivax Wilson and Martill, 2001. SMNS 64276, holotype.
2514	
2515	66.2. Phylogenetic justification
2516	
2517	F. vivax is "morphologically indistinguishable" (Wilson and Martill, 2001) from extant
2518	Japygoidea, sharing characters such as 40-segmented antennules, abdominal tergites 1-8 with a
2519	median suture, abdominal tergite 9 significantly shorter, conical abdominal styli, and forcipate cerci
2520	with curved inner margins and lacking obvious denticles (Wilson and Martill, 2001). Monophyly of
2521	Japygoidea has been considered "beyond doubt" (Koch, 2009; Fig. 3 therein for cladogram), so a
2522	phylogenetic position for this fossil either within or closely related to that clade would place it within
2523	crown Diplura.
2524	
2525	66.3. Age justification
2526	
	98

2527 As for 29.3. 2528 2529 67. Crown Insecta 2530 2531 This clade comprises Microcoryphia (jumping bristletails), Zygentoma (silverfish) and Pterygota 2532 (winged insects), their last common ancestor and all of its descendants (Fig. 17). Monophyly is 2533 established by phylogenetic analysis of nuclear protein-coding genes (Regier et al., 2010, 2005; 2534 Sasaki et al., 2013), transcriptomes (Dell'Ampio et al., 2014; Misof et al., 2014), and morphology 2535 (Legg et al., 2013). 2536 2537 67.1. Fossil specimens 2538 2539 Rhyniognatha hirsti Tillyard, 1928. BMNH IN. 38234, holotype, preserving the mandibles and 2540 their articulation (Fig. 18d). Redescribed and imaged by Engel and Grimaldi (2004). 2541 2542 67.2. Phylogenetic justification 2543 2544 The only known specimen (the holotype) of R. hirsti demonstrates that the preserved pair of 2545 mandibles articulate at two points, i.e. are dicondylic (Engel and Grimaldi, 2004). Dicondylic mandibles 2546 are a diagnostic synapomorphy of Insecta (including Microcoryphia; Blanke et al., 2015). Although R. 2547 hirsti has not been included in numerical phylogenetic analyses, its mandibular shape implies 2548 "metapterygote" affinities (Engel and Grimaldi, 2004) and accordingly crown group membership within 2549 Insecta. 2550 2551 67.3. Age justification 2552

2553 As for 58.3.

2554

2555 67.4. Discussion

2556

A complete body fossil of a putative insect, *Strudiella devonica* Garrouste et al., 2012, was described from the Fammenian (372-359 Ma) of Strud, Belgium. Apomorphies supporting an insect affinity (such as the structure of the mandibles and the number of legs), however, are poorly preserved and potentially over-interpreted (Hörnschemever et al., 2013).

2561

### 2562 **68. Crown Microcoryphia**

2563

2564 This clade comprises the families 'Machilidae' and Meinertillidae, their last common ancestor, 2565 and all of its descendants (Fig. 17). This clade is commonly referred to as Microcoryphia in taxonomic 2566 literature and Archaeognatha in phylogenetic literature (Gaju-Richart et al., 2015). Recently it was clarified that Archaeognatha includes the completely extinct order Monura (compound eves not fused, 2567 2568 paracercus only) and Microcoryphia (very small head vertex due to their fused compound eyes, 2569 terminalia composed of a median paracercus and two lateral cerci), and thus the crown group refers to 2570 Microcoryphia only (Gaju-Ricart et al., 2015). Monophyly is supported by phylogenetic analysis of 2571 transcriptomes (Misof et al., 2014), nuclear protein-coding genes (Regier et al., 2010), and 2572 morphology (Legg et al., 2013). Synapomorphies are discussed and mapped on cladograms by Larink 2573 (1997) and Koch (2003). 2574 2575 68.1. Fossil specimens 2576

2577 *Cretaceomachilis libanensis* Sturm and Poinar, 1998 (collection Milki No. 194/35, deposited at 2578 the American University of Beirut, Beirut, Lebanon), holotype, male in amber (**Fig. 18b**).

# 2580 68.2. Phylogenetic justification

2581

*C. libanensis* shares morphological characters with the extant family Meinertillidae. These
include the the absence of scales on the scapus, pedicellus and flagellum, and the presence of a
characteristic hook near the distal end of article 2 of the male maxillary palp (Sturm and Poinar, 1998).
The latter character is a synapomorphy of crown Meinertillidae (Sturm and Poinar, 1998), therefore the
fossil is within crown Microcoryphia.

2587

2588 68.3. Age justification

2589

*C. libanensis* was discovered in Cretaceous amber, from a locality in Lebanon that was not recorded (Sturm and Poinar, 1998). We therefore use a minimum age constraint from the youngest of the several known Lebanese amber localities, which all bear the same age within the early Barremian (Maksoud et al., 2016). The upper boundary of the early Barremian is proposed to be the first appearance of the ammonite *Ancyloceras vandenheckii* (Ogg et al., 2012). Cyclostratigraphy dates the *A. vandenheckii* Zone beginning at 129.41 Ma (Ogg et al., 2012), providing a minimum age for Jezzine Lebanese amber fossils.

- 2597 Soft maximum as for 26.3.
- 2598

2599 *68.4. Discussion* 

2600

Body imprint and trackway trace fossils from the Pennsylvanian have been attributed to both Archaeognatha and Zygentoma (Getty et al., 2013). Experiments with extant species of both clades indicate that archaeognathans produced fossil body imprints, as well as trackways exhibiting opposite symmetry (Getty et al., 2013). However, it is not possible to distinguish specific crown group

apomorphies for these traces.

2606 Dasyleptidae, a diverse fossil group known from the Carboniferous-Triassic, has been 2607 proposed as the sister group of Ectognatha (Collembola, Diplura, Protura) as well as part of 2608 Archaeognatha. Recent classifications place Dasyleptidae in Monura, a separate extinct suborder of 2609 Archaeognatha, and thus outside its crown group (Bechly and Stockar, 2011; Gaju-Ricart et al., 2015). 2610 2611 69. Crown Zygentoma 2612 2613 This clade comprises the families Lepismatidae, Nicoletiidae, Lepidotrichidae, Maindroniidae, 2614 and Protrinemuridae, their last common ancestor and all of its descendants (Fig. 17). Phylogenetic 2615 analyses of transcriptomes (Misof et al., 2014), protein-coding genes (Regier et al., 2010; Sasaki et 2616 al., 2013), morphology (Blanke et al., 2014), and combined molecular and morphological data (Kjer et 2617 al., 2006) with partial taxon sampling support monophyly. 2618 2619 69.1. Fossil specimens 2620 2621 Burmalepisma cretacicum Mendes and Poinar, 2008 (specimen B-TH-1 deposited in the Poinar 2622 amber collection maintained at Oregon State University; B-TH refers to Burma-Thysanura), holotype, a 2623 female in amber (Fig. 18c). 2624 2625 69.2. Phylogenetic justification 2626 2627 Although it has not been included in a phylogenetic analysis, *B. cretacicum* bears several 2628 morphological similarities to the extant family Lepismatidae. These include the presence of compound 2629 eyes, absence of ocelli, coxal, femur, and tarsal morphology, absence of a pronotal setal collar, and 2630 presence of only smooth macrochaetae (Mendes and Poinar, 2008). A phylogenetic position either on

2631	the stem or within the crown of Lepismatidae is within the crown group of Zygentoma.
2632	
2633	69.3. Age justification
2634	
2635	As for 33.3.
2636	
2637	69.4 Discussion
2638	
2639	A possible Zygentoma fossil has been recorded from the older Aptian Crato Formation of Brazil
2640	(Sturm, 1998), but is not sufficiently characterized to be a calibration fossil. Another fossil from
2641	Burmese amber, Cretolepisma kachinicum Mendes and Wunderlich, 2013, is also identified as
2642	Lepismatidae. This fossil is of equal age and affinity, and is therefore also an acceptable calibration for
2643	Zygentoma.
2644	
2645	70. Crown Pterygota
2646	
2647	This clade comprises Palaeoptera (mayflies, dragonflies) and Neoptera (flexible winged
2648	insects), their last common ancestor and all of its descendants (Fig. 17). Monophyly is established
2649	based on phylogenetic analysis of nuclear protein-coding genes (Regier et al., 2010, 2005; Sasaki et
2650	al., 2013), transcriptomes (Misof et al., 2014; Simon et al., 2012), and morphology (Legg et al., 2013).
2651	
2652	70.1. Fossil specimens
2653	
2654	Delitzschala bitterfeldensis Brauckmann and Schneider, 1996 (BGR X 9216), holotype,
2655	preserving a forewing, a hindwing, cerci, and part of the abdomen (Fig. 18a).
2656	
	103

2657 70.2. Phylogenetic justification

2658

2659 D. bitterfeldensis is considered a member of the family Spilapteridae, in the clade 2660 Palaeodictyopterida (Brauckmann and Schneider, 1996). Morphological characters supporting this 2661 relationship include the concave anterior wing margin and deeply bifurcate MA vein ending with two 2662 long branches (Brauckmann and Schneider, 1996; Li et al., 2013b). Other fossils of Spilapteridae have also preserved the distinctive colour patterns and long cerci observed in D. bitterfeldensis (Li et al., 2663 2664 2013b). Palaeodictyoptera have previously assumed to be related to extant Palaeoptera as they share 2665 the inability to fold their wings over the abdomen (a character observed in *D. bitterfeldensis*). However, 2666 a recent morphological phylogenetic analysis controversially recognized Palaeodictyopterida as the 2667 fossil sister group of Neoptera (Sroka et al., 2015). In this evolutionary scenario, palaeopterous wings 2668 are presumably a symplesiomorphy. Nonetheless, the position of Palaeodictyoptera suggested by 2669 Sroka et al. (2015) remains within crown Pterygota.

2670

2671 70.3. Age justification

2672

*D. bitterfeldensis* was preserved in a core extracted from the locality Bore WISABAW 1315, in the Sandersdorf Formation of Bitterfeld, Germany (Brauckmann and Schneider, 1996). The core was correlated with the E2 ammonite zone, i.e. Arnsbergian (middle Namurian A) based on the cooccurrence of ostracods and conchostracans (Brauckmann et al., 1994). The Arnsbergian is further correlated to the late Serpukhovian stage at the end of the Mississippian (Pointon et al., 2012). The upper boundary of the Serpukhovian (base of the Pennsylvanian) is estimated at 323.23 Ma  $\pm$  0.4 Myr (Davydov et al., 2012), giving a minimum age of 322.83 Ma.

2680 Soft maximum as for 26.3.

2681

2682 70.4. Discussion

An undescribed Namurian A (latest Mississippian) member of Archaeorthoptera was initially attributed to Orthoptera (Prokop et al., 2005). It was noted that the veins are strongly deformed, enough so that the authors were reluctant to make a formal systematic description (Prokop et al., 2005). Therefore, we regard the fossil as insufficiently characterized for dating. See section 67.4 for refutation of the even older *Strudiella devonica* (Garrouste et al., 2012).

2689

## 2690 **71. Crown Palaeoptera**

2691

2692 This clade comprises Euplectoptera (mayflies) and Odonata (dragonflies), their last common 2693 ancestor and all of its descendants (Fig. 17). Monophyly of this group has been challenged by 2694 morphology (Kristensen 1981) and some transcriptome data (Simon et al., 2012, 2009), though recent 2695 analyses of nuclear protein-coding genes (Regier et al., 2010) and transcriptomes have supported 2696 Palaeoptera (Misof et al., 2014; von Reumont et al., 2012), the former weakly, only in maximum 2697 likelihood analyses of the total dataset. Recent detailed morphological analyses of head morphology 2698 corroborate the monophyly of Palaeoptera (Blanke et al., 2013, 2012). Although a morphological 2699 phylogenetic analysis (Sroka et al., 2015) claims to reject palaeopteran monophyly, its constituent 2700 extant members, Euplectoptera and Odonata, are each others' closest living relative and named 2701 therein as a new clade, Euhydropalaeoptera. We therefore cautiously endorse Palaeoptera as a clade 2702 of interest for dating.

2703

2704 71.1. Fossil specimens

2705

2706 Oligotypus huangheensis Li et al., 2013a (CNU-NX2006003), holotype, a forewing.

2707

2708 71.2. Phylogenetic justification

2710 This species was originally described as *Sinomeganeura huangheensis* within the family 2711 Meganeuridae, part of Protodonata (Ren et al., 2008). Meganeurids include the "giant" dragonflies 2712 (with wings up to 710 mm), though O. huangheensis is much smaller at 70 mm (Ren et al., 2008). 2713 Despite the size difference, wing venation characters are consistent with classification in Protodonata, 2714 including the fusion of stems of CuP and CuA to a single obligue vein, distinctly stronger than the 2715 crossveins (Ren et al., 2008). This character, previously assumed to be synapomorphic for 2716 Meganeuridae, is more widespread within Protodonata (Li et al., 2013a). The group "Protodonata" 2717 itself is a paraphyletic stem group to crown Odonata, together within the total group Odonatoptera, 2718 defined by the simple MP vein (Sroka et al., 2015). Regardless of the precise relationship of 2719 Protodonata to crown Odonata, its members are definitively within crown Palaeoptera. 2720 2721 71.3. Age justification 2722 2723 The insect beds where this species was located are near Xiaheyan Village in the Qilianshan 2724 Mountains, Zhongwei County, Ningxia Huizu Autonomous Region, northwest China (Zhang et al., 2725 2013). The insect fossil deposits are within the uppermost unit of the upper Tupo Formation 2726 (synonyms Hongtuwa or Zhongwei Formation). The presence of the ammonoids Reticuloceras 2727 reticulatum, Gastrioceras listeri and G. montgomervense and conodonts Declingnathodus noduliferous 2728 and Neognathodus symmetricus indicate a Namurian B/C age (Xie et al., 2004; Yang, 1987; Yang et 2729 al., 1988; Zhang et al., 2013). The (late) Namurian-(early) Westphalian boundary is defined by the 2730 earliest occurrence of the goniatite Gastrioceras subcrenatum (Waters and Davies, 2006), but lacks a precise isotopic date. Pointon et al. (2012) estimated an age of c. 319.9 Ma for the base of the 2731 2732 Westphalian (top of the Namurian, only slightly younger than the Marsdenian) based on Milankovitch 2733 cycles of sedimentation, giving a minimum age for Xiaheyan fossils. 2734 Soft maximum as for 26.3.

# 2736 71.4. Discussion

2737

Due to the controversial status of Palaeoptera as a clade, there are several fossil groups that have been considered for membership: Palaeodictyopterida, Paoliida, stem mayflies (Ephemeroptera, see section 72), and stem dragonflies (Protodonata, including Geroptera) (Grimaldi and Engel, 2005). Each is discussed below.

2742 Palaeodictyopterida, an abundant clade from the Carboniferous and Permian, have been 2743 assumed to be related to extant Palaeoptera as they share the inability to fold their wings over the 2744 abdomen. The oldest member, Delitzschala bitterfeldensis, predates all other Palaeoptera (and all 2745 other Pterygota with preserved wings), as it is from the Mississippian (Brauckmann et al., 1994; 2746 Pointon et al., 2012). In cladodograms in which Palaeodictyopterida is the fossil sister group of 2747 Neoptera (Sroka et al., 2015), palaeopterous wings are presumably a symplesiomorphy. The presence 2748 of nymphal wing pads is probably also a symplesiomorphy of Pterygota (Haug et al., 2016). Therefore 2749 Palaeodictyopterida may be outside the crown and even stem group of Palaeoptera.

Paoliida is an extinct clade known mainly from wings of the Westphalian A stage of the Pennsylvanian. The group has been attributed to the Palaeodictyoptera and later removed (Prokop et al., 2012; Prokop and Nel, 2007). It has been subsequently proposed that Paoliida is the fossil sister group of Dictyoptera (Prokop et al., 2014), and thus are within crown Polyneoptera. This would refute a relationship with Palaeoptera or any of its members.

A full body impression of a putative Carboniferous (Westphalian B/C) mayfly is subject to controversy (Benner et al., 2013; Knecht et al., 2011; Marden, 2013a, 2013b). *Bojophlebia prokopi* Kukalová-Peck, 1985 (Westphalian C) is likely outside of Palaeoptera, according to descriptions and phylogenetic analysis (Prokop et al., 2010; Sroka et al., 2015; Staniczek et al., 2011). The Stephanian B/C fossil *Triplosoba pulchella* Brongniart, 1883, originally described as a mayfly, has been redescribed as Palaeodictyopterida (Prokop and Nel, 2009). The oldest body fossils belonging to the

2761 mayfly stem group are therefore members of the Syntonopteroidea. The oldest Syntonopteroidea are 2762 Lithoneura lameerei Carpenter, 1938 and Syntonoptera schucherti Handlirsch, 1911, from the 2763 Westphalian D Mazon Creek (younger than Xiaheyan) (Nicholson et al., 2015; Prokop et al., 2010). 2764 Putative older members of Odonatoptera are Geroptera, represented by the species 2765 Eugeropteron lunatum and Geropteron arcuatum (both Riek and Kukalová-Peck, 1984), are known 2766 from the late Namurian of Argentina (Gutiérrez et al., 2000; Riek and Kukalová-Peck, 1984). G. 2767 arcuatum was included in a morphological phylogenetic analysis, but was resolved outside 2768 Protodonata, in a polytomy with Odonata, Ephemeroptera, and Neoptera, thus outside Palaeoptera 2769 (Bybee et al., 2008). It need, however, be noted that morphological characters were polarized a priori 2770 with respect to G. arcuatum (Bybee et al., 2008).

2771

## 2772 **72. Crown Euplectoptera**

2773

2774 This clade comprises the families Siphluriscidae, Baetidae, Isonychiidae, Ametropodidae, 2775 Acanthametropodidae, Coloburiscidae, Siphlaenigmatidae, Ameletopsidae, Heptageniidae, 2776 Metretopodidae, Siphlonuridae, Oniscigastridae, Rallidentidae, Nesameletidae, and the larger clades 2777 Carapacea and Furcatergalia, their last common ancestor and all of its descendants (Fig. 17). A 2778 variety of different classification schemes have been proposed (Kluge, 2004, 1998; McCafferty, 1991; 2779 Ogden and Whiting, 2005), but we follow the consensus based on combined phylogenetic analysis of 2780 two nuclear genes, two mitochondrial genes, and morphology (Ogden et al., 2009). Although the 2781 extant members are often referred to as Ephemeroptera, that clade includes a number of extinct 2782 members forming a paraphyletic grade (Kluge, 2004, 1998). As membership of fossil species within a 2783 crown group is only possible if they branch along the stem lineage of a living clade that is part of the 2784 crown itself, we treat crown 'Ephemeroptera' as equivalent to the clade Euplectoptera sensu Tillyard 2785 (1932).

2786 Monophyly has been supported by the aforementioned combined data study (Ogden et al.,
2787 2009), as well as analyses of transcriptomes (with limited but representative taxon sampling: Misof et 2788 al., 2014) and morphology (Ogden et al., 2009 Fig. 4: note this is monophyletic, but the root is shown 2789 intervening).

2790

2791 72.1. Fossil specimens

2792

*Triassonurus doliiformis* Sinitshenkova et al., 2005 (part of the private Louis Grauvogel
 collection, Ringendorf, Bas-Rhin, France, No. 9304), holotype, an incomplete nymph (Fig. 18e).
 2795

2796 72.2. Phylogenetic justification

2797

2798 T. doliiformis has not been explicitly included in a phylogenetic analysis. It bears several 2799 morphological characters indicating affinity with the extant family Siphlonuridae: a large nymph with a 2800 non-flattened body, head longer than short prothorax, massive mesothorax with considerably shorter 2801 metathorax, large and wide forewing pads almost completely covering the hind ones, short and 2802 slender legs, abdominal segments without sharp denticles, large rounded tergaliae, and cerci and 2803 paracercus long (Sinitshenkova et al., 2005). The family Siphlonuridae is not accepted as 2804 monophyletic by all authors (J.-D. Huang et al., 2008; Kluge, 2004; McCafferty, 1991) although it is 2805 supported in total evidence and morphological analyses of Odgen et al. (2009). Siphlonuridae is within 2806 the crown of Euplectoptera, in the clade of families outside Carapacea + Furcatergalia (Ogden et al., 2807 2009). Therefore, *T. doliiformis* is also crown Euplectoptera.

2808

2809 72.3. Age justification

2810

2811 The fossil is derived from the silt-clay Grès à Meules unit (lowermost layer) of the Grès-a-2812 Voltzia Formation, Vosges, northeastern France (Gall and Grauvogel-Stamm, 1993). Grès à Meules

represents the last stage of the fluviatile facies prevalent in the Buntsandstein (Gall, 1985). Based on sequence stratigraphy, Bourquin et al. (2007, 2006) correlate the Grès-a-Voltzia Formation to the middle Anisian stage of the Triassic. Globally, the uppermost boundary of the Anisian is  $241.5 \pm 1$  Ma (Ogg, 2012), providing a minimum age at 240.5 Ma.

2817 Because the monophyly of Palaeoptera is under debate (Simon et al., 2012, 2009), we assign 2818 a soft maximum age that allows its constituent extant orders to be older than the Rhynie Chert, as for 2819 26.3.

2820

2821 **72.4**. *Discussion* 

2822

2823 The Permian fossils *Protereisma permianum* Sellards, 1907 and *Kukalova americana* 

2824 Demoulin, 1970 were coded in the morphology matrix (larval and adult characters) of Odgen et al.

2825 (2009), but their relationships to the crown remain uncertain. *P. permianum* was resolved on the stem

2826 lineage of the extant families Euthyplociidae, Ephemeridae, and Potamanthidae with morphology only,

2827 but outside crown Euplectoptera in a total evidence analysis (Ogden et al., 2009). More generally,

2828 Kluge (Kluge, 2004, 1998) considered the Permian-Triassic members to form a plesion,

2829 Permoplectoptera, outside the crown group Euplectoptera. The relationship of Permoplectoptera to the

2830 crown group remains to be tested by morphological phylogenetics.

Furthermore, many mayfly fossils are of nymphs, and linking characters between fossil and extant nymphs (or fossil nymphs and extant adults) is challenging, though not impossible (e.g. Haug et al., 2016; Wolfe and Hegna, 2014). The nymphal fossils include *Fuyous gregarius* and *Shantous lacustris* (both Zhang and Kluge, 2007), two species from the Jurassic Daohugou biota that have been used as crown group calibrations in previous divergence time analyses (Thomas et al., 2013). They are, however, younger than *T. doliiformis*.

2837

### 2838 **73. Crown Odonata**

2840 This clade comprises Epiprocta (dragonflies; comprising Anisozygoptera and Anisoptera) and 2841 Zygoptera (damselflies), their last common ancestor and all of its descendants (Fig. 17). Monophyly of 2842 Odonata is supported by phylogenetic analysis of transcriptomes (Misof et al., 2014), combined 2843 morphology and housekeeping genes (Bybee et al., 2008), and a supertree including morphological 2844 and molecular input trees (Davis et al., 2011). 2845 2846 73.1. Fossil specimens 2847 2848 Triassothemis mendozensis Carpenter, 1960. MACN No. 18040, holotype, preserving the distal 2849 portion of two wings. 2850 2851 73.2. Phylogenetic justification 2852 2853 T. mendozensis is the oldest known member of the fossil family Triassolestidae (Nel et al., 2854 2002; Nicholson et al., 2015). A family-level supertree, incorporating molecular and morphological 2855 input trees, found Triassolestidae within crown group Epiprocta (Davis et al., 2011, largest tree in their 2856 Fig. 1). This fossil is therefore also a member of crown group Odonata. Of all the fossil families 2857 included in the supertree analysis and placed within crown Odonata (Davis et al., 2011), 2858 Triassolestidae (represented by T. mendozensis) has the oldest member. Furthermore, this family (and 2859 its approximate date) was used to calibrate Odonata in multiple recent divergence time analyses 2860 (Rota-Stabelli et al., 2013a; Thomas et al., 2013). 2861 2862 73.3. Age justification 2863 2864 T. mendozensis was discovered in dark grey siltstone of the Potrerillos Formation, at Quebrada

del Durazno, Mendoza Province, Argentina (Martins-Neto et al., 2008). The insect-bearing beds are from the upper part of the Potrerillos Formation. U-Pb SHRIMP dates have been measured for zircons from tuff layers in the middle section of the Potrerillos Formation. The uppermost tuff layer estimated an age of 230.3 Ma  $\pm$  2.3 Myr (Spalletti et al., 2009), corresponding to the Carnian, late Triassic. Thus a minimum age of *T. mendozensis* is 228.0 Ma.

Because the monophyly of Palaeoptera is under debate (Simon et al., 2009, 2012), we assign a soft maximum age that allows its constituent extant orders to be older than the Rhynie Chert, as for 2872 26.3.

2873

2874 **73.4**. *Discussion* 

2875

The internal taxonomy and placement of odonate fossils is highly contentious. Triassic members of the fossil family Triadophlebiidae are of approximately equal age to *T. mendozensis* (i.e. Carnian; Nicholson et al., 2015), however, they appear outside the crown group of Odonata in a supertree (Davis et al., 2011). Triadophlebiidae were not included in the total evidence analysis of Bybee et al. (2008). Most fossils in the latter analysis that had membership within crown Odonata were Jurassic or younger (Bybee et al., 2008).

2882 The Madygen fauna of Kyrgyzstan yields two possible calibrations for crown group Odonata. Triassolestodes asiaticus Pritykina, 1981 (family Triassolestidae, preserving a hindwing) was recently 2883 2884 justified as the oldest odonate by Kohli et al. (2016). As well, fossil members of Lestidae, crown group 2885 Odonata in the analysis of Bybee et al. (2008), are inferred from oviposition scars on plant fossils from 2886 Madygen (Moisan et al., 2012). Aside from challenges associated with interpreting crown group 2887 affinities of trace fossils, the Madygen fauna is, according to our stratigraphy, dated to the Carnian 2888 (see section 90.3), substantially younger than the 237 Ma age argued by Kohli et al. (2016) based on 2889 megaflora. Our age would give a minimum age of 226.4 Ma for Madygen fossils, which is very slightly 2890 younger than the 228.0 Ma estimated for T. mendozensis. Note, however, that the mean age estimate

2891	for Madygen is 228.4 Ma	(also	vounger than	the mean of :	230.3 Ma f	for the Potrerillos	Formation).
		· · · · ·					/

2892Triassolestes epiophlebioides Tillyard, 1918, a member of Triassolestidae used as a calibration2893fossil by Rota-Stabelli et al. (2013), is also known from the Carnian (Nicholson et al., 2015). Another

2894 fossil, *Pseudotriassothemis nipponensis* Bechly, 1997 (formerly *Triassoneura okafujii*), from the

2895 Carnian of Japan is also approximately coeval. We select *T. mendozensis* because its preservation is

2896 better, and radiometric dates for the Potrerillos Formation may be more precise.

2897

### 2898 **74. Crown Neoptera**

2899

This clade comprises Polyneoptera (**Figs. 19 and 20**) and Eumetabola, their last common ancestor and all of its descendants (**Fig. 21**). Monophyly is supported by phylogenetic analysis of transcriptomes (Letsch and Simon, 2013; Misof et al., 2014), protein-coding genes (Ishiwata et al., 2011; Sasaki et al., 2013), and combined molecular and morphological data (Terry and Whiting, 2005).

2904

# 2905 74.1. Fossil specimens

2906

2907 *Protoprosbole straeleni* Laurentiaux, 1952. IRSNB a9885, holotype, preserving a forewing.
 2908 Figured in Nel et al. (A. Nel et al., 2012), Fig. 3h.

2909

2910 74.2. Phylogenetic justification

2911

The original description of *P. straeleni* as a member of Hemiptera by Laurentiaux (1952) has been rejected several times (Hennig, 1981; A. Nel et al., 2012; Shcherbakov, 1995). Nel et al. (2012) summarize the phylogenetic position of *P. straeleni* as being within Paraneoptera (a clade unsupported by recent molecular studies, but comprising Psocodea and Condylognatha). The cua-cup contact with CuP and the flexion or nodal line following the course of RA are both similar to those observed in extant Hemiptera (A. Nel et al., 2012). However, the presence of three veins in the anal
area is argued as a hemipteran autapomorphy that is lacking in *P. straeleni* (A. Nel et al., 2012).
Conservatively, this fossil species can be thus assigned to the stem group of Condylognatha, and thus
crown Eumetabola and Neoptera.

2921

2922 74.3. Age justification

2923

2924 P. straeleni was discovered in Charbonnage de Monceau-Fontaine, Charleroi Coal Basin, 2925 Belgium (Brauckmann et al., 1994). The specimen was likely found in latest Marsdenian strata about 3 2926 m below the base of the Yeadonian (discussed by Brauckmann et al., 1994). The fossil-bearing 2927 deposits are assigned to the late Namurian B (Marsdenian) based on the *Bilinguites superbilinguis* 2928 R2c2 subzone of goniatite ammonoid stratigraphy (Brauckmann et al., 1994). The (late) Namurian-2929 (early) Westphalian boundary is defined by the earliest occurrence of the goniatite Gastrioceras 2930 subcrenatum (Waters and Davies, 2006), but lacks a precise isotopic date. Pointon et al. (2012) estimated an age of c. 319.9 Ma for the base of the Westphalian (top of the Namurian, only slightly 2931 2932 younger than the Marsdenian) based on Milankovitch cycles of sedimentation, giving a minimum age 2933 for P. straeleni. 2934 Soft maximum as for 26.3.

2935

2936 74.4. Discussion

2937

2938 *Qilianiblatta namurensis* Zhang et al., 2013 has an equal claim to being the earliest record of 2939 Neoptera (as *Q. namurensis* is a member of crown Polyneoptera), but it is of equal age to *P. straeleni*. 2940 The Qilianshan entomofauna at Xiaheyan, China, yields many other likely neopterans (e.g. Béthoux et 2941 al., 2011; Liu et al., 2009a; Prokop and Nel, 2007; Zhang et al., 2013).

2942 *Ctenoptilus elongatus* Béthoux and Nel, 2005 from the Stephanian B/C of France has been

2943	used as the putative oldest calibration fossil for crown Neoptera (e.g. O'Reilly et al., 2015). However,
2944	the Stephanian is a European stage of the Pennsylvanian, corresponding to the globally used
2945	Gzhelian, which is substantially younger than the Bashkirian age of both <i>P. straeleni</i> and <i>Q.</i>
2946	namurensis (with an upper boundary of 298.75 Ma).
2947	
2948	75. Crown Polyneoptera
2949	
2950	This clade comprises Zoraptera (ground lice), Dermaptera (earwigs), Plecoptera (stoneflies),
2951	Orthoptera (crickets, katydids), Notoptera, Eukinolabia and Dictyoptera, their last common ancestor
2952	and all of its descendants (Fig. 19). Monophyly has been demonstrated by phylogenetic analysis of
2953	transcriptomes (Letsch and Simon, 2013; Misof et al., 2014), protein-coding genes (Ishiwata et al.,
2954	2011), and wing morphology (Yoshizawa, 2011). This clade is not recognized in GenBank taxonomy.
2955	
2956	75.1. Fossil specimens
2957	
2958	Qilianiblatta namurensis Zhang et al., 2013. GMCB 04GNX1001-1, holotype, preserving the
2959	right forewing. We also refer to a second specimen (CNU-NX1-303; Fig. 20a), preserving paired
2960	forewings and hindwings (Guo et al., 2013).
2961	
2962	75.2. Phylogenetic justification
2963	
2964	Q. namurensis has not been included in formal phylogenetic analysis, but the fossil exhibits
2965	some apomorphic characters uniting it with crown group Blattodea, specifically presence of a deeply
2966	concave CuP in the forewing (Prokop et al., 2014). Additional data from forewings of the CNU
2967	specimen shows the RA with branches translocated to RP, as in cockroaches, suggesting this species

2968 could be stem Blattodea (Guo et al., 2013). However, there has not been a cladistic analysis of wing

2969 venation characters for both fossil and extant Blattodea and/or Dictyoptera, thus we agree with the 2970 more conservative view (Kjer et al., 2015; Legendre et al., 2015; Prokop et al., 2014) that roachoids 2971 likely represent a diverse and speciose fauna on the stem group of Dictyoptera. See also section 82.4. 2972 Nonetheless, placement of *Q. namurensis* on the stem lineage of Dictyoptera identifies it as a member 2973 of crown Polyneoptera. 2974 2975 75.3. Age justification 2976 2977 Minimum as for 71.3. 2978 A soft maximum age is estimated from *R. praecursor*, the oldest hexapod, from the Early 2979 Devonian (Pragian) Rhynie Chert of Aberdeenshire, Scotland. Spore assemblages of the Windyfield 2980 and stratigraphically underlying Rhynie Chert are dated to the early but not earliest Pragian to early 2981 (earliest?) Emsian (polygonalis-emsiensis Spore Assemblage Biozone) (Parry et al., 2011). 2982 Radiometric dating of the underlying Milton of Noth Andesite at ca. 411 Ma (Parry et al., 2013, 2011) has been subject to a dispute over its temporal relationship to hot spring activity associated with the 2983 2984 cherts (Mark et al., 2013, 2011) and predates the biostratigraphic dating of the Rhynie Chert relative to 2985 the global dating of the base of the Pragian Stage. Therefore, a soft maximum constraint may be 2986 defined at 411 Ma for the Rhynie Chert. 2987 2988 76. Crown Dermaptera 2989 2990 This clade comprises Protodermaptera and Epidermaptera, their last common ancestor and all 2991 of its descendants (Fig. 19). Monophyly is supported based on phylogenetic analysis of 2992 transcriptomes (Misof et al., 2014), nuclear genes (Kocarek et al., 2013), and combined molecular and

2993 morphological data (Jarvis et al., 2005).

2994

*Rhadinolabis phoenicica* Engel et al., 2011. Holotype preserving a female in amber, 1013 in the
private collection of D. Azar in Fanar (Matn), Lebanon (Fig. 20e). Provisionally housed at MNHN.
76.2. Phylogenetic justification

3001

*R. phoenicica* is assigned only to Neodermaptera (= Protodermaptera + Epidermaptera), and
 not to any extant family. Membership within Neodermaptera is based on the presence of
 morphological characters: trimerous tarsi, absence of a well-developed ovipositor, and tarsal structure
 (Engel et al., 2011). These characters are sufficient to confirm the fossil belongs within crown
 Dermaptera.

3007

3008 76.3. Age justification

3009

3010 This fossil was discovered in amber from the Mdeyrij-Hammana outcrop of the Baabda district. 3011 Mount Lebanon (Azar et al., 2010). Recent revision of the stratigraphy of Lebanese amber deposits 3012 places the Hammana fossils in the upper interval of the Grès du Liban (Maksoud et al., 2016). This is 3013 below the Jezzinian regional stage (Maksoud et al., 2014) and above the Banc de Mrejatt subunit 3014 (indicated as Ba3-Ba4 in Fig. 4 of Maksoud et al., 2016). Despite the lack of microfossils to further 3015 constrain the oldest boundary of the Jezzinian within the late Barremian, there is evidence that later 3016 Lebanese amber deposits bear the same age as Jezzine amber (see 26.3) because the amber itself 3017 has been reworked (Maksoud et al., 2016). We adopt the early Barremian minimum age proposed by 3018 Maksoud et al. (2016). The upper boundary of the early Barremian is proposed to be the first 3019 appearance of the ammonite Ancyloceras vandenheckii (Ogg et al., 2012). Cyclostratigraphy dates the 3020 A. vandenheckii Zone beginning at 129.41 Ma (Ogg et al., 2012), providing a minimum age for Jezzine

- 3021 Lebanese amber fossils. 3022 Soft maximum as for 75.3. 3023 3024 77. Crown Plecoptera 3025 3026 This clade comprises Antarctoperlaria, Euholognatha and Systellognatha, their last common 3027 ancestor and all of its descendants (Fig. 19). This classification and its morphological evidence is 3028 reviewed by Zwick (2000). Monophyly of Plecoptera is supported by phylogenetic analysis of 3029 transcriptomes (Misof et al., 2014) and combined ribosomal genes, H3, and morphology (Terry and 3030 Whiting, 2005). 3031 3032 77.1. Fossil specimens 3033 3034 Palaeotaeniopteryx elegans Sharov, 1961. PIN 1197/333, holotype, preserving a forewing. 3035 3036 77.2. Phylogenetic justification 3037 P. elegans is classified in the fossil family Palaeonemouridae, suborder Nemourina 3038 3039 (Sinitshenkova, 1987). At that time, Nemourina was one of only two suborders, the other being Perlina 3040 (Rasnitsyn and Quicke, 2002). Zwick (2000) summarized Nemourina as containing the (extant) 3041 families Notonemouridae, Nemouridae, Taeniopterygidae, Capniidae, and Leuctridae, therefore 3042 equivalent to the new suborder Euholognatha. Grimaldi and Engel (2005; Fig. 7.6) prefer a placement 3043 of Palaeonemouridae outside the crown group of Plecoptera, on the basis that diagnostic characters 3044 for crown group suborders within Plecoptera are rarely preserved (e.g. muscles, cellular structures). 3045 While no formal phylogenetic hypothesis illustrates the relationship of Palaeonemouridae to other 3046 Euholognatha, synapomorphies are identified linking *P. elegans* to the crown group of Plecoptera
  - 118

3047 (Béthoux, 2005, pers. comm.).

3048

3049 77.3. Age justification

3050

3051 The oldest specimen of *P. elegans* was discovered from the Mitino Horizon at the Kaltan 3052 locality in the Kuznetsk Basin, Kemerovo, Russia (Sharov, 1961; Shcherbakov, 2000). Correlation of 3053 insect faunas suggests the Kaltan locality is late early Kazanian (Lozovsky et al., 2009; Shcherbakov, 3054 2008). The Kazanian is a regional stage of the Russian Permian, which has been correlated to both 3055 the Wordian (Menning et al., 2006) and the Roadian global Stages (Lozovsky et al., 2009). Evidence 3056 for an age in the Roadian is stronger, demarcated by presence of ammonites such as Sverdrupites 3057 harkeri and S. amundseni (Lozovsky et al., 2009). These ammonites, and associated conodonts 3058 Kamagnathus khalimbadzhai and K. volgensis, correlate globally to the Roadian (Barskov et al., 2014; 3059 Leonova, 2007; Leonova and Shilovsky, 2007). The upper boundary of the Roadian is  $268.8 \text{ Ma} \pm 0.5$ 3060 Myr, so a minimum age is 268.3 Ma.

3061 Soft maximum as for 75.3.

3062

3063 77.4. Discussion

3064

3065 *Gulou carpenteri* Béthoux et al., 2011, from the Pennsylvanian Qilianshan entomofauna of 3066 China, is identified as a member of the stem group to Plecoptera (Béthoux et al., 2011), and thus 3067 cannot be used to calibrate a minimum age of the crown group. Moreover, other Permian plecopterans 3068 had terrestrial nymphs; an aquatic nymph is a symapomorphy uniting crown group Plecoptera (Zwick, 3069 2000), relegating any fossil without it to the stem group.

O. Béthoux (pers. comm.) cautioned that a Jurassic minimum age for crown Plecoptera, as
 used by Misof et al. (2014), would underestimate their age significantly. The calibrating fossil
 *Pronemoura angustithorax* Liu et al., 2011 used by Misof et al. (2014), from the Daohugou Beds, is

3073	likely a member of total group Euholognatha (Liu et al., 2011). Other crown Plecoptera groups are also
3074	known from the same locality (Liu et al., 2009b), suggesting diversification of the crown group was
3075	significantly earlier.
3076	
3077	78. Crown Orthoptera
3078	
3079	This clade comprises Ensifera (crickets, katydids) and Caelifera (grasshoppers), their last
3080	common ancestor and all of its descendants (Fig. 19). Monophyly is demonstrated by phylogenetic
3081	analysis of transcriptomes (Misof et al., 2014), mitochondrial genomes plus four nuclear genes (Song
3082	et al., 2015), morphology (Béthoux and Nel, 2002), and combined molecular and morphological data
3083	(Terry and Whiting, 2005).
3084	
3085	78.1. Fossil specimens
3086	
3087	Raphogla rubra Béthoux et al., 2002. Ld LAP 415 B, holotype, preserving the counterpart of a
3088	forewing ( <b>Fig. 20c</b> ).
3089	
3090	78.2. Phylogenetic justification
3091	
3092	Although no cladistic analysis exists combining extant and fossil Enserifa, R. rubra may be
3093	assigned to crown Enserifa based on forewing venation characters (Béthoux et al., 2002). It likely
3094	belongs to the stem group of the clade (Gryllidea + Tettigoniidea), based on the following characters:
3095	very broad area between anterior margin and Sc; RS moderately long basal of a short fusion with the
3096	anterior branch MA1a of MA; MP + CuA1 with only one simple anterior branch (Béthoux et al., 2002).
3097	As both Gryllidea and Tettigoniidea are crown clades within crown Enserifa, R. rubra is within crown
3098	group Orthoptera.

# 3100 78.3. Age justification

3102	R. rubra was found at the fossiliferous site F21 D, at "Le Moural D", in the basal Mérifrons
3103	Member of the Salagou Formation (Saxonian Group), near village Octon, Lodève Basin, Hérault,
3104	France (Béthoux et al., 2002; Nel et al., 1999; Schneider et al., 2006). U-Pb dates have been recently
3105	measured from zircons lying in tuff beds near the lower two-thirds of the Salagou Formation (Octon
3106	Member), in the Artinskian (Michel et al., 2015). The Mérifrons Member, overlying the Octon, is
3107	therefore inferred to be Artinskian at its base but continuing up through the Kungurian (Michel et al.,
3108	2015). As the exact stratum of the F21 site is not indicated within the Mérifrons member (Michel et al.,
3109	2015; Schneider et al., 2006), we apply a conservative minimum estimate from the upper boundary of
3110	the Kungurian (272.3 Ma $\pm$ 0.5 Myr), at 271.8 Ma.
3111	Soft maximum as for 75.3.
3112	
3113	78.4. Discussion
3114	
3115	An undescribed Namurian member of Archaeorthoptera was initially attributed to crown group
3116	Orthoptera (Prokop et al., 2005). However, an affinity with Archaeorthoptera is supported in the stem
3117	group of Orthoptera based on phylogenetic analysis (Béthoux and Nel, 2002), thus it cannot be used
3118	to calibrate the crown. Similarly, Oedischia williamsoni Brongniart, 1885, from the Pennsylvanian of
3119	France, is recognized as a stem group member of Orthoptera by cladistic analysis (Béthoux and Nel,
3120	2002). Together these fossils suggest a long stem branch for Orthoptera.
3121	The fossil Eolocustopsis primitiva Riek, 1976 from Natal, South Africa was listed as the oldest
3122	crown group member of Caelifera, and thus another Permian crown group member of Orthoptera
3123	(Song et al., 2015). However, the fossil comes from strata of the Normandien Formation,
3124	Changhsingian stage, latest Permian (due to the co-occurrence of the vertebrate fossil Dicynodon;

3125	e.g. Catuneanu et al., 2	2005), which is v	vounger than	the Kungurian.

3126	
3127	79. Crown Notoptera
3128	
3129	This clade comprises Mantophasmatodea (rock crawlers) and Grylloblattodea (ice crawlers),
3130	their last common ancestor and all of its descendants (Fig. 19). The monophyly of Notoptera is
3131	supported by phylogenetic analysis of transcriptomes (Misof et al., 2014), morphology (Wipfler et al.,
3132	2011), and combined molecular and morphological data (Terry and Whiting, 2005).
3133	
3134	79.1. Fossil specimens
3135	
3136	Juramantophasma sinica D. Huang et al., 2008. NIGP 142171, holotype, preserving a nearly
3137	complete adult female ( <b>Fig. 20g</b> ).
3138	
3139	79.2. Phylogenetic justification
3140	
3141	J. sinica has several characters in common with crown Mantophasmatodea. These include: a
3142	third tarsomere with a sclerotized elongated dorsal process, enlarged and fanlike pretarsal arolia, last
3143	tarsomere at right angle to the others, female gonoplacs short and claw shaped, and egg with a
3144	circular ridge (D. Huang et al., 2008). As no morphological matrix exists for Mantophasmatodea,
3145	relationships to extant lineages are not possible to test (D. Huang et al., 2008). The fossil is excluded
3146	from the crown group of Grylloblattodea as it lacks segmented cerci. Thus, conservatively, a position
3147	on the stem lineage of Mantophasmatodea is likely (although J. sinica could be amended to within the
3148	crown of Mantophasmatodea). This would, in any case, mean it is a member of crown Notoptera.
3149	
3150	79.3. Age justification

3152	This fossil was found in deposits of the Daohugou Beds, Ningcheng County, Inner Mongolia,
3153	China (D. Huang et al., 2008). There has been controversy about the accuracy and precise age and
3154	stratigraphic position of the Daohugou Beds (Gao and Ren, 2006; Wang et al., 2005; Zhang, 2015).
3155	The beds consist of 100–150 m thick succession of grey-white or locally reddish, thinly bedded
3156	claystones, shales, siltstones and sandy mudstones with intercalated ash-fall tuffs and ignimbrites.
3157	Ages have been proposed from Aalenian (Middle Jurassic) to Early Cretaceous (Liu et al., 2014; Wang
3158	et al., 2000), with several studies converging on Callovian-Oxfordian (Late Jurassic; Zhang, 2015).
3159	Radiometric dating of the ignimbrites with 40Ar/39Ar and SHRIMP U-Pb variously yields dates
3160	between 165 Ma $\pm$ 2.5 Myr and 158.7 Ma $\pm$ 0.6 Myr (Chang et al., 2009b; Gao and Ren, 2006; He et
3161	al., 2004; Peng et al., 2012). The fossiliferous shales overlay the volcanic deposits (Gao and Ren,
3162	2006), and are thus younger. The isotopic dates nonetheless provide a reasonable refutation of
3163	Cretaceous age estimates. Furthermore, the Daohugou Beds may be correlated to sediments from
3164	Oxfordian localities in China and Kazakhstan (Zhang, 2015). The most conservative (i.e. youngest) of
3165	the direct radiometric dates is 158.1 Ma (within the Oxfordian), giving a minimum age.
3166	Soft maximum as for 75.3.
3167	

3168 **79.4**. *Discussion* 

3169

Stem group Grylloblattodea are uncommon, and extant grylloblattids (and mantophasmids) are wingless (Wipfler et al., 2014). A putative grylloblattid insect was described from the Pennsylvanian Montceau-les-Mines Lagerstatte, about 130 Myr older than *J. sinica* (Béthoux and Nel, 2010); however, the fossil preserved only the wings. We take the parsimonious view that there was a single loss of wings in the common ancestor of Grylloblattodea and Mantophasmatodea, i.e. in the crown group of Notoptera (Grimaldi and Engel, 2005). Therefore, any fossil bearing wings, such as the Pennyslvanian and Permian members, would be on the stem branch of Notoptera.

3177	
3178	80. Crown Eukinolabia
3179	
3180	This clade comprises Embioptera (webspinners) and Phasmatodea (stick and leaf insects),
3181	their last common ancestor and all of its descendants (Fig. 19). Monophyly of Eukinolabia is
3182	supported by phylogenetic analyses of transcriptomes (Letsch and Simon, 2013; Misof et al., 2014)
3183	and ribosomal and H3 sequences (Terry and Whiting, 2005).
3184	
3185	80.1. Fossil specimens
3186	
3187	Cretophasmomima melanogramma Wang et al., 2014. CNU-PHA-NN2012002, holotype,
3188	preserving a male ( <b>Fig. 20d</b> ).
3189	
3190	80.2. Phylogenetic justification
3191	
3192	C. melanogramma shares the 'shoulder pad' structure, and twig-like appearance (elongated
3193	meso- and metathorax) diagnostic of total group Phasmatodea (Wang et al., 2014). Crown
3194	membership within Phasmatodea is questionable, as important synapomorphies, the vomer and
3195	forceps-like extensions of the 10th abdominal tergum, are absent from C. melanogramma (Wang et
3196	al., 2014). The position of C. melanogramma on the stem lineage of Phasmatodea therefore places it
3197	within the crown group of Eukinolabia.
3198	
3199	80.3. Age justification
3200	
3201	As for 76.3.
3202	

3203	80.4. Discussion
3204	
3205	Renphasma sinica Nel and Delfosse, 2011 is of equal age, also from the Yixian Formation, and
3206	also a member of stem Phasmatodea, and thus crown Eukinolabia.
3207	
3208	81. Crown Phasmatodea
3209	
3210	This clade comprises Timematodea and Euphasmatodea, their last common ancestor and all
3211	of its descendants (Fig. 19). Monophyly of Phasmatodea is supported by phylogenetic analyses of
3212	transcriptomes (Misof et al., 2014), ribosomal and H3 sequences (Terry and Whiting, 2005), and
3213	morphology (Friedemann et al., 2012).
3214	
3215	81.1 Fossil specimens
3216	
3217	Echinosomiscus primoticus Engel et al., 2016c. NIGP 163536, holotype, preserving a male in
3218	amber ( <b>Fig. 20f</b> ).
3219	
3220	81.2 Phylogenetic justification
3221	
3222	Until recently, no Mesozoic fossil qualified for membership in the crown group of Phasmatodea
3223	(Bradler and Buckley, 2011). E. primoticus bears morphological characters shared with extant
3224	members of Euphasmatodea, in particular Heteropterygidae and Aschiphasmatidae, but lack the area
3225	apicalis on the tibiae (Engel et al., 2016c). It also shares characters with Lonchodinae, such as absent
3226	areole on all tibiae, comparatively long antennae, the absence of wings, and the division of the tenth
3227	abdominal tergum into moveable hemitergites (Engel et al., 2016c). Although a new family was
3228	erected to accommodate the unique character combination for <i>E. primoticus</i> , it is very clearly within

3229	Euphasmatodea (Phasmatidae s.l.), and thus a member of crown Phasmatodea (Engel et al., 2016c).
3230	
3231	81.3 Age justification
3232	
3233	Minimum as for 12.3. Soft maximum as for 75.3.
3234	
3235	82. Crown Dictyoptera
3236	
3237	This clade comprises Mantodea (praying mantids) and Blattodea (cockroaches, termites), their
3238	last common ancestor and all of its descendants (Fig. 19). Phylogenetic analysis of transcriptomes
3239	(Misof et al., 2014), mitochondrial genes (Legendre et al., 2015), and combined molecular and
3240	morphological data (Djernæs et al., 2015; Ware et al., 2008), support monophyly of Dictyoptera.
3241	
3242	82.1. Fossil specimens
3243	
3244	Valditermes brenanae Jarzembowski, 1981. BMNH In. 64588, holotype, preserving a forewing.
3245	
3246	82.2. Phylogenetic justification
3247	
3248	The position of V. brenanae was confirmed by morphological phylogenetic analysis (Engel et
3249	al., 2009). V. brenanae was resolved on the stem lineage of Mastotermitidae (Engel et al., 2009). This
3250	position was separately found for a congeneric species in the combined morphological and molecular
3251	phylogeny of Ware et al. (2010). Mastotermitidae is a monotypic family, sister to all other termites
3252	(Djernæs et al., 2015; Ware et al., 2010), so this phylogeny would also place V. brenanae in the
3253	crowns of Isoptera and Blattodea.
3254	

3255 82.3. Age justification

3256

3257 The fossil is from the Clockhouse Brickworks pit site, Surrey, England (Jarzembowski, 1981). 3258 The Clockhouse Brickworks belongs to the Lower Weald Clay, as indicated by the presence of the 3259 ostracods Cytheridea clavata, C. tuberculata, and C. valdensis (Anderson, 1985). Of these, C. 3260 tuberculata has the narrowest range, and is restricted to the middle portion of the Lower Weald Clay, 3261 at BGS Bed 3a (Anderson, 1985; Ross and Cook, 1995). This faunal Zone is now assigned to the 3262 lower portion of the C. pumila Subzone of the Theriosynoecum fittoni Zone (Horne, 1995). Based on 3263 palynomorph stratigraphy, the boundary between Lower and Upper Weald Clay at the base of BGS 3264 Bed 3a corresponds accurately to the boundary between the Hauterivian and Barremian Stages (Ross 3265 and Cook, 1995). The upper boundary of the Hauterivian is 130.8 Ma  $\pm$  0.5 Myr (Ogg et al., 2012a). 3266 therefore a minimum age of the Lower Weald Clay is 130.3 Ma. 3267 Soft maximum as for 75.3. 3268 3269 82.4. Discussion 3270 3271 There is ongoing debate over whether various Palaeozoic "roachoid" fossils, such as 3272 Qilianiblatta namurensis and Homocladus grandis Carpenter, 1966 (known only from wing venation characters), truly represent crown group members of Dictyoptera (e.g. Guan et al., 2016; Kjer et al., 3273 3274 2015; Legendre et al., 2015; Tong et al., 2015). If roachoids are indeed within crown group 3275 Dictyoptera, their antiquity may push back the origins of crown Dictyoptera and crown Polyneoptera by 3276 80-88 Myr (Legendre et al., 2015; Tong et al., 2015). However, wing venation alone may be insufficient 3277 to place most fossils within the crown group of Blattodea or even Dictyoptera. Particularly in 3278 cockroaches, asymmetry at the individual level and convergence at higher taxonomic levels are 3279 impediments to wing venation taxonomy, as well as the paucity of comparative venation data for extant 3280 species (e.g. Béthoux et al., 2010; Béthoux and Wieland, 2009; Garwood and Sutton, 2010; Gorochov,

3281 2013; Guan et al., 2016).

3282 In the absence of detailed cladistic analysis of fossil roachoid wings together with extant 3283 Dictyoptera and other outgroups, we take the conservative view (Guan et al., 2016; Kier et al., 2015; 3284 Prokop et al., 2014) that roachoids (including the family Anthracoptilidae/Strephocladidae, containing 3285 H. grandis) likely represent a diverse and speciose fauna on the stem group of Dictyoptera, perhaps with some members on the stem group of Neoptera or Polyneoptera (Grimaldi and Engel. 2005). At 3286 3287 least some such roachoids may be used to calibrate crown group Polyneoptera (as done herein by 3288 assigning Q. namurensis), but they cannot calibrate crown Dictyoptera. As a consequence, many 3289 recent analyses have begun to rewrite the traditional assumption of extremely old crown ages for 3290 Dictyoptera, with crown origins likely in the Jurassic (Misof et al., 2014).

3291 Morphological phylogenetic analyses have excluded all Cretaceous fossils from the crown 3292 group of Mantodea, although they remain as likely crown Dictyoptera (Delclòs et al., 2016; Grimaldi, 3293 2003). Given that the analysed morphological matrix has fewer characters than taxa and has 3294 substantial missing data, it is not definitive (Delclos et al., 2016). A recently discovered fossil from 3295 Crato (Aptian of Brazil), Cretophotina santanensis Lee, 2014, may be a stem group Chaeteessidae, 3296 which may be the most basal crown family of Mantodea (Svenson and Whiting, 2009). The position of 3297 Chaeteessidae may be within polyphyletic Mantidae (Legendre et al., 2015), but we exercise caution 3298 and do not place *C. santanensis* in the crown group, as recommended by Lee (2014).

3299

### 3300 83. Crown Blattodea

3301

This clade comprises Lamproblattidae, Blaberoidea, Blattidae, Nocticolidae, Polyphagidae, Cryptocercidae and Isoptera, their last common ancestor and all of its descendants (**Fig. 19**). The position of Isoptera (termites) within a paraphyletic Blattodea was first identified by Inward et al. (2007) with six molecular loci. Further support for the monophyly of the new concept of Blattodea comes from transcriptomes (Misof et al., 2014), mitochondrial genes (Legendre et al., 2015), housekeeping genes

3307	(Djernæs et al., 2012), and combined molecular and morphological data (Djernæs et al., 2015; Ware
3308	et al., 2008).
3309	
3310	83.1. Fossil specimens
3311	
3312	As for 82.1.
3313	
3314	83.2. Phylogenetic justification
3315	
3316	As for 82.2.
3317	
3318	83.3. Age justification
3319	
3320	As for 82.3.
3321	
3322	83.4. Discussion
3323	
3324	Baissatermes lapideus Engel et al., 2007 is a crown group member of Isoptera, and
3325	Mastotermes nepropadyom Vršanský and Aristov, 2014 is crown Blattodea (Engel et al., 2016a); both
3326	have been used to calibrate Isoptera and Blattodea (Djernæs et al., 2015; Ware et al., 2010). Note that
3327	fossil Mastotermes are likely polyphyletic (Engel et al., 2016a). Although these are appropriate
3328	calibration fossils, they are not the oldest Blattodea. B. lapideus is from the Zaza Formation
3329	(Transbaikalian Russia), and <i>M. nepropadyom</i> is from Chernovskie Kopi, also in Transbaikalia and
3330	similar in age to the Turga Formation (Sukatsheva and Vassilenko, 2011; Vršanskỳ and Aristov, 2014).
3331	The Turga Formation has been correlated to the Baissa locality, Zaza Formation; this is based on
3332	shared presence of Asteropollis asteroides spores (Vakhrameev and Kotova, 1977). As discussed in

section 86.3, the Zaza Formation may be much younger than initially described, with a minimum age
of Campanian (71.9 Ma). Therefore both Russian fossils are younger than *V. brenanae*.

3335

## 3336 84. Crown Eumetabola

3337

3338 This clade comprises Condylognatha, Psocodea and Holometabola, their last common 3339 ancestor and all of its descendants (Fig. 21). Monophyly of the clade is supported by transcriptomes 3340 (Letsch and Simon, 2013; Misof et al., 2014) and protein-coding genes (Ishiwata et al., 2011). Some 3341 morphological analyses do not support monophyly of Eumetabola (Kristensen, 1981; Wheeler et al., 2001), although it is recovered (Kristensen, 1991; Kukalová-Peck, 1991) and assumed (Yoshizawa 3342 3343 and Saigusa, 2001) in other analyses. Note also that support for Psocodea as the sister clade of 3344 Holometabola was statistically weak in analyses of transcriptomes (Misof et al., 2014), although 3345 monophyly of Eumetabola was well supported.

3346

3347 84.1. Fossil specimens

3348

- As for 74.1.
- 3350
- 3351 84.2. Phylogenetic justification
- 3352
- 3353 As for 74.2.
- 3354
- 3355 84.3. Age justification
- 3356
- 3357 Minimum as for 74.3. Soft maximum as for 75.3.
- 3358

3359	85. Crown	Condvlognatha
5557		oonayiognaana

3361 This clade comprises Hemiptera (true bugs) and Thysanoptera (thrips), their last common 3362 ancestor and all of its descendants (Fig. 21). Monophyly is determined by phylogenetic analysis of 3363 transcriptomes (Misof et al., 2014), nuclear protein-coding genes (Ishiwata et al., 2011), and wing 3364 morphology (Yoshizawa and Saigusa, 2001). 3365 3366 85.1. Fossil specimens 3367 3368 Aviorrhyncha magnifica Nel et al., 2013, holotype Avion No. 2 (provisionally stored in the 3369 collection of Entomological Laboratory, MNHN; to be deposited in the Musée Géologique Pierre Vetter, 3370 Decazeville, France), preserving a single forewing (Fig. 22a). 3371 3372 85.2. Phylogenetic justification 3373 3374 Nel et al. (2013) diagnose A. magnifica as stem Euhemiptera (the clade sister to 3375 Sternorrhyncha containing all other living Hemiptera; Cryan and Urban, 2012; Cui et al., 2013). At least 3376 two forewing characters in A. magnifica are synapomorphies of Euhemiptera, including presence of an 3377 ambient vein and a well-developed concave CP (its presence is a synapomorphy) (Nel et al., 2013). 3378 Unlike many extant Euhemiptera, the cua-cup vein is not zigzagged. Given that much of fossil insect 3379 taxonomy is conducted with only preserved wings, an assignment to the crown group of Hemiptera 3380 and thus Condylognatha is reasonable. 3381 3382 85.4. Age justification 3383 A. magnifica was found in "Terril No. 7", a layer containing rocks from the slag heap of coal 3384

3385	mines 3 and 4 of Liévin, in the Avion outcrop of Pas-de-Calais, France (Nel et al., 2013). The coal
3386	mines are dated to the Westphalian C/D, or Bolsovian/Asturian, which has a youngest boundary
3387	equivalent to the latest Moscovian stage of the Pennsylvanian (Nel et al., 2013; Richards, 2013). As
3388	the upper boundary of the Moscovian is 307.0 Ma $\pm$ 0.1 Myr, this provides a minimum age of 306.9
3389	Ma.
3390	Soft maximum as for 75.3.
3391	
3392	86. Crown Thysanoptera
3393	
3394	This clade comprises Tubulifera and Terebrantia, their last common ancestor and all of its
3395	descendants (Fig. 21). Monophyly is established based on phylogenetic analysis of transcriptomes
3396	(Misof et al., 2014) and five nuclear protein-coding genes (Buckman et al., 2013). There is no
3397	adequate phylogenetic test of thysanopteran monophyly using morphology (reviewed by Mound and
3398	Morris, 2007).
3399	
3400	86.1. Fossil specimens
3401	
3402	Fusithrips crassipes Shmakov, 2009. PIN 3064/8547, holotype, preserving a female body (Fig.
3403	<b>22</b> b).
3404	
3405	86.2. Phylogenetic justification
3406	
3407	F. crassipes has not been included in a phylogenetic analysis, however, Shmakov (2009)
3408	describes characters placing it in the crown of Thysanoptera. In particular, Rs1 and M2 as crossveins
3409	rather than oblique veins suggest membership in the family Aeolothripidae (Shmakov, 2009). Whether
3410	crown or stem Aeolothripidae, the family is a part of Terebrantia, indicating crown group membership in

3411 Thysanoptera.

3412

3413 86.3. Age justification

3414

3415 The fossil F. crassipes was found in Layer 31 on the left bank of the Vitim River, 3 km 3416 downstream from the mouth of the Baissa River, Buryatia, Transbaikalian Russia (Shmakov, 2009). 3417 The fossiliferous lacustrine deposits are part of the Zaza Formation, Baissa locality. The Zaza 3418 Formation was once assigned to the Valanginian, based on correlation of fossil insect species, 3419 however palynological data from the appearance of Asteropollis spores suggests a younger date 3420 (O'Reilly et al., 2015; Zherikhin et al., 1998). A. asteroides, one of the earliest angiosperms, has a 3421 worldwide distribution during the Early and mid Cretaceous (Friis et al., 2005), and has been 3422 biostratigraphically assigned to the Barremian-Aptian (Friis et al., 1999; Zherikhin et al., 1998). This 3423 range has since been completely revised to Albian-Campanian, on the basis of pollen morphology 3424 (Doyle and Endress, 2014) and younger appearances of Asteropollis (Dettmann and Thomson, 1987; 3425 Eklund et al., 2004; Martínez et al., 2013). A minimum age can thus be estimated by the upper 3426 boundary of the Campanian, 72.1 Ma  $\pm$  0.2 Myr, or 71.9 Ma. 3427 Soft maximum as for 75.3. 3428 3429 86.4. Discussion 3430

3431 Triassothrips virginicus Grimaldi et al., 2004 was described from the Late Triassic of Virginia.
3432 Although it was used as a calibration for Thysanoptera by Misof et al. (2014), *T. virginicus* is found in a
3433 basal polytomy outside of any crown group members in a morphological phylogeny (P. Nel et al.,
3434 2012). Liassothrips crassipes Martynov, 1927 is known from the Late Jurassic of Kazakhstan, but is
3435 classified in an extinct family, Liassothripidae (Shmakov, 2008). While Shmakov (2008) suggests
3436 Liassothripidae is the oldest family in the Tubulifera, making it crown Thysanoptera, characters are

3437	also listed linking it with Terebrantia; without a phylogenetic analysis it is difficult to assess their
3438	polarity and thus crown affinity.
3439	
3440	87. Crown Hemiptera
3441	
3442	This clade comprises Sternorrhyncha (aphids, scale insects), Fulgoromorpha (planthoppers),
3443	Cicadomorpha (cicadas, leafhoppers, treehoppers), Coleorrhyncha (moss bugs) and Heteroptera
3444	(typical bugs), their last common ancestor and all of its descendants (Fig. 21). Monophyly of
3445	Hemiptera is established by phylogenetic analysis of housekeeping genes (Cryan and Urban, 2012),
3446	whole mitochondrial genomes (Cui et al., 2013), transcriptomes (Misof et al., 2014; Simon et al.,
3447	2012), and wing morphology (Yoshizawa and Saigusa, 2001).
3448	
3449	87.1. Fossil specimens
3450	
3451	As for 85.1.
3452	
3453	87.2. Phylogenetic justification
3454	
3455	As for 85.2.
3456	
3457	87.3. Age justification
3458	
3459	As for 85.3.
3460	
3461	88. Crown Psocodea
3462	
	134

3463	This clade comprises Psocoptera (barklice) and Phthiraptera (true lice), their last common
3464	ancestor and all of its descendants (Fig. 21). Monophyly of this clade is supported by phylogenies of
3465	transcriptomes (Misof et al., 2014), nuclear protein-coding genes (Ishiwata et al., 2011), mitochondrial
3466	genes (Yoshizawa and Johnson, 2003), and morphology (Lyal, 1985).
3467	
3468	88.1. Fossil specimens
3469	
3470	Cretoscelis burmitica Grimaldi and Engel, 2006. AMNH Bu912, holotype, female in amber.
3471	
3472	88.2. Phylogenetic justification
3473	
3474	In a morphological phylogenetic analysis, C. burmitica was a stem group member of
3475	Liposcelididae (Grimaldi and Engel, 2006). Liposcelididae is an extant family of Psocoptera, thus
3476	within the crown group of Psocodea.
3477	
3478	88.3. Age justification
3479	
3480	As for 81.3.
3481	
3482	89. Crown Holometabola
3483	
3484	This clade comprises Hymenoptera (sawflies, ants, bees, wasps) and Aparaglossata, their last
3485	common ancestor and all of its descendants (Figs. 23 and 24). Support for monophyly comes from
3486	phylogenetic analysis of transcriptomes (Misof et al., 2014; Peters et al., 2014), morphology (Beutel et
3487	al., 2011), and morphology plus molecules (Oakley et al., 2013). This clade exists in GenBank, but as
3488	Endopterygota.

3490 89.1. Fossil specimens

3491

3492 *Westphalomerope maryvonneae* Nel et al., 2007. MNHN-LP-R.55181, holotype, preserving a 3493 hindwing. Pictured in Nel et al. (2007; Fig. 1a).

3494

3495 89.2. Phylogenetic justification

3496

3497 W. maryvonneae has not been included in a phylogenetic analysis, nor have any other 3498 members of its family, Protomeropidae. Mostly Permian members of Protomeropidae have been 3499 proposed to have affinities with a variety of holometabolan clades, including the total groups of 3500 Trichoptera, Mecoptera, and more generally Amphiesmenoptera or Antliophora (Grimaldi and Engel, 3501 2005; Kukalova-Peck and Willmann, 1990; Morse, 1997; Nel et al., 2013, 2007; Sukatsheva et al., 3502 2007). Crown amphiesmenopteran (and thus trichopteran) affinity may be unlikely, as Protomeropidae 3503 lack a key synapomorphy, a true 'double-Y loop' arrangement of the anal veins on the forewing 3504 (Labandeira, 2011; Minet et al., 2010). However, Permian Protomeropidae possess Carpenter's 3505 organs in the male, a probable apomorphy for total group Mecoptera (Minet et al., 2010). 3506 Protomeropidae (with a younger date) was subsequently used to calibrate the basal split of 3507 Mecopterida for divergence time estimation (Rehm et al., 2011). Pending phylogenetic analysis of 3508 wing morphology, it is difficult to assign a specific placement for Protomeropidae, however, even with a 3509 conservative view all these possibilities are within crown Aparaglossata, and therefore crown 3510 Holometabola. 3511

3512 89.3. Age justification

3513

3514 *W. maryvonneae* was collected from black shales in the "Terril no. 5" horizon at the "Faisceau

3515 de Modeste", "Veine Maroc" locality in Bruay-la-Bussière, Pas-de-Calais, France (Nel et al., 2007). 3516 The locality is dated as early Langsettian (Nel et al., 2007), equivalent to the Westphalian A stage 3517 (Pointon et al., 2012). There is a SHRIMP U-Pb date within the middle Langsettian estimated at 3518  $317.63 \text{ Ma} \pm 0.12 \text{ Myr}$ , however, the stratigraphy of Bruay-la-Bussière is not precise enough to 3519 determine when in the Westphalian A the fossil occurred (Nel et al., 2007; Pointon et al., 2012). 3520 Therefore, we use a date inclusive of the upper boundary of the Westphalian A, which is the upper 3521 boundary of Westphalian B. U-Pb dating of zircons constrains the upper boundary of the Westphalian 3522 B to 313.78 Ma ± 0.08 Myr (Pointon et al., 2012), so a minimum age for W. maryvonneae is 313.70 3523 Ma. 3524 Soft maximum as for 75.3. 3525 3526 89.4. Discussion 3527 3528 Srokalarva berthei Haug et al., 2015 is a putative holometabolan larva, from the Mazon Creek 3529 and thus younger than W. maryvonneae. S. berthei has been interpreted as both an antliophoran (Labandeira, 2011) and a neuropterid (Haug et al., 2015), both positions within the crown group of 3530 3531 Holometabola. S. berthei, however, remains informative about the evolutionary timing of insect 3532 metamorphosis. 3533 3534 90. Crown Hymenoptera

3535

This clade comprises Symphyta (sawflies) and Apocrita (itself comprising Apoidea, Formicidae, and a paraphyletic group of wasps), their last common ancestor and all of its descendants (**Fig. 23**). Monophyly is supported by phylogenetic analysis of transcriptomes (Misof et al., 2014), morphology (Beutel et al., 2011), and morphology analysed together with molecular data (Ronquist et al., 2012).

3541	90.1.	Fossil	specimens
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3543 *Triassoxyela foveolata* Rasnitsyn, 1964. PIN 2070/1, holotype (**Fig. 25a**).

3544

3545 90.2. Phylogenetic justification

3546

In the total-evidence phylogenetic analysis of Ronquist et al. (2012), *T. foveolata* was found as a stem group member of the family Xyelidae. As Xyelidae is a crown group family of sawflies, it is thus crown Hymenoptera.

3550

3551 90.3. Age justification

3552

3553 T. foveolata was found in the Madygen Formation, south of the Fergana Valley, Kyrgyzstan. 3554 Key plant fossils Scytophyllum and Neocalamites correlate the Madygen to the Scytophyllum flora of 3555 the upper Keuper lithographic unit, of Ladinian-Carnian age (Dobruskina, 1995). The Scytophyllum 3556 flora is correlated with the Cortaderitian Stage of Gondwana due to the abundance of Scytophyllum 3557 (Morel et al., 2003). The Cortaderitian Stage is divided into 3 Biozones; a 40Ar/39Ar radiometric date 3558 for the middle biozone of the Cortaderitian Stage of 228.5 Ma  $\pm$  0.3 Myr was measured by Rogers et 3559 al. (1993), falling within the Carnian (O'Reilly et al., 2015). The Gondwanan Puesto Viejo Formation, 3560 part of the Barrealian Stage underlying the Cortaderitian Stage (and therefore the Scytophyllum flora) 3561 has been radiometrically dated to 232 Ma ± 4 Myr, also within the Carnian (Valencio et al., 1975). 3562 Recently calculated SHRIMP U-Pb dates dispute this age, instead constraining the Puesto Viejo 3563 Formation to 235.8 Ma  $\pm$  2.0 Myr (Ottone et al., 2014). This suggests the Cortaderitian Stage is no 3564 older than 237.8 Ma, and therefore the Scytophyllum flora and Madygen Formation can be no older 3565 than this age, still within the Carnian. Note that a GSSP for the Carnian-Norian boundary has not yet 3566 been identified; radioisotopic ages may suggest a younger boundary at ~220 Ma (Lucas et al., 2012).

3567	Nevertheless, a commonly accepted date for the Carnian upper boundary is estimated at 228.4 Ma $\pm$
3568	2 Myr based on cyclostratigraphy and a candidate GSSP (e.g. Ogg, 2012; Ogg et al., 2014), so this
3569	provides a minimum age at 226.4 Ma.
3570	Soft maximum as for 75.3.
3571	
3572	90.1 Discussion
3573	
3574	Previous work has suggested Archexyela ipswichensis Engel, 2005 from the Mt. Crosby
3575	Formation, Ipswich Coal Measures of Queensland, Australia may be the oldest hymenopteran (e.g.
3576	Nicholson et al., 2015). However, the stratigraphy of the Ipswich Basin also provides a minimum age
3577	of uppermost Carnian (Purdy and Cranfield, 2013), thus we calibrate crown Hymenoptera with the
3578	equally old T. foveolata, which has been included in landmark total-evidence phylogenies (O'Reilly et
3579	al., 2015; Ronquist et al., 2012).
3580	
3581	91. Crown Aparaglossata
3582	
3583	This clade comprises Neuropterida, Coleopterida and Mecopterida, their last common ancestor
3584	and all of its descendants (Fig. 23). The clade was first named by Peters et al. (2014) based on
3585	support from phylogenetic analysis of transcriptomes.
3586	
3587	91.1. Fossil specimens
3588	
3589	As for 89.1.
3590	
3591	91.2. Phylogenetic justification
3592	
	139

3593	As for 89.2.
3594	
3595	91.3. Age justification
3596	
3597	As for 89.3.
3598	
3599	92. Crown Neuropterida
3600	
3601	This clade comprises Raphidioptera (snakeflies), Megaloptera (fishflies), Neuroptera (net-
3602	winged insects), their last common ancestor and all of its descendants (Fig. 23). Monophyly is
3603	established by phylogenetic analysis of transcriptomes (Misof et al., 2014; Peters et al., 2014), protein-
3604	coding genes (Wiegmann et al., 2009), morphology (Beutel et al., 2011), and combined molecular and
3605	morphological data (Winterton et al., 2010).
3606	
3607	92.1. Fossil specimens
3608	
3609	Elmothone martynovae Carpenter, 1976. MCZ 5585, holotype, a forewing (Fig. 25b). Figured
3610	by Prokop et al. (2015; Fig. 7A).
3611	
3612	92.2. Phylogenetic justification
3613	
3614	A morphological phylogenetic analysis placed the Permithonidae sensu lato as a stem group to
3615	the extant Neuroptera (Ren et al., 2009; shown in supplementary information therein). A position on
3616	the stem lineage of Neuroptera is thus part of the crown group of Neuropterida. As the coding was
3617	done at a family level, we note with caution that monophyly of the Permithonidae and the exact
3618	relationships of its member species with Neuroptera has not been examined in a phylogenetic context
	140

3619 and remain obscure (Prokop et al., 2015). Nonetheless, most members of Permithonidae possess the 3620 character states coded by Ren et al. (2009), so we take the oldest well-described member, E. 3621 *martynovae*, as a calibration fossil. 3622 3623 92.3. Age justification 3624 3625 This fossil occurs in the Carlton Limestone Member of the Wellington Formation in the Sumner 3626 Group of Elmo, Dickinson County, central Kansas (Prokop et al., 2015; Zambito et al., 2012). The 3627 insect-bearing locality is correlated with the Leonardian regional Stage (Sawin et al., 2008; Zambito et 3628 al., 2012) on the basis of conchostracan biostratigraphy (Tasch, 1962). The Leonardian spans the 3629 Artinskian and the younger Kungurian Stage (Henderson et al., 2012). The upper boundary of the 3630 Kungurian is 272.3 Ma  $\pm$  0.5 Myr, thus providing a conservative minimum age estimate of 271.8 Ma. 3631 Soft maximum as for 75.3. 3632 3633 92.4. Discussion 3634 3635 A younger member of the Permithonidae, Permithone belmontensis Tillyard, 1922 3636 (Changhsingian or latest Permian of Belmont, Australia), was previously used as a calibration fossil for 3637 Neuropterida (Misof et al., 2014). 3638 3639 93. Crown Megaloptera 3640 3641 This clade comprises Sialidae and Corydalidae, their last common ancestor and all of its 3642 descendants (Fig. 23). Monophyly is established by phylogenetic analysis of full mitochondrial 3643 genomes (Wang et al., 2012), transcriptomes (Misof et al., 2014), and morphology of the wing base 3644 (Zhao et al., 2014).

3645	
3646	93.1. Fossil specimens
3647	
3648	Eochauliodes striolatus Liu et al., 2012. CNU-MEG-NN2011004 P/C, holotype part/counterpart,
3649	laterally preserving an adult including forewing and hindwing (Fig. 25c).
3650	
3651	93.2. Phylogenetic justification
3652	
3653	E. striolatus was included in a phylogenetic analysis of morphology, encompassing characters
3654	from wing venation, adult genitalia, and larval morphology where possible (Liu et al., 2012). E.
3655	striolatus was found within the crown Corydalidae, at the base of the 'Protochauliodes clade'
3656	(comprising extant species). This position is therefore within crown Megaloptera. The bifurcated
3657	anterior branch of the Rs vein is a relevant synapomorphy (Liu et al., 2012).
3658	
3659	93.3. Age justification
3660	
3661	As for 79.3.
3662	
3663	93.4. Discussion
3664	
3665	Another fossil from the Daohugou fauna, Jurochauliodes ponomarenkoi Wang and Zhang,
3666	2010 was found in a slightly more basal position within the Corydalidae (and thus Megaloptera) crown
3667	group (Liu et al., 2012). As it is of equal age to <i>E. striolatus</i> , it is also an acceptable calibration fossil
3668	for this clade.
3669	
3670	94. Crown Neuroptera

3672 This clade comprises Hemerobiiformia, Nevrorthiformia and Myrmeleontiformia, their last 3673 common ancestor and all of its descendants (Fig. 23). Monophyly is supported by phylogenetic 3674 analysis of ribosomal and mitochondrial genes (Haring and Aspöck, 2004), housekeeping genes 3675 (Wiegmann et al., 2009), and morphology (Beutel et al., 2011; Zhao et al., 2014). 3676 3677 94.1. Fossil specimens 3678 3679 Liassochrysa stigmatica Ansorge and Schlüter, 1990. MBA.I 5046 (formerly from the Ansorge 3680 collection, Dobbertin, Germany: No. LDA301), holotype, preserving a forewing. Imaged in (Wedmann 3681 and Makarkin, 2007: Fig. 5a). 3682 3683 94.2. Phylogenetic justification 3684 3685 L. stigmatica was coded in the morphological matrix for the total evidence phylogeny of Liu et 3686 al. (2015). In that tree, it was a member of crown group Mantispidae, a family within Hemerobiiformia, 3687 and therefore crown Neuroptera (Liu et al., 2015). This fossil was also the oldest calibration used for 3688 Neuroptera in the divergence time analysis of Winterton et al. (2010). 3689 3690 94.3. Age justification 3691 3692 The fossil was recovered from the former clay pit of Schwinz, near Dobbertin, Mecklenburg, 3693 northeast Germany (Ansorge and Schlüter, 1990). Multiple associated ammonites (Eleganticeras 3694 elegantulum, Lobolytoceras siemensi, Harpoceras capellatum) indicate that the locality is correlated to 3695 the lower part of the *H. falciferum* ammonite Zone, early Toarcian (Ansorge and Schlüter, 1990; 3696 O'Reilly et al., 2015; Pálfy et al., 2002, 2000). The Boreal falciferum Zone is equivalent to the Tethyan

3697	H. serpentinum ammonoid Zone (Macchioni, 2002), and succeeded by the Hildoceras bifrons
3698	ammonoid Zone. The base of the <i>bifrons</i> Zone has been dated to 180.36 Ma $\pm$ 0.7 Myr (Ogg et al.,
3699	2012b). From this, an upper boundary of the falciferum Zone can be derived, and thus a minimum age
3700	for Dobbertin, at 179.66 Ma.
3701	Soft maximum as for 75.3.
3702	
3703	95. Crown Coleopterida
3704	
3705	This clade comprises Strepsiptera (twisted wing parasites) and Coleoptera (beetles), their last
3706	common ancestor and all of its descendants (Fig. 23). Monophyly of this clade is an extremely well-
3707	examined question in systematics, often used to illustrate the principle of long branch attraction (e.g.
3708	Boussau et al., 2014; Carmean and Crespi, 1995; Huelsenbeck, 1998, 1997; Niehuis et al., 2012;
3709	Siddall and Whiting, 1999; Whiting et al., 1997; Wiegmann et al., 2009). However, recent analyses of
3710	genomes and transcriptomes have consistently converged on a sister group relationship between
3711	Strepsiptera and Coleoptera (Boussau et al., 2014; Misof et al., 2014; Niehuis et al., 2012).
3712	
3713	95.1. Fossil specimens
3714	
3715	Adiphlebia lacoana Scudder, 1885. USNM 38140, holotype, preserving a forewing. Imaged in
3716	Béthoux (2009: Fig. 1(3-5)).
3717	
3718	95.2. Phylogenetic justification
3719	
3720	A. lacoana has not been included in formal cladistic analysis to test its phylogenetic position.
3721	Variation in forewing venation within species provides a challenge to homology statements (Béthoux,
3722	2009; Garwood and Sutton, 2010). However, A. lacoana shares a forewing character with the crown
	144
3723 beetle suborder Archostemata, specifically: "the areas between ScP, RA, branches of RP, M, branches 3724 of CuA, and AA filled with a regular network of guadrangular to pentagonal cells forming intercalary 3725 longitudinal pseudo-veins" (Béthoux, 2009). Intercalary pseudo-veins are also observed in fossils 3726 throughout Pterygota, suggesting this is either a symplesiomorphic or homoplastic state. However, 3727 some of the wing regions exhibiting intercalary veins (ScP and RA) are restricted to fossil Coleoptera 3728 (Béthoux, 2009). A. lacoana has thus been designated as a sister group to all crown Coleoptera, i.e. a 3729 member of its stem lineage (Béthoux, 2009), and thus a crown group member of Coleopterida. This 3730 assignment is also supported by putative larval material (Labandeira, 2011). 3731 There has been debate, however, about the taphonomy of the network of wing veins, 3732 suggesting they are clumps of clay instead of morphological characters (Kukalova-Peck and Beutel, 3733 2012). Alternative placements were on the stem lineage of Neuroptera or Neuropterida (Kukalova-3734 Peck and Beutel, 2012), or outside Holometabola altogether (Guan et al., 2016; Nel et al., 2013). 3735 3736 95.3. Age justification 3737 3738 Minimum as for 31.3. Soft maximum as for 75.3. 3739 3740 96. Crown Coleoptera 3741 3742 This clade comprises Archostemata, Myxophaga, Adephaga (ground beetles, tiger beetles, 3743 diving beetles, whirliging beetles) and Polyphaga (ladybugs, longhorn beetles, weevils, fireflies, 3744 scarabs, stag beetles, rove beetles), their last common ancestor and all of its descendants (Fig. 23). 3745 Monophyly is supported by phylogenetic analysis of nuclear protein-coding genes (McKenna et al., 3746 2015) and morphology (Beutel et al., 2011). 3747 3748 96.1. Fossil specimens

3749	
3750	Triadogyrus sternalis Ponomarenko, 1977. PIN 3320/13, holotype (Fig. 25d), an exoskeleton
3751	without head, prothorax, or legs (Arnol'di et al., 1992).
3752	
3753	96.2. Phylogenetic justification
3754	
3755	In the morphological phylogenetic analysis of Beutel et al. (2013), <i>T. sternalis</i> is a stem group
3756	member of the family Gyrinidae. As Gyrinidae is part of Adephaga, crown membership within both
3757	Adephaga and Coleoptera is justified.
3758	
3759	96.3. Age justification
3760	
3761	T. sternalis was recovered from the mouth of Bereni River near Garazhokva settlement,
3762	Khar'kov oblast, Izyum region, Ukraine (Arnol'di et al., 1992). Fossiliferous strata are lacustrine
3763	claystone, part of the Protopivka Formation, estimated as Late Carnian-Early Norian age within the
3764	late Triassic (Arnol'di et al., 1992; Rasnitsyn and Quicke, 2002; Shcherbakov, 2008). The upper Norian
3765	boundary is estimated at ~208.5 Ma, so this provides a conservative minimum age.
3766	Soft maximum as for 75.3.
3767	
3768	96.4. Discussion
3769	
3770	The Pennsylvanian (Mazon Creek) fossil A. lacoana is a member of the stem lineage of
3771	Coleoptera (Béthoux, 2009). Recent divergence time analyses (McKenna et al., 2015; Misof et al.,
3772	2014) have therefore elected not to calibrate the crown group of Coleoptera with A. lacoana. Resulting
3773	age estimates for crown Coleoptera ranged from 250-280 Ma, substantially younger than A. lacoana
3774	itself.

The Permian *Coleopsis archaica* Kirejtshuk et al., 2014 was noted as a stem group fossil, potentially Protocoleoptera (stem Coleoptera) (McKenna et al., 2015). Thus it was not used as a calibration. However, using younger internal calibrations (the oldest from Madygen, 225 Ma in their dataset), the crown origin of Coleoptera was estimated around 250 Ma (McKenna et al., 2015). Accounting for error bars, the crown group may have originated shortly before (or shortly after) the end-Permian extinction, timing that is compatible with *C. archaica* as a very early representative.

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### 3782 **97. Crown Mecopterida**

3783

3784 This clade comprises Amphiesmenoptera and Antliophora, their last common ancestor and all 3785 of its descendants (Fig. 24). Phylogenetic support for monophyly of Mecopterida comes from 3786 genomes (Niehuis et al., 2012), transcriptomes (Misof et al., 2014) and morphology (Beutel et al., 3787 2011). Note that the clade we refer to as Mecopterida was called Panorpida by Grimaldi and Engel 3788 (2005), because they used Mecopterida to refer to paraphyletic Mecoptera containing Siphonaptera 3789 (and excluding Diptera). Our clade Mecopterida was also referred to as Panorpoidea by several 3790 sources, including Ren et al. (2009). Analyses relying on molecular data alone do not support the 3791 paraphyly of Mecoptera (Misof et al., 2014; Peters et al., 2014; Wiegmann et al., 2009), and these 3792 tend to utilize our conception of Mecopterida.

3793

3794 97.1. Fossil specimens

3795

3796 *Permopanorpa inaequalis* Tillyard, 1926. YPM IP 005058, holotype, a wing (**Fig. 25e**).

3797

3798 97.2. Phylogenetic justification

3799

3800 *P. inaequalis* is the oldest member of the family Permopanorpidae, which was coded (at the

family level) in the morphological matrix of Ren et al. (2009). In that tree, it was part of the total group of Antliophora (although the figure label indicated it was inside crown Antliophora, the topology clearly indicates it was on the stem lineage; Ren et al., 2009). As a stem group member of Antliophora, *P. inaequalis* is thus crown group Mecopterida.

3805

3806 97.3. Age justification

3807

3808 As for 92.3.

3809

3810 97.4. Discussion

3811

*W. maryvonneae* (family Protomeropidae), from the Bashkirian of France, has been proposed as an "amphiesmenopteran or antliophoran", which may mean it belongs on the stem lineage of one of those clades and thus in crown Mecopterida. It has also been drawn onto a phylogram as a stem member of Mecoptera (Nel et al., 2013). However, the evidence for any particular placement within Mecopterida is ambiguous, and thus it is possible the fossil is only stem Mecopterida. See 89.2 for greater detail.

Conversely, the early to middle Permian family Kaltanidae has been included in a phylogenetic analysis, and shown to fall on the stem lineage of Amphiesmenoptera (Ren et al., 2009). Although Kaltanidae have been previously discussed as calibration fossils for Mecopterida (e.g. Benton and Donoghue, 2007), their oldest members are from the Kungurian Stage of Russia, the same age as Elmo (Bashkuev, 2008). Additionally, the family Belmontiidae is within crown Mecopterida in a phylogenetic analysis (Ren et al., 2009), but its oldest fossil is from the late Permian (Changhsingian) of Australia (Grimaldi and Engel, 2005).

3825

#### 3826 **98. Crown Amphiesmenoptera**

3828 This clade comprises Trichoptera (caddisflies) and Lepidoptera (butterflies, moths), their last 3829 common ancestor and all of its descendants (Fig. 24). Monophyly is supported by phylogenetic 3830 analysis of transcriptomes (Misof et al., 2014), nuclear protein-coding genes (Wiegmann et al., 2009), 3831 and morphology (Beutel et al., 2011; Kristensen, 1991). 3832 3833 98.1. Fossil specimens 3834 3835 Archaeolepis mane Whalley, 1985. BMNH In. 59397, holotype, preserving a hindwing (Fig. 3836 25f). 3837 3838 98.2. Phylogenetic justification 3839

A. mane has been used to calibrate the lepidopteran root in previous molecular dating analyses (e.g. Wahlberg et al., 2013), where this relationship is based on two lines of evidence: wing scales and wing venation. The preservation of extremely rare scales completely covering the hindwing excludes *A. mane* from crown Trichoptera (Whalley, 1986, 1985) because Trichoptera only bear scales on the forewing. The presence of scales across the entirety of a wing with panorpoid venation can only signal amphiesmenopteran affinity.

The Sc vein (with one visible branch) of *A. mane* is unlikely to represent the ancestral state for Lepidoptera, as the number of Sc vein branches varies in early-diverging moths, but is usually two branches, and this vein is multi-branched ancestrally in Amphiesmenoptera (Kukalova-Peck and Willmann, 1990; Minet et al., 2010; Sukatsheva and Vassilenko, 2011; Schachat and Brown, 2016). Although Trichoptera tend to have more wing veins than Lepidoptera, it is likely that fewer veins were lost by ancestral moths than is currently accepted in the literature, making distinctions between amphiesmenopteran branches difficult for Mesozoic fossils (Schachat and Brown, 2015, 2016). As

3853 reconstructed by Whalley (1986), the wing venation of A. mane differs markedly from the venation of crown Lepidoptera: there is a single, branched Cubitus vein, with CuP apparently absent, and all three 3854 3855 branches of the anal vein reach the dorsum. In contrast, basal crown Lepidoptera nearly always have 3856 a CuP vein, and the anal vein becomes fused before reaching the dorsum (Common, 1973; Schachat 3857 and Brown, 2016). A position for A. mane within the crown group of Lepidoptera thus cannot be 3858 confirmed, but an identity as stem Lepidoptera is highly likely based on the wing scales in particular, in 3859 agreement with Whalley (1986). This fossil would therefore be within the crown group of 3860 Amphiesmenoptera. 3861

3862 98.3. Age justification

3863

Whalley (1985) noted the locality as Black Ven, Charmouth, Dorset, on the Jurassic Coast of England. This was further specified as calcareous flatstone, probably from Bed 75a, of the *Caenisites turneri* ammonoid Zone (Sohn et al., 2012), or *Microderoceras birchi* Nodular of the "Shales with Beef" (Lang et al., 1923). Chemostratigraphy places the *C. turneri* (and *M. birchi*) Zones within the middle Sinemurian (Jenkyns et al., 2002). The upper boundary of the *C. turneri* Zone is thus dated to 195.31 Ma (Ogg et al., 2012b), providing a minimum age.

3870 Soft maximum as for 75.3.

3871

## 3872 99. Crown Trichoptera

3873

3874This clade comprises 'Spicipalpia', Annulipalpia and Integripalpia their last common ancestor3875and all of its descendants (**Fig. 24**). Monophyly is supported by phylogenetic analysis of

transcriptomes (Misof et al., 2014), housekeeping genes (Kjer et al., 2002, 2001; Malm et al., 2013),

and morphology (Beutel et al., 2011).

3878

3879	99.1. Fossil specimens
3880	
3881	Liadotaulius maior Handlirsch, 1906. Handlirsch (1906) did not designate a holotype, thus we
3882	refer to three specimens figured by Ansorge (2002): (Ansorge collection, to be deposited at MBA: LGA
3883	1995; Fig. 25g), female forewing, (LGA 672), male forewing, and (LGA 1710), hindwing.
3884	
3885	99.2. Phylogenetic justification
3886	
3887	Taxonomic placement of <i>L. maior</i> requires apomorphies from the male wings, as female wings
3888	have many plesiomorphic venation characters (Ansorge, 2002). Further studies of a younger
3889	congeneric, L. daohugouensis Wu and Huang, 2012, reveal new characters shared with crown group
3890	Trichoptera. These include the apical part of Cu2 bending towards the wing margin, its
3891	desclerotisation, and complete anal veins (Ansorge, 2002; Wu and Huang, 2012). These apomorphies
3892	place the genus Liadotaulius in Philopotamidae, a family within crown group Annulipalpa, and thus
3893	Trichoptera (Wu and Huang, 2012).
3894	
3895	99.3. Age justification
3896	
3897	The fossils were recovered from Grimmen, northeast Germany (Ansorge, 2002). Further age
3898	information as for 94.3.
3899	
3900	99.4. Discussion
3901	
3902	Possible caddisfly larval cases were recently described from the early Permian of Brazil (Mouro
3903	et al., 2016). The cases are tubular in form, and particulate matter is stuck to some of the cases
3904	(Mouro et al., 2016). Of the two most basal extant trichopteran families that construct larval cases, the

3905	Hydroptilidae construct tubular cases and the Glossosomatidae construct their cases from particulate
3906	matter (Malm et al., 2013). However, various types of larval cases, including tubular cases, are
3907	constructed by caddisflies belonging to distantly-related lineages (Malm et al., 2013); at present, it
3908	cannot be assumed that tubular larval cases have originated only once within the Trichoptera.
3909	Assuming the Permian fossils are indeed insect larval cases, therefore, does not confirm the
3910	phylogenetic position of their inhabitants within crown versus stem Trichoptera, as larval cases might
3911	have evolved in the stem group.
3912	
3913	100. Crown Lepidoptera
3914	
3915	This clade comprises Zeugloptera, Aglossata, Heterobathmiina and Glossata (itself comprising
3916	six infraorders, over 100 families, and over 160,000 species), their last common ancestor and all of its
3917	descendants (Fig. 24). The list of lepidopteran subclades comes from a recently published consensus
3918	(van Nieukerken et al., 2011), although some molecular analyses have not recovered these clades
3919	(Regier et al., 2013). Monophyly is supported by nuclear protein-coding genes (Regier et al., 2013),
3920	transcriptomes (Misof et al., 2014), and morphology (Beutel et al., 2011).
3921	
3922	100.1. Fossil specimens
3923	
3924	Parasabatinca aftimacrai Whalley, 1978. Although the holotype (the specimen to which we
3925	refer; Fig. 25h) and two paratypes were attributed to the NHMUK (Sohn et al., 2012), they are now
3926	housed as part of the Acra collection, curated by D. Azar, pending construction of a fossil museum at
3927	the Lebanese University in Fanar (Matn), Lebanon (D. Azar, pers. comm.).
3928	
3929	100.2. Phylogenetic justification
3930	

3931 Although not included in formal phylogenetic analysis, morphological characters (morphology 3932 of the antennae with ascoids, number and shape of tibial spurs, mouthpart and maxillary palp 3933 morphology) support the position of *P. aftimacrai* in what was formerly known as the 'Sabatinca' group 3934 of genera within Micropterigidae (Kristensen and Skalski, 1998; D. Azar, pers. comm.). As P. aftimacrai 3935 has an unbranched R vein and because Rs<sub>4</sub> terminates below the apex, the wing venation of P. 3936 aftimacrai most closely resembles that of the extant species Austromartyria porphyrodes, which 3937 belongs to what is now known as the 'Southern sabatincoid' lineage of Micropterigidae (Gibbs, 2010). 3938 Based on the above morphological characters, P. aftimacrai is supported as the oldest crown group 3939 member in multiple summaries of the fossil record of Lepidoptera (Grimaldi and Engel, 2005, Fig. 3940 13.13; Sohn et al., 2015, Fig. 2). Membership either within the crown or stem of Micropterigidae places 3941 the fossil within crown Zeugloptera and crown Lepidoptera. 3942 3943 100.3. Age justification 3944 3945 As for 76.3. 3946 3947 3948 100.4. Discussion 3949 3950 A number of older fossils have been assigned to Lepidoptera, but their position within the 3951 crown is ambiguous. A. mane, from the Early Jurassic of Dorset, England, has been used to calibrate 3952 the lepidopteran root in previous molecular dating analyses (e.g. Wahlberg et al., 2013). See 98.2 for 3953 exclusion of *A. mane* from the lepidopteran crown. 3954 Sohn et al. (2015) suggested that two undescribed fossil species are members of the 3955 Micropterigidae stem lineage (and thus crown Zeugloptera and crown Lepidoptera). These are from 3956 the Toarcian (Early Jurassic) Grüne Series of Grimmen, Germany (Ansorge, 2002), but they are too

3957 poorly characterized to be confidently used as calibration fossils.

3958 3959 **101. Crown Antliophora** 3960 3961 This clade comprises Siphonaptera (fleas), Mecoptera (scorpionflies) and Diptera (flies), their 3962 last common ancestor and all of its descendants (Fig. 24). Support for monophyly comes from 3963 phylogenetic analysis of transcriptomes (Misof et al., 2014; Peters et al., 2014) and morphology 3964 (Beutel et al., 2011). A recent analysis of mitochondrial genomes finds Amphiesmenoptera within 3965 Antliophora under some analytical conditions, potentially challenging antliophoran monophyly (Song et 3966 al., 2016). 3967 3968 101.1. Fossil specimens 3969 3970 Pseudonannochorista willmanni Novokshonov, 1994. PIN 966/21, holotype, preserving a 3971 forewing (Fig. 25i). 3972 3973 101.2. Phylogenetic justification 3974 3975 Pseudonannochoristinae is a subfamily of the Permochoristidae (Bashkuey, 2011; 3976 Novokshonov, 1994), however, a morphological phylogenetic analysis indicates polyphyly of this family 3977 (Ren et al., 2009). While the Permochoristinae (the other subfamily of Permochoristidae) fall on the 3978 stem lineage of Antliophora, Pseudonannochoristinae are part of the stem lineage of Mecoptera (Ren 3979 et al., 2009). Therefore, P. willmanni, as a member of Pseudonannochoristinae, is part of the crown 3980 group of Antliophora. 3981 3982 101.3. Age justification

3984 Minimum as for 77.3. Soft maximum as for 75.3.

3985

3986 101.4. Discussion

3987

3988 Other fossils from the families Permotanyderidae, Permotipulidae, and Nannochoristinae are 3989 all demonstrably within crown group Antliophora (Ren et al., 2009). However, the localities from which 3990 they are known are younger, of Changhsingian age (Belmont, Australia and Mooi River, South Africa). 3991 Fossils of Siphonaptera from the Jurassic (Gao et al., 2012) and Cretaceous (Gao et al., 2014; 3992 Huang, 2015), suggested to parasitise dinosaurs, have been excluded from the crown group in a 3993 recent molecular phylogenetic analysis (Zhu et al., 2015). The molecular clock analysis (which was 3994 calibrated with better established fossils from Dominican and Baltic amber, of Miocene and Eocene 3995 age, respectively) estimated the origins of crown Siphonaptera in the Valanginian to Aptian stages of 3996 the Early Cretaceous (Zhu et al., 2015). Furthermore, none of the Mesozoic fossils possess a 3997 diagnostic character combination for the crown group (Dittmar et al., 2016). As siphonapteran 3998 parasites of dinosaurs would require a strong assumption that piercing mouthparts must be used for 3999 blood-feeding (Dittmar et al., 2016), we do not include any crown fossil calibrations.

4000

## 4001 **102. Crown Mecoptera**

4002

This clade comprises Apteropanorpidae, Bittacidae, Boreidae, Choristidae, Eomeropidae, Meropeidae, Nannochoristidae, Panorpidae, and Panorpodidae, their last common ancestor and all of its descendants (**Fig. 24**). Paraphyly of the traditional concept of Mecoptera (i.e. inclusion of Siphonaptera) was proposed by Whiting (2002) on the basis of four nuclear genes. This was, however, contradicted by analysis of six nuclear genes (Wiegmann et al., 2009), transcriptomes (Misof et al., 2014; Peters et al., 2014), and morphology (Beutel et al., 2011). Each of the latter studies recovered a

4009	monophyletic	Mecoptera	as the	sister	group	o of Si	iphona	ptera.
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4010	
4011	102.1. Fossil specimens
4012	
4013	Burmomerope eureka Grimaldi and Engel, 2013 (collection of James Zigras, available for study
4014	at AMNH: JZC Bu-84), holotype in amber.
4015	
4016	102.2. Phylogenetic justification
4017	
4018	B. eureka was assigned to the stem group of the extant family Meropeidae, based on several
4019	wing venation characters, including loss of slanted portion of CuA in forewing and R-Rs fork basal
4020	(Grimaldi and Engel, 2013). A position on the stem lineage of Meropeidae is therefore within the crown
4021	group of Mecoptera.
4022	
4023	102.3. Age justification
4024	
4025	As for 87.3.
4026	
4027	103. Crown Diptera
4028	
4029	This clade comprises Tipulomorpha (crane flies), Psychodomorpha (moth flies, sand flies),
4030	Culicomorpha (mosquitoes, black flies), Bibionomorpha (march flies, fungus gnats) and Brachycera
4031	(horse flies, robber flies, fruit flies, house flies, blow flies, etc.), their last common ancestor and all of
4032	its descendants (Fig. 24). Monophyly of Diptera has been supported in many phylogenetic analyses,
4033	including those based on transcriptomes (Misof et al., 2014), mitochondrial genomes and microRNA
4034	presence (Wiegmann et al., 2011), and morphology (Beutel et al., 2011; Wiegmann et al., 2011).

4035	
4036	103.1. Fossil specimens
4037	
4038	Grauvogelia arzvilleriana Krzeminski et al., 1994 (part of the private Louis Grauvogel collection,
4039	Ringendorf, Bas-Rhin, France, No. 5514), holotype (Fig. 25j).
4040	
4041	103.2. Phylogenetic justification
4042	
4043	G. arzvilleriana was included in the morphological cladistic analysis of Blagoderov et al. (2007).
4044	In that analysis, it was supported on the stem group of Psychodomorpha (Blagoderov et al., 2007).
4045	Although the original description assigned G. arzvilleriana to its own family, several wing venation
4046	characters were noted as similarities with families of Psychodomorpha (Krzeminski et al., 1994). The
4047	stem group of Psychodomorpha is within crown Diptera.
4048	
4049	103.3. Age justification
4050	
4051	Minimum as for 72.3. Soft maximum as for 75.3.
4052	
4053	103.4. Discussion
4054	
4055	A number of other dipteran fossils have been described from Grès à Voltzia; of special interest
4056	is Voltziapupa tentata Lukashevich et al., 2010, known only from well-preserved pupae, while G.
4057	arzvilleriana is known only from adult wings. The venation of the wing sheath in V. tentata is not well
4058	preserved, preventing a clear link of characters with G. arzvilleriana (Lukashevich et al., 2010).
4059	
4060	104. Conclusions

4062 Based on this compilation, qualitative trends in the fossil record of arthropod crown group 4063 members can be described. Patchiness in our taxonomic coverage results from differential 4064 preservation potential, with a notable scarcity of taxa living in habitats with poorly preserved facies 4065 (e.g. intertidal barnacles or pelagic copepods). More completely preserved fossils representing ancient 4066 divergences are well represented in our list of calibrations, perhaps owing to the attention devoted to 4067 phylogenetic analysis of deep fossil relationships within arthropods (e.g. Garwood and Dunlop, 2014; 4068 Lee et al., 2013; Legg et al., 2013; Oakley et al., 2013; Rota-Stabelli et al., 2011). However because 4069 our review is focused on crown groups, about half of our calibrations are from mid-Palaeozoic 4070 localities, making them much more numerous than those from Cambrian Burgess Shale-type biotas. 4071 Throughout the dataset, there is less of a relationship between 'hard part' preservation (calcified body 4072 parts, such as ostracod carapaces) and phylogenetic accuracy than might be expected.

4073 Particular Konservat-Lagerstätten, such as Herefordshire (Silurian), Rhynie Chert (Devonian), 4074 Mazon Creek (Carboniferous), Crato (Cretaceous) and Burmese amber (Cretaceous), provide several 4075 calibrations representing different arthropod clades, presumably owing to their preservation of non-4076 biomineralised tissues required to identify arthropods to the ordinal level. These sites are critically 4077 important for the arthropod fossil record because of their relatively low preservation potential of many 4078 groups, as is particularly the case for terrestrial arthropods, being less well mineralised than many of 4079 the marine groups. This is reflected in the low level of congruence between the order of appearance of 4080 lineages in the fossil record (stratigraphic appearance) and the order of phylogenetic branching (Wills, 4081 2001; O'Connor and Wills, 2016) in arthropods, as compared to more congruent datasets such as 4082 tetrapods (Benton et al., 1999, 2000; Norell and Novacek, 1992). Clustering of calibrations at 4083 Konservat-Lagerstätten localities may lead to highly variable lengths of ghost lineages for the different 4084 taxa that are preserved together at these sites, and indeed many of the clades in our database have 4085 soft maxima that are substantially older than their hard minimum date. Konservat-Lagerstätten 4086 localities are, however, fairly regularly spaced throughout the Middle to Late Palaeozoic and the

4061

4087 Mesozoic, and interim periods of time are punctuated by numerous other fossil localities yielding fewer 4088 calibration points. This results in our database having good coverage throughout the Phanaerozoic 4089 with fossil localities occurring on average every 4-10 million years. A notable exception is the 43.2 4090 million year gap in the Ordovician, during which no definite earliest appearances of any crown-group 4091 orders have been identified in our study, despite this period being known as the Ordovician 4092 biodiversification event (Servais et al., 2008, 2010). Numerous arthropod stem lineage taxa were 4093 abundant during the Ordovician (e.g. trilobites), while the possible crown group taxa that have been 4094 described, e.g. ostracods (Siveter et al., 2014; Williams et al., 2008), barnacles (Van Roy et al., 2010), 4095 pycnogonids (Rudkin et al., 2013), xiphosurans (Lamsdell, 2013; Rudkin et al., 2008; Van Roy et al., 4096 2010), and acariform mites (Bernini et al., 2002) do not meet the rigorous standards employed herein 4097 for determining calibration points. From the Late Devonian through the Mississippian (382.7 to 323.2 4098 Ma) our dataset has another large gap during which we have only one calibration point, which 4099 interestingly corresponds with one of the largest mass extinctions events known in the fossil record 4100 (McGhee, 2013).

4101 The field of divergence time estimation itself is rapidly advancing. New methodologies to 4102 incorporate fossil morphology and stratigraphy into the model of diversification (Heath et al., 2014; 4103 Wilkinson et al., 2011) and the phylogenetic topology itself ('tip-dating'; Ronguist et al., 2012) are 4104 growing in popularity. Precision and accuracy of date estimates are improved with the inclusion of as 4105 many a priori justified fossils as possible in tip- (Lee et al., 2013; Ronquist et al., 2012; Zhang et al., 4106 2016) or node-dating studies (Heath et al., 2014; Ho and Phillips, 2009; Warnock et al., 2012, 2015; 4107 Yang and Rannala, 2006). When examined in the context of geological and evolutionary history, the 4108 distribution of fossil calibrations in our dataset are comprehensive, and have been rigorously vetted to 4109 ensure they meet a priori requirements (Parham et al., 2012; Warnock et al., 2015). Following their 4110 use in molecular clock analyses, a posteriori methods such as cross-validation could be employed to 4111 explore the impact of calibrations on the resulting divergence time estimates (e.g. Battistuzzi et al., 4112 2015; Dornburg et al., 2011; Marshall, 2008; Near et al., 2005), although these methods cannot justify

- 4113 removal of individual constraints (Warnock et al., 2015). Fossils mentioned in Discussion sections
- 4114 occupy key positions along clade stems, and should also be considered in divergence time
- 4115 applications. To this end, we have compiled a robust list of over 100 fossil calibrations covering much
- 4116 of the arthropod Tree of Life. We hope this summary will inspire further work clarifying the
- 4117 phylogenetic relationships of fossil arthropods, and morphological studies of characters linking them to
- 4118 their crown clades.
- 4119
- 4120

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4138	
4139	
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## 5976 FIGURE CAPTIONS

5977

5978 **Fig. 1.** Calibration diagram for Ecdysozoa (nodes 2-5, 22-23, 34, 41). Altocrust. = Altocrustacea.

5979 Numbers in this and all other calibration diagrams are ages in Ma.

5980

- 5981 **Fig. 2.** Major fossil calibrations for (A) nodes 2-3: *Rusophycus* trace fossils, GSC 85983, scale bar
- 5982 20mm, image credit M. Coyne; (B-C) nodes 4, 22, 34, 41: Yicaris dianensis, YKLP 10840, scale bars
- 5983 100µm, images credit X. Zhang; (B) whole specimen; (C) detail of epipodites; (D) node 5:
- 5984 Wisangocaris barbarahardyae, SAM P43679a, scale bar 5mm; (E) nodes 23-25, 27: Cowiedesmus
- 5985 eroticopodus, AMS F.64845, scale bar 2mm, image credit Y. Zhen; (F) nodes 64-65: *Rhyniella*
- 5986 *praecursor*, BMNH In.38228, scale bar 200µm, image credit NHMUK.

5987

5988 **Fig. 3.** Calibration diagram for non-arachnid Chelicerata (nodes 6-8).

5989

5990 Fig. 4. Calibration diagram for non-tetrapulmonate Arachnida (nodes 9-16). Pseudos. =

5991 Pseudoscorpiones.

5992

5993 Fig. 5. Chelicerate fossil calibrations for (A) node 6: Haliestes dasos, OUM C.29571, scale bar 500µm, 5994 image credit D. Siveter, M. Sutton, D. Briggs & D. Siveter; (B) node 7: Chasmataspis-like resting 5995 traces, MBA 1084, scale bar 20mm, image credit J. Dunlop; (C) node 13: Protofeaella peetersae, 5996 NHMII3115, scale bar 500µm, image credit H. Henderickx; (D) node 10: Eophalangium sheari, PBM 5997 3503, scale bar 1mm, image credit J. Dunlop; (E) node 14: Electrokoenenia yaksha, NIGP 163263, 5998 scale bar 500µm, image credit M. Engel: (F) node 15: Cratosolpuga wunderlichi, SMNK 1268PAL, 5999 scale bar 5mm, image credit P. Selden; (G) node 9: Eramoscorpius brucensis, holotype ROM 5324, 6000 scale bar 10mm, image credit D. Rudkin & J. Waddington; (H) node 9: Palaeophonus loudonensis, 6001 NMS 1897.122.196, scale bar 20mm, image credit: J. Lamsdell; (I-J) node 12: Cornupalpatum

6002 *burmanicum*, scale bars 100 μm, image credit G. Poinar; (I) Holotype A-10-160; (J) Paratype A-10-261;

6003 (K) node 11: *Protacarus crani*, BMNH In.24665, scale bar 100µm, image credit NHMUK.

6004

6005 **Fig. 6.** Calibration diagram for Tetrapulmonata (nodes 17-21).

6006

**Fig. 7.** Tetrapulmonata fossil calibrations for (A) nodes 17-19: *Parageralinura naufraga*, LWL Ar.K.1,

scale bar 5mm, image credit C. Brauckmann; (B) node 20: *Graeophonus anglicus*, BMNH In 31233,

scale bar 5mm, image credit J. Dunlop; (C, D) node 21: Palaeothele montceauensis, images credit P.

6010 Selden; (C) Holotype MNHN 51961, scale bar 2mm; (D) Reconstructed specimen BMNH In.62050,

scale bar 0.2mm; (E) node 21: *Arthrolycosa* sp., PIN 5431/9, scale bar 1mm, image credit P. Selden.

6012

6013 **Fig. 8.** Calibration diagram for Myriapoda (nodes 24-33). Chilogn. = Chilognatha, Scutigerom. =

6014 Scutigeromorpha, Geophilom. = Geophilomorpha.

6015

6016 **Fig. 9.** Myriapod fossil calibrations for (A-B) node 26: *Electroxenus jezzinensis*, MNHN JS 231/1, scale

6017 bar 0.5mm, image credit D. Azar; (C-E) node 28: *Crussolum* sp., images credit L. Anderson; (C)

6018 Forcipular segment, slide AUGD 12308, scale bar 0.5mm; (D) Prefemur of a trunk leg, slide AUGD

6019 12307, scale bar 0.2mm; (E) Tibia of a trunk leg, slide AUGD 12307, scale bar 0.2mm; (F) node 29:

6020 Fulmenocursor tenax, SMNS 64275, scale bar 5mm, image credit G. Bechly; (G-H) node 30:

6021 Devonobius delta, scale bars 0.1mm, images credit W. Shear; (G) Head and anterior part of trunk,

6022 AMNH slide 411-15-AR18; (H) Forcipular segment, AMNH slide 4329-AR4; (I) nodes 31-32:

6023 Mazoscolopendra richardsoni, FMNH PE29002, scale bar 5mm, image credit J. Wittry; (J-K) node 33:

6024 Kachinophilus pereirai, AMNH Bu-Ba41a; (J) Head and anterior part of trunk, scale bar 0.3 mm; (K)

6025 Posterior body segments, scale bar 0.1mm.

6026

6027 **Fig. 10.** Calibration diagram for Oligostraca (nodes 35-40).

Fig. 11. Oligostraca fossil calibrations for (A) nodes 35-36: *Boeckelericambria pelturae*, UB W116,
scale bar 50µm, image credit D. Waloszek; (B) nodes 37, 39-40: *Luprisca incuba*, YPM IP 307300,
scale bar 500µm, image credit D. Siveter, G. Tanaka, U. Farrell, M. Martin, D. Siveter & D. Briggs; (CE) node 38: *Cytherellina submagna*, ZPAL O.60/001, images credit E. Olempska; (C) steinkern left
lateral view, scale bar 200 µm; (D) soft anatomy of posterior region, scale bar 100µm; (E) walking legs
and presumed furca, scale bar 50µm.

6035

6036 **Fig. 12.** Calibration diagram for Copepoda and Thecostraca (nodes 42-47).

6037

Fig. 13. Calibration diagram for Malacostraca (nodes 48-56). Verunip. = Verunipeltata, Tanaid =
Tanaidacea.

6040

6041 Fig. 14. Multicrustacea fossil calibrations for (A) node 42: Arenosicaris inflata, PRI 10130, scale bar 6042 10mm, image credit J. Collette; (B) node 43: Kabatarina pattersoni, NHMUK 63466, scale bar 100µm, 6043 image credit G. Boxshall; (C-D) node 44: Rhamphoverritor reduncus, OUM C.29587, scale bars 6044 500µm, image credit D. Briggs, M. Sutton, D. Siveter & D. Siveter; (C) lateral views with (left) and 6045 without (right) head shield; (D) transverse section before serial grinding; (E) nodes 45-46: Illilepas 6046 damrowi, FMNH P32055, scale bar 5mm, image credit J. Wittry; (F-G) node 48: Cinerocaris magnifica. 6047 images credit D. Briggs, M. Sutton, S. Siveter & D. Siveter; (F) OUM C.29566, reconstruction in lateral 6048 view with (top) and without (bottom) head shield, scale bar 2mm; (G) holotype C.29565, sub-6049 transverse section, scale bar 1mm; (H-I) nodes 49, 55-56: Palaeopalaemon newberryi, KSU 3484, 6050 scale bars 5mm, image credit W. Jones; (H) left view; (I) right view; (J) nodes 52-53: Hesslerella 6051 shermani, FMNH PE 16527, latex cast whitened with ammonium chloride, scale bar image credit T. 6052 Hegna; (K) node 50: Anaspidites antiguus, AMS F64765, scale bar 5mm, image credit S. Ahyong; (L-6053 M) node 54: Alavatanais carabe, scale bars 500 µm, images credit A. Sánchez-Garcia; (L) holotype

6054 MCNA 9537; (M) MCNA 13888 lateral view.

6055

6056 **Fig. 15.** Calibration diagram for Allotriocarida (nodes 57-63).

6057

Fig. 16. Allotriocarida fossil calibrations for (A) node 57: *Rehbachiella kinnekullensis*, UB 611, scale
bar 200μm, image credit D. Waloszek; (B) node 58: *Lepidocaris rhyniensis*, NHMUK In. 24493, scale
bar 200μm, image credit NHMUK; (C) node 60: *Chenops yixianensis*, CNU-CAL-HP-2009001, scale
bar 10mm, image credit T. Hegna; (D) node 61: *Leaia chinensis*, NIGP 51786, scale bar 1mm, image
credit Y. Shen; (E) node 62: *Dundgobiestheria mandalgobiensis*, ED-A-14-1, scale bar 1 mm, image
credit G. Li; (F) node 63: *Smirnovidaphnia smirnovi*, PIN 1873/100, scale bar 200 μm, image credit A.

6065

Fig. 17. Calibration diagram for non-neopteran Hexapoda (nodes 64-73). Microc. = Microcoryphia,
Zygent. = Zygentoma, Euplect. = Euplectoptera.

6068

6069 Fig. 18. Hexapoda fossil calibrations for (A) node 70: Delitzschala bitterfeldensis, BGR X 9216, scale 6070 bar 2mm, image credit C. Brauckmann; (B) node 68: Cretaceomachilis libanensis, Milki No. 194/35, 6071 scale bar 500µm, image credit G. Poinar; (C) node 69: Burmalepisma cretacicum, B-TH-1, scale bar 500µm, image credit G. Poinar; (D) node 67: Rhyniognatha hirsti, BMNH IN. 38234, scale bar 200µm, 6072 6073 image credit NHMUK; (E) node 72: Triassonurus doliiformis, Louis Grauvogel collection No. 9304, 6074 scale bar 10mm, image credit L. Grauvogel-Stamm. 6075 6076 Fig. 19. Calibration diagram for Polyneoptera (nodes 75-83). Dermap. = Dermaptera, Notop. = 6077 Notoptera, Phasm. = Phasmatodea.

6078

6079 Fig. 20. Polyneoptera fossil calibrations for (A) node 75: Qilianiblatta namurensis, CNU-NX1-303,

6080 scale bar 5mm, image credit D. Ren; (B) node 77: Palaeotaeniopteryx elegans, PIN 1197/333, scale 6081 bar 1mm, image credit N. Sinitshenkova; (C) node 78: Raphogla rubra, Ld LAP 415 B, scale bar 5 6082 mm, image credit S. Fouché; (D) node 80: Cretophasmomima melanogramma, CNU-PHA-6083 NN2012002, scale bar 10mm, image credit D. Ren; (E) node 76: Rhadinolabis phoenicica, Azar 6084 collection 1013, scale bar 500µm, image credit M. Engel;; (F) node 81: Echinosomiscus primoticus, 6085 NIGP 163536, scale bar 2mm, image credit M. Engel; (G) node 79: Juramantophasma sinica, NIGP 6086 142171, scale bar 10mm, image credit D. Huang. 6087 6088 Fig. 21. Calibration diagram for Condylognatha and Psocodea (nodes 74, 84-88). 6089 6090 Fig. 22. Condylognatha fossil calibrations for (A) nodes 85, 87: Aviorrhyncha magnifica, holotype 6091 MNHN Avion No. 2, scale bar 1mm, image credit A. Nel; (B) node 86: Fusithrips crassipes, PIN 6092 3064/8547, scale bar 200µm, image credit A. Rasnitsyn. 6093 6094 Fig. 23. Calibration diagram for Hymenoptera, Neuropterida, and Coleopterida (nodes 89-96). 6095 Hymenopt. = Hymenoptera, Mec. = Mecopterida, Megalopt. = Megaloptera. 6096 6097 **Fig. 24.** Calibration diagram for Mecopterida (nodes 97-103). Mecopt. = Mecoptera. 6098 6099 Fig. 25. Holometabola fossil calibrations for (A) node 90: Triassoxyela foveolata, PIN 2070/1, scale bar 6100 1mm, image credit A. Rasnitsyn; (B) node 92: Elmothone martynovae, MCZ 5585, scale bar 2mm, 6101 image credit Museum of Comparative Zoology, Harvard University (©President and Fellows of Harvard 6102 College); (C) node 93: Eochauliodes striolatus, CNU-MEG-NN2011004 P/C, scale bar 5mm, image 6103 credit D. Ren; (D) node 96: Triadogyrus sternalis, PIN 3320/13, scale bar 2mm, image credit A. 6104 Rasnitsyn; (E) node 97: Permopanorpa inaequalis, YPM IP 005058, scale bar 1mm, image credit J. 6105 Utrup; (F) node 98: Archaeolepis mane, BMNH In. 59397, scale bar 2mm, image credit NHMUK; (G)

- 6106 node 99: *Liadotaulius maior*, LGA 1995, scale bar 2mm, image credit J. Ansorge; (H) node 100:
- 6107 Parasabatinca aftimacrai, holotype, scale bar 2mm, image credit D. Azar; (I) node 101:
- 6108 *Pseudonannochorista willmanni,* PIN 966/21, scale bar 1mm, image credit A. Bashkuev; (J) node 103:
- 6109 *Grauvogelia arzvilleriana*, Louis Grauvogel collection No. 5514, scale bar 1mm, image credit L.
- 6110 Grauvogel-Stamm.

\*Revised manuscript with no changes marked Click here to view linked References

## 1 **1. Introduction**

2

3 Accurate and precise systematic placement and dating of fossils underpins most efforts to infer a chronology for the Tree of Life. Arthropods, as a whole or in part, have received considerable focus 4 5 owing to their incredible morphological disparity, species richness, and (relative to much of the Tree of Life) excellent fossil record. A growing number of recent studies have constructed timetrees for 6 7 arthropods as a whole or for major groups therein (e.g. Bellec and Rabet, 2016; Bond et al., 2014; 8 Bracken-Grissom et al., 2014, 2013; Djernæs et al., 2015; Fernández et al., 2016, 2014; Fernández 9 and Giribet, 2015; Garrison et al., 2016; Garwood et al., 2014; Giribet and Edgecombe, 2013; Herrera 10 et al., 2015; Klopfstein et al., 2015; Legendre et al., 2015; Malm et al., 2013; McKenna et al., 2015; 11 Misof et al., 2014; Oakley et al., 2013; Rehm et al., 2011; Schwentner et al., 2013; Song et al., 2015; 12 Sun et al., 2015; Thomas et al., 2013; Tsang et al., 2014; Wahlberg et al., 2013; Wiegmann et al., 13 2011; Wood et al., 2013; Xu et al., 2015; Zhu et al., 2015). These studies vary in how well they have 14 adhered to best practices for selecting calibration fossils, as many previous calibrations assume that 15 fossil taxonomy accurately reflects phylogeny. Compounding the issue is the expansion of divergence 16 time studies for a variety of comparative questions far beyond systematics and biogeography, 17 including habitat shifts (Letsch et al., 2016; Lins et al., 2012; Rota-Stabelli et al., 2013a; Yang et al., 18 2013), genome evolution (Cao et al., 2013; Schwarz et al., 2014; Starrett et al., 2013; Wissler et al., 19 2013; Yuan et al., 2016), origins of novel characters and behaviours (Rainford et al., 2014; Sanggaard 20 et al., 2014; Wheat and Wahlberg, 2013), evolution of parasites and disease (Ibarra-Cerdeña et al., 21 2014; Palopoli et al., 2014; Rees et al., 2014; Zhou et al., 2014), rate of diversification and its 22 relationship to morphology and ecology (Lee et al., 2013; Wiens et al., 2015), coevolution (Kaltenpoth 23 et al., 2014; Shelomi et al., 2016; Wilson et al., 2013), conservation (Owen et al., 2015), and the use 24 of arthropods as a model for methodological development (O'Reilly et al., 2015; Ronquist et al., 2012; 25 Warnock et al., 2012; Zhang et al., 2016).

26

Recent consensus on best practices for selecting calibration fossils comes with several

27 requirements. There must be references to specific fossil specimen(s), phylogenetic or morphological 28 evidence justifying placement of the fossil, and stratigraphic and/or radiometric dating information for 29 the fossil (Parham et al., 2012). The importance of accurate phylogenetic knowledge of calibration 30 fossils is underscored by recent controversies in dating the evolution of insects, where arguments 31 hinge on the classification of particular 'roachoid' fossils on the stem lineage of Dictyoptera, with 32 resulting differences on the order of 100 Myr (Kjer et al., 2015; Tong et al., 2015). With the explosion of 33 taxonomic sampling in molecular phylogenies due to improvements in sequencing technology, 34 improving the coverage of fossil calibrations is equally important. Recommendations include, for 35 example, including as many as one fossil per ten extant taxa for precise ages, with a varied 36 distribution across lineages and clade depth (Bracken-Grissom et al., 2014). As a response, we have 37 compiled an atlas of 80 rigorously scrutinized calibration fossils for 102 key nodes in arthropod 38 phylogeny. These represent four basal ecdysozoan and arthropod clades, 17 chelicerates, 12 39 myriapods, 30 non-hexapod pancrustaceans, and 39 hexapod clades.

40 Where possible, we favour clade topologies resulting from a phylogenetic analysis of the 41 largest total dataset. If phylogenomic analysis of genomes or transcriptomes has been performed but 42 conflicts with morphology, a strongly supported molecular result is presented (e.g. putative clades 43 such as Oligostraca that do not yet have identified morphological autapomorphies). If, however, 44 molecular phylogenies have been constructed with few genes (e.g. clades such as Peracarida) or with 45 highly conflicting results (e.g. Arachnida), morphological results are given greater weight. Where 46 relevant, we discuss clade names with respect to NCBI's GenBank taxonomy (as recommended by 47 the Fossil Calibrations Database: Polly et al., 2015), as this review is intended to be used by molecular 48 biologists who are interested in dating the evolution of arthropod groups.

As there are >1.2 million species of arthropods, our calibrations are limited to fossils from the Palaeozoic and Mesozoic. Many extant clades have their oldest fossils in Cenozoic ambers such as the Eocene Baltic amber but are predicted to be vastly older based on fossils of allied taxa (e.g.

52 Symphyla and Pauropoda relative to Chilopoda and Diplopoda).

53 While acknowledging the complexity of estimating an age prior for a fossil species known from 54 multiple deposits, we use the oldest (e.g. section 28.3) and/or best known (e.g. section 51.3) horizons 55 to provide minimum age constraints with the narrowest and most accurate age interval. Where there is 56 substantial variation in age estimates for a fossil species, this issue is noted in the text. To 57 accommodate the possibility of older fossils not yet discovered, we provide generous soft maxima (Ho 58 and Phillips, 2009). Accordingly, when conducting divergence time analyses, prior distributions 59 accounting for the large probability tail (e.g. gamma or lognormal) of an older undiscovered fossil may 60 be appropriate. All fossil calibrations described herein are listed with their age information in Table A.1. 61 formatted for adding age constraints in BEAST or PhyloBayes. 62 63 2. Crown Ecdysozoa 64 65 This clade comprises Euarthropoda, Onychophora (velvet worms), Tardigrada (water bears), 66 Nematoida (itself comprising Nematoda and Nematomorpha), and Scalidophora (itself comprising 67 Kinorhyncha, Loricifera, and Priapulida), their last common ancestor and all of its descendants (Fig. 68 1). Monophyly has been demonstrated on the basis of coding and non-coding molecular data 69 (Campbell et al., 2011). 70

- 71 2.1. Fossil specimens
- 72

*Rusophycus* trace fossils in Member 2 of the Chapel Island Formation of the southwestern
Burin Peninsula of southeastern Newfoundland, defining the base of the *R. avalonensis* Biozone.
Arbitrarily, we fix this calibration on a specimen (**Fig. 2a**) from this unit figured by Narbonne et al.
(1987: Fig. 6I; GSC 85983), as in Benton et al. (2015).

77

78 2.2. Phylogenetic justification

80 *Rusophycus* trace fossils are widely accepted to have been produced by arthropod-grade 81 organisms, showing bilateral symmetry and evidence of segmented limbs used in their construction, 82 the latter an apomorphy of Euarthropoda (Budd and Jensen, 2000).

83

84 2.3. Age justification

85

86 Rusophycus occurs well below the first animal body fossils in Cambrian sections around the 87 world (Crimes, 1987; Crimes and Jiang, 1986; Goldring and Jensen, 1996; MacNaughton and 88 Narbonne, 1999; Weber and Zhu, 2003). In many of these regions, records of Rusophycus begin with 89 proximity to the base of the Cambrian. However, their ages are only well constrained in sections in 90 Newfoundland, Canada, and Yunnan, China. Of these, records of Rusophycus begin low in Member 2 91 of the Chapel Island Formation of the southwestern Burin Peninsula of southeastern Newfoundland, 92 defining the base of the *R. avalonensis* Biozone (Narbonne et al., 1987). The Biozone is itself dated 93 through correlations to a section in New Brunswick where the younger ash bed has been dated by U-94 Pb series to 530.02 Ma ± 1.2 Myr (Isachsen et al., 1994; Peng et al., 2012), thus providing for a 95 minimum constraint of 528.82 Ma.

A soft maximum constraint is based on that used by Benton et al. (2015), the maximum age interpretation of the Lantian Biota (Yuan et al., 2011). This, together with the Doushantuo Biota (Yuan et al., 2002), provides a series of Konservat-Lagerstätten preserving the biota in Orsten- and Burgess Shale-like modes of fossilization. None of these Lagerstätten, least of all the Lantian, preserves anything that could possibly be interpreted as even a total group eumetazoan and on this basis we define our soft maximum constraint at 635.5 Ma  $\pm$  0.6 Myr (Condon et al., 2005) and, thus, 636.1 Ma.

103 **3. Crown Arthropoda** 

104

105	This clade comprises Euarthropoda and Onychophora (sensu Ortega-Hernández, 2016), their
106	last common ancestor and all of its descendants (Fig. 1). This clade has traditionally been called
107	Panarthropoda (Nielsen, 1995), however, this latter name is most often used to refer to a group
108	encompassing Arthropoda and Tardigrada, but we exclude tardigrades from our current grouping.
109	Monophyly of this clade has been established through phylogenetic analysis of both non-coding and
110	protein-coding gene datasets (Campbell et al., 2011), and morphological data sets (Legg et al., 2013),
111	although it has been challenged by other recent morphological analyses that endorsed a rival sister
112	group relationship between Euarthropoda and Tardigrada (e.g. Smith and Ortega-Hernández, 2014).
113	Note the name Arthropoda in GenBank refers to what we consider Euarthropoda; there is no GenBank
114	taxonomy ID for the clade comprising Euarthropoda and Onychophora.
115	
116	3.1. Fossil specimens
117	
118	As for 2.1.
119	
120	3.2. Phylogenetic justification
121	
122	As for 2.2.
123	
124	3.3. Age justification
125	
126	As for 2.3.
127	
128	4. Crown Euarthropoda
129	
130	This clade comprises Chelicerata, Myriapoda and Pancrustacea, their last common ancestor

131	and all of its descendants (Fig. 1). The monophyly of Euarthropoda, comprising the sister clades
132	Chelicerata and Mandibulata (itself comprising Myriapoda and Pancrustacea) has been established on
133	the basis of protein-coding and noncoding molecular data, as well as morphological data (Rota-Stabelli
134	et al., 2011). Note that in Benton et al. (2015) this node was named Arthropoda (likely with reference
135	to GenBank taxonomy). Here we follow the naming conventions outlined by Ortega-Hernández (2016).
136	
137	4.1. Fossil specimens
138	
139	Yicaris dianensis Zhang et al., 2007. YKLP 10840, holotype (Fig. 2b,c), consisting of an almost
140	complete articulated specimen (Zhang et al., 2007).
141	
142	4.2. Phylogenetic justification
143	
144	Several phylogenetic analyses of morphology (Edgecombe, 2010; Legg et al., 2013; Wolfe and
145	Hegna, 2014) and morphology plus molecules (Oakley et al., 2013) place Y. dianensis within the
146	crown group of Pancrustacea. Key characters include the presence of epipodites on the thoracic
147	limbs; paddle-shaped mandibular and maxillary exopods; and the protopodite of post-mandibular limbs
148	elongated as soft, setiferous endites. Any position supported within the crown group of Pancrustacea
149	is within crown Euarthropoda.
150	
151	4.3. Age justification
152	
153	Y. dianensis was recovered from the Yu'anshan Formation at Xiaotan section, Yongshan,
154	Yunnan Province, attributed to the Eoredlichia-Wutingaspis Biozone (Zhang et al., 2007). Chinese
155	Cambrian stratigraphy has been revised substantially and the Eoredlichia – Wutingaspis Biozone is no
156	longer recognized (Peng, 2009, 2003). However, Eoredlichia is known to co-occur with Hupeidiscus,
	6

157	which is diagnostic of the Hupeidiscus-Sinodiscus Biozone, which is formally recognised as the
158	second biozone of the Nangaoan Stage of the Qiandongian Series of the Cambrian of China (Peng
159	and Babcock, 2008). The Nangaoan is the proposed third stage of the Cambrian System for the
160	International Geologic Timescale (Peng et al., 2012). Thus, a minimum constraint can be established
161	on the age of the top of the Nangaoan, which has been dated to 514 Ma (Peng et al., 2012; Peng and
162	Babcock, 2008).
163	Soft maximum as for 2.3.
164	
165	4.4. Discussion
166	
167	There are older records of euarthropods than Y. dianensis, notably trilobites, but their
168	phylogenetic position within Arthropoda is contested (it is unclear whether trilobites are stem-
169	Euarthropoda, stem-Chelicerata or stem-Mandibulata). Wujicaris muelleri Zhang et al., 2010 has an
170	equal claim to being the earliest record of Arthropoda, but it is of equal age to the holotype of Y.
171	dianensis.
172	
173	5. Crown Chelicerata
174	
175	This clade comprises Pantopoda (sea spiders) and Euchelicerata, their last common ancestor
176	and all of its descendants (Figs. 1, 3 and 4). Monophyly of this clade has been established by
177	phylogenetic analysis of nuclear protein-coding genes (Regier et al., 2010), transcriptomes
178	(Meusemann et al., 2010; Rota-Stabelli et al., 2011), and morphology (Legg et al., 2013).
179	
180	5.1. Fossil specimens
181	
182	Wisangocaris barbarahardyae Jago, García-Bellido and Gehling, 2016. SAM P45427,
	7

183 holotype, almost complete specimen (**Fig. 2d**).

184

185 5.2. Phylogenetic justification

186

187 Few recent phylogenetic studies have addressed the stem-lineage of Euchelicerata (notable 188 exceptions being Lamsdell, 2013; Legg, 2014; Legg et al., 2013). Including W. barbarahardyae in the 189 dataset of Legg (2014), this species was resolved in most shortest cladograms as sister taxon to the 190 middle Cambrian Sanctacaris and Sidnevia, and in all shortest cladograms as more closely related to 191 Euchelicerata than Pantopoda, i.e. as crown group Chelicerata (Jago et al., 2016). This relationship is 192 supported by the shared presence of pediform cephalic exites, multi-partite trunk exites, and a trunk 193 composed of a posterior limb-less abdomen in both crown euchelicerates and the Cambrian taxa. 194 195 5.3. Age justification 196 197 W. barbarhardyae was collected from the Emu Bay Shale on Kangaroo Island, South Australia. 198 Trilobite biostratigraphy correlates this unit with the upper part of the *Pararaia janeae* Zone in 199 mainland South Australia (Jell in Bengtson et al., 1990; Fig. 2 in Jago et al., 2012), equivalent to the 200 Canglangpuan Stage in South China and the late Botoman in Siberia (Gehling et al., 2011, Fig. 9). 201 This dates the Emu Bay Shale to Cambrian Series 2, Stage 4, providing a minimum constraint of 509 202 Ma. 203 Soft maximum as for 2.3. 204 205 5.4. Discussion 206 207 208 Until recently the oldest evidence of chelicerates in the fossil record were thought to be

209 represented by Chasmataspis-like trace fossils from the Furongian of Texas (Dunlop et al., 2004), and 210 a putative pycnogonid larva from the Furongian of Sweden (Waloszek and Dunlop, 2002). However, in 211 a number of recent phylogenetic analyses (e.g. Legg, 2014; Legg et al., 2013), a number of taxa from 212 the middle Cambrian Burgess Shale Formation, namely Sanctacaris uncata Briggs and Collins, 1988. 213 Sarotrocercus oblita Whittington, 1981, and Sidneyia inexpectans Walcott, 1911, have been resolved 214 as stem-lineage representatives of Euchelicerata. These relationships are preserved with the addition 215 of the older W. barbarahardyae to the dataset (Jago et al., 2016). Although another purported species 216 of Sidneyia (S. sinica Zhang et al., 2002) is known from the older Chengijang biota, it lacks many 217 diagnostic features of this genus, and could therefore not be reliably used for calibration purposes. It 218 should also be noted that Sidneyia only resolved as a stem representative of Euchelicerata under 219 some iterations of the analysed data set of Legg (2014), specifically only when all characters were 220 weighted equally, and therefore its exact phylogenetic position is equivocal.

221

## 222 6. Crown Pantopoda

223

This clade comprises Ammotheidae, Austrodecidae, Callipallenidae, Colossendeidae, Endeididae, Nymphonidae, Pallenopsidae, Phoxichilidiidae, Pycnogonidae and Rhynchothoracidae, their last common ancestor and all of its descendants (**Fig. 3**). Phylogenetic analyses of proteincoding genes (Arabi et al., 2010) or protein-coding genes combined with morphology (Arango and Wheeler, 2007) indicate monophyly.

229

230 6.1. Fossil specimens

231

Haliestes dasos Siveter et al., 2004. OUM C.29571, holotype (Fig. 5a). As the reconstruction of
 Herefordshire fossils requires serial grinding and photography of 20 µm sections (Sutton et al., 2002),
 the holotype figured in Siveter et al. (2004) and herein was thus destroyed in preparation.

235 Morphological data for Herefordshire fossils are published as 3D models of the thin section236 photographs.

237

238 6.2. Phylogenetic justification

239

240 Arango and Wheeler (2007) resolved H. dasos as sister to part of Ammotheidae (nested within 241 clade of Ammotheidae, Callipallenidae, Nymphonidae, Pallenopsidae, Phoxichilidiidae, 242 Rhynchothoracidae), i.e. as crown-group Pantopoda. *H. dasos* was classified separately from extant 243 pycnogonids (Pantopoda) as an Order Nectopantopoda by Bamber (2007), although without explicit 244 phylogenetic justification. It should be noted that H. dasos was included in the phylogenetic analysis of 245 Legg et al. (2013), and resolved as sister-taxon to Palaeopantopus, which in turn resolved as sister-246 taxon to extant pycnogonids, however, just three extant exemplars were included in this study and as 247 this was not extensive enough to determine the exact position of these fossil taxa with respect to 248 crown-group exemplars, we continue to follow Arango and Wheeler (2007) in their placement. 249 250 6.3. Age justification 251 252 This fossil is preserved as a carbonate concretion from the volcaniclastic Herefordshire 253 Lagerstätte of Herefordshire, England, at the Sheinwoodian-Homerian stage boundary, within the 254 Early Silurian Wenlock Series (Siveter, 2008). As the Homerian begins at 430.5 Ma  $\pm$  0.7 Myr, a 255 minimum age constraint for the Herefordshire can thus be placed at 429.8 Ma. 256 Soft maximum as for 2.3. 257 258 6.4. Discussion 259 260 Although *H. dasos* is the oldest assignable crown group pycnogonid, there is an older fossil,

261	Cambropycnogon klausmuelleri Waloszek and Dunlop, 2002, from the Cambrian Orsten biota
262	(minimally 497 Ma). C. klausmuelleri, however, is known only from larval stages, and does not share
263	specific apomorphies with any extant larva. Without such characters, it is not possible to adequately
264	confirm crown group affinity. Another fossil species, Palaeomarachne granulata Rudkin et al., 2013
265	from the Late Ordovician of Manitoba, is specifically noted as a stem pantopod due to its likely
266	plesiomorphic head tagmosis.
267	
268	7. Crown Euchelicerata
269	
270	This clade comprises Xiphosurida (horseshoe crabs) and Arachnida, their last common
271	ancestor and all of its descendants (Fig. 3). Monophyly is established on the basis of phylogenetic
272	analysis of transcriptomes (Rota-Stabelli et al., 2011; Sharma et al., 2014) and morphology (Legg et
273	al., 2013). Note that monophyly of Euchelicerata is challenged by a recent morphological phylogeny, a
274	result attributed to outgroup sampling (Garwood and Dunlop, 2014). Euchelicerata is not recognized in
275	GenBank taxonomy.
276	
277	7.1. Fossil specimens
278	
279	Chasmataspis-like resting trace fossils (MBA 1084), Fig 5b. Described and illustrated in
280	Dunlop et al. (2004, Figs. 9 and 10).
281	
282	7.2. Phylogenetic justification
283	
284	The assignment of the traces to Chasmataspida is based on impressions of plate-like
285	opisthosomal opercula, one of the characters used to define Euchelicerata (Dunlop et al., 2004)
286	Furthermore, recent phylogenetic analyses of morphology place chasmataspid body fossil species
	11

within Euchelicerata, as sister group to eurypterids (Garwood and Dunlop, 2014; Legg et al., 2013) or
sister group to a clade composed of eurypterids and arachnids (Lamsdell, 2013; Lamsdell et al., 2015;
Selden et al., 2015).

290

291 7.3. Age justification

292

293 The Chasmataspis-like resting traces were found in the Cambrian Hickory Sandstone Member 294 of the Riley Formation, Texas (Dunlop et al., 2004). The top of the Hickory Sandstone preserves 295 trilobite representatives of the Bolaspidella Zone and the Cedarina Zone (Miller et al., 2012; Palmer, 296 1954). These trilobite biozones are assigned to the lowermost Marjumiid Biomere in the Marjuman 297 Stage of the Lincolnian Series (Miller et al., 2012). The early Marjuman itself is correlated to the 298 Drumian Stage of Cambrian Series 3 (Taylor et al., 2012). The end of the Drumian is dated to 500.5 299 Ma, providing a minimum age for *Chasmataspis*-like trace fossils. 300 Soft maximum as for 2.3. 301 302 8. Crown Xiphosurida 303 304 This clade comprises four extant species, all members of the family Limulidae: Carcinoscorpius 305 rotundicauda, Limulus polyphemus, Tachypleus gigas and Tachypleus tridentatus, their last common 306 ancestor and all of its descendants (Fig. 3). Monophyly is established by phylogenetic analyses of 307 housekeeping genes (Obst et al., 2012) and morphology (Lamsdell and McKenzie, 2015). 308 309 8.1. Fossil specimens 310 311 Tachypleus gadeai Vía Boada and de Villalta, 1966. MGSB 19195, holotype. 312
- 313 8.2. Phylogenetic justification
- 314

315 Heterolimulus gadeai Vía Boada and de Villalta, 1966 was reassigned to the extant genus 316 Tachypleus by Diedrich (2011), who cited the presence of lateral immobile opisthosomal spines as 317 evidence. This was validated by the phylogenetic analysis of Lamsdell and McKenzie (2015), who 318 resolved T. gadeai as sister-taxon to a clade composed of all other members of Tachypleus. This more 319 inclusive clade in turn resolved as sister-taxon to the extant genus Carcinoscorpius. 320 321 8.3. Age justification 322 323 T. gadeai was discovered in the Alcover unit of the Montral site, Tarragona province, Catalonia, 324 Spain (Vía Boada and de Villalta, 1966). Based on sequence stratigraphy, the Alcover dolomite unit is 325 dated to the late Muschelkalk, a European regional stage of the Triassic (Calvet and Tucker, 1995; Vía 326 Boada and de Villalta, 1966). The middle and late Muschelkalk correspond to the global Ladinian 327 stage (Calvet and Tucker, 1995). The upper boundary of the Ladinian is  $237.0 \text{ Ma} \pm 1 \text{ Myr}$  (Ogg, 328 2012), thus, a minimum age of 236.0 Ma.

329 Soft maximum as for 2.3.

330

333 We note that morphological phylogenetic analysis has suggested paraphyly of Xiphosura

334 (crown Xiphosurida plus several fossil genera), and resolved synziphosurines as basal euchelicerates

- 335 (Lamsdell, 2013). A subsequent morphological phylogeny resolved synziphosurines as polyphyletic
- 336 (Garwood and Dunlop, 2014). Some other morphological phylogenies resolve the traditional

monophyletic Xiphosura (Briggs et al., 2012; Legg et al., 2013).

338 Crown xiphosurid affinities of older fossils cannot be confirmed. For example, an undescribed

<sup>331 8.4.</sup> Discussion

<sup>332</sup> 

Early Ordovician fossil from Morocco (Van Roy et al., 2010) exhibits fused opisthosomal tergites, a synapomorphy of Xiphosurida *sensu* Lamsdell (2013), but its position with respect to the crown has not been tested in a phylogeny. The Late Ordovician *Lunataspis aurora* Rudkin et al., 2008 and the Pennsylvanian genus *Euproops* are resolved on the stem group of Xiphosurida in a morphological phylogeny (Lamsdell, 2013).

344 Morphological conservatism in the evolution of Xiphosura (as illustrated by a Jurassic member 345 assigned to a living genus) has led to use of the misnomer 'living fossil' for the clade, despite 346 continued molecular evolution throughout its history (Avise et al., 1994; Obst et al., 2012). The more 347 appropriate term of 'stabilomorph' was proposed with the discovery of Limulus darwini (Kin and 348 Blażejowski, 2014); it refers to morphological stability over evolutionary history, at the genus level. 349 However, long branches unbroken by unsampled extinct species may have significantly 350 underestimated divergence times among crown Xiphosurida (Lamsdell and McKenzie, 2015), though 351 this assertion has not yet been tested with a divergence time analysis.

352

#### 353 9. Crown Arachnida

354

355 This clade comprises Acariformes (acariform mites), Opiliones (harvestmen), Palpigradi 356 (microwhip scorpions), Parasitiformes (parasitiform mites, ticks), Pseudoscorpiones, Ricinulei (hooded 357 tickspiders), Schizomida, Scorpiones, Solifugae (camel spiders), and Tetrapulmonata, their last common ancestor and all of its descendants (Fig. 4). Monophyly is established on the basis of 358 359 phylogenetic analysis of transcriptomes (Rota-Stabelli et al., 2013a), nuclear protein-coding genes 360 (Regier et al., 2010), strong support from morphology (Garwood and Dunlop, 2014; Legg et al., 2013; 361 Rota-Stabelli et al., 2011; Shultz, 2007), and combined morphological and molecular data (Giribet et 362 al., 2002; Lee et al., 2013). Some recent phylogenetic analyses of transcriptomes have failed to 363 resolve a monophyletic Arachnida; instead Xiphosurida is variably placed within the traditional 364 arachnids (Sharma et al., 2014; von Reumont et al., 2012).

## 366 9.1. Fossil specimens

367

368	Palaeophonus loudonensis Laurie, 1899. NMS 1897.122.196 (holotype), a dorsally preserved
369	specimen lacking walking legs and telson (Fig. 5h). For additional anatomical detail, we refer to
370	Eramoscorpius brucensis Waddington et al., 2015. ROM 53247, holotype (Fig. 5g).

371

### 372 9.2. Phylogenetic justification

373

374 The genus Dolichophonus Petrunkevitch, 1949, was erected for P. loudonensis, based on the 375 increased length of the prosoma compared to other palaeophonids, namely P. nuncius Thorell and 376 Lindström, 1885, and P. caledonicus Hunter, 1886. An examination (by D.A.L.) of the single known 377 specimen of *P. loudonensis* could not confirm this character because the specimen is very poorly 378 preserved, and the junction between the prosoma and mesosoma is not easily distinguished. We 379 retain the holotype within Palaeophonus. It is even possible that this specimen may belong to one of 380 the other currently recognised species of *Palaeophonus*, although more material would be required. P. 381 loudonensis was included in a phylogenetic analysis by Legg et al. (2013), in which it resolved 382 amongst total-group Scorpiones. Other Siluro-Devonian fossil scorpions such as Proscorpius osborni 383 Whitfield, 1885 and Palaeoscorpius devonicus Lehmann, 1944 have been placed in the stem group of 384 Orthosterni (crown-group Scorpiones) (e.g. Legg et al., 2013; Garwood and Dunlop, 2014), which are 385 therefore crown group members of Arachnida.

386

387 9.3. Age justification

388

*P. loudonenesis* was recovered from the Gutterford Burn section of the "Eurypterid Bed"
 (Reservoir Formation) in the Pentland Hills, Midlothian, Scotland (Kjellesvig-Waering, 1986), which

391	has been dated as Late Llandovery. The associated graptolite fauna suggests a late Llandovery
392	(Telychian) age for this formation, within the Oktavites spiralis Biozone (Bull and Loydell, 1995). A
393	spline-fit age for the upper boundary of the O. spiralis Biozone provides a minimum age constraint of
394	435.15 Ma (Melchin et al., 2012).
395	Soft maximum as for 2.3.
396	
397	10. Crown Opiliones
398	
399	This clade comprises Cyphophthalmi and Phalangida (itself comprising Laniatores, Dyspnoi
400	and Eupnoi), their last common ancestor and all of its descendants (Fig. 4). Monophyly has been
401	demonstrated by phylogenetic analysis of transcriptomes (Sharma et al., 2014), morphology (Garwood
402	et al., 2011), and combined morphology and molecules (Garwood et al., 2014; Giribet et al., 2002).
403	
404	10.1. Fossil specimens
405	
406	Eophalangium sheari Dunlop et al., 2003. PBM slide no. 3503, holotype (Fig. 5d), consisting of
407	a lateral thin section outlining nearly the entire female body (Dunlop et al., 2003).
408	
409	10.2. Phylogenetic justification
410	
411	In a phylogenetic analysis of morphology, E. sheari was placed in a polytomy with members of
412	Phalangida, to the exclusion of Cyphophthalmi (Garwood and Dunlop, 2014). In combined analysis of
413	molecules and morphology, E. sheari was resolved as a stem group Cyphophthalmi (Garwood et al.,
414	2014). Both positions, however, fall within the crown group of Opiliones.
415	
416	10.3. Age justification

418	This fossil is known from the Early Devonian (Pragian) Rhynie Chert of Aberdeenshire,
419	Scotland. Spore assemblages of the Windyfield and stratigraphically underlying Rhynie Chert are
420	dated to the early but not earliest Pragian to early (earliest?) Emsian (polygonalis-emsiensis Spore
421	Assemblage Biozone) (Parry et al., 2011). Radiometric dating of the underlying Milton of Noth
422	Andesite at ca. 411 Ma (Parry et al., 2013, 2011) has been subject to a dispute over its temporal
423	relationship to hot spring activity associated with the cherts (Mark et al., 2013, 2011) and predates the
424	biostratigraphic dating of the Rhynie Chert relative to the global dating of the base of the Pragian
425	Stage. Therefore, a minimum age constraint may be defined at 405.0 Ma for the Rhynie Chert, using
426	the Pragian-Emsian boundary (407.6 Ma $\pm$ 2.6 Myr) as a reference.
427	A soft maximum constraint comes from the oldest chelicerate W. barbarhardyae from the Emu
428	Bay Shale on Kangaroo Island, South Australia, which has been correlated based on trilobite
429	biostratigraphy to the upper part of the Pararaia janeae Zone in mainland South Australia (Jell in
430	Bengtson et al., 1990; Fig. 2 in Jago et al., 2012). As this is equivalent to the Canglangpuan Stage in
431	South China and the late Botoman in Siberia (Gehling et al., 2011, Fig. 9), the Emu Bay Shale can be
432	dated to Cambrian Series 2, Stage 4, providing a maximum age of ~514 Ma.
433	
434	11. Crown Acariformes
435	
436	This clade comprises Sarcoptiformes, Trombidiformes and 'Endeostigmata', their last common
437	ancestor and all of its descendants (Fig. 4). Monophyly is established by phylogenetic analysis of
438	nuclear ribosomal genes (Pepato and Klimov, 2015), morphology (Garwood and Dunlop, 2014), and
439	combined molecular and morphological data (Pepato et al., 2010).
440	
441	11.1. Fossil specimens

443	Protacarus crani Hirst, 1923. BMNH In. 24665, holotype, preserving a nearly complete
444	individual in chert ( <b>Fig. 5k</b> ).
445	
446	11.2. Phylogenetic justification
447	
448	Originally described as a single species (Hirst, 1923), P. crani from the Rhynie Chert was
449	subsequently treated as five species belonging to five different genera (Dubinin, 1962). P. crani itself,
450	as exemplified by the holotype, was described as a member of Eupodidae, within Trombidiformes
451	(Hirst, 1923), or potentially more basal within the Acariformes (Bernini, 1986). While the specifics of its
452	classification may be debatable due to the lack of preserved diagnostic characters, the fan-like setae
453	observed dorsally in <i>P. crani</i> support a relationship with endeostigmatids within crown group
454	Acariformes (Bernini, 1986; Dunlop and Selden, 2009).
455	
456	11.3. Age justification
457	
458	As for 10.3.
459	
460	11.4. Discussion
461	
462	Bernini et al. (2002) figured a putative oribatid mite from terrestrial sediments dated to the Early
463	Ordovician of Sweden. However, its age and systematic placement were queried by Dunlop (2010, p.
464	134) and this species is not used for calibration herein.
465	Arguments that P. crani is a Recent contaminant (Crowson, 1985) have been countered by
466	Kühne and Schlüter (1985) and Greenslade (1988). Other species of fossil Acariformes have also
467	been described from the Rhynie Chert (all originally P. crani), including Protospeleorchestes
468	pseudoprotacarus, Pseudoprotacarus scoticus, Palaeotydeus devonicus, and Paraprotocarus hirsti (all

469 Dubinin, 1962). 470 471 **12. Crown Parasitiformes** 472 473 This clade comprises Opilioacariformes, Ixodida (hard and soft ticks), Holothyrida and 474 Mesostigmata, their last common ancestor and all of its descendants (Fig. 4). Monophyly is 475 established by phylogenetic analysis of nuclear ribosomal genes (Pepato and Klimov, 2015) and 476 morphology (Garwood and Dunlop, 2014). 477 478 12.1. Fossil specimens 479 480 Cornupalpatum burmanicum Poinar and Brown, 2003. Holotype larva (accession number A-10-481 260; Fig. 5i) and paratype (accession number A-10-261; Fig. 5j) deposited in the Poinar amber 482 collection maintained at Oregon State University, later to be deposited at the California Academy of 483 Sciences (Poinar, 2015; Poinar and Brown, 2003). 484 485 12.2. Phylogenetic justification 486 487 Morphological characters such as the subcircular body with a marginal groove, free coxae, 488 ventral anal opening, the presence of a capitulum and Haller's organ, absence of an anal groove, and 489 elongate four-segmented palpi are all suggestive of Parasitiformes affinity for C. burmanicum (Poinar 490 and Brown, 2003). A particularly diagnostic character, suggesting placement within at least total-group 491 Ixodida (and thus crown Parasitiformes), is the presence of claws on palpal segment 3 in the larva 492 (Poinar and Brown, 2003). Putative morphologies similar to bacterial pathogens exclusive to modern 493 Ixodida were recently described from the paratype (Poinar, 2015). 494

497 This fossil is sourced from amber mines in the Hukawng Valley of Kachin State, northern 498 Myanmar (formerly Burma). The depositional age of Burmese amber was estimated from U-Pb dating 499 of zircons from the volcaniclastic matrix surrounding the amber (Shi et al., 2012). Shi et al. (2012) 500 argue the amber is not older than its associated sediments, as burial and preservation would have to 501 be rapid for survival of organic material, so the amber was probably formed at, but not earlier than the 502 U-Pb date: at 98.79 Ma ± 0.62 Myr. Therefore, a minimum age for any fossil from Burmese amber 503 deposits is 98.17 Ma. 504 Soft maximum as for 10.3. 505 506 **13. Crown Pseudoscorpiones** 507 508 This clade comprises Feaelloidea, Chthonioidea, Neobisiodea, Garypoidea, Sternophoroidea 509 and Cheliferoidea, their last common ancestor and all of its descendants (Fig. 4). While relationships 510 between superfamilies remain unclear, monophyly of Pseudoscorpiones was demonstrated with wide 511 taxon sampling and three genes (Murienne et al., 2008). More limited taxon sampling supports 512 monophyly with morphology (Garwood and Dunlop, 2014) and morphology combined with ribosomal

- 513 genes (Pepato et al., 2010).
- 514

#### 515 13.1. Fossil specimens

516

517 *Protofeaella peetersae* Henderickx in Henderickx and Boone, 2016. NHM II 3115, holotype, 518 near complete specimen preserved in amber (**Fig. 5c**).

519

520 13.2. Phylogenetic justification

522 Although P. peetersae has not been included in a formal phylogenetic analysis, it was assigned 523 to the extant family Feaellidae by Henderickx and Boone (2016:8), based on its narrow cephalothorax, 524 granulated abdomen, and presence of small pedipalps with narrow coxa and small hands. Whilst 525 these features are certainly found in both P. peetersae and feaellids, other features, such as slender 526 pedipalp fingers, and the overall shape of the cephalic shield are more like those of pseudogarypids 527 (Harvey, 1992). Both the feaellid and pseudogarypids belong to the superfamily Feaelloidea (sensu 528 Harvey, 1992), and thus it is still likely *P. peetersae* belongs within the pseudoscorpion crown-group. 529 530 13.3. Age justification 531 532 As for 12.3. 533 534 535 13.4. Discussion 536 537 Dracochela deprehendor Schawaller et al., 1991 from the Middle Devonian of Gilboa, New

York State, was originally interpreted as a crown-group pseudoscorpion but was reassigned to the pseudoscorpion stem group (Judson, 2012). Preliminary morphological phylogenetic analyses by one of us (D.A.L.), however, suggest that *D. deprehendor* may be within the crown group. If so, this would drastically extend the range of crown Pseudoscorpiones by over 280 Myr (to a minimum age of 382.7 Ma; Richardson et al., 1993).

543 Note that other Cretaceous pseudoscorpions have been preserved in amber (older from 544 Lebanon and Spain; younger from France, New Jersey and Alberta), but these have yet to be fully 545 described or examined for their systematic positions (Judson, 2009). If the Lebanese or Spanish 546 fossils were found to be members of the crown group, they could extend the range of

<ul> <li>14. Crown Palpigradi</li> <li>This clade comprises the families Eukoeneniidae and Prokoeneniidae, their last common ancestor and all of its descendants (Fig. 4). Monophyly has been supported by a phylogenetic analysis of two nuclear ribosomal and one mitochondrial gene (Giribet et al., 2014).</li> <li>14.1. Fossil specimens</li> <li>Electrokoenenia yaksha Engel et al., 2016b. NIGP 163253, holotype in amber (Fig. 5e).</li> </ul>
<ul> <li>14. Crown Palpigradi</li> <li>This clade comprises the families Eukoeneniidae and Prokoeneniidae, their last common ancestor and all of its descendants (Fig. 4). Monophyly has been supported by a phylogenetic analysis of two nuclear ribosomal and one mitochondrial gene (Giribet et al., 2014).</li> <li>14.1. Fossil specimens</li> <li>Electrokoenenia yaksha Engel et al., 2016b. NIGP 163253, holotype in amber (Fig. 5e).</li> </ul>
This clade comprises the families Eukoeneniidae and Prokoeneniidae, their last common ancestor and all of its descendants ( <b>Fig. 4</b> ). Monophyly has been supported by a phylogenetic analysis of two nuclear ribosomal and one mitochondrial gene (Giribet et al., 2014). <i>14.1. Fossil specimens</i> <i>Electrokoenenia yaksha</i> Engel et al., 2016b. NIGP 163253, holotype in amber ( <b>Fig. 5e</b> ).
This clade comprises the families Eukoeneniidae and Prokoeneniidae, their last common ancestor and all of its descendants ( <b>Fig. 4</b> ). Monophyly has been supported by a phylogenetic analysis of two nuclear ribosomal and one mitochondrial gene (Giribet et al., 2014). <i>14.1. Fossil specimens</i> <i>Electrokoenenia yaksha</i> Engel et al., 2016b. NIGP 163253, holotype in amber ( <b>Fig. 5e</b> ).
ancestor and all of its descendants ( <b>Fig. 4</b> ). Monophyly has been supported by a phylogenetic analysis of two nuclear ribosomal and one mitochondrial gene (Giribet et al., 2014). <i>14.1. Fossil specimens</i> <i>Electrokoenenia yaksha</i> Engel et al., 2016b. NIGP 163253, holotype in amber ( <b>Fig. 5e</b> ).
analysis of two nuclear ribosomal and one mitochondrial gene (Giribet et al., 2014). 14.1. Fossil specimens Electrokoenenia yaksha Engel et al., 2016b. NIGP 163253, holotype in amber ( <b>Fig. 5e</b> ).
14.1. Fossil specimens Electrokoenenia yaksha Engel et al., 2016b. NIGP 163253, holotype in amber ( <b>Fig. 5e</b> ).
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<i>Electrokoenenia yaksha</i> Engel et al., 2016b. NIGP 163253, holotype in amber ( <b>Fig. 5e</b> ).
Electrokoenenia yaksha Engel et al., 2016b. NIGP 163253, holotype in amber (Fig. 5e).
14.2. Phylogenetic justification
E. yaksha was classified within the extant family Eukoeneniidae (Engel et al., 2016b). This was
justified with morphological characters, in particular the rounded lateral "arms" to the frontal organ of
the propeltidium, as seen in the extant genus Leptokoenenia (Engel et al., 2016b). Thus E. yaksha is
within the crown group of Palpigradi.
14.3. Age justification
As for 12.3.
15. Crown Solifugae
This clade comprises Ammotrechidae, Ceromidae, Daesiidae, Eremobatidae, Galeodidae,
22

573	Gylippidae, Hexisopodidae, Karschiidae, Melanoblossidae, Mummuciidae, Rhagodidae and
574	Solpugidae, their last common ancestor and all of its descendants (Fig. 4). No phylogenetic analysis
575	has yet included all families, but limited taxon sampling has shown monophyly with morphology
576	(Garwood and Dunlop, 2014; Shultz, 2007) and morphology combined with nuclear genes (Giribet et
577	al., 2002; Pepato et al., 2010). Extensive morphological work on the homology of cheliceral characters
578	was recently published by Bird et al. (2015).
579	
580	15.1. Fossil specimens
581	
582	Cratosolpuga wunderlichi Selden and Shear, 1996 (Sol. 1 in the private Wunderlich collection,
583	Straubenhardt, Germany), holotype. An additional specimen (SMNK 1268 PAL; Fig. 5f), not a
584	paratype, is also deposited.
585	
586	15.2. Phylogenetic justification
587	
588	C. wunderlichi was assigned to the extant family Ceromidae on the basis of shape of the
589	cheliceral flagellum, shape of the propeltidium, eye tubercle, and leg spination (Selden and Shear,
590	1996). Only a single tarsal segment is present on the legs (Selden and Shear, 1996). A position in
591	total-group Ceromidae would therefore be within crown-group Solifugae.
592	
593	15.3. Age justification
594	
595	This fossil was recovered from the Nova Olinda Member of the Crato Formation in the Araripe
596	Basin, northeastern Brazil. This unit is generally agreed to be around the Aptian/Albian border (Martill
597	et al., 2007). Batten (2007) suggests that if assemblages in the upper layers are consistent across the
598	lower layers, a late Aptian date should be considered. The Crato formation has been dated using
	23

599	palynomorphs (Pons et al., 1990) to the Aptian, though an accurate date for the Nova Olinda Member
600	is not available. The upper boundary of the Aptian, at 113.0 Ma $\pm$ 0.4 Myr, gives a minimum date of
601	112.6 Ma.
602	Soft maximum as for 10.3.
603	
604	15.4. Discussion
605	
606	The Pennsylvanian Protosolpuga carbonaria Petrunkevitch, 1913, the only older possible fossil
607	solifuge, was discounted from the crown group of Solifugae in the same paper as described C.
608	wunderlichi (Selden and Shear, 1996). It is too poorly preserved to assign to the crown group without
609	additional phylogenetic justification.
610	
611	16. Crown Scorpiones
612	
613	This clade comprises Buthida and Iurida, their last common ancestor and all of its descendants
614	(Fig. 4). The composition of Buthida and Iurida are as detailed in Sharma et al. (2015). Monophyly has
615	been supported by phylogenetic analysis of transcriptomes (Sharma et al., 2015, 2014), morphology
616	(Garwood and Dunlop, 2014; Shultz, 2007), and combined ribosomal sequences and morphology
617	(Pepato et al., 2010).
618	
619	16.1. Fossil specimens
620	
621	Protoischnurus axelrodurum Carvalho and Lourenço, 2001. MN-7601-I, holotype, a male. We
622	also refer to the specimen SMNS 65534, which preserves phylogenetically relevant details of the
623	pedipalps (Fig. 3c in Menon, 2007).
624	
	24

- 625 16.2. Phylogenetic justification
- 626

627 Menon (2007) placed *P. axelrodurum* in the extant family Hemiscorpiidae, based on, amongst 628 other things, an inverse Y-shape on sulcus on the cephalic shield, the placement of Est trichobothria 629 on the pedipalp chela, and the placement of carinae V2 and V3 in the pedipalp chela, all of which are 630 diagnostic of the hemiscorpidid subfamily Hormurinae (Soleglad et al., 2005). Hemiscorpiidae is 631 classified within lurida (Sharma et al., 2015), and is thus crown group Scorpiones. 632 633 16.3. Age justification 634 635 As for 15.3. 636 637 16.4. Discussion 638 639 A number of fossil taxa have been placed within crown group scorpion families, including 640 Protobuthus elegans Lourenço and Gall, 2004, from the Early Triassic Buntsanstein of France. It was 641 assigned to the superfamily Buthoidea, however, a subsequent study (Baptista et al., 2006), 642 considered this taxon and Archaeobuthus from the Early Cretaceous of Lebanon, outside the crown-643 group based on trichobothrial arrangement. 644 Araripescorpius ligabuei Campos, 1986 is coeval to P. axelrodurum, and from the same locality. Menon (2007) placed A. ligabuei in the extant family Chactidae based on general habitus and 645 646 trichobothrial pattern. Therefore it is also a member of the crown group of Scorpiones, albeit a less 647 well-preserved species. 648 649 17. Crown Tetrapulmonata 650

651	This clade comprises Pedipalpi and Araneae (spiders), their last common ancestor and all of its
652	descendants (Fig. 6). Monophyly is supported by phylogenetic analysis of transcriptomes (Sharma et
653	al., 2014), nuclear protein-coding genes (Regier et al., 2010), and morphology (Garwood and Dunlop,
654	2014; Legg et al., 2013; Shultz, 2007). This clade is not recognized in GenBank taxonomy.
655	
656	17.1. Fossil specimens
657	
658	Parageralinura naufraga (Tetlie and Dunlop, 2008), LWL Ar.K.1 (Fig. 7a). Counterpart in the
659	private collection of W. Elze, Ennepetal, Germany.
660	
661	17.2. Phylogenetic justification
662	
663	Tetlie and Dunlop (2008) interpreted Coal Measures uropygids to comprise a plesion on the
664	stem of the extant Thelyphonidae, the sole extant family of Thelyphonida. A subchelate pedipalp is
665	considered apomorphic of the crown group but is lacking in Geralinura and P. naufraga. This identifies
666	them as crown Uropygi, and thus, Tetrapulmonata.
667	
668	17.3. Age justification
669	
670	Of the uropygid fossils, the oldest are P. naufraga (formerly Prothelyphonus naufragus) from
671	deposits of "Ziegelei-Grube," Hagen-Vorhalle, Nordrhein-Westphalia, Germany (Brauckmann and
672	Koch, 1983; Tetlie and Dunlop, 2008). The fossil-bearing deposits are assigned to the Namurian B
673	(Marsdenian) based on the Bilinguites metabilinguis R2c1 subzone of ammonoid stratigraphy
674	(Brauckmann et al., 1994; Tetlie and Dunlop, 2008). The (late) Namurian-(early) Westphalian
675	boundary is defined by the earliest occurrence of the goniatite Gastrioceras subcrenatum (Waters and
676	Davies, 2006), but lacks a precise isotopic date. Pointon et al. (2012) estimated an age of c. 319.9 Ma

677	for the base of the Westphalian (top of the Namurian, only slightly younger than the Marsdenian)
678	based on Milankovitch cycles of sedimentation, giving a minimum age for <i>P. naufraga</i> .
679	Soft maximum as for 10.3.
680	
681	18. Crown Pedipalpi
682	
683	This clade comprises Amblypygi (tailless whip scorpions) and Uropygi, their last common
684	ancestor and all of its descendants (Fig. 6). Monophyly is supported by phylogenetic analysis of
685	transcriptomes (Sharma et al., 2014), nuclear protein-coding genes (Regier et al., 2010), and
686	morphology (Garwood and Dunlop, 2014; Legg et al., 2013; Shultz, 2007). This clade is not
687	recognized in GenBank taxonomy.
688	
689	18.1. Fossil specimens
690	
691	As for 17.1.
692	
693	18.2. Phylogenetic justification
694	
695	As for 17.2.
696	
697	18.3. Age justification
698	
699	As for 17.3.
700	
701	19. Crown Uropygi
702	
	27

703	This clade comprises Thelyphonida (whip scorpions) and Schizomida, their last common
704	ancestor and all of its descendants (Fig. 6). Monophyly is supported by phylogenetic analysis of
705	nuclear protein-coding genes (Regier et al., 2010), and morphology (Garwood and Dunlop, 2014;
706	Legg et al., 2013; Shultz, 2007).
707	
708	19.1. Fossil specimens
709	
710	As for 17.1.
711	
712	19.2. Phylogenetic justification
713	
714	As for 17.2.
715	
716	19.3. Age justification
717	
718	As for 17.3.
719	
720	20. Crown Amblypygi
721	
722	This clade comprises Paracharontidae, Charinidae, Charontidae, Phrynichidae and Phrynidae,
723	their last common ancestor and all of its descendants (Fig. 6). Monophyly of Amblypygi has not been
724	fully investigated with phylogenetic analysis; however, monophyly has been shown for at least some
725	families with morphological data (Garwood and Dunlop, 2014; Shultz, 2007) and morphology
726	combined with nuclear genes (Pepato et al., 2010).
727	
728	20.1. Fossil specimens

729 730 Graeophonus anglicus Pocock, 2011. BMNH In. 31233, holotype (Fig. 7b). Figured in Dunlop 731 et al. (2007: Fig. 1 a,b). 732 733 20.2. Phylogenetic justification 734 735 G. anglicus was redescribed by Dunlop et al. (2007) as a member of the Amblypygi crown 736 group. This was based on several morphological character comparisons to living members, such as 737 the pedipalp femur with dorsal spination similar to Paracharon (the monotypic extant species of the 738 family Paracharontidae). G. anglicus, unlike Paracharon, has a pear-shaped ocular tubercle, 739 suggesting it was not blind. G. anglicus is inferred to be on the stem lineage of Paracharontidae, and 740 thus, crown group Amblypygi (Dunlop et al., 2007). 741 742 20.3. Age justification 743 744 The genus *Graeophonus* was originally described from the Sydney Basin, Cape Breton 745 Carboniferous Coal Measures, Nova Scotia, Canada, which corresponds to Westphalian in age 746 (Dunlop et al., 2007; Giles et al., 2002; Scudder, 1890a). Further studies are needed on the Canadian 747 material, so the minimum age was taken from the oldest European specimen (which is roughly the 748 same age as the Cape Breton specimen) from the British Middle Coal Measures (Coseley, 749 Stafffordshire), which is Westphalian B (or Duckmantian) at the youngest (Waters et al., 1994; Waters 750 and Davies, 2006). U-Pb dating of zircons constrains the upper boundary of the Duckmantian to 751 313.78 Ma ± 0.08 Myr (Pointon et al., 2012), so a minimum age for G. anglicus is 313.70 Ma. 752 Soft maximum as for 10.3. 753

- 754 **21. Crown Araneae** 
  - 29

755	
756	This clade comprises Mesothelae, Mygalomorphae (tarantulas, funnel-web spiders) and
757	Araneomorphae (most spiders), their last common ancestor and all of its descendants (Fig. 6).
758	Monophyly is established by phylogenetic analysis of transcriptomes (Fernández et al., 2014a;
759	Garrison et al., 2016) and morphology (Garwood and Dunlop, 2014; Legg et al., 2013; Shultz, 2007).
760	
761	21.1. Fossil specimens
762	
763	Palaeothele montceauensis Selden, 2000. Muséum d'Histoire naturelle, Autun: 51961
764	(holotype; Fig. 7c), and BMNH 62050, second specimen (not a paratype, Fig. 7d; Selden, 1996). We
765	also compare to Arthrolycosa sp. B Selden et al. 2014. PIN 5431/9 (Fig. 7e).
766	
767	21.2. Phylogenetic justification
768	
769	The deep, narrow sternum of P. montceauensis (formerly Eothele montceauensis Selden,
770	1996) is shared by extant members of Mesothelae (Selden, 1996). Several other characters that are
771	symplesiomorphic within Araneae, such as spinnerets, suggest a position within crown Araneae, and
772	perhaps on the stem lineage of Mesothelae (Selden, 1996).
773	
774	21.3. Age justification
775	
776	P. montceauensis was found in the Montceau Lagerstätte, Montceau-les-Mines, Massif
777	Central, France. The nodule-rich layer is just above the first seam in the Great Seams Formation (late
778	Stephanian) (Perrier and Charbonnier, 2014). The age within the Stephanian has been assigned to
779	Stephanian B, with some biostratigraphic evidence for Stephanian C (Racheboeuf et al., 2002). The
780	Stephanian B/C is a European stage of the Pennsylvanian, straddling the boundary of the globally

781	used Kasimovian and Gzhelian (Richards, 2013). The upper boundary of the Gzhelian is 298.9 Ma $\pm$
782	0.15 Myr, hence the minimum age of the Montceau Lagerstätte is 298.75 Ma.
783	Soft maximum as for 10.3.
784	
785	21.4 Discussion
786	
787	A possible older spider, Arthrolycosa sp. B Selden et al., 2014, is known from the
788	Krasnodonsky Horizon of Rostov Province, Russia (Duckmantian, ~313 Ma). It shares characters with
789	extant Mesothelae, such as the position and morphology of the eye tubercles, but lacks spinnerets, so
790	the inference is largely based on better-known Arthrolycosa from other localities (Selden et al., 2014).
791	Because phylogenetic evidence for crown group membership is largely indirect, we maintain P.
792	montceauensis as the oldest well-supported Araneae.
793	
794	22. Crown Mandibulata
795	
796	This clade comprises Myriapoda and Pancrustacea, their last common ancestor and all of its
797	descendants (Fig. 1). Monophyly has been independently demonstrated based on protein-coding
798	genes and microRNAs, as well as morphological data (Rota-Stabelli et al., 2011).
799	
800	22.1. Fossil specimens
801	
802	As for 4.1.
803	
804	22.2. Phylogenetic justification
805	
806	As for 4.2.
	31

807	
808	22.3. Age justification
809	
810	As for 4.3.
811	
812	22.4. Discussion
813	
814	Wujicaris muelleri Zhang et al., 2010 has an equal claim to being the earliest record of
815	Mandibulata, but it is of equal age to the holotype of Y. dianensis.
816	
817	23. Crown Myriapoda
818	
819	This is the clade comprising Chilopoda (centipedes) and Progoneata, their last common
820	ancestor and all of its descendants (Fig. 1). Monophyly has been demonstrated by morphology
821	(Edgecombe, 2004; Legg et al., 2013; Rota-Stabelli et al., 2011), nuclear protein-coding genes (Regier
822	et al., 2010; Zwick et al., 2012), transcriptomes (Rehm et al., 2014), and combined analysis of
823	molecules and morphology (Lee et al., 2013).
824	
825	23.1. Fossil specimens
826	
827	Cowiedesmus eroticopodus Wilson and Anderson, 2004. AMS F.64845, holotype (Fig. 2e).
828	
829	23.2. Phylogenetic justification
830	
831	Membership of <i>C. eroticopodus</i> in Diplopoda is indicated by its strict diplosegmentation,
832	whereas its cuticular mineralization supports membership in the subgroup Chilognatha, and its
	32

833 modified legs on trunk segment 8 support membership in Helminthomorpha. C. eroticopodus is

resolved as total-group Helminthomorpha in the morphological cladistic analysis of Fernández et al.

835 (2016) and is accordingly a member of the crown-groups of Chilognatha, Diplopoda, Progoneata and836 Myriapoda.

837

838 23.3. Age justification

839

840 The earliest myriapods in the body fossil record are three species of Diplopoda from the 841 Dictyocaris Member of the Cowie Formation at Cowie Harbour, near Stonehaven, Aberdeenshire, 842 Scotland, one of which is C. eroticopodus (Wilson and Anderson, 2004). Based on associated spores, 843 the Cowie Formation taxa are late Wenlock to early Ludlow in age (Marshall, 1991; Wellman, 1993) 844 and the Early Ludlow upper boundary (Gorstian-Ludfordian boundary) is 425.6 Ma ± 0.9 Myr, so the 845 minimum age for Myriapoda is 424.7 Ma. 846 Soft maximum as for 2.3. 847 848 23.4. Discussion 849 850 Albadesmus almondi and Pneumodesmus newmani (both described by Wilson and Anderson, 851 2004) have an equal claim to being the oldest myriapod, sourced from the same locality and unit as C. 852 eroticopodus. The latter was selected because it has been explicitly coded in a morphological cladistic 853 analysis (Fernández et al., 2016). We have not used trace fossil evidence suggestive of Ordovician 854 diplopods (Wilson, 2006) for dating.

855

856 24. Crown Progoneata

857

This clade comprises Diplopoda (millipedes), Pauropoda and Symphyla, their last common

859	ancestor and all of its descendants (Fig. 8). Monophyly is supported by phylogenetic analysis of
860	nuclear protein-coding genes (Regier et al., 2010; Zwick et al., 2012), whole mitochondrial genomes
861	(Brewer et al., 2013), and morphology (Edgecombe, 2004; Legg et al., 2013). Two recent molecular
862	phylogenies reject monophyly of Progoneata in favour of a putative clade of Chilopoda and Diplopoda:
863	one based on three protein-coding genes (Miyazawa et al., 2014) and one on transcriptomes (Rehm
864	et al., 2014). This clade is not recognized in GenBank taxonomy.
865	
866	24.1. Fossil specimens
867	
868	As for 23.1.
869	
870	24.2. Phylogenetic justification
871	
872	As for 23.2.
873	
874	24.3. Age justification
875	
876	As for 23.3.
877	
878	24.4. Discussion
879	
880	As for 23.4.
881	
882	25. Crown Diplopoda
883	
884	This clade comprises Penicillata (bristly millipedes) and Chilognatha, their last common

885	ancestor and all of its descendants (Fig. 8). Monophyly is supported by morphological analyses
886	(Blanke and Wesener, 2014), nuclear protein-encoding genes (Regier et al., 2010), and
887	transcriptomes (Fernández et al., 2016; Rehm et al., 2014).
888	
889	25.1. Fossil specimens
890	
891	As for 23.1.
892	
893	25.2. Phylogenetic justification
894	
895	As for 23.2.
896	
897	25.3. Age justification
898	
899	As for 23.3.
900	
901	25.4. Discussion
902	
903	As for 23.4.
904	
905	26. Crown Penicillata
906	
907	This clade comprises Polyxenoidea and Synxenoidea, their last common ancestor and all of its
908	descendants (Fig. 8). Monophyly has been defended based on the shared presence of serrate setae
909	arranged in lateral and caudal tufts (Enghoff, 1984).
910	
	35

911	26.1.	Fossil	specimens

*Electroxenus jezzinensis* Nguyen Duy-Jacquemin and Azar, 2004 (Acra collection, provisionally
 deposited at MNHN: JS 231/1), holotype (Fig. 9a,b), adult in amber (Nguyen Duy-Jacquemin and
 Azar, 2004, Fig. 1A, B).

916

917 26.2. Phylogenetic justification

918

Cretaceous amber penicillates are readily assigned to two of the three extant families,
Polyxenidae and Synxenidae (Nguyen Duy-Jacquemin and Azar, 2004; classification of Penicillata
following Short in Enghoff et al., 2015). *E. jezzinensis* preserves diagnostic characters of Polyxenidae
such as lateral extensions of the gnathochilarial palps. Membership in an extant family indicates status
as crown Penicillata.

924

925 26.3. Age justification

926

927 *E. jezzinensis* was discovered in amber from the Jouar Ess-Souss locality, in the Jezzine area, 928 South Lebanon (Azar et al., 2010). Previous work suggested a Neocomian (Valanginian-Hauterivian) 929 age for the Jezzine area (Azar et al., 2010). However, Lebanese stratigraphy has recently been 930 revised; the Jouar Ess-Souss locality is now recognized as part of the lowermost interval of the Grès 931 du Liban (Maksoud et al., 2016). The lower interval lies below a shale layer bearing the echinoid fossil 932 Heteraster oblongus, and below a pisolitic interval bearing charyophyte fossils (Maksoud et al., 2016). 933 The charyophyte layer is associated to the Cruciata-Paucibracteatus Zone of Martín-Closas et al. 934 (2009) in the late Barremian-early Aptian, but this layer is also older than the Banc de Mrejatt subunit 935 within Lebanon, thus Jezzine amber is older than the Ba2 layer in Fig. 6 of Maksoud et al. (2016). 936 Jezzine amber is therefore no younger than early Barremian. The upper boundary of the early

Barremian is proposed to be the first appearance of the ammonite *Ancyloceras vandenheckii* (Ogg et al., 2012). Cyclostratigraphy dates the *A. vandenheckii* Zone beginning at 129.41 Ma (Ogg et al., 2012), providing a minimum age for Jezzine Lebanese amber fossils.

940 A soft maximum age is obtained from the oldest mandibulate, Y. dianensis, which was 941 recovered from the Yu'anshan Formation at Xiaotan section, Yongshan, Yunnan Province, attributed to 942 the Eoredlichia–Wutingaspis Biozone (Zhang et al., 2007). Chinese Cambrian stratigraphy has been 943 revised substantially and the *Eoredlichia – Wutingaspis* Biozone is no longer recognized (Peng, 2009, 944 2003). However, *Eoredlichia* is known to co-occur with *Hupeidiscus*, which is diagnostic of the 945 Hupeidiscus-Sinodiscus Biozone, which is formally recognised as the second biozone of the 946 Nangaoan Stage of the Qiandongian Series of the Cambrian of China (Peng and Babcock, 2008). The 947 Nangaoan is the proposed third stage of the Cambrian System for the International Geologic 948 Timescale (Peng et al., 2012). Thus, a soft maximum constraint can be established on the age of the 949 lower boundary of the Nangaoan, which has been dated to 521 Ma (Peng et al., 2012; Peng and 950 Babcock, 2008).

951

952 **26.4**. *Discussion* 

953

Another species of Polyxenidae from Lebanese amber, *Libanoxenus hammanaensis* Nguyen Duy-Jacquemin and Azar, 2004, is likewise known from a single specimen, from the Mdeiriji/Hammana locality in Central Lebanon. Its age data are similar to those of the more completely known *E. jezzinensis*, so the latter is used for calibration.

958

## 959 27. Crown Chilognatha

960

961 This clade comprises Pentazonia (pill millipedes) and Helminthomorpha (long-bodied
 962 millipedes), their last common ancestor and all of its descendants (Fig. 8). Monophyly is supported by

963	morphological analyses (Blanke and Wesener, 2014), nuclear coding genes (Miyazawa et al., 2014),
964	and transcriptomes (Fernández et al., 2016). Chilognthan monophyly has rarely been opposed: some
965	analyses of nuclear protein coding genes by Regier et al. (2005) found weak support for an
966	unconventional grouping of Penicillata with Pentazonia, but others retrieved Chilognatha.
967	
968	27.1. Fossil specimens
969	
970	As for 23.1.
971	
972	27.2. Phylogenetic justification
973	
974	As for 23.2.
975	
976	27.3. Age justification
977	
978	Minimum as for 23.3. Soft maximum as for 26.3.
979	
980	27.4. Discussion
981	
982	As for 23.4.
983	
984	28. Crown Chilopoda
985	
986	This clade comprises Scutigeromorpha (house centipedes) and Pleurostigmophora, their last
987	common ancestor and all of its descendants (Fig. 8). Monophyly is robustly supported by
988	morphological analyses (Edgecombe and Giribet, 2004; Murienne et al., 2010), nuclear protein-coding

989 genes (Miyazawa et al., 2014; Regier et al., 2010; Zwick et al., 2012), and transcriptomics (Fernández 990 et al., 2016; Rehm et al., 2014). 991 992 28.1. Fossil specimens 993 994 Crussolum sp. Jeram et al., 1990. DE 1.3.2/50 (Fig. 1N) and DE 3.1.1/88 (Fig. 1P; Jeram et al., 995 1990). As mentioned below, we also refer to material from the Windyfield Chert (AUGD 12307-12308; 996 Anderson and Trewin, 2003) for morphological details (Fig. 9c-e). 997 998 28.2. Phylogenetic justification 999 1000 Crussolum was resolved as stem-group Scutigeromorpha in the morphological cladistic 1001 analysis of Fernández et al. (2016). Codings were a composite of material described as *Crussolum* sp. 1002 from the Windyfield Chert (Pragian) of the Dryden Flags Formation, Aberdeenshire, Scotland (figured 1003 by Anderson and Trewin, 2003), and the one formally named species of the genus, C. crusseratum 1004 (Shear et al., 1998), known from isolated and fragmentary legs from the Middle Devonian Gilboa 1005 locality, Schoharie County, New York State (Givetian). 1006 1007 28.3. Age justification 1008 1009 The oldest examples of Crussolum are isolated legs from Ludford Lane in England (Shear et 1010 al., 1998), which come from a horizon 0.15-0.20 m above the base of the Ludlow Bone Bed Member, 1011 in the Downtown Castle Sandstone Formation. The Ludlow Bone Bed Member is early Pridoli in age 1012 (Jeram et al., 1990), that stage having an upper boundary of 419.2 Ma ± 3.2 Myr, providing a minimum 1013 age of 416.0 Ma. Crussolum as currently delimited crosses the Silurian-Devonian boundary. 1014 Soft maximum as for 2.3. 39

1015	
1016	29. Crown Scutigeromorpha
1017	
1018	This clade comprises Scutigeridae, Scutigerinidae and Psellioididae, their last common
1019	ancestor and all of its descendants (Fig. 8). Monophyly is robustly supported by morphological
1020	analyses (Edgecombe and Giribet, 2004), targeted gene sequencing (Murienne et al., 2010), and
1021	transcriptomics (Fernández et al., 2016).
1022	
1023	29.1. Fossil specimens
1024	
1025	Fulmenocursor tenax Wilson, 2001. SMNS 64275, holotype (Fig. 9f), nearly complete
1026	specimen (Wilson, 2001, Pl. 1, Fig. 2).
1027	
1028	29.2. Phylogenetic justification
1029	
1030	Wilson (2001) assigned F. tenax to the extant family Scutigeridae based on the proportions of
1031	its antennal articles and its styliform male gonopods. Paired spine-bristles on the tibia of the second
1032	maxilla (synapomorphy of Pselliodidae + Scutigeridae) are consistent with this interpretation
1033	(Edgecombe, 2011). These affinities place the genus in crown-group Scutigeromorpha.
1034	
1035	29.3. Age justification
1036	
1037	Minimum as for 15.3. Soft maximum as for 26.3.
1038	
1039	29.5 Discussion
1040	

1041 A total-group scutigeromorph from the Carboniferous Mazon Creek deposits, Latzelia 1042 primordialis Scudder, 1890b, cannot be reliably assigned to the scutigeromorph crown group 1043 (Edgecombe, 2011; J. T. Haug et al., 2014) and is accordingly not used for dating that clade. 1044 1045 **30. Crown Pleurostigmophora** 1046 1047 This clade comprises Craterostigmomorpha and Amalpighiata, their last common ancestor and 1048 all of its descendants (Fig. 8); membership is identical if the internal relationships of the clade are 1049 resolved as Lithobiomorpha + Phylactometria. Monophyly is supported by morphological analyses 1050 (Edgecombe and Giribet, 2004), nuclear ribosomal and mitochondrial genes, and their combination 1051 with morphology (Giribet and Edgecombe, 2006; Murienne et al., 2010), nuclear protein coding genes 1052 (Regier et al., 2010), and transcriptomics (Fernández et al., 2016, 2014b). 1053 1054 30.1. Fossil specimens 1055 1056 Devonobius delta Shear and Bonamo, 1988. AMNH slide 411-15-AR18, holotype (Fig. 9g), 1057 complete head with 15 or 16 trunk segments. We also refer to AMNH slide 4329-AR4 (Fig. 9h). 1058 1059 30.2. Phylogenetic justification 1060 1061 D. delta was resolved in a trichotomy with Craterostigmus and Epimorpha in the morphological 1062 cladistic analysis of (Edgecombe and Giribet, 2004, Fig. 9), and as sister group to extant 1063 Phylactometria when those data were combined with sequence data from four genes (Edgecombe 1064 and Giribet, 2004, Fig. 14). Published analyses agree on it being more closely related to Epimorpha 1065 than to Lithobiomorpha (Shear and Bonamo, 1988, Fig. 1; Murienne et al., 2010, Fig. 2; Fernández et 1066 al., 2016) and it is accordingly crown Pleurostigmophora.

1068 30.3. Age justification

1069

1070	D. delta occurs in the Middle Devonian Gilboa locality, Schoharie County, New York State,
1071	USA. Fossils come from the upper part of the Panther Mountain Formation, dated to the Tioughniogan
1072	regional Stage, Givetian in the global time scale. Palynomorphs are consistent with a Givetian age
1073	(Richardson et al., 1993). Accordingly, minimum date for the end of the Givetian/base of the Frasnian
1074	is applied (382.7 Ma).
1075	Soft maximum as for 26.3.
1076	
1077	31. Crown Amalpighiata
1078	
1079	This clade comprises Lithobiomorpha (stone centipedes) and Epimorpha, their last common
1080	ancestor and all of its descendants (Fig. 8). Monophyly is supported by targeted gene sequencing
1081	(Regier et al., 2010) and transcriptomics (Fernández et al., 2016, 2014b).
1082	
1083	31.1. Fossil specimens
1084	
1085	Mazoscolopendra richardsoni Mundel, 1979. FMNH PE 22936, holotype, nearly complete
1086	specimen in siderite concretion (J. T. Haug et al., 2014; Mundel, 1979). We also refer to FMNH PE
1087	29002 ( <b>Fig. 9i</b> ).
1088	
1089	31.2. Phylogenetic justification
1090	
1091	M. richardsoni was coded by Fernández et al. (2016) for its morphological data based on
1092	descriptions and figures of Mundel (1979) and Haug et al. (J. T. Haug et al., 2014), and personal

1093	observation by G.D.E. of type and other material in the Field Museum. It was resolved as total-group
1094	Scolopendromorpha based on possession of autapomorphies of that order (e.g. single tergite on the
1095	forcipular/first leg-bearing segments, 21 pairs of trunk legs) but cannot be placed more precisely with
1096	regards to whether it is a stem- or crown-group scolopendromorph. Nonetheless, its membership in
1097	Scolopendromorpha assigns it to crown Amalpighiata. The same calibration would apply were the
1098	putative clade Phylactometria endorsed in lieu of Amalpighiata.
1099	
1100	31.3. Age justification
1101	
1102	Specimens are derived from the Francis Creek Shale Member of the Carbondale Formation,
1103	Mazon Creek, Illinois, of Westphalian D age (Baird et al., 1985; Shabica and Hay, 1997). The
1104	Westphalian D is equivalent to the latest Moscovian stage of the Pennsylvanian (Richards, 2013). As
1105	the upper boundary of the Moscovian is 307.0 Ma $\pm$ 0.1 Myr, this provides a minimum age of 306.9
1106	Ma.
1107	Soft maximum as for 26.3.
1108	
1109	32. Crown Epimorpha
1110	
1111	This clade comprises Scolopendromorpha and Geophilomorpha, their last common ancestor
1112	and all of its descendants (Fig. 8). Monophyly is supported by morphological analyses (Fernández et
1113	al., 2016; Murienne et al., 2010) and transcriptomics (Fernández et al., 2016, 2014b).
1114	
1115	32.1. Fossil specimens
1116	
1117	As for 31.1.
1118	
	42

1119	32.2. Phylogenetic justification
1120	
1121	As for 31.2.
1122	
1123	32.3. Age justification
1124	
1125	As for 31.3.
1126	
1127	33. Crown Geophilomorpha
1128	
1129	This clade comprises Placodesmata and Adesmata, their last common ancestor and all of its
1130	descendants (Fig. 8). Monophyly is supported by morphological analyses, targetted sequencing, and
1131	combination of molecular and morphological data (Bonato et al., 2014a; Fernández et al., 2014b;
1132	Murienne et al., 2010) and transcriptomics (Fernández et al., 2016).
1133	
1134	33.1. Fossil specimens
1135	
1136	Kachinophilus pereirai Bonato et al., 2014b. AMNH Bu-Ba41a, holotype (Fig. 9j,k), complete
1137	adult male in amber (Bonato et al., 2014b, Fig. 1A-B, 2).
1138	
1139	33.2. Phylogenetic justification
1140	
1141	K. pereirai was originally assigned to the extant family Geophilidae based on a combination of
1142	characters that is unique to that family. More precisely it compares most closely to a subgroup within
1143	Geophilidae that has been classified as subfamilies Chilenophilinae or Pachymeriinae. K. pereirai was
1144	coded by Fernández et al. (2016) for its morphological data based on original observations on the type
	44

1145 material. It was resolved as more closely related to extant Geophilidae (sensu Bonato et al., 2014a) 1146 than to members of any of the other sampled geophilomorph family, as predicted by its original 1147 classification. Thus it is unambiguously a member of crown Adesmata and accordingly crown 1148 Geophilomorpha. 1149 1150 33.3. Age justification 1151 1152 Minimum as for 12.3. Soft maximum as for 26.3. 1153 1154 33.4. Discussion 1155 1156 A total-group geophilomorph from the Late Jurassic of Germany, Eogeophilus jurassicus 1157 Schweigert and Dietl, 1997 (refigured by J. T. Haug et al., 2014), is too inadequately known to 1158 establish whether or not it is a member of the geophilomorph crown-group. 1159 1160 34. Crown Pancrustacea 1161 1162 This clade comprises Oligostraca, Multicrustacea, and Allotriocarida, their last common 1163 ancestor and all of its descendants (Fig. 1). The inclusion of Hexapoda in a paraphyletic 'Crustacea' 1164 (and hence, erection of the clade Pancrustacea; Zrzavý and Štys, 1997) has been supported by 1165 numerous phylogenetic analyses, including those based on nuclear protein-coding genes (Regier et 1166 al., 2010, 2005), transcriptomes (Andrew, 2011; Meusemann et al., 2010; Rota-Stabelli et al., 2011;

1167 von Reumont et al., 2012), morphology (Legg et al., 2013; Schram and Koenemann, 2004; Strausfeld

and Andrew, 2011) and combined morphological and molecular data (Oakley et al., 2013).

1169 This clade has also been named Tetraconata (Dohle, 2001) referring to the shared apomorphy 1170 of four cone cells within the compound eye; however this character is absent in many members of the

1171	clade, with multiple possible reconstructions of homology (Oakley, 2003; T. Oakley, pers. comm.).
1172	Terminology that does not rely on the homology of cone cell arrangement is thus preferred. More
1173	recently, an amended version of 'Crustacea' has been proposed (Haug and Haug, 2015) to avoid a
1174	different application of the 'Pan-' prefix (Lauterbach, 1989). While this concept of Crustacea is in our
1175	view valid, for this purpose we favour the original use of Pancrustacea referring to the crown group
1176	members only (Zrzavỳ and Štys, 1997). Haug and Haug (2015) argue that fossils such as
1177	Phosphatocopina would need to be included within Pancrustacea, however recent phylogenetic
1178	analyses show the sister group to crown Pancrustacea is in fact crown Myriapoda, with all other fossils
1179	outside (Legg et al., 2013). Pancrustacea is the clade name implemented in GenBank, and is the most
1180	commonly used name among molecular workers.
1181	
1182	34.1. Fossil specimens
1183	
1184	As for 4.1.
1185	
1186	34.2. Phylogenetic justification
1187	
1188	As for 4.2.
1189	
1190	34.3. Age justification
1191	
1192	As for 4.3.
1193	
1194	34.4. Discussion
1195	
1196	As for 22.4.
	46

# **35. Crown Oligostraca**

1200	This clade comprises Ostracoda (seed shrimp), Branchiura (fish lice), Pentastomida (tongue
1201	worms), and Mystacocarida, their last common ancestor and all of its descendants (Fig. 10).
1202	Monophyly of this clade has been demonstrated with nuclear protein-coding genes (Regier et al.,
1203	2010; Zwick et al., 2012) and combined phylogenetic analysis of molecules and morphology (Lee et
1204	al., 2013; Oakley et al., 2013; Zrzavỳ et al., 1998). GenBank taxonomy does not recognize this clade.
1205	Instead GenBank prefers the Maxillopoda hypothesis (Branchiura, Pentastomida, Mystacocarida,
1206	Thecostraca and Copepoda), which has not been recovered in molecular analyses (Abele et al., 1992;
1207	Regier et al., 2005) despite support from morphology (Legg et al., 2013).
1208	
1209	35.1. Fossil specimens
1210	
1211	Boeckelericambria pelturae Walossek and Müller, 1994. UB W116, holotype, consisting of a
1212	complete larva (Fig. 11a).
1213	
1214	35.2. Phylogenetic justification
1215	
1216	B. pelturae is likely a stem group pentastomid, based especially on the diagnostic
1217	synapomorphy of a head with two pairs of grasping hooks (similar to the extant Reighardia larva;
1218	Walossek and Müller, 1994, Fig. 25a). This species is a member of the round headed (as opposed to
1219	hammer headed) morphotype (Walossek and Müller, 1994). It was resolved in the pentastomid stem-
1220	group in a cladistic analysis that sampled the extant genera by Almeida and Christoffersen (Almeida
1221	and Christoffersen, 1999). Its pentastomid identity is not dependent on whether pentastomids are
1222	interpreted as Ichthyostraca (Møller et al., 2008; Regier et al., 2010; Sanders and Lee, 2010) or early

1223	diverging euarthropods (e.g. Castellani et al., 2011). Because we accept crown pentastomids as sister
1224	group to crown branchiurans on the basis of strong support from molecular data, B. pelturae must
1225	therefore be within crown Oligostraca.
1226	
1227	35.3. Age justification
1228	
1229	The Orsten fossils come from the lowest zone of the late Cambrian Alum Shale, formally called
1230	the Agnostus pisiformis Zone or Zone 1, previously corresponding to the Uppermost Zone of the
1231	Middle Cambrian (Babcock et al., 2005). The Agnostus pisiformis Zone was recently redefined as the
1232	uppermost zone of the Guzhangian, at the upper boundary of Cambrian Series 3 (Nielsen et al.,
1233	2014). This age of the uppermost stage of the Cambrian Series 3 is 499 Ma $\pm$ 2 Myr. Thus the
1234	minimum age applied to Oligostraca is 497 Ma.
1235	Soft maximum as for 2.3.
1236	
1237	36. Crown Ichthyostraca
1238	
1239	This clade comprises Branchiura and Pentastomida, their last common ancestor and all of its
1240	descendants (Fig. 10). It was first proposed based on sperm ultrastructure (Wingstrand, 1972).
1241	Subsequent analyses of morphology combined with protein-coding genes (Zrzavỳ et al., 1998) or with
1242	transcriptomes (Oakley et al., 2013), as well as molecular data on their own (Møller et al., 2008;
1243	Regier et al., 2010) have supported monophyly of this clade.
1244	
1245	36.1. Fossil specimens
1246	
1247	As for 35.1.
1248	
	48
1249	36.2. Phylogenetic justification
------	--
1250	
1251	As for 35.2.
1252	
1253	36.3. Age justification
1254	
1255	As for 35.3.
1256	
1257	37. Crown Ostracoda
1258	
1259	This clade comprises Myodocopa, Podocopa (including Palaeocopida), their last common
1260	ancestor and all its descendants (Fig. 10). Monophyly of this clade has been demonstrated by
1261	phylogenetic analysis of a dataset including nuclear protein-coding genes, transcriptomes, and
1262	morphology (Oakley et al., 2013). Additional phylogenetic analyses of morphology alone (Legg et al.,
1263	2013; Wolfe and Hegna, 2014) also support monophyly.
1264	
1265	37.1. Fossil specimens
1266	
1267	Luprisca incuba Siveter et al., 2014. YPM IP 307300, holotype, consisting of a complete
1268	pyritized specimen in ventral aspect (Fig. 11b).
1269	
1270	37.2. Phylogenetic justification
1271	
1272	To date, <i>L. incuba</i> is yet to be included in an extensive phylogenetic analysis, but a number of
1273	features confirm both its placement within Myodocopida, and therefore Myodocopa. Specifically, the
1274	arrangement of setae on the antenula of L. incuba is currently only observed amongst extant

1275 myodocopid ostracods (Kornicker, 1981).

1276

1277 37.3. Age justification

1278

1279 The holotype of L. incuba was collected from siltstone of the Original Trilobite Bed, Walcott 1280 Quarry of Beecher's Trilobite Bed, in the Frankfort Shale of upstate New York (Siveter et al., 2014). 1281 Beecher's site within the Frankfort Shale is within the Lorraine Group, part of the regional Maysvillian 1282 Stage of the Cincinnatian Series (Farrell et al., 2011, 2009). Globally, the Maysvillian (Amplexograptus 1283 manitoulinensis Graptolite Zone) corresponds to the early Katian Stage, from the base of the 1284 Diplacanthograptus caudatus Graptolite Zone to the base of the Pleurograptus linearis Graptolite Zone (Bergström et al., 2009). The upper boundary of the Katian is 445.2 Ma ± 1.4 Myr, providing a 1285 1286 minimum age of 443.8 Ma.

1287 As in Oakley et al. (2013), we suggest the maximum age of ostracods must be 509 Ma, the 1288 age of the Burgess Shale. Myodocope ostracods possess bivalved, calcified carapaces, which are 1289 preserved from many other Burgess Shale arthropods. There is no taphonomic reason why they would 1290 not have been preserved from ostracods. The Burgess Shale type locality is from Unit 3 of the Collins 1291 Quarry on Mount Stephen in the Canadian Rocky Mountains, British Columbia, which falls within the 1292 Kicking Horse Shale Member of the "thick" Stephen Formation (Aitkin, 1997; Caron et al., 2010; 1293 Stewart, 1991), also referred to as the Burgess Shale Formation (Fletcher and Collins, 2003, 1998). 1294 This unit yields trilobites from the Polypleuraspis insignis Subzone of the Glossopleura Zone (Fletcher 1295 and Collins, 1998), and is the oldest soft-bodied fossil excavation of the Burgess Shale sites. The age 1296 of the Glossopleura Zone corresponds to the Cambrian Series 3 Stage 5, giving a maximum constraint 1297 of 509 Ma.

1298

1299 37.4. Discussion

1300

1301 Older fossils, from the Tremadocian (~40 Myr older) have been reported from numerous 1302 localities across the current and Ordovician world: Argentina, Australia, China, Iran, Norway, Sweden, 1303 and the UK (Williams et al., 2008). However, all of these fossils are known solely from carapaces, 1304 which are known to be highly homoplastic (Siveter et al., 2013). The affinities of Tremadocian 1305 ostracods are therefore ambiguous. Other bivalved crustacean-like taxa from the Cambrian, such as 1306 bradoriids and phosphatocopines, are demonstrably not closely related to ostracods, or even 1307 Oligostraca, based on phylogenetic analyses (Hou et al., 2010; Legg et al., 2013; Oakley et al., 2013; 1308 Wolfe and Hegna, 2014).

1309

# 1310 **38. Crown Podocopa**

1311

This clade comprises Palaeocopida, Podocopida and Platycopida, their last common ancestor and all of its descendants (**Fig. 10**). Monophyly has been demonstrated by phylogenetic analysis of morphology (Horne et al., 2005), and morphology combined with nuclear protein-coding genes and transcriptomes (Oakley et al., 2013). Although the sole living representative of Palaeocopida, *Manawa staceyi*, has to date only been represented by a single ribosomal sequence and morphology, bootstrap support for its position as a sister to the remaining Podocopa is strong (Oakley et al., 2013).

1318

1319 38.1. Fossil specimens

1320

1321 *Cytherellina submagna* Krandijevsky, 1963. For phylogenetically relevant details, we refer to 1322 ZPAL O.60/001 (**Fig. 11c-e**), preserving soft anatomy, and ZPAL O.60/002, preserving adductor 1323 muscle scars (Olempska et al., 2012).

1324

1325 38.2. Phylogenetic justification

1326

1327 C. submagna is very similar to modern podocopes, particularly sigilloideans and

1328 darwinuloideans, with which it shares a particular adductor muscle scar pattern, long terminal seta on

1329 the seventh limb pair, and a furca with large distal setae (Olempska et al., 2012).

1330

1331 38.3. Age justification

1332

1333 Specimens of *C. submagna* were recovered from two localities in Podolia, Ukraine: Kasperovcy 1334 village, left border of the river Seret (type locality), and from the right escarpment of the River Dniester 1335 near the village Ivanye Zlote (Olempska et al., 2012). The type locality, part of the Chortkov/Chortkiv 1336 Horizon, underlies the second locality, which is part of the Ivanye Horizon (Filipiak et al., 2012; 1337 Olempska et al., 2012). Thus we must use the Chortkiv age as a minimum constraint on the age of C. 1338 submagna, to provide the narrowest interval of clade divergence. The Chortkiv Horizon comfortably 1339 lies within the middle Lochkovian stage of the Early Devonian (Filipiak et al., 2012; Małkowski et al., 1340 2009; Plotnick, 1999). Conodont biostratigraphy places the upper boundary of the Chortkiv Horizon at the end of the Caudicriodus postwoschmidti Biozone, the oldest conodont Biozone within the 1341 1342 Devonian (Drygant and Szaniawski, 2012). Spline fits on radiometric ages for the Devonian place the 1343 C. postwoschmidti Biozone at 417.27 Ma with a duration of 1.89 Myr (Becker et al., 2012). Thus the 1344 end of the C. postwoschmidti Biozone, and a minimum age for the first appearance of C. submagna, is 1345 415.38 Ma.

1346 Soft maximum as for 37.3.

- 1347
- 1348 38.4. Discussion

1349

Although isolated ostracod carapace valves are incredibly abundant in the fossil record, the morphology of carapaces has been shown to have little systematic value (Siveter et al., 2013). For this reason we have selected a taxon with soft-tissue preservation, of which *C. submagna* is the oldest

1353	recognized example, although other species of Cytherellina are known from older deposits including
1354	the later Silurian of Ludlow, England, with only the carapaces preserved (Olempska et al., 2012).
1355	These older species cannot be ruled out as myodocopes or stem members of any of Podocopa,
1356	Myodocopa, or even Ostracoda, as they lack diagnostic soft parts.
1357	
1358	39. Crown Myodocopa
1359	
1360	This clade comprises Myodocopida and Halocyprida, their last common ancestor and all of its
1361	descendants (Fig. 10). Monophyly has been demonstrated by phylogenetic analysis of morphology
1362	(Horne et al., 2005), and morphology combined with nuclear protein-coding genes and transcriptomes
1363	(Oakley et al., 2013).
1364	
1365	39.1. Fossil specimens
1366	
1367	As for 37.1.
1368	
1369	39.2. Phylogenetic justification
1370	
1371	As for 37.2.
1372	
1373	39.3. Age justification
1374	
1375	As for 37.3.
1376	
1377	40. Crown Myodocopida
1378	
	53

1379	This clade comprises Cylindroleberidoidea, Cypridinoidea and Sarsielloidea, their last common
1380	ancestor and all of its descendants (Fig. 10). Monophyly has been demonstrated by phylogenetic
1381	analysis of morphology (Horne et al., 2005), and morphology combined with nuclear protein-coding
1382	genes and transcriptomes (Oakley et al., 2013).
1383	
1384	40.1. Fossil specimens
1385	
1386	As for 37.1.
1387	
1388	40.2. Phylogenetic justification
1389	
1390	As for 37.2.
1391	
1392	40.3. Age justification
1393	
1394	As for 37.3.
1395	
1396	41. Crown Altocrustacea
1397	
1398	This clade comprises Multicrustacea and Allotriocarida, their last common ancestor and all of
1399	its descendants (Fig. 1). Monophyly has been supported by phylogenetic analysis of nuclear protein-
1400	coding genes (Regier et al., 2010; Zwick et al., 2012), transcriptomes (von Reumont et al., 2012), and
1401	combined analysis of morphology and nuclear protein-coding genes (Lee et al., 2013) or morphology
1402	and transcriptomes (Oakley et al., 2013). However, this clade has been challenged as paraphyletic
1403	(containing Oligostraca) by Rota-Stabelli et al. (2013b), and has not been supported by morphological
1404	data alone. It is not recognized in GenBank taxonomy.

1405 1406 41.1. Fossil specimens 1407 1408 As for 4.1. 1409 1410 41.2. Phylogenetic justification 1411 1412 As for 4.2. 1413 1414 41.3. Age justification 1415 1416 As for 4.3. 1417 1418 41.4. Discussion 1419

1420 A series of disarticulated Small Carbonaceous Fossils (Harvey and Butterfield, 2008) from the 1421 early Cambrian Mount Cap Formation, Northwest Territories, Canada, have been cited as calibration 1422 fossils within Altocrustacea or even Allotriocarida (e.g. Rehm et al., 2011; Sun et al., 2015). These 1423 fossils were argued by Harvey (2008) to comprise part of the feeding apparatus of a single crustacean 1424 taxon. The Mount Cap arthropod fossils would have represented structures each specialized for 1425 precise feeding functions. The fossil species may have initially scraped food with saw-toothed and 1426 hooked setae, further processed particles with filter plates and other delicate setal associations, then 1427 macerated with mandibular molar surfaces and passed to the mouth with long fringing setae (Harvey 1428 and Butterfield, 2008). Estimates of the body size of the animal, based on regression of body length 1429 versus molar surface length (from extant crustaceans) suggest the Mount Cap arthropod was, in total, 1430 about the same size as an adult cladoceran or anostracan (Harvey and Butterfield, 2008). While direct synapomorphies linking the Mount Cap arthropod to crown group branchiopods are lacking, the
evidence together suggests affinity along the stem lineage of Altocrustacea (Harvey, 2008, Fig. 5.6).

1433

# 1434 **42. Crown Multicrustacea**

1435

1436 This clade comprises Copepoda, Thecostraca (barnacles) and Malacostraca, their last 1437 common ancestor and all of its descendants (Figs. 12 and 13). Monophyly was first demonstrated by 1438 nuclear protein-coding genes (Regier et al., 2010) and supported by transcriptomes (von Reumont et 1439 al., 2012) and combined analysis of molecular and morphological data (Lee et al., 2013; Oakley et al., 1440 2013). This clade has, however, not been recovered in any morphology-only phylogenetic analyses, 1441 presumably owing to widespread support for Malacostraca as sister to much of the rest of 1442 Pancrustacea (the Entomostraca hypothesis, e.g. Walossek and Müller, 1998). See Wolfe and Hegna 1443 (2014) for a morphological deconstruction of Entomostraca. Neither Multicrustacea nor Entomostraca 1444 is recognized in GenBank taxonomy. 1445 1446 42.1. Fossil specimens 1447 1448 Arenosicaris inflata Collette and Hagadorn, 2010a. PRI 10130), holotype from the Elk Mound 1449 Group (Fig. 14a), which is difficult to date (see 42.3). Therefore, we refer to a second specimen, 1450 UWGM 745.

1451

1452 42.2. Phylogenetic justification

1453

1454 A. inflata was identified within the Archaeostraca, the likely fossil sister group to extant

1455 Leptostraca (together comprising 'Phyllocarida') and included in the morphological cladistic analysis of

- 1456 Collette and Hagadorn (2010b). In that analysis, the exceptionally preserved fossils *Nahecaris stuertzi* 
  - 56

1457 Jaeckel, 1921 and Cinerocaris magnifica Briggs et al., 2004 were also included within Archaeostraca 1458 (Collette and Hagadorn, 2010b). A separate extensive combined molecular and morphological 1459 analysis placed C. magnifica within crown Malacostraca (as is traditionally assumed for members of 1460 Archaeostraca), while N. stuertzi was equivocally stem Leptostraca or stem Malacostraca (Oakley et 1461 al., 2013), suggesting non-monophyly of Archaeostraca. C. magnifica was also crown Malacostraca in 1462 another morphological analysis that omitted N. stuertzi (Legg et al., 2013). A. inflata is within the same 1463 archaeostracan clade as N. stuertzi (Pephricaridina + Rhinocaridina) while C. magnifica is in a 1464 separate archaeostracan group (Echinocaridina; Collette and Hagadorn, 2010b). Given the uncertainty 1465 of crown affinities and potential monophyly of Archaeostraca, we conservatively assign A. inflata to 1466 crown-group Multicrustacea, but not Malacostraca.

1467

#### 1468 42.3. Age justification

1469

1470 A. inflata is found in the Elk Mound Group (holotype) and in the Lodi Member of the St. 1471 Lawrence Formation, both in Wisconsin (Collette and Hagadorn, 2010a). Although the Elk Mound 1472 Group is the older of these, no biostratigraphically useful fossils co-occur with A. inflata, limiting the 1473 ability to determine the formation to which they belong (Collette and Hagadorn, 2010a). The St. 1474 Lawrence Formation is younger, containing Saukia Zone trilobites, which mark it as late Sunwaptan 1475 within the Furongian (Collette and Hagadorn, 2010a; Raasch, 1951). The Sunwaptan is the second 1476 latest stage of the Furongian, postdated by the Skullrockian (which extends into the Early Ordovician; 1477 Peng et al., 2012). The Sunwaptan-Skullrockian boundary is determined by the appearance of 1478 conodonts in the Hirsutodontus hirsutus Subzone of the Cordylodus proavus Zone (Peng et al., 2012). Based on the correlation diagram of Peng et al. (2012), the Sunwaptan-Skullrockian boundary is 1479 1480 approximately 487 Ma, providing a minimum age estimate.

- 1481 Soft maximum as for 2.3.
- 1482
- 57

- **43. Crown Copepoda**

1485	This clade comprises Calanoida, Cyclopoida, Gelyelloida, Harpacticoida (benthic copepods),
1486	Misophrioida, Mormonilloida, Platycopioida and Siphonostomatoida (fish parasites), their last common
1487	ancestor and all of its descendants (Fig. 12). Members of Calanoida, Cyclopoida, and
1488	Siphonostomatoida were included in a large combined analysis of transcriptomes and morphology,
1489	forming a monophyletic group (Oakley et al., 2013). Phylogenetic analysis of morphology (Huys and
1490	Boxshall, 1991; Ho, 1994), mitochondrial genes (Minxiao et al., 2011), and ribosomal genes combined
1491	with morphology (Huys et al., 2007) suggest this sampling covers distant lineages of Copepoda,
1492	although omitting Platycopioida, the presumed most basal order (Huys and Boxshall, 1991). Molecular
1493	data remain unavailable from Platycopioida, although comparative morphological investigations
1494	support copepod monophyly (Dahms, 2004).
1495	
1496	43.1. Fossil specimens
1497	
1498	Kabatarina pattersoni Cressey and Boxshall, 1989. BMNH IN. 63466, holotype, preserving the
1499	cephalothorax, mouthparts, oral cone, and first and second thoracic limbs (Fig. 14b). This specimen
1500	likely represents an adult female, recovered from the gills of a fossil teleost fish (Cressey and
1501	Boxshall, 1989).
1502	

1503 43.2. Phylogenetic justification

*K. pattersoni* has not been included in a formal phylogenetic analysis. Cressey and Boxshall
(1989) detail one apomorphy shared by the fossil and recent members of the family Dichelesthiidae,
which is a medial groove delimiting the distal part of the maxillary claw. A number of other characters
are shared more generally with copepods, such as the shape of the oral cone (typical for fish parasitic

1509 copepods), and biramous thoracic limbs with a 2-segmented protopod, joined by the intercoxal plate

1510 (Cressey and Boxshall, 1989). Dichelesthiidae is a family belonging to the Siphonostomatoida. Even a

1511 position for *K. pattersoni* on the stem of Dichelesthiidae or stem Siphonostomatoida would be within

1512 crown group Copepoda.

1513

1514 43.3. Age justification

1515

*K. pattersoni* was found in the Cretaceous Santana Formation, Serra do Araripe, Ceará, Brazil (Cressey and Boxshall, 1989), which is mainly famous for concretions enclosing fossil fishes. The age of the Santana Formation is poorly constrained (as it lacks biostratigraphic index fossils and igneous rocks for radiometric dating); dates have been suggested that range from the Aptian to the Albian or Cenomanian (Martill, 2007). In order to ensure a minimum date, the upper boundary of the Cenomanian, which is 93.7 Ma (from 93.9 Ma  $\pm$  0.2 Myr; Ogg et al., 2012), is used. Soft maximum as for 26.3.

1523

1524 *43.4. Discussion* 

1525

1526 Despite their overwhelming abundance in modern aquatic ecosystems, copepods have a poor 1527 fossil record, likely due to their small size, unsclerotized cuticle, and planktonic ecology. Apart from K. 1528 pattersoni, putative copepod appendages have been reported from much older sediments in the 1529 Pennsylvanian (Selden et al., 2010) and even the Cambrian (Harvey et al., 2012; Harvey and Pedder, 1530 2013; These fossils each bear one to four characters found in crown copepods, from partial maxillae 1531 (Selden et al., 2010) and partial or complete mandibular gnathal edges (Harvey et al., 2012; Harvey 1532 and Pedder, 2013). Relationships between feeding habits and mandibular morphology have been 1533 observed in extant copepods (Michels and Schnack-Schiel, 2005), and variation may occur among 1534 closely related species (Sano et al., 2015). It is therefore extremely unlikely that mandibular characters 1535 have not experienced any homoplasy since the Cambrian.

1536 Nevertheless, divergence time analyses suggest Devonian-Carboniferous (calibrated with *K*. 1537 *pattersoni*; (Rota-Stabelli et al., 2013a), Carboniferous (calibrated with external fossils from other 1538 pancrustacean clades; Oakley et al., 2013), or Permian (external fossils; Wheat and Wahlberg, 2013) 1539 origins for crown Copepoda. These analyses do not conflict stratigraphically with a crown assignment 1540 for the Pennsylvanian fossils (Selden et al., 2010). Therefore we must caution that a Cretaceous age 1541 is likely a severe underestimate of crown copepod antiquity.

1542

# 1543 **44. Crown Thecostraca**

1544

This clade comprises Facetotecta (y-larvae), Ascothoracida, and Cirripedia, their last common ancestor and all of its descendants (**Fig. 12**). Monophyly of Thecostraca has been demonstrated by separate analysis of nuclear housekeeping genes and morphology (Pérez-Losada et al., 2009a). All included clades have complex (sometimes only partially known) life histories, but particularly strong morphological support comes from a shared larval stage, the cyprid.

More recently, the enigmatic parasitic Tantulocarida were added within Thecostraca based on analysis of a single ribosomal gene (Petrunina et al., 2014), however, other relationships within Pancrustacea differed significantly from those outlined herein. In light of the paucity of data other than ribosomal genes, we remain ambivalent about including Tantulocarida. As tantulocarids have no known fossil record, if further evidence supports their position within Thecostraca, this calibration may be modified to include them as well.

1556

1557 44.1. Fossil specimens

1558

1559 *Rhamphoverritor reduncus* Briggs et al., 2005. OUM C.29587, holotype (**Fig. 14c,d**),

1560 preserving a cyprid larva in a volcaniclastic concretion. As the reconstruction of Herefordshire fossils

requires serial grinding and photography of 20 µm sections (Sutton et al., 2002), the holotype (figured
in Briggs et al., 2005: Fig. 1) was thus destroyed in preparation. Morphological data for Herefordshire
fossils are published as 3D models of the thin section photographs.

1564

1565 44.2. Phylogenetic justification

1566

1567 In a phylogenetic analysis of morphology, R. reduncus is the sister group of two species of 1568 Thoracica (both are members of Balanomorpha) (Legg et al., 2013). This is a position likely within the 1569 crown group of Thecostraca, however, no other thecostracans (such as Facetotecta and 1570 Ascothoracida) were included. Generally, the cyprid larval morphotype (with an elongated head shield, 1571 six swimming thoracopods, and robust modified antennules) is considered a synapomorphy of 1572 Thecostraca (Høeg et al., 2004). *R. reduncus* differs from cirripede cyprids as it lacks attachment 1573 discs, and its abdomen extends past the head shield; a differentiated abdomen is a condition of 1574 Ascothoracida (Briggs et al., 2005; Høeg et al., 2009a). Based on the presence of five shell plates in a 1575 juvenile specimen, Høeg et al. (2009b) suggested that *R. reduncus* may be placed on the cirripede 1576 stem lineage. In combination with the phylogenetic analysis of Legg et al. (2013), these apomorphies 1577 indicate that *R. reduncus* is very likely a member of crown group Thecostraca, and likely on the stem 1578 of Cirripedia. 1579 1580 44.3. Age justification

1581

1582 Minimum as for 6.3. Soft maximum as for 26.3.

1583

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1584 45. Crown Cirripedia
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1585

1586 This clade comprises Acrothoracica, Rhizocephala and Thoracica (barnacles), their last

1587	common ancestor and all of its descendants (Fig. 12). Monophyly has been demonstrated by separate
1588	phylogenetic analysis of nuclear housekeeping genes and morphology (Pérez-Losada et al., 2009a).
1589	
1590	45.1. Fossil specimens
1591	
1592	Illilepas damrowi Schram, 1986. FMNH P32055, holotype (Fig. 14e).
1593	
1594	45.2. Phylogenetic justification
1595	
1596	Schram (1975) described this fossil as Praelepas damrowi, a congener of P. jaworskii
1597	Chernyshev, 1930. Restudy led to the transfer of this fossil to the new genus Illilepas under the
1598	combination I. damrowi, as the original description of a carina more closely resembled a tergum, and
1599	the original tergum was more likely an enlarged spine along the margin of the aperture, similar to that
1600	seen in Ibliformes (Thoracica) (Buckeridge and Newman, 2006; Schram, 1986). However, both
1601	molecular and morphological data place Ibla as the most basal clade of Thoracica (Pérez-Losada et
1602	al., 2009a, 2008), which, if I. damrowi is on the Ibliformes stem lineage, would still situate the fossil
1603	within the crown group of Cirripedia.
1604	
1605	45.3. Age justification
1606	
1607	As for 31.3.
1608	
1609	45.4. Discussion
1610	
1611	A possible Early Ordovician stalked barnacle (Pedunculata: Lepadomorpha?) was illustrated in
1612	Fig. 2c and S3h of Van Roy et al. (2010). It has not been formally described and its affinities are
	62

1613 unclear.

1614 P. jaworskii is in some ways a more appropriate fossil calibration than I. damrowi. It is 1615 approximately coeval to *I. damrowi*, and was coded in a morphological phylogenetic analysis (Glenner 1616 et al., 1995), where it was placed within Thoracica (sister to all other Thoracica except Ibla). P. 1617 jaworskii has been used as a calibration fossil for Thoracica and Cirripedia (Pérez-Losada et al., 1618 2009b, 2008; Rees et al., 2014). However, no specimen information was available in the original 1619 publication, nor was any significant stratigraphic data beyond Carboniferous of the Kusnetzk Basin, 1620 Russia (Chernyshev, 1930). As the papers using P. jaworskii for calibration estimate its age at 306.5-1621 311.7 Ma (e.g. Rees et al., 2014), substitution of the slightly younger *I. damrowi* will not significantly 1622 violate the minimum age.

1623

# 1624 **46. Crown Thoracica**

1625

1626 This clade comprises Ibliformes, 'Pedunculata' (goose barnacles) and Sessilia (acorn 1627 barnacles), their last common ancestor and all of its descendants (Fig. 12). Pedunculata is no longer 1628 supported as monophyletic (Buckeridge and Newman, 2006; Pérez-Losada et al., 2009a; Rees et al., 1629 2014). Ibliformes is identified as the sister group of all other Thoracica (Pérez-Losada et al., 2009a). 1630 Monophyly has been established by phylogenetic analysis of nuclear housekeeping genes (Pérez-1631 Losada et al., 2009a), although a morphological phylogenetic analysis in the same paper resolves all 1632 studied members of Rhizocephala and Thoracica together in a polytomy. This is because only larval 1633 characters can be scored for Rhizocephala, with missing data for all adult characters due to their 1634 parasitic lifestyle.

1635

1636 46.1. Fossil specimens

1637

1638 As for 45.1.

1639	
1640	46.2. Phylogenetic justification
1641	
1642	As for 45.2.
1643	
1644	46.3. Age justification
1645	
1646	As for 31.3.
1647	
1648	46.4. Discussion
1649	
1650	As for 45.4.
1651	
1652	47. Crown Sessilia
1653	
1654	This clade comprises Verrucomorpha and Balanomorpha, their last common ancestor and all
1655	of its descendants (Fig. 12). Monophyly is supported by phylogenetic analysis of nuclear protein-
1656	coding and ribosomal genes (Pérez-Losada et al., 2008; Rees et al., 2014).
1657	
1658	47.1. Fossil specimens
1659	
1660	Brachylepas fallax Withers, 1935. For calibration, we refer to the stratigraphically oldest
1661	specimen (SM 704275), which is undescribed (A. Gale, pers. comm.).
1662	
1663	47.2. Phylogenetic justification
1664	

1665 This species was originally described from disarticulated material by Darwin (1851) as 1666 Pollicipes fallax. Withers (1935, 1914) recognized it was a sessile, rather than pedunculate barnacle, 1667 and that it had similarities to the basal sessilian genus Pycnolepas in overall form and plate 1668 development. Synapomorphies shared by *B. fallax* and all crown Sessilia include: the absence of a 1669 peduncle, presence of an operculum, and absence of all lateral plates (Gale and Sørensen, 2015). B. fallax shares with crown Balanomorpha a low, hemiconical carina and rostrum (Gale and Sørensen, 1670 1671 2015). On the basis of these characters, a recent cladogram depicts *B. fallax* as one of the most 1672 distant stem lineages of Balanomorpha, which is therefore a position within the crown group of 1673 Sessilia (Gale and Sørensen, 2015).

1674

1675 47.3. Age justification

1676

1677 The oldest known locality from which *B. fallax* has been recovered is Pit No. 125 (Brydone, 1678 1912), close to junction of Barnet Side Lande and King's Lane, Froxfield, Hampshire, England (A. Gale, pers. comm.). This locality bears fossils of Holaster (Sternotaxis) planus, and is thus part of the 1679 1680 S. planus echinoid zone, which is the uppermost zone of the Turonian in English Chalk (Gale, 1996; 1681 Mortimore, 2011). The GSSP defining the global upper boundary of the Turonian remains debated (due to difficulty in identifying its index ammonite fossil, Forresteria (Harleites) petrocoriensis (Ogg et 1682 1683 al., 2012). Currently, the upper boundary of the Turonian is dated to 89.8 Ma  $\pm$  0.3 Myr, providing a 1684 minimum age of 89.5 Ma.

- 1685 Soft maximum as for 26.3.
- 1686
- 1687 47.4. Discussion
- 1688

1689 The Albian-Cenomanian *Verruca withersi* Schram and Newman, 1980 has been shown not to 1690 be a cirripede (Jagt and Buckeridge, 2005) and cannot be used as a minimum. *Proverruca* (coded at

1691 the genus level) was included in a morphological phylogenetic analysis, where it was placed in a 1692 polytomy with the fossil *Eoverruca* and the crown family Verrucidae (Glenner et al., 1995), and 1693 subsequently used as a calibration fossil for divergence time analysis (Pérez-Losada et al., 2014, 1694 2008). However, the placement of *Proverruca* was based on similarities to the extant genus 1695 Neoverruca, which was shown in molecular analyses to fall outside Sessilia entirely, instead within the 1696 Scalpelliformes (Pérez-Losada et al., 2008; Rees et al., 2014). More recent morphological 1697 phylogenetic analyses confirm the convergence between Neoverruca + Proverruca and crown 1698 Verrucomorpha (Gale, 2015; Gale and Sørensen, 2015).

The Albian *Pycnolepas rigida* Sowerby, 1836 was included in a morphological phylogenetic analysis, where it was placed on the stem lineage of Verrucomorpha (Gale, 2015). However, that analysis did not include members of Balanomorpha, so the topology did not explicitly exclude a position on the stem lineage of Sessilia. In fact, this species was referred to stem Sessilia (Gale, 2015, p. 770). Unlike crown group Sessilia, it retains the pedunculate character of a lateral plate, the tall upper latus (Gale, 2015).

*Verruca tasmanica tasmanica* (Buckeridge, 1983), a previously used calibration fossil at the
base of Verrucomorpha (Herrera et al., 2015; Linse et al., 2013; Pérez-Losada et al., 2014, 2008;
Rees et al., 2014), is known from the Santonian Gingin Chalk Formation of Dandaragan, Western
Australia (as well as type material from younger Oligocene strata of Oamaru, New Zealand;
Buckeridge, 1979). As it is both younger than *B. fallax* and has not been studied in a phylogenetic

1710 context, it is not used herein.

1711

# 1712 **48. Crown Malacostraca**

1713

This clade comprises Leptostraca and Eumalacostraca, their last common ancestor and all of its descendants (**Fig. 13**). Its monophyly is one of the least contested matters in arthropod phylogeny; it has been demonstrated by phylogenetic analysis of morphology (Legg et al., 2013; Wills et al.,

1717	1998), nuclear ribosomal and protein-coding genes (Giribet et al., 2001; Regier et al., 2010, 2005),
1718	transcriptomes (von Reumont et al., 2012), and combined analysis of molecular and morphological
1719	data (Lee et al., 2013; Oakley et al., 2013).
1720	
1721	48.1. Fossil specimens
1722	
1723	Cinerocaris magnifica Briggs et al., 2004. OUM C.29565 (holotype; Fig. 14g), and OUM
1724	C.29566 (serially ground and reconstructed specimen; Fig. 14f). Morphological data for Herefordshire
1725	fossils are published as 3D models of thin section photographs.
1726	
1727	48.2. Phylogenetic justification
1728	
1729	C. magnifica was found to be a member of the stem group of Leptostraca (therefore crown
1730	group Malacostraca) in analyses of morphology (Legg et al., 2013) and morphology combined with
1731	molecules (Oakley et al., 2013).
1732	
1733	48.3. Age justification
1734	
1735	As for 44.3.
1736	
1737	48.4. Discussion
1738	
1739	The position of other fossil phyllocarids with respect to extant malacostracans (and the
1740	monophyly of phyllocarids themselves) have not been significantly investigated. The position of the
1741	Devonian phyllocarid Nahecaris stuertzi in a phylogenetic analysis (Oakley et al., 2013) was
1742	equivocally stem Leptostraca or stem Malacostraca, casting doubt on the position of at least rhinocarid

1743 phyllocarids within crown Malacostraca. As *N. stuertzi* has the same relationship to crown

1744 Malacostraca as A. inflata (at least in the analysis of Collette and Hagadorn, 2010b), neither fossil can

1745 be confidently placed within crown-group Malacostraca. Recent reinvestigation of *Ceratiocaris* cf.

1746 macroura (related to A. inflata and N. stuertzi in the analysis of Collette and Hagadorn, 2010b)

1747 suggests this Silurian 'phyllocarid' may be a stem eumalacostracan due to possession of an antennal

scale, casting further doubt on the monophyly of fossil phyllocarids (Jones et al., 2015). The C.

1749 macroura study, however, assumes malacostracan identity of phyllocarids (partly defined by biramous

1750 antennules), which, as discussed above (section 42.2), may not be robust to phylogenetic analysis. If,

1751 however, *Ceratiocaris* is within crown Malacostraca (either alone or with other archaeostracans), the

1752 oldest Malacostraca would be amended to Ceratiocaris winneshiekensis Briggs et al., 2015 from the

1753 Darriwilian Winneshiek Lagerstätte of Iowa (~14 Myr older than *C. magnifica*).

1754 Thylacocephalans are an enigmatic fossil arthropod clade ranging from the Silurian to the 1755 Cretaceous (C. Haug et al., 2014; Schram, 2014). Some Cambrian fossils have been proposed as 1756 thylacocephalans, but their membership is generally discounted (Schram, 2014; Vannier et al., 2006). 1757 Thylacocephalans have been compared to several extant arthropod clades, including the 1758 malacostracan stomatopods and decapods (Schram, 2014; Schram et al., 1999; Secrétan and Riou, 1759 1983; Vannier et al., 2016), which would extend the minimum age of Malacostraca slightly older within 1760 the Silurian (~433 Ma). The Jurassic thylacocephalan *Dollocaris ingens* Van Straelen, 1923 was coded 1761 in a morphological matrix, and found to be a stem eumalacostracan (therefore crown malacostracan) 1762 by phylogenetic analysis (Legg et al., 2013). However, their malacostracan affinities have been 1763 questioned, especially by C. Haug et al. (2014) studying a Silurian species, noting divergent trunk 1764 tagmosis and similarities to remipedes. Continued uncertainty over thylacocephalan affinites make 1765 them poor calibration fossils.

1766

1767 **49. Crown Eumalacostraca** 

1768

1769 This clade comprises Verunipeltata (mantis shrimp, partial total group called Stomatopoda), 1770 Peracarida, 'Syncarida' (itself comprising Anaspidacea and Bathynellacea) and Eucarida, their last 1771 common ancestor and all of its descendants (Fig. 13). Monophyly is demonstrated by phylogenetic 1772 analysis of morphology (Legg et al., 2013; Richter and Scholtz, 2001), nuclear ribosomal and protein-1773 coding genes (Regier et al., 2010), transcriptomes (von Reumont et al., 2012), and combined analysis 1774 of molecular and morphological data (Lee et al., 2013; Oakley et al., 2013; Wills et al., 2009). Although 1775 stomatopods and/or syncarids were not sampled in some of the above analyses, the best taxon 1776 sampling still resulted in eumalacostracan monophyly (Legg et al., 2013; Wills et al., 2009). 1777 1778 49.1. Fossil specimens 1779 1780 Palaeopalaemon newberryi Whitfield, 1880. The holotype at the AMNH, figured by Schram et 1781 al. (1978: Plate 3 #1-3), has been lost (B. Hussaini, pers. comm.), thus we refer to specimen KSU 1782 3484 (Fig. 14h.i). 1783 1784 49.2. Phylogenetic justification 1785 Schram and Dixon (2004) coded P. newberryi into the morphological matrix of Dixon et al. 1786 1787 (2003), finding it sister to a clade including Anomura, Brachyura, and Achelata to the exclusion of 1788 Astacidea, Axiidea, Gebiidea and Glypheidea. This position is within the crown group of Reptantia, 1789 hence within the crown groups of Decapoda and Eumalacostraca. 1790 1791 49.3. Age justification 1792 1793 The specimen of *P. newberryi* was found in gray shale near "Paine's Creek," LeRoy, Lake 1794 County, Chagrin (Erie) Shale, northeastern Ohio, USA (Feldmann et al., 1978; Schram et al., 1978). 69

1795	The Chagrin Shale is dated to the late Fammenian based on presence of the index alga Foerstia
1796	(Murphy, 1973), which in Ohio lies 40-70 m below surface outcrops (Feldmann et al., 1978). The upper
1797	boundary of the Fammenian is 358.9 Ma $\pm$ 0.4 Myr, giving a minimum of 358.5 Ma.
1798	Soft maximum as for 26.3.
1799	
1800	50. Crown Anaspidacea
1801	
1802	This clade comprises the families Anaspididae, Koonungidae, Psammaspididae and
1803	Stygocarididae, their last common ancestor and all of its descendants (Fig. 13). Phylogenetic studies
1804	including Anaspidacea are extremely rare, but morphology (Schram, 1984) and mitochondrial 16S
1805	sequences (Camacho et al., 2002) indicated monophyly of the clade.
1806	
1807	50.1. Fossil specimens
1808	
1809	Anaspidites antiquus Chilton, 1929. AMS F64765, holotype, complete specimen (Fig. 14k).
1810	
1811	50.2. Phylogenetic justification
1812	
1813	Although not included in a formal phylogenetic analysis, Schram (1984) justified the
1814	membership of A. antiquus as essentially indistinguishable from living Anaspididacea. Fusion of the
1815	first thoracomere into the cephalon, uniramous pleopods, and absence of an antennal scale are noted
1816	as diagnostic characters (Schram, 1984). As the fossil lacks preservation of diagnostic mouthparts,
1817	exact family affinities within total-group Anaspidacea are uncertain.
1818	
1819	50.3. Age justification
1820	

A. antiquus was found in the Hawkesbury Sandstone at the former Brookvale Brick Quarry, New South Wales, Australia (Schram, 1984). The Hawkesbury Sandstone overlies the Narrabeen Group and underlies the Wianamatta Group (Herbert, 1997). Sequence stratigraphy places the Hawkesbury in Sequence F, including the appearance of *Aratrisporites parvispinosus* spores (Helby, 1825 1973; Herbert, 1997). The *A. parvispinosus* spore zone indicates an age during the Anisian (middle Triassic) (Herbert, 1997). The upper boundary of the Anisian is estimated at 241.5 ± 1 Ma (Ogg, 2012), providing a minimum age at 240.5 Ma.

- 1828 Soft maximum as for 26.3.
- 1829

1830 *50.4. Discussion* 

1831

1832 'Syncarida', the traditional taxon containing Anaspidacea, is purposely excluded from this 1833 review, as its monophyly has been substantially challenged. In phylogenetic analyses, syncarid 1834 monophyly was only supported by the morphological dataset of Richter and Scholtz (2001). 1835 emphasizing the absence of a dorsal carapace in Anaspidacea and Bathynellacea ('Syncarida'). Each 1836 of a partial mitochondrial gene (Camacho et al., 2002), two mitochondrial genes and morphology 1837 (Jenner et al., 2009) and morphology including putative syncarid fossils (Schram and Hof, 1998; Wills 1838 et al., 2009) failed to recover a sister group relationship bewteen Anaspidacea and Bathynellacea. 1839 Wills et al. (2009) suggested that a paraphyletic grade of 'Syncarida', including fossils (Acanthotelson,

1840 Palaeocaris) represented the first divergences of Eumalacostraca.

1841

# 1842 **51. Crown Verunipeltata**

1843

1844 This is the clade comprising Bathysquilloidea, Erythrosquilloidea, Eurysquilloidea,

1845 Parasquilloidea, Gonodactyloidea, Lysiosquilloidea and Squilloidea, their last common ancestor and

all of its descendants (Fig. 13). Although the extant members are often referred to Stomatopoda, that

1847 clade includes a number of extinct members forming a paraphyletic grade (Fig. 1 of Haug et al., 2010).

1848 As membership of fossil species within a crown group is only possible if they branch along the stem

1849 lineage of a living clade that is part of the crown itself, we agree with the assertion that crown

1850 'Stomatopoda' is equivalent to the clade Verunipeltata *sensu* Haug et al. (2010). The stomatopod

1851 clade as a whole may be defined by several apomorphies, such as five pairs of maxillipeds, and

1852 modification of the first two pleopods as gonopods (Richter and Scholtz, 2001).

All living members form a clade in analyses of morphology including both fossil and extant taxa (Ahyong, 1997; Ahyong and Harling, 2000). Analysis of combined molecular and morphological data, with limited sampling of verunipeltatan clades, strongly supports monophyly of those members (Jenner et al., 2009). As well, representatives of Gonodactyloidea, Lysiosquilloidea and Squilloidea were sequenced for six housekeeping genes; these were monophyletic in a diverse sample of

1858 Pancrustacea (Bybee et al., 2011).

1859

1860 51.1. Fossil specimens

1861

*Ursquilla yehoachi* Remy and Avnimelech, 1955. For calibration, we refer to two specimens. Based on new phylogenetically relevant details, we use a new specimen (SMNS 67703) from Fig. 1 and 2 of Haug et al. (2013). The SMNS specimen, however, lacks locality and stratigraphic information beyond "Late Cretaceous Negev Desert, Israel" as it was privately donated (Haug et al., 2013). We also therefore refer to the holotype (MNHN R. 62691).

1867

1868 51.2. Phylogenetic justification

1869

1870 The uropod morphology of *U. yehoachi* indicates its membership in the crown group of

1871 Verunipeltata. The uropodal exopod of *U. yehoachi* specimen SMNS 67703 is bipartite, a

1872 synapomorphy of Verunipeltata (Haug et al., 2013). Furthermore, U. yehoachi shares several

characters with Squillidae (Squilloidea), such as prelateral lobes, submedian teeth with fixed apices
and a subquadrate telson (Haug et al., 2013). As *U. yehoachi* has not been included in a phylogenetic
analysis, it is uncertain whether it falls within crown Squilloidea (Haug et al., 2013) or on its stem;
either position would remain within the crown group of Verunipeltata.

1877

1878 51.3. Age justification

1879

The holotype of *U. yehoachi* was collected from a chert bank in the Chert Member of the Mishash Formation, near the city of Arad, Israel (Hof, 1998). The chert banks are within the *Hoplitoplacenticeras marroti* ammonite biiozone (Reiss et al., 1986). *H. marroti* co-occurs with *Baculites* sp. (smooth) (Lehmann and Murphy, 2001), which is dated to the uppermost early Campanian. Based on a spline-fit of interbedded bentonites, the base of the Tethyan *Baculites* sp. (smooth) Zone is dated to 79.64 Ma, with a duration of 0.63 Myr (Ogg et al., 2012), thus the minimum age of *U. yehoachi* is 79.01 Ma.

1887 Soft maximum as for 26.3.

1888

## 1889 **52. Crown Peracarida**

1890

1891 This clade comprises Amphipoda (scuds/beach fleas), Isopoda (wood lice/pill bugs), Cumacea, 1892 Lophogastrida, Bochusacea, Mictacea, Mysida (opossum shrimp), Stygiomysida, Spelaeogriphacea, 1893 Tanaidacea and Thermosbaenacea, their last common ancestor and all of its descendants (Fig. 13). 1894 Monophyly has been demonstrated by phylogenetic analysis of morphology (Jones et al., 2016; 1895 Poore, 2005; Richter and Scholtz, 2001; Wills et al., 2009; Wirkner and Richter, 2010), and combined 1896 morphology and molecular data (Jenner et al., 2009). Molecular phylogenies based on ribosomal 1897 genes reject the inclusion of Mysida within Peracarida (Jenner et al., 2009; Meland and Willassen, 1898 2007; Spears et al., 2005), while Lophogastrida and Stygiomysida are removed from Mysidacea and

1899	found comfortably within Peracarida (Meland and Willassen, 2007; Meland et al., 2015). Note
1900	ribosomal genes alone are insufficient markers for deep divergences (Giribet and Ribera, 2000), so we
1901	cautiously include Mysida within Peracarida pending multilocus investigations.
1902	
1903	52.1. Fossil specimens
1904	
1905	Hesslerella shermani Schram, 1970. FMNH PE 16527, holotype, lateral view (illustrated in
1906	Wilson, 2012 and <b>Fig. 14j</b> ).
1907	
1908	52.2. Phylogenetic justification
1909	
1910	H. shermani was included in a morphological cladistic analysis by Wilson (2012). It occurred at
1911	the base of Phreatoicidea (Wilson, 2012), a position within the crown group of Isopoda and thus,
1912	crown Peracarida. Note that the assignment of our calibration fossil to crown Isopoda means that
1913	exclusion of Mysida from Peracarida (Jenner et al., 2009; Meland and Willassen, 2007; Spears et al.,
1914	2005) will not change the date assessed for Peracarida.
1915	
1916	52.3. Age justification
1917	
1918	As for 31.3.
1919	
1920	52.4. Discussion
1921	
1922	Pygocephalomorpha is a eumalacostracan fossil clade with a number of symplesiomorphic
1923	characters. Pygocephalomorpha were proposed as members of Peracarida; however, a recent
1924	phylogeny depicted them in a polytomy in any of three positions: sister to Mysidacea (Mysida +
	74
	17

Lophogastrida), sister to all non-Mysidacea peracarids, or on the peracarid stem lineage (Jones et al.,
2016). Note also the molecular analyses discussed above that exclude Mysida from Peracarida (e.g.
Jenner et al., 2009), which would mean two of three equally parsimonious positions for
Pygocephalomorpha may be outside the peracarid crown group. If Pygocephalomorpha were shown
to be more likely within the crown group of Peracarida (e.g. as sister to non-mysid peracarids), one
species in this clade, *Tealliocaris walloniensis* Gueriau et al., 2014, would become the oldest peracarid
(from the Fammenian stage of the Devonian ~50 Myr older; Gueriau et al., 2014).

1932 Within Peracarida, several orders have putative Mesozoic calibration fossils that do not fully 1933 meet our requirements. Putative Lophogastrida fossils were described from the middle Triassic Falang 1934 Formation of China (Taylor et al., 2001) and Grès à Voltzia, France (Bill, 1914). These were attributed 1935 to the extant family Eucopiidae (Taylor et al., 2001), although they resolved outside crown 1936 Lophogastrida in an older phylogeny including only the French species (Taylor et al., 1998). Putative 1937 Mysida were described from the Late Jurassic Solnhofen Plattenkalk of Germany, but are poorly 1938 preserved (Schram, 1986). Fossils separately attributed to each of Lophogastrida and Mysida have 1939 also been described from the Middle Jurassic La Voulte-sur-Rhône of France (Secrétan and Riou, 1940 1986). Other fossils noted as "mysidaceans" have been mentioned, but not yet described, from the 1941 middle Triassic Luoping Biota of China (Feldmann et al., 2015; Hu et al., 2010). None of these fossils 1942 have been evaluated in the context of molecular discoveries, i.e. they assume a sister relationship 1943 between Mysida and Lophogastrida. Therefore, none can be used as calibrations until their 1944 relationships with respect to potential polyphyletic Mysidacea have been assessed. 1945 Fossils allied to Spelaeogriphacea have been described from the Cretaceous Yixian Formation 1946 of China (Shen et al., 1998; section 60.3 for revised stratigraphy) and Las Hoyas of Spain (Jaume et al., 2013). However, poor preservation of diagnostic characters indicates these are stem 1947

1948 spelaeogriphaceans (Jaume et al., 2013).

1949Although several Mesozoic fossils have been assigned to Amphipoda, none have sufficient or1950accurate morphological placement (Starr et al., 2016; Vonk and Schram, 2007). Thus no known

1951 Mesozoic fossil qualifies as a crown group amphipod.

# **53. Crown Isopoda**

1955	This clade comprises Asellota, Phoratopodidea, Cymothoida, Microcereberidea, Limnoridea,
1956	Sphaeromatidea, Valvifera, Oniscidea (wood lice/pill bugs), Phreatoicidea, Calabozoidea and
1957	Tainisopidea, their last common ancestor and all of its descendants (Fig. 13). The list of isopod
1958	suborders is derived from Boyko et al. (2008). Isopod monophyly was recovered in phylogenetic
1959	analysis of four housekeeping genes (Lins et al., 2012) and of combined ribosomal genes and
1960	morphology (Wilson, 2009).
1961	
1962	53.1. Fossil specimens
1963	
1964	As for 52.1.
1965	
1966	53.2. Phylogenetic justification
1967	
1968	As for 52.2.
1969	
1970	53.3. Age justification
1971	
1972	As for 31.3.
1973	
1974	54. Crown Tanaidacea
1975	
1976	This clade comprises Apseudomorpha, Neotanaidomorpha and Tanaidomorpha, their last

1977	common ancestor and all of its descendants (Fig. 13). Phylogenetic analysis of three molecular loci
1978	demonstrated monophyly of Apseudomorpha and Tanaidomorpha; Neotanaidomorpha could not be
1979	included (Drumm, 2010). More expansive outgroup sampling (without Neotanaidomorpha) did not
1980	recover monophyletic Tanaidacea with ribosomal and morphological data (Wilson, 2009). However, a
1981	nuclear ribosomal analysis including Neotanaidomorpha supported monophyly (Kakui et al., 2011).
1982	
1983	54.1. Fossil specimens
1984	
1985	Alavatanais carabe Vonk and Schram, 2007. MCNA 9537, holotype in amber, male (Fig. 14I).
1986	For additional morphological details, we also refer to MCNA 9846a and MCNA 13888 (Fig. 14m), both
1987	males.
1988	
1989	54.2. Phylogenetic justification
1990	
1991	Spanish amber tanaids were originally misidentified as amphipods (Alonso et al., 2000). The
1992	fossils were placed in a new family, Alavatanaidae, part of the superfamily Paratanaoidea within
1993	Tanaidomorpha (Sánchez-García et al., 2015; Vonk and Schram, 2007). Characters supporting affinity
1994	within Tanaidomorpha include the presence of an articulated ischium, articulation of the last two
1995	pleopods (may be reduced in males), and seven or fewer antennal articles (Sánchez-García et al.,
1996	2015).
1997	
1998	54.3. Age justification
1999	
2000	Amber inclusions bearing arthropod fossils were discovered from the Peñacerrada I outcrop,
2001	Basque-Cantabrian Basin, Álava, Spain (Alonso et al., 2000; Peñalver and Delclòs, 2010). The
2002	Peñacerrada I outcrop itself is divided into three intervals, with the lowest bearing the amber (Barrón

et al., 2015). Earlier palynological study assigned Peñacerrada I to the Escucha Formation, in the late Aptian (Barrón et al., 2001). Recent restudy, however, amended this outcrop to the Utrillas Group (Barrón et al., 2015). The presence of marine palynomorphs characterized by *Chichaouadinium vestitum* and *Palaeohystrichophora infusorioides*, and the terrestrial *Distaltriangulisporites mutabilis* and *Senectotetradites varireticulatus* together constrain a late Albian age for the Peñacerrada I (Barrón et al., 2015). The upper boundary of the Albian stage is 100.5 Ma  $\pm$  0.4 Myr (Ogg et al., 2012), providing a minimum estimate for Álava amber fossils at 100.1 Ma.

- 2010 Soft maximum as for 26.3.
- 2011

# 2012 **55. Crown Eucarida**

2013

2014 This clade comprises Euphausiacea (krill) and Decapoda (crabs, shrimp, lobsters), their last 2015 common ancestor and all of its descendants (Fig. 13). Monophyly of Euphausiacea and Decapoda is 2016 supported by phylogenetic analysis of transcriptomes (von Reumont et al., 2012), ribosomal genes 2017 (Spears et al., 2005), and combined molecular and morphological data (Jenner et al., 2009; Wills et 2018 al., 2009). Amphionidacea was represented as its own order within Eucarida based on morphology 2019 (Jenner et al., 2009; Wills et al., 2009), but recently the first molecular sequence data have become 2020 available, indicating that Amphionidacea are larval stages of Caridea (i.e. within Decapoda) (De Grave 2021 et al., 2015).

- 2022
- 2023 55.1. Fossil specimens
- 2024
- 2025 As for 49.1.
- 2026
- 2027 55.2. Phylogenetic justification
- 2028
- 78

2029 As for 49.2.
2030
2031 55.3. Age justification
2032
2033 As for 49.3.
2034
2035 56. Crown Decapoda

2036

2037 This clade comprises Dendrobranchiata (shrimp/prawns) and Pleocyemata (caridean shrimp, 2038 mud shrimp, true crabs, hermit and king crabs, lobsters, spiny lobsters, etc.), their last common 2039 ancestor and all of its descendants (Fig. 13). Decapod monophyly is established by phylogenetic 2040 analysis of protein-coding genes (Bracken et al., 2009; Bybee et al., 2011; Timm and Bracken-2041 Grissom, 2015), morphology (Legg et al., 2013; Richter and Scholtz, 2001), and combined 2042 morphology and molecular data (Jenner et al., 2009). Analyses of whole mitochondrial genomes place 2043 Euphausiacea (krill) within Decapoda (Shen et al., 2015), a result congruent with acquisition of a 2044 nauplius larval stage (though this is accepted as convergent: (Jirikowski et al., 2013; Scholtz, 2000). 2045 We apply caution in interpreting deep splits inferred from mitochondrial DNA (Simon and Hadrys, 2046 2013); hence, we accept decapod monophyly to the exclusion of krill. 2047 2048 56.1. Fossil specimens 2049 2050 As for 49.1. 2051 2052 56.2. Phylogenetic justification 2053 2054 As for 49.2.

2055	
2056	56.3. Age justification
2057	
2058	As for 49.3.
2059	
2060	57. Crown Allotriocarida
2061	
2062	This clade comprises Branchiopoda, Cephalocarida, Remipedia, and Hexapoda, their last
2063	common ancestor and all of its descendants (Fig. 15). Monophyly of this clade was proposed by a
2064	combined phylogenetic analysis of transcriptomes, nuclear protein-coding genes, and morphology
2065	(Oakley et al., 2013). As of this writing, a transcriptome remains to be sequenced for Cephalocarida.
2066	This clade is not recognized in GenBank taxonomy.
2067	
2068	57.1. Fossil specimens
2069	
2070	Rehbachiella kinnekullensis Müller, 1983. UB 644, holotype, consisting of a complete larva
2071	(Fig. 16a). This species has been extensively documented by Walossek (1993).
2072	
2073	57.2. Phylogenetic justification
2074	
2075	Recent phylogenetic analyses including R. kinnekullensis have strongly indicated a position on
2076	the branchiopod stem lineage (morphology: Legg et al., 2013; combined morphology and molecular:
2077	Oakley et al., 2013) or the cephalocarid stem lineage (morphology: Wolfe and Hegna, 2014). Either
2078	relationship (or a strict consensus position on the stem of Branchiopoda + Cephalocarida) would still
2079	be within the crown group of Allotriocarida.
2080	

2081	57.3. Age justification
2082	
2083	As for 35.3.
2084	
2085	58. Crown Branchiopoda
2086	
2087	This clade comprises Anostraca (fairy/brine shrimp), Notostraca (tadpole shrimp) and
2088	Diplostraca, their last common ancestor and all of its descendants (Fig. 15). Monophyly of this clade is
2089	established by phylogenetic analysis of protein-coding genes (Regier et al., 2010; Spears and Abele,
2090	2000), transcriptomes (von Reumont et al., 2012), morphology (Legg et al., 2013), and combined
2091	molecular and morphological data (Oakley et al., 2013).
2092	
2093	58.1. Fossil specimens
2094	
2095	Lepidocaris rhyniensis Scourfield, 1926. BMNH IN. 24493, holotype (Fig. 16b).
2096	
2097	58.2. Phylogenetic justification
2098	
2099	L. rhyniensis has been included in several phylogenetic analyses, coded from a composite of
2100	holotype and paratype material (Scourfield, 1926). With morphology only, L. rhyniensis is sister to
2101	extant Anostraca (Hegna, 2012; Legg et al., 2013); with morphology and molecular data, it is within
2102	Anostraca (Oakley et al., 2013). Therefore, it is unequivocally a crown group member of
2103	Branchiopoda.
2104	
2105	58.3. Age justification
2106	
	81

2107 Minimum as for 10.3. Soft maximum as for 26.3.

2108

2109 **58.4**. Discussion

2110

2111 R. kinnekullensis has been frequently used to polarize the evolution of Branchiopoda. Its fossils 2112 are known only from larval stages, which may confound discussions of its morphology (Wolfe and 2113 Hegna, 2014). Recent phylogenetic analyses have indicated a position on the branchiopod stem 2114 lineage (Legg et al., 2013; Oakley et al., 2013) or the cephalocarid stem lineage (Wolfe and Hegna, 2115 2014), excluded from the branchiopod crown. Nevertheless, divergence time analyses suggest 2116 Cambrian origins for crown Branchiopoda (Oakley et al., 2013), such that molecular clock estimates 2117 do not conflict with branchiopod affinities for Cambrian filter plate fossils (Harvey and Butterfield, 2008) 2118 or *R. kinnekullensis*. 2119 2120 **59. Crown Anostraca** 2121 2122 This clade comprises Artemiidae, Branchinectidae, Branchipodidae, Chirocephalidae, 2123 Parartemiidae, Streptocephalidae, Tanymastigidae and Thamnocephalidae, their last common 2124 ancestor and all of its descendants (Fig. 15). Monophyly of five sampled families is established by 2125 phylogenetic analysis of six housekeeping genes and morphology (Richter et al., 2007). Full sampling 2126 of families produced monophyletic Anostraca in an analysis of one ribosomal gene (Weekers et al., 2127 2002). 2128 2129 59.1. Fossil specimens 2130 2131 Palaeochirocephalus rasnitsyni Trussova, 1975. TsGM 7a/10303 and 9/10303, preserving male 2132 antennae, and TsGM 2/10303, preserving a female body. The holotype does not preserve any

2133 diagnostic characters for the Anostraca crown group.

2134

2135 59.2. Phylogenetic justification

2136

*P. rasnitsyni* (formerly *Chirocephalus rasnitsyni* Trussova, 1971) has not been included in a
phylogenetic analysis. Taxonomic placement of its family, Palaeochirocephalidae, implicitly relates
them to the extant family Chirocephalidae, though this family is considered *incertae sedis* by Rogers
(2013). Morphological characters (shared with Chirocephalidae) supporting this relationship include 11
thoracic appendages bearing two pre-epipodites, the nine-segmented abdomen, and the basally
separated two-segmented antennae in males (Trussova, 1971). A possible position on the stem
lineage of Chirocephalidae would therefore place *P. rasnitsyni* within the crown group of Anostraca.

2144

# 2145 59.3. Age justification

2146

2147 The type locality of *P. rasnitsyni*, briefly described by Trussova (1971), is the left bank of Daya 2148 River, upstream from Shiviya Falls, in eastern Transbaikal, Russia. This locality, within the Unda-Daya 2149 Basin, has been assigned to the Glushkovo Formation (Sinitshenkova, 2005). The age of the 2150 Glushkovo Formation is poorly constrained, suggested as Late Jurassic (Sinitsa and Starukhina, 2151 1986), Early Cretaceous (Sinitshenkova, 2005; Zherikhin et al., 1998), or perhaps at the 2152 Jurassic/Cretaceous boundary (Rasnitsyn and Quicke, 2002). However, P. rasnitsyni itself (along with 2153 palaeopteran insects such as Proameletus caudatus and Equisetum undense) correlates the 2154 Glushkovo Formation to the Baigul locality, also in Transbaikalia (Ignatov et al., 2011). The Baigul 2155 locality preserves fossil Bryokhutuliinia jurassica, one of only five known genera of Jurassic mosses 2156 (Ignatov et al., 2011). Thus Baigul can be correlated to the Ulugey Formation of Mongolia, which also 2157 preserves Bryokhutuliinia fossils (Ignatov, 1992). The Ulugey Formation, in turn, is correlated to the La 2158 Cabrúa (Sierra del Montsec, Pyrenees, Spain) locality based on the shared presence of the

2159 coleopteran genus Gobicar (Gratshev and Zherikhin, 2000; Legalov, 2010; Soriano et al., 2006). Fossil 2160 charophyte algae (Atopochara trivolvis triguetra) indicate an age of late Hauterivian-early Barremian 2161 for the freshwater deposits of La Cabrúa (Gomez et al., 2002; Martín-Closas and López-Morón, 1995). 2162 Although it has been proposed that a minimum age of the Montsec limestone may be as young as the 2163 end Maastrichtian (O'Reilly et al., 2015), recent biostratigraphic work proposes the last appearance of 2164 A. trivolvis triguetra is correlated to the Deshayesites weissi ammonite Zone at its youngest (Martín-2165 Closas et al., 2009). Revision of Tethyan ammonite dates indicates the D. weissi Zone, now the D. 2166 forbesi Zone, had an upper boundary of 125.71 Ma (Ogg et al., 2012a). This age is early Aptian, and 2167 provides a minimum for the correlated Glushkovo Formation. 2168 Soft maximum as for 26.3.

- 2169
- 2170 **59.4**. Discussion
- 2171

2172 Oakley et al. (2013) placed the Early Devonian *L. rhyniensis* in the crown group of Anostraca, 2173 having sampled extant members of Artemiidae and Streptocephalidae. Earlier descriptions (Sanders, 2174 1963; Scourfield, 1940a, 1926; Walossek, 1993) support this position. However, the most extensively 2175 sampled morphological analyses of Hegna (2012) consistently place *L. rhyniensis* as sister to all 2176 extant Anostraca. The Late Devonian *Haltinnaias serrata* Gueriau et al., 2016, described from both 2177 sexes, likely also belongs to the total group of Anostraca.

Other fossils from the Late Jurassic Daohugou Beds of China (Huang et al., 2006; Shen and Huang, 2008) and Early Cretaceous Koonwarra Formation of Australia are likely to belong to the crown group of Anostraca, as they have been included in a morphological phylogenetic analysis (Hegna, 2012), but these have not been described in detail.

2182

# 2183 **60. Crown Notostraca**

2184
2185	This clade comprises two extant genera, <i>Triops</i> and <i>Lepidurus</i> , their last common ancestor and				
2186	all of its descendants (Fig. 15). Monophyly is established by phylogenetic analysis of housekeeping				
2187	genes (Mathers et al., 2013), morphology (Lagebro et al., 2015), and combined morphological and				
2188	molecular data (Richter et al., 2007).				
2189					
2190	60.1. Fossil specimens				
2191					
2192	Chenops yixianensis Hegna and Ren, 2010. CNU-CAL-HP-2009001 (part; Fig. 16c) and CNU-				
2193	CAL-HP-2009002 (counterpart), holotype.				
2194					
2195	60.2. Phylogenetic justification				
2196					
2197	In the morphological phylogenetic analysis of Lagebro et al. (2015), C. yixianensis was in a				
2198	polytomy with other crown Notostraca, including Lepidurus batesoni. The equal size of thoracic				
2199	endopods and fourth and fifth endites may exclude C. yixianensis from crown Notostraca (Hegna and				
2200	Ren, 2010). However, in previous morphological phylogenies (Hegna, 2012), C. yixianensis was sister				
2201	taxon to the extant L. batesoni. This is because L. batesoni lacks elongated endites on the first				
2202	thoracic appendage, suggesting a synapomorphy between C. yixianensis and the extant species, and				
2203	perhaps membership in an entirely different genus (Hegna, 2012; Hegna and Ren, 2010). If indeed C.				
2204	yixianensis is, based on phylogenies and endite morphology, a sister group of L. batesoni, it would				
2205	remain within the crown Notostraca.				
2206					
2207	60.3. Age justification				
2208					
2209	This fossil was discovered in the Yixian Formation of northeastern China (Hegna and Ren,				
2210	2010). The Yixian Formation lies between the overlying Jiufotang Formation and underlying Tuchengzi				
	85				

2211 Formation; together they comprise the Jehol Group (e.g. Chang et al., 2009a; Zhou, 2006). Dating of 2212 the Jehol Group has been contentious, varying from Late Jurassic to Early Cretaceous based on 2213 biostratigraphic and radiometric techniques. Recent 40Ar/39Ar dates yielded ages of 129.7 Ma ± 0.5 2214 Myr for basaltic lava from the bottom of the Yixian Formation and 122.1 Ma  $\pm$  0.3 Myr for tuff layers at 2215 the bottom of the overlying Jiufotang Formation (Chang et al., 2009a). Other age estimates have fallen 2216 within this range (reviewed by Zhou, 2006). This debate underscores the point that reasonably precise 2217 radiometric dates may still be quite inaccurate. We conservatively use the younger of these estimates, 2218 so a minimum age for Yixian fossils is 121.8 Ma.

Soft maximum as for 26.3.

2220

2221 *60.4. Discussion* 

2222

2223 *Strudops goldenbergi* Lagebro et al., 2015 was recently described from the Late Devonian, 2224 which would be the oldest notostracan. In a morphological phylogenetic analysis, however, it could 2225 only be identified as a member of the total group (Lagebro et al., 2015), and thus cannot assign a 2226 minimum age to crown Notostraca.

Morphological conservatism (i.e. Permian and Triassic fossils erroneously attributed to the extant species *Triops cancriformis*) has led to the misleading name 'living fossil' for Notostraca (Hegna, 2012; Mathers et al., 2013). Once touted as the 'oldest living species,' *T. cancriformis permiensis*, from the Permian of France, is more similar to the co-occurring *Lepidurus occitaniacus* than extant *Triops* (Lagebro et al., 2015). Decay experiments on living *T. cancriformis* confirm that carapace characters and elongated endites of the first thoracic limb are phylogenetically meaningful, thus rejecting a referral of any fossil to the extant species (Hegna, 2012).

2234

2235 61. Crown Diplostraca

2236

2237	This clade comprises Laevicaudata, Spinicaudata, Cyclestherida (these three collectively:
2238	'clam shrimp') and Cladocera (water fleas), their last common ancestor and all of its descendants (Fig.
2239	15). Monophyly is supported by phylogenetic analysis of transcriptomes (von Reumont et al., 2012)
2240	and 62 nuclear protein-coding genes (Regier et al., 2010), and combined molecules and morphology
2241	(Oakley et al., 2013) although Cyclestherida was not sampled in these analyses. Smaller molecular
2242	analyses (Richter et al., 2007 with indel costs) and morphological analyses (Hegna, 2012; Legg et al.,
2243	2013; Olesen, 2009, 1998; Richter et al., 2007) including data for Cyclestherida also support
2244	monophyly of Diplostraca.
2245	
2246	61.1. Fossil specimens
2247	
2248	Leaia chinensis Shen, 1983. NIGP 51786, holotype, preserving a left valve (Fig. 16d).
2249	

- 2250 61.2. Phylogenetic justification
- 2251

2252 L. chinensis has not been treated in a phylogenetic context. It is placed within the fossil family 2253 Lealidae primarily based on carapace shape, including the nearly straight ventral edge (Shen, 1978; 2254 Tasch, 1987). However, congeneric fossils, L. gondwanella Tasch, 1987 and L. canadensis Shen and 2255 Schram, 2014, may have preserved soft parts (Shen and Schram, 2014). These include biramous 2256 antennae, mandibles, as well as putative shell glands and digestive tubes, and radiating carinae (Shen 2257 and Schram, 2014). The short and delicate antennal flagella and radiating carinae of L. chinensis, in 2258 particular, are similar to extant Spinicaudata and Cyclestherida; the presence of growth lines is only 2259 known from Spinicaudata (Shen and Schram, 2014). However, the head shape of L. chinensis is more 2260 similar to Laevicaudata. This suggests phylogenetic positions either on the stem of Onychocaudata 2261 (Spinicaudata, Cyclestherida, and Cladocera) or on the stem of Laevicaudata. A position as stem 2262 Diplostraca would mean growth lines are ancestral for all diplostracans, and have been lost twice (in

the ancestors of Laevicaudata and Cyclestherida + Cladocera), which is unparsimonious. Hence we
 support *L. chinensis* within crown Diplostraca.

2265

2266 61.3. Age justification

2267

2268 L. chinensis was found in sediments of the Guitou Group, near Chengma village, Hepu county, 2269 Guangxi Zhuang Autonomous Region, southern China (Shen, 1978). The upper subgroup of the 2270 Guitou Group, bearing conchostracan fossils, has purple-grey sandy shales within mudstone 2271 lamination, and is overlain by the Tungkangling Formation (Shen, 1978). The brachiopod 2272 Stringocephalus, the stromatoporoid corals Endophyllum and Sunophyllum, and the ostracods 2273 Samarella crassa and Tuberokloedenia bituberculata together indicate a Givetian age for the upper 2274 Tungkangling Formation (Liao and Ruan, 2003). The underlying Yingtang Formation (as well as the 2275 lower Tungkangling Formation) are correlated to the Eifelian Stage by the ostracods Bairdocypris 2276 biesenbachi and Flatiella subtrapezoidalis (Liao and Ruan, 2003), the brachiopod Bornhardtina and 2277 the conodonts Polygnathus australis, P. costatus, and P. partitus (Ma et al., 2009). As the 2278 conchostracan-bearing sediments underlie the Tungkangling Formation, they are no younger than 2279 Eifelian in age. The upper boundary of the Eifelian is  $387.7 \text{ Ma} \pm 0.8 \text{ Myr}$ , providing a minimum age of 2280 386.9 Ma.

Soft maximum as for 26.3.

2282

# 2283 **62. Crown Spinicaudata**

2284

This clade comprises Leptestheriidae, Cyzicidae and Limnadiidae, their last common ancestor and all of its descendants (**Fig. 15**). Clade names are defined in Schwentner et al. (2009). Monophyly is established by phylogenetic analysis of morphology (Hegna, 2012; Olesen, 1998; Richter et al., 2007), three housekeeping genes (Schwentner et al., 2009), and six housekeeping genes plus

2289	morphology (Richter et al., 2007).
2290	
2291	62.1. Fossil specimens
2292	
2293	Dundgobiestheria mandalgobiensis Li et al., 2014. ED-A-14-1, holotype (Fig. 16e).
2294	
2295	62.2. Phylogenetic justification
2296	
2297	Phylogenetic analysis of spinicaudatan fossils is rare, owing to difficulty in character
2298	identification (Astrop and Hegna, 2015; see also 62.3). Members of Leptestheriidae appear to share
2299	emergence of dendritic reticulation and anastomizing ridge ornamentation with the fossil spinicaudatan
2300	family Loxomegaglyptidae (Astrop and Hegna, 2015; Shen, 1994). D. mandalgobiensis is perhaps the
2301	oldest definitive Loxomegaglyptidae, based on large-sized reticulate ornamentation and weakly
2302	defined growth lines, shared with other members of the family (Li et al., 2014). Due to the above
2303	ornamentation characters (Astrop and Hegna, 2015; T. Astrop, pers. comm.), it can be placed on the
2304	stem lineage of Leptestheriidae, and thus within crown Spinicaudata.
2305	
2306	62.3. Age justification
2307	
2308	D. mandalgobiensis is from the Eedemt Formation, Khootiin Khotgor coal mine region,
2309	Dundgobi Province, southeast Mongolia (Li et al., 2014). The spinicaudatan genus Triglypta (co-
2310	occurring with D. mandalgobiensis) provides a biostratigraphic constraint on the Eedemt Formation, as
2311	Triglypta species also occur in both the (older) Euestheria ziliujingensis fauna and (younger)
2312	Sinokontikia fauna in lacustrine sequences of northwestern China (Li et al., 2014; Li and Matsuoka,
2313	2012). First, the E. ziliujingensis fauna is distributed throughout east Asia, dated to a Bajocian-
2314	Bathonian (Jurassic) age by the occurrence of Euestheria trotternishensis (Chen et al., 2007). E.

2315 trotternishensis co-occurs in the Skyestheria spinicaudatan fauna of Skye, Scotland; the Bajocian-2316 Bathonian date for this locality comes from ammonite and palynological index fossils (Chen and 2317 Hudson, 1991). Although the Sinokontikia fauna was once thought stratigraphically equal to the late E. 2318 ziliujingensis fauna (Chen et al., 2007; Li and Matsuoka, 2012), Sinokontikia has been determined to 2319 be younger based on occurrence in the Qiketai Formation of the Turpan Basin, northwest China. The 2320 Qiketai Formation is constrained only to the Callovian. As Chinese Triglypta (the index genus for the 2321 Eedemt Formation) is absent from any higher strata, a minimum age comes from the upper boundary 2322 of the Sinokontikia fauna (Li et al., 2014). The upper boundary of the Callovian is 163.5 Ma ± 1.0 Myr. 2323 giving a minimum age for the Eedemt Formation of 162.5 Ma.

Soft maximum as for 26.3.

2325

# 2326 **62.4**. Discussion

2327

2328 Preservation of the calcified spinicaudatan carapace is extremely common (some fossil species are used as biostratigraphic indices), but characters diagnostic for extant taxa (i.e. soft parts) are 2329 2330 rarely preserved (Hegna, 2012; Orr and Briggs, 1999). Uniquely among 'conchostracans' (and indeed 2331 most arthropods), Spinicaudata do not moult their carapace, instead preserving growth lines. The 2332 number of growth lines necessarily increases through ontogeny, so it is a poor character to 2333 demonstrate phylogenetic relationships. Therefore relationships among fossil taxa have been 2334 determined based on ornamentation of the carapace (e.g. Gallego, 2010); however, these characters 2335 have not yet been integrated with morphological study of extant carapaces. Ongoing work seeks to 2336 demonstrate the utility of carapace ornamentation as valid phylogenetic characters (Astrop and 2337 Hegna, 2015). Furthermore, integration of past descriptive work is hindered by language barriers 2338 between different workers (Chinese, Russian, and English; summarized by Astrop and Hegna, 2015). 2339 For example, some poorly known fossils from the Middle Devonian of Antarctica, described as 2340 members of the genus Cyzicus (Euestheria), may be assigned to Spinicaudata (Tasch, 1987), possibly

2341 on the stem lineage of 'non-Australian Cyzicidae' sensu Schwentner et al. (2009). Characters linking 2342 the Antarctic fossils to the living clade, however, are dubious. There are reports of uncertain Late 2343 Devonian stem group members for Limnadiidae (Liu and Gao, 1985), and much more likely Permian 2344 stem Limnadiidae (Novojilov, 1970), but these fossils are insufficiently described, leaving any specific 2345 crown spinicaudatan character states debatable. Therefore we must caution that Jurassic age is likely 2346 a severe underestimate of crown spinicaudatan antiquity. Finally, the Sinemurian Afrolimnadia 2347 sibiriensis Tasch, 1987 was used to calibrate crown Spinicaudata in a divergence time analysis, but 2348 with limited justification of characters for Limnadiidae (Bellec and Rabet, 2016).

2349

#### 2350 63. Crown Cladocera

2351

This clade comprises Anomopoda, Ctenopoda, Onychopoda and Haplopoda, their last common ancestor and all of its descendants (**Fig. 15**). Monophyly of this clade is supported by phylogenetic analysis of housekeeping genes alone (Stenderup et al., 2006), morphology (Hegna, 2012; Olesen, 2009, 2007, 1998), and six housekeeping genes plus morphology (Richter et al., 2007).

2357 63.1. Fossil specimens

2358

2359 *Smirnovidaphnia smirnovi* Kotov, 2007, illustrated by two specimens: PIN 1873/100 (holotype, 2360 preserving the second antenna; **Fig. 16f**) and PIN 1873/105 (paratype, preserving both second 2361 antennae and mandibles).

2362

2363 63.2. Phylogenetic justification

2364

The setal armature of the second antenna is similar to that found in extant Ctenopoda (Kotov,
2007). In morphological phylogenetic analyses, *S. smirnovi* was either found in a basal polytomy with

2367	all of crown Cladocera, or it was sister to all Cladocera except Anomopoda (Hegna, 2012). The
2368	polytomy could indicate a stem cladoceran position, but the analyses in which S. smirnovi was within
2369	crown Cladocera included a lesser amount of missing data, and thus may be more robust.
2370	Furthermore, Ctenopoda itself was not recovered as monophyletic in these analyses, but S. smirnovi
2371	was related to taxa that have been previously included in Ctenopoda (Hegna, 2012).
2372	
2373	63.3. Age justification
2374	
2375	S. smirnovi was found on the right bank of the Angara River, downstream of Ust'-Baley village
2376	in the Olonkovsky District of Asian Russia (Kotov, 2007). According to the presence of
2377	Osmundacidites-type plant spores, the Ust'-Baley outcrop of the Cheremkhovo or Cheremkhovskaya
2378	Formation is correlated to the late Toarcian stage of the Early Jurassic (Akulov et al., 2015). The upper
2379	boundary of the Toarcian is 174.1 Ma $\pm$ 1.0 Myr, therefore giving a minimum age of 173.1 Ma.
2380	Soft maximum as for 26.3.
2381	
2382	63.4. Discussion
2383	
2384	Ebullitiocaris oviformis Anderson et al., 2003 from the Devonian Rhynie Chert and E. elatus
2385	Womack et al., 2012 from Carboniferous chert have both been described as Cladocera.
2386	Fragmentation patterns of both fossils are inconsistent with those observed from decay experiments,
2387	therefore casting doubt on their cladoceran membership (Hegna, 2012).
2388	Other Jurassic/Cretaceous members of the fossil family Prochydoridae are known from
2389	Mongolia and Asian Russia (Kotov, 2009). However, the Prochydoridae have been proposed as a
2390	member of the stem lineage of Anomopoda, the stem of all non-Anomopoda Cladocera, as well as the
2391	stem of Cladocera itself (Kotov, 2013, 2009). Thus crown-group affinity cannot be confirmed.
2392	

2393	64.	Crown	Hexapoda
-070		•••••••	

2395 This clade comprises Collembola (springtails), Protura (cone heads), Diplura (two-pronged 2396 bristletails) and Insecta (insects), their last common ancestor and all of its descendants (Fig. 17). 2397 Monophyly of Hexapoda is established by phylogenetic analysis of nuclear protein-coding genes 2398 (Regier et al., 2010, 2005; Sasaki et al., 2013), transcriptomes (Dell'Ampio et al., 2014; Misof et al., 2399 2014), and morphology (Legg et al., 2013). 2400 2401 64.1. Fossil specimens 2402 2403 Rhyniella praecursor Hirst and Maulik, 1926. NHMUK IN. 27765, lectotype (fide Ross and York, 2404 2003), head capsule with mouthparts in chert (Fig. 2f). Paralectyotypes NHMUK IN. 38225-38227.

2405

2406 64.2. Phylogenetic justification

2407

2408 The Rhynie Chert taxon *R. praecursor* Hirst and Maulik, 1926, was originally identified as an 2409 insect. Re-identification as a poduromorph collembolan was made by Tillyard (1928). Additional 2410 material was examined by Scourfield (1940a, 1940b), who considered R. praecursor to be a possible 2411 entomobryomorph rather than a poduromorph. Subsequent studies, including some additional 2412 specimens, were made by Massoud (1967), Whalley and Jarzembowski (1981), Greenslade (1988), 2413 and Greenslade and Whalley (1986). The most recent of these investigations favour membership of at 2414 least some specimens assigned to R. praecursor in the extant entomobryomorph family Isotomidae 2415 (Greenslade and Whalley, 1986). Greenslade (1988) indicated that three species could be 2416 represented in the sample that is currently assigned to *R. praecursor*. Identification as an 2417 entomobryomorph underpins an assignment to the crown groups of Collembola and Hexapoda. Other 2418 taxa from the Rhynie Chert (Rhyniognatha and Leverhulmia; Engel and Grimaldi, 2004; Fayers and

2419	Trewin, 2005) and thus as old as <i>R. praecursor</i> have also been identified as Hexapoda, and more				
2420	precisely as Insecta.				
2421					
2422	64.3. Age justification				
2423					
2424	As for 58.3.				
2425					
2426	65. Crown Collembola				
2427					
2428	This clade comprises Entomobryomorpha, Neelipleona, Poduromorpha, Symphypleona and				
2429	Tomoceroidea, their last common ancestor and all of its descendants (Fig. 17). Most studies with				
2430	substantial outgroup sampling are based on only one or two subclades of Collembola; however,				
2431	phylogenetic analysis of ribosomal genes including all subclades (Gao et al., 2008; Xiong et al., 2008)				
2432	demonstrated monophyly. Additional support with limited sampling of Collembola subclades comes				
2433	from transcriptomes (Dell'Ampio et al., 2014), mitochondrial genomes (Carapelli et al., 2007), and				
2434	morphology (D'Haese, 2003).				
2435					
2436	65.1. Fossil specimens				
2437					
2438	As for 64.1.				
2439					
2440	65.2. Phylogenetic justification				
2441					
2442	As for 64.2.				
2443					
2444	65.3. Age justification				
	94				

2445	
2446	As for 58.3.
2447	
2448	66. Crown Diplura
2449	
2450	This clade comprises Projapygoidea, Japygoidea and Campodeoidea, their last common
2451	ancestor and all of its descendants (Fig. 17). Monophyly of Diplura has been demonstrated by
2452	phylogenetic analysis of ribosomal genes (Gao et al., 2008), whole mitochondrial genomes (Chen et
2453	al., 2014), and morphology (Koch, 1997).
2454	
2455	66.1. Fossil specimens
2456	
2457	Ferrojapyx vivax Wilson and Martill, 2001. SMNS 64276, holotype.
2458	
2459	66.2. Phylogenetic justification
2460	
2461	F. vivax is "morphologically indistinguishable" (Wilson and Martill, 2001) from extant
2462	Japygoidea, sharing characters such as 40-segmented antennules, abdominal tergites 1-8 with a
2463	median suture, abdominal tergite 9 significantly shorter, conical abdominal styli, and forcipate cerci
2464	with curved inner margins and lacking obvious denticles (Wilson and Martill, 2001). Monophyly of
2465	Japygoidea has been considered "beyond doubt" (Koch, 2009; Fig. 3 therein for cladogram), so a
2466	phylogenetic position for this fossil either within or closely related to that clade would place it within
2467	crown Diplura.
2468	
2469	66.3. Age justification
2470	
	95

2471 As for 29.3. 2472 2473 67. Crown Insecta 2474 2475 This clade comprises Microcoryphia (jumping bristletails), Zygentoma (silverfish) and Pterygota 2476 (winged insects), their last common ancestor and all of its descendants (Fig. 17). Monophyly is 2477 established by phylogenetic analysis of nuclear protein-coding genes (Regier et al., 2010, 2005; 2478 Sasaki et al., 2013), transcriptomes (Dell'Ampio et al., 2014; Misof et al., 2014), and morphology 2479 (Legg et al., 2013). 2480 2481 67.1. Fossil specimens 2482 2483 Rhyniognatha hirsti Tillyard, 1928. BMNH IN. 38234, holotype, preserving the mandibles and 2484 their articulation (Fig. 18d). Redescribed and imaged by Engel and Grimaldi (2004). 2485 2486 67.2. Phylogenetic justification 2487 2488 The only known specimen (the holotype) of R. hirsti demonstrates that the preserved pair of 2489 mandibles articulate at two points, i.e. are dicondylic (Engel and Grimaldi, 2004). Dicondylic mandibles 2490 are a diagnostic synapomorphy of Insecta (including Microcoryphia; Blanke et al., 2015). Although R. 2491 hirsti has not been included in numerical phylogenetic analyses, its mandibular shape implies 2492 "metapterygote" affinities (Engel and Grimaldi, 2004) and accordingly crown group membership within 2493 Insecta. 2494 2495 67.3. Age justification 2496

2497 As for 58.3.

2498

2499 **67.4**. Discussion

2500

A complete body fossil of a putative insect, *Strudiella devonica* Garrouste et al., 2012, was described from the Fammenian (372-359 Ma) of Strud, Belgium. Apomorphies supporting an insect affinity (such as the structure of the mandibles and the number of legs), however, are poorly preserved and potentially over-interpreted (Hörnschemever et al., 2013).

2505

#### 2506 **68. Crown Microcoryphia**

2507

2508 This clade comprises the families 'Machilidae' and Meinertillidae, their last common ancestor, 2509 and all of its descendants (Fig. 17). This clade is commonly referred to as Microcoryphia in taxonomic 2510 literature and Archaeognatha in phylogenetic literature (Gaju-Richart et al., 2015). Recently it was clarified that Archaeognatha includes the completely extinct order Monura (compound eyes not fused, 2511 2512 paracercus only) and Microcoryphia (very small head vertex due to their fused compound eyes, 2513 terminalia composed of a median paracercus and two lateral cerci), and thus the crown group refers to 2514 Microcoryphia only (Gaju-Ricart et al., 2015). Monophyly is supported by phylogenetic analysis of 2515 transcriptomes (Misof et al., 2014), nuclear protein-coding genes (Regier et al., 2010), and 2516 morphology (Legg et al., 2013). Synapomorphies are discussed and mapped on cladograms by Larink 2517 (1997) and Koch (2003). 2518 2519 68.1. Fossil specimens 2520 2521 Cretaceomachilis libanensis Sturm and Poinar, 1998 (collection Milki No. 194/35, deposited at

the American University of Beirut, Beirut, Lebanon), holotype, male in amber (**Fig. 18b**).

# 2524 68.2. Phylogenetic justification

2525

*C. libanensis* shares morphological characters with the extant family Meinertillidae. These
include the the absence of scales on the scapus, pedicellus and flagellum, and the presence of a
characteristic hook near the distal end of article 2 of the male maxillary palp (Sturm and Poinar, 1998).
The latter character is a synapomorphy of crown Meinertillidae (Sturm and Poinar, 1998), therefore the
fossil is within crown Microcoryphia.

2531

2532 68.3. Age justification

2533

*C. libanensis* was discovered in Cretaceous amber, from a locality in Lebanon that was not recorded (Sturm and Poinar, 1998). We therefore use a minimum age constraint from the youngest of the several known Lebanese amber localities, which all bear the same age within the early Barremian (Maksoud et al., 2016). The upper boundary of the early Barremian is proposed to be the first appearance of the ammonite *Ancyloceras vandenheckii* (Ogg et al., 2012). Cyclostratigraphy dates the *A. vandenheckii* Zone beginning at 129.41 Ma (Ogg et al., 2012), providing a minimum age for Jezzine Lebanese amber fossils.

- 2541 Soft maximum as for 26.3.
- 2542

2543 **68.4**. Discussion

2544

Body imprint and trackway trace fossils from the Pennsylvanian have been attributed to both Archaeognatha and Zygentoma (Getty et al., 2013). Experiments with extant species of both clades indicate that archaeognathans produced fossil body imprints, as well as trackways exhibiting opposite symmetry (Getty et al., 2013). However, it is not possible to distinguish specific crown group apomorphies for these traces.

2550 Dasyleptidae, a diverse fossil group known from the Carboniferous-Triassic, has been 2551 proposed as the sister group of Ectognatha (Collembola, Diplura, Protura) as well as part of 2552 Archaeognatha. Recent classifications place Dasyleptidae in Monura, a separate extinct suborder of 2553 Archaeognatha, and thus outside its crown group (Bechly and Stockar, 2011; Gaju-Ricart et al., 2015). 2554 2555 69. Crown Zygentoma 2556 2557 This clade comprises the families Lepismatidae, Nicoletiidae, Lepidotrichidae, Maindroniidae, 2558 and Protrinemuridae, their last common ancestor and all of its descendants (Fig. 17). Phylogenetic 2559 analyses of transcriptomes (Misof et al., 2014), protein-coding genes (Regier et al., 2010; Sasaki et 2560 al., 2013), morphology (Blanke et al., 2014), and combined molecular and morphological data (Kjer et 2561 al., 2006) with partial taxon sampling support monophyly. 2562 2563 69.1. Fossil specimens 2564 2565 Burmalepisma cretacicum Mendes and Poinar, 2008 (specimen B-TH-1 deposited in the Poinar 2566 amber collection maintained at Oregon State University; B-TH refers to Burma-Thysanura), holotype, a 2567 female in amber (Fig. 18c). 2568 2569 69.2. Phylogenetic justification 2570 2571 Although it has not been included in a phylogenetic analysis, *B. cretacicum* bears several 2572 morphological similarities to the extant family Lepismatidae. These include the presence of compound 2573 eyes, absence of ocelli, coxal, femur, and tarsal morphology, absence of a pronotal setal collar, and 2574 presence of only smooth macrochaetae (Mendes and Poinar, 2008). A phylogenetic position either on

2575	the stem or within the crown of Lepismatidae is within the crown group of Zygentoma.				
2576					
2577	69.3. Age justification				
2578					
2579	As for 33.3.				
2580					
2581	69.4 Discussion				
2582					
2583	A possible Zygentoma fossil has been recorded from the older Aptian Crato Formation of Brazil				
2584	(Sturm, 1998), but is not sufficiently characterized to be a calibration fossil. Another fossil from				
2585	Burmese amber, Cretolepisma kachinicum Mendes and Wunderlich, 2013, is also identified as				
2586	Lepismatidae. This fossil is of equal age and affinity, and is therefore also an acceptable calibration for				
2587	Zygentoma.				
2588					
2589	70. Crown Pterygota				
2590					
2591	This clade comprises Palaeoptera (mayflies, dragonflies) and Neoptera (flexible winged				
2592	insects), their last common ancestor and all of its descendants (Fig. 17). Monophyly is established				
2593	based on phylogenetic analysis of nuclear protein-coding genes (Regier et al., 2010, 2005; Sasaki et				
2594	al., 2013), transcriptomes (Misof et al., 2014; Simon et al., 2012), and morphology (Legg et al., 2013).				
2595					
2596	70.1. Fossil specimens				
2597					
2598	Delitzschala bitterfeldensis Brauckmann and Schneider, 1996 (BGR X 9216), holotype,				
2599	preserving a forewing, a hindwing, cerci, and part of the abdomen (Fig. 18a).				
2600					
	100				

2601 70.2. Phylogenetic justification

2602

2603 D. bitterfeldensis is considered a member of the family Spilapteridae, in the clade 2604 Palaeodictyopterida (Brauckmann and Schneider, 1996). Morphological characters supporting this 2605 relationship include the concave anterior wing margin and deeply bifurcate MA vein ending with two 2606 long branches (Brauckmann and Schneider, 1996; Li et al., 2013b). Other fossils of Spilapteridae have 2607 also preserved the distinctive colour patterns and long cerci observed in D. bitterfeldensis (Li et al., 2608 2013b). Palaeodictyoptera have previously assumed to be related to extant Palaeoptera as they share 2609 the inability to fold their wings over the abdomen (a character observed in *D. bitterfeldensis*). However, 2610 a recent morphological phylogenetic analysis controversially recognized Palaeodictyopterida as the 2611 fossil sister group of Neoptera (Sroka et al., 2015). In this evolutionary scenario, palaeopterous wings 2612 are presumably a symplesiomorphy. Nonetheless, the position of Palaeodictyoptera suggested by 2613 Sroka et al. (2015) remains within crown Pterygota.

2614

2615 70.3. Age justification

2616

*D. bitterfeldensis* was preserved in a core extracted from the locality Bore WISABAW 1315, in the Sandersdorf Formation of Bitterfeld, Germany (Brauckmann and Schneider, 1996). The core was correlated with the E2 ammonite zone, i.e. Arnsbergian (middle Namurian A) based on the cooccurrence of ostracods and conchostracans (Brauckmann et al., 1994). The Arnsbergian is further correlated to the late Serpukhovian stage at the end of the Mississippian (Pointon et al., 2012). The upper boundary of the Serpukhovian (base of the Pennsylvanian) is estimated at 323.23 Ma  $\pm$  0.4 Myr (Davydov et al., 2012), giving a minimum age of 322.83 Ma.

Soft maximum as for 26.3.

2625

2626 70.4. Discussion

An undescribed Namurian A (latest Mississippian) member of Archaeorthoptera was initially attributed to Orthoptera (Prokop et al., 2005). It was noted that the veins are strongly deformed, enough so that the authors were reluctant to make a formal systematic description (Prokop et al., 2005). Therefore, we regard the fossil as insufficiently characterized for dating. See section 67.4 for refutation of the even older *Strudiella devonica* (Garrouste et al., 2012).

2633

# 2634 **71. Crown Palaeoptera**

2635

2636 This clade comprises Euplectoptera (mayflies) and Odonata (dragonflies), their last common 2637 ancestor and all of its descendants (Fig. 17). Monophyly of this group has been challenged by 2638 morphology (Kristensen 1981) and some transcriptome data (Simon et al., 2012, 2009), though recent 2639 analyses of nuclear protein-coding genes (Regier et al., 2010) and transcriptomes have supported 2640 Palaeoptera (Misof et al., 2014; von Reumont et al., 2012), the former weakly, only in maximum 2641 likelihood analyses of the total dataset. Recent detailed morphological analyses of head morphology 2642 corroborate the monophyly of Palaeoptera (Blanke et al., 2013, 2012). Although a morphological 2643 phylogenetic analysis (Sroka et al., 2015) claims to reject palaeopteran monophyly, its constituent 2644 extant members, Euplectoptera and Odonata, are each others' closest living relative and named 2645 therein as a new clade, Euhydropalaeoptera. We therefore cautiously endorse Palaeoptera as a clade 2646 of interest for dating.

2647

2648 71.1. Fossil specimens

2649

2650 Oligotypus huangheensis Li et al., 2013a (CNU-NX2006003), holotype, a forewing.

2651

2652 71.2. Phylogenetic justification

2654 This species was originally described as *Sinomeganeura huangheensis* within the family 2655 Meganeuridae, part of Protodonata (Ren et al., 2008). Meganeurids include the "giant" dragonflies 2656 (with wings up to 710 mm), though O. huangheensis is much smaller at 70 mm (Ren et al., 2008). 2657 Despite the size difference, wing venation characters are consistent with classification in Protodonata, 2658 including the fusion of stems of CuP and CuA to a single obligue vein, distinctly stronger than the crossveins (Ren et al., 2008). This character, previously assumed to be synapomorphic for 2659 2660 Meganeuridae, is more widespread within Protodonata (Li et al., 2013a). The group "Protodonata" 2661 itself is a paraphyletic stem group to crown Odonata, together within the total group Odonatoptera, 2662 defined by the simple MP vein (Sroka et al., 2015). Regardless of the precise relationship of 2663 Protodonata to crown Odonata, its members are definitively within crown Palaeoptera. 2664 2665 71.3. Age justification

2666

2667 The insect beds where this species was located are near Xiaheyan Village in the Qilianshan 2668 Mountains, Zhongwei County, Ningxia Huizu Autonomous Region, northwest China (Zhang et al., 2669 2013). The insect fossil deposits are within the uppermost unit of the upper Tupo Formation 2670 (synonyms Hongtuwa or Zhongwei Formation). The presence of the ammonoids Reticuloceras 2671 reticulatum, Gastrioceras listeri and G. montgomervense and conodonts Declingnathodus noduliferous 2672 and Neognathodus symmetricus indicate a Namurian B/C age (Xie et al., 2004; Yang, 1987; Yang et 2673 al., 1988; Zhang et al., 2013). The (late) Namurian-(early) Westphalian boundary is defined by the 2674 earliest occurrence of the goniatite Gastrioceras subcrenatum (Waters and Davies, 2006), but lacks a 2675 precise isotopic date. Pointon et al. (2012) estimated an age of c. 319.9 Ma for the base of the 2676 Westphalian (top of the Namurian, only slightly younger than the Marsdenian) based on Milankovitch 2677 cycles of sedimentation, giving a minimum age for Xiaheyan fossils. 2678 Soft maximum as for 26.3.

### 2680 71.4. Discussion

2681

Due to the controversial status of Palaeoptera as a clade, there are several fossil groups that have been considered for membership: Palaeodictyopterida, Paoliida, stem mayflies (Ephemeroptera, see section 72), and stem dragonflies (Protodonata, including Geroptera) (Grimaldi and Engel, 2005). Each is discussed below.

2686 Palaeodictyopterida, an abundant clade from the Carboniferous and Permian, have been 2687 assumed to be related to extant Palaeoptera as they share the inability to fold their wings over the 2688 abdomen. The oldest member, Delitzschala bitterfeldensis, predates all other Palaeoptera (and all 2689 other Pterygota with preserved wings), as it is from the Mississippian (Brauckmann et al., 1994; 2690 Pointon et al., 2012). In cladodograms in which Palaeodictyopterida is the fossil sister group of 2691 Neoptera (Sroka et al., 2015), palaeopterous wings are presumably a symplesiomorphy. The presence 2692 of nymphal wing pads is probably also a symplesiomorphy of Pterygota (Haug et al., 2016). Therefore 2693 Palaeodictyopterida may be outside the crown and even stem group of Palaeoptera.

Paoliida is an extinct clade known mainly from wings of the Westphalian A stage of the Pennsylvanian. The group has been attributed to the Palaeodictyoptera and later removed (Prokop et al., 2012; Prokop and Nel, 2007). It has been subsequently proposed that Paoliida is the fossil sister group of Dictyoptera (Prokop et al., 2014), and thus are within crown Polyneoptera. This would refute a relationship with Palaeoptera or any of its members.

A full body impression of a putative Carboniferous (Westphalian B/C) mayfly is subject to controversy (Benner et al., 2013; Knecht et al., 2011; Marden, 2013a, 2013b). *Bojophlebia prokopi* Kukalová-Peck, 1985 (Westphalian C) is likely outside of Palaeoptera, according to descriptions and phylogenetic analysis (Prokop et al., 2010; Sroka et al., 2015; Staniczek et al., 2011). The Stephanian B/C fossil *Triplosoba pulchella* Brongniart, 1883, originally described as a mayfly, has been redescribed as Palaeodictyopterida (Prokop and Nel, 2009). The oldest body fossils belonging to the

2705 mayfly stem group are therefore members of the Syntonopteroidea. The oldest Syntonopteroidea are 2706 Lithoneura lameerei Carpenter, 1938 and Syntonoptera schucherti Handlirsch, 1911, from the 2707 Westphalian D Mazon Creek (younger than Xiaheyan) (Nicholson et al., 2015; Prokop et al., 2010). 2708 Putative older members of Odonatoptera are Geroptera, represented by the species 2709 Eugeropteron lunatum and Geropteron arcuatum (both Riek and Kukalová-Peck, 1984), are known 2710 from the late Namurian of Argentina (Gutiérrez et al., 2000; Riek and Kukalová-Peck, 1984). G. 2711 arcuatum was included in a morphological phylogenetic analysis, but was resolved outside 2712 Protodonata, in a polytomy with Odonata, Ephemeroptera, and Neoptera, thus outside Palaeoptera 2713 (Bybee et al., 2008). It need, however, be noted that morphological characters were polarized a priori 2714 with respect to G. arcuatum (Bybee et al., 2008).

2715

# 2716 **72. Crown Euplectoptera**

2717

2718 This clade comprises the families Siphluriscidae, Baetidae, Isonychiidae, Ametropodidae, Acanthametropodidae, Coloburiscidae, Siphlaenigmatidae, Ameletopsidae, Heptageniidae, 2719 2720 Metretopodidae, Siphlonuridae, Oniscigastridae, Rallidentidae, Nesameletidae, and the larger clades 2721 Carapacea and Furcatergalia, their last common ancestor and all of its descendants (Fig. 17). A 2722 variety of different classification schemes have been proposed (Kluge, 2004, 1998; McCafferty, 1991; 2723 Ogden and Whiting, 2005), but we follow the consensus based on combined phylogenetic analysis of 2724 two nuclear genes, two mitochondrial genes, and morphology (Ogden et al., 2009). Although the 2725 extant members are often referred to as Ephemeroptera, that clade includes a number of extinct 2726 members forming a paraphyletic grade (Kluge, 2004, 1998). As membership of fossil species within a 2727 crown group is only possible if they branch along the stem lineage of a living clade that is part of the 2728 crown itself, we treat crown 'Ephemeroptera' as equivalent to the clade Euplectoptera sensu Tillyard 2729 (1932).

2730 Monophyly has been supported by the aforementioned combined data study (Ogden et al.,

2731 2009), as well as analyses of transcriptomes (with limited but representative taxon sampling: Misof et 2732 al., 2014) and morphology (Ogden et al., 2009 Fig. 4: note this is monophyletic, but the root is shown 2733 intervening).

2734

2735 72.1. Fossil specimens

2736

2737 *Triassonurus doliiformis* Sinitshenkova et al., 2005 (part of the private Louis Grauvogel
 2738 collection, Ringendorf, Bas-Rhin, France, No. 9304), holotype, an incomplete nymph (Fig. 18e).
 2739

2740 72.2. Phylogenetic justification

2741

2742 T. doliiformis has not been explicitly included in a phylogenetic analysis. It bears several 2743 morphological characters indicating affinity with the extant family Siphlonuridae: a large nymph with a 2744 non-flattened body, head longer than short prothorax, massive mesothorax with considerably shorter 2745 metathorax, large and wide forewing pads almost completely covering the hind ones, short and 2746 slender legs, abdominal segments without sharp denticles, large rounded tergaliae, and cerci and 2747 paracercus long (Sinitshenkova et al., 2005). The family Siphlonuridae is not accepted as 2748 monophyletic by all authors (J.-D. Huang et al., 2008; Kluge, 2004; McCafferty, 1991) although it is 2749 supported in total evidence and morphological analyses of Odgen et al. (2009). Siphlonuridae is within 2750 the crown of Euplectoptera, in the clade of families outside Carapacea + Furcatergalia (Ogden et al., 2751 2009). Therefore, *T. doliiformis* is also crown Euplectoptera.

2752

2753 72.3. Age justification

2754

The fossil is derived from the silt-clay Grès à Meules unit (lowermost layer) of the Grès-aVoltzia Formation, Vosges, northeastern France (Gall and Grauvogel-Stamm, 1993). Grès à Meules

represents the last stage of the fluviatile facies prevalent in the Buntsandstein (Gall, 1985). Based on sequence stratigraphy, Bourquin et al. (2007, 2006) correlate the Grès-a-Voltzia Formation to the middle Anisian stage of the Triassic. Globally, the uppermost boundary of the Anisian is  $241.5 \pm 1$  Ma (Ogg, 2012), providing a minimum age at 240.5 Ma.

2761 Because the monophyly of Palaeoptera is under debate (Simon et al., 2012, 2009), we assign 2762 a soft maximum age that allows its constituent extant orders to be older than the Rhynie Chert, as for 2763 26.3.

2764

2765 **72.4**. Discussion

2766

2767 The Permian fossils *Protereisma permianum* Sellards, 1907 and *Kukalova americana* 

2768 Demoulin, 1970 were coded in the morphology matrix (larval and adult characters) of Odgen et al.

2769 (2009), but their relationships to the crown remain uncertain. *P. permianum* was resolved on the stem

2770 lineage of the extant families Euthyplociidae, Ephemeridae, and Potamanthidae with morphology only,

2771 but outside crown Euplectoptera in a total evidence analysis (Ogden et al., 2009). More generally,

2772 Kluge (Kluge, 2004, 1998) considered the Permian-Triassic members to form a plesion,

2773 Permoplectoptera, outside the crown group Euplectoptera. The relationship of Permoplectoptera to the

crown group remains to be tested by morphological phylogenetics.

Furthermore, many mayfly fossils are of nymphs, and linking characters between fossil and extant nymphs (or fossil nymphs and extant adults) is challenging, though not impossible (e.g. Haug et al., 2016; Wolfe and Hegna, 2014). The nymphal fossils include *Fuyous gregarius* and *Shantous lacustris* (both Zhang and Kluge, 2007), two species from the Jurassic Daohugou biota that have been used as crown group calibrations in previous divergence time analyses (Thomas et al., 2013). They are, however, younger than *T. doliiformis*.

2781

#### 2782 **73. Crown Odonata**

2784 This clade comprises Epiprocta (dragonflies; comprising Anisozygoptera and Anisoptera) and 2785 Zygoptera (damselflies), their last common ancestor and all of its descendants (Fig. 17). Monophyly of 2786 Odonata is supported by phylogenetic analysis of transcriptomes (Misof et al., 2014), combined 2787 morphology and housekeeping genes (Bybee et al., 2008), and a supertree including morphological 2788 and molecular input trees (Davis et al., 2011). 2789 2790 73.1. Fossil specimens 2791 2792 Triassothemis mendozensis Carpenter, 1960. MACN No. 18040, holotype, preserving the distal 2793 portion of two wings. 2794 2795 73.2. Phylogenetic justification 2796 2797 T. mendozensis is the oldest known member of the fossil family Triassolestidae (Nel et al., 2798 2002; Nicholson et al., 2015). A family-level supertree, incorporating molecular and morphological 2799 input trees, found Triassolestidae within crown group Epiprocta (Davis et al., 2011, largest tree in their 2800 Fig. 1). This fossil is therefore also a member of crown group Odonata. Of all the fossil families 2801 included in the supertree analysis and placed within crown Odonata (Davis et al., 2011), 2802 Triassolestidae (represented by T. mendozensis) has the oldest member. Furthermore, this family (and 2803 its approximate date) was used to calibrate Odonata in multiple recent divergence time analyses 2804 (Rota-Stabelli et al., 2013a; Thomas et al., 2013). 2805 2806 73.3. Age justification 2807 2808 T. mendozensis was discovered in dark grey siltstone of the Potrerillos Formation, at Quebrada

del Durazno, Mendoza Province, Argentina (Martins-Neto et al., 2008). The insect-bearing beds are from the upper part of the Potrerillos Formation. U-Pb SHRIMP dates have been measured for zircons from tuff layers in the middle section of the Potrerillos Formation. The uppermost tuff layer estimated an age of 230.3 Ma  $\pm$  2.3 Myr (Spalletti et al., 2009), corresponding to the Carnian, late Triassic. Thus a minimum age of *T. mendozensis* is 228.0 Ma.

Because the monophyly of Palaeoptera is under debate (Simon et al., 2009, 2012), we assign a soft maximum age that allows its constituent extant orders to be older than the Rhynie Chert, as for 2816 26.3.

2817

2818 **73.4**. *Discussion* 

2819

The internal taxonomy and placement of odonate fossils is highly contentious. Triassic members of the fossil family Triadophlebiidae are of approximately equal age to *T. mendozensis* (i.e. Carnian; Nicholson et al., 2015), however, they appear outside the crown group of Odonata in a supertree (Davis et al., 2011). Triadophlebiidae were not included in the total evidence analysis of Bybee et al. (2008). Most fossils in the latter analysis that had membership within crown Odonata were Jurassic or younger (Bybee et al., 2008).

2826 The Madygen fauna of Kyrgyzstan yields two possible calibrations for crown group Odonata. 2827 Triassolestodes asiaticus Pritykina, 1981 (family Triassolestidae, preserving a hindwing) was recently 2828 justified as the oldest odonate by Kohli et al. (2016). As well, fossil members of Lestidae, crown group 2829 Odonata in the analysis of Bybee et al. (2008), are inferred from oviposition scars on plant fossils from 2830 Madygen (Moisan et al., 2012). Aside from challenges associated with interpreting crown group 2831 affinities of trace fossils, the Madygen fauna is, according to our stratigraphy, dated to the Carnian 2832 (see section 90.3), substantially younger than the 237 Ma age argued by Kohli et al. (2016) based on 2833 megaflora. Our age would give a minimum age of 226.4 Ma for Madygen fossils, which is very slightly 2834 younger than the 228.0 Ma estimated for T. mendozensis. Note, however, that the mean age estimate

2835	for Madygen is 228.4 Ma	(also younger than the mea	n of 230.3 Ma for the Potrerillos Formation).

2836 *Triassolestes epiophlebioides* Tillyard, 1918, a member of Triassolestidae used as a calibration

fossil by Rota-Stabelli et al. (2013), is also known from the Carnian (Nicholson et al., 2015). Another

2838 fossil, *Pseudotriassothemis nipponensis* Bechly, 1997 (formerly *Triassoneura okafujii*), from the

2839 Carnian of Japan is also approximately coeval. We select *T. mendozensis* because its preservation is

2840 better, and radiometric dates for the Potrerillos Formation may be more precise.

2841

# **2842 74. Crown Neoptera**

2843

This clade comprises Polyneoptera (**Figs. 19 and 20**) and Eumetabola, their last common ancestor and all of its descendants (**Fig. 21**). Monophyly is supported by phylogenetic analysis of transcriptomes (Letsch and Simon, 2013; Misof et al., 2014), protein-coding genes (Ishiwata et al., 2011; Sasaki et al., 2013), and combined molecular and morphological data (Terry and Whiting, 2005). 2848

#### 2849 74.1. Fossil specimens

2850

*Protoprosbole straeleni* Laurentiaux, 1952. IRSNB a9885, holotype, preserving a forewing.
 Figured in Nel et al. (A. Nel et al., 2012), Fig. 3h.

2853

2854 74.2. Phylogenetic justification

2855

The original description of *P. straeleni* as a member of Hemiptera by Laurentiaux (1952) has been rejected several times (Hennig, 1981; A. Nel et al., 2012; Shcherbakov, 1995). Nel et al. (2012) summarize the phylogenetic position of *P. straeleni* as being within Paraneoptera (a clade unsupported by recent molecular studies, but comprising Psocodea and Condylognatha). The cua-cup contact with CuP and the flexion or nodal line following the course of RA are both similar to those observed in extant Hemiptera (A. Nel et al., 2012). However, the presence of three veins in the anal
area is argued as a hemipteran autapomorphy that is lacking in *P. straeleni* (A. Nel et al., 2012).
Conservatively, this fossil species can be thus assigned to the stem group of Condylognatha, and thus
crown Eumetabola and Neoptera.

2865

2866 74.3. Age justification

2867

2868 P. straeleni was discovered in Charbonnage de Monceau-Fontaine, Charleroi Coal Basin, 2869 Belgium (Brauckmann et al., 1994). The specimen was likely found in latest Marsdenian strata about 3 2870 m below the base of the Yeadonian (discussed by Brauckmann et al., 1994). The fossil-bearing 2871 deposits are assigned to the late Namurian B (Marsdenian) based on the *Bilinguites superbilinguis* 2872 R2c2 subzone of goniatite ammonoid stratigraphy (Brauckmann et al., 1994). The (late) Namurian-2873 (early) Westphalian boundary is defined by the earliest occurrence of the goniatite Gastrioceras 2874 subcrenatum (Waters and Davies, 2006), but lacks a precise isotopic date. Pointon et al. (2012) 2875 estimated an age of c. 319.9 Ma for the base of the Westphalian (top of the Namurian, only slightly 2876 younger than the Marsdenian) based on Milankovitch cycles of sedimentation, giving a minimum age 2877 for P. straeleni.

Soft maximum as for 26.3.

2879

2880 **74.4**. Discussion

2881

2882 *Qilianiblatta namurensis* Zhang et al., 2013 has an equal claim to being the earliest record of 2883 Neoptera (as *Q. namurensis* is a member of crown Polyneoptera), but it is of equal age to *P. straeleni*. 2884 The Qilianshan entomofauna at Xiaheyan, China, yields many other likely neopterans (e.g. Béthoux et 2885 al., 2011; Liu et al., 2009a; Prokop and Nel, 2007; Zhang et al., 2013).

2886 *Ctenoptilus elongatus* Béthoux and Nel, 2005 from the Stephanian B/C of France has been

2887	used as the putative oldest calibration fossil for crown Neoptera (e.g. O'Reilly et al., 2015). However,
2888	the Stephanian is a European stage of the Pennsylvanian, corresponding to the globally used
2889	Gzhelian, which is substantially younger than the Bashkirian age of both <i>P. straeleni</i> and <i>Q.</i>
2890	namurensis (with an upper boundary of 298.75 Ma).
2891	
2892	75. Crown Polyneoptera
2893	
2894	This clade comprises Zoraptera (ground lice), Dermaptera (earwigs), Plecoptera (stoneflies),
2895	Orthoptera (crickets, katydids), Notoptera, Eukinolabia and Dictyoptera, their last common ancestor
2896	and all of its descendants (Fig. 19). Monophyly has been demonstrated by phylogenetic analysis of
2897	transcriptomes (Letsch and Simon, 2013; Misof et al., 2014), protein-coding genes (Ishiwata et al.,
2898	2011), and wing morphology (Yoshizawa, 2011). This clade is not recognized in GenBank taxonomy.
2899	
2900	75.1. Fossil specimens
2901	
2902	Qilianiblatta namurensis Zhang et al., 2013. GMCB 04GNX1001-1, holotype, preserving the
2903	right forewing. We also refer to a second specimen (CNU-NX1-303; Fig. 20a), preserving paired
2904	forewings and hindwings (Guo et al., 2013).
2905	
2906	75.2. Phylogenetic justification
2907	
2908	Q. namurensis has not been included in formal phylogenetic analysis, but the fossil exhibits
2909	some apomorphic characters uniting it with crown group Blattodea, specifically presence of a deeply
2910	concave CuP in the forewing (Prokop et al., 2014). Additional data from forewings of the CNU
2911	specimen shows the RA with branches translocated to RP, as in cockroaches, suggesting this species

- 2912 could be stem Blattodea (Guo et al., 2013). However, there has not been a cladistic analysis of wing
  - 112

2913	venation characters for both fossil and extant Blattodea and/or Dictyoptera, thus we agree with the
2914	more conservative view (Kjer et al., 2015; Legendre et al., 2015; Prokop et al., 2014) that roachoids
2915	likely represent a diverse and speciose fauna on the stem group of Dictyoptera. See also section 82.4.
2916	Nonetheless, placement of Q. namurensis on the stem lineage of Dictyoptera identifies it as a member
2917	of crown Polyneoptera.
2918	
2919	75.3. Age justification
2920	
2921	Minimum as for 71.3.
2922	A soft maximum age is estimated from <i>R. praecursor</i> , the oldest hexapod, from the Early
2923	Devonian (Pragian) Rhynie Chert of Aberdeenshire, Scotland. Spore assemblages of the Windyfield
2924	and stratigraphically underlying Rhynie Chert are dated to the early but not earliest Pragian to early
2925	(earliest?) Emsian (polygonalis-emsiensis Spore Assemblage Biozone) (Parry et al., 2011).
2926	Radiometric dating of the underlying Milton of Noth Andesite at ca. 411 Ma (Parry et al., 2013, 2011)
2927	has been subject to a dispute over its temporal relationship to hot spring activity associated with the
2928	cherts (Mark et al., 2013, 2011) and predates the biostratigraphic dating of the Rhynie Chert relative to
2929	the global dating of the base of the Pragian Stage. Therefore, a soft maximum constraint may be
2930	defined at 411 Ma for the Rhynie Chert.
2931	
2932	76. Crown Dermaptera
2933	
2934	This clade comprises Protodermaptera and Epidermaptera, their last common ancestor and all
2935	of its descendants (Fig. 19). Monophyly is supported based on phylogenetic analysis of
2936	transcriptomes (Misof et al., 2014), nuclear genes (Kocarek et al., 2013), and combined molecular and
2937	morphological data (Jarvis et al., 2005).
2938	

2939	76.1.	Fossil	specime	ens

2941 *Rhadinolabis phoenicica* Engel et al., 2011. Holotype preserving a female in amber, 1013 in the 2942 private collection of D. Azar in Fanar (Matn), Lebanon (**Fig. 20e**). Provisionally housed at MNHN. 2943

2944 76.2. Phylogenetic justification

2945

*R. phoenicica* is assigned only to Neodermaptera (= Protodermaptera + Epidermaptera), and
not to any extant family. Membership within Neodermaptera is based on the presence of
morphological characters: trimerous tarsi, absence of a well-developed ovipositor, and tarsal structure
(Engel et al., 2011). These characters are sufficient to confirm the fossil belongs within crown
Dermaptera.

2951

2952 76.3. Age justification

2953

2954 This fossil was discovered in amber from the Mdeyrij-Hammana outcrop of the Baabda district. 2955 Mount Lebanon (Azar et al., 2010). Recent revision of the stratigraphy of Lebanese amber deposits 2956 places the Hammana fossils in the upper interval of the Grès du Liban (Maksoud et al., 2016). This is 2957 below the Jezzinian regional stage (Maksoud et al., 2014) and above the Banc de Mrejatt subunit 2958 (indicated as Ba3-Ba4 in Fig. 4 of Maksoud et al., 2016). Despite the lack of microfossils to further 2959 constrain the oldest boundary of the Jezzinian within the late Barremian, there is evidence that later 2960 Lebanese amber deposits bear the same age as Jezzine amber (see 26.3) because the amber itself 2961 has been reworked (Maksoud et al., 2016). We adopt the early Barremian minimum age proposed by 2962 Maksoud et al. (2016). The upper boundary of the early Barremian is proposed to be the first 2963 appearance of the ammonite Ancyloceras vandenheckii (Ogg et al., 2012). Cyclostratigraphy dates the 2964 A. vandenheckii Zone beginning at 129.41 Ma (Ogg et al., 2012), providing a minimum age for Jezzine

2965	Lebanese amber fossils.
2966	Soft maximum as for 75.3.
2967	
2968	77. Crown Plecoptera
2969	
2970	This clade comprises Antarctoperlaria, Euholognatha and Systellognatha, their last common
2971	ancestor and all of its descendants (Fig. 19). This classification and its morphological evidence is
2972	reviewed by Zwick (2000). Monophyly of Plecoptera is supported by phylogenetic analysis of
2973	transcriptomes (Misof et al., 2014) and combined ribosomal genes, H3, and morphology (Terry and
2974	Whiting, 2005).
2975	
2976	77.1. Fossil specimens
2977	
2978	Palaeotaeniopteryx elegans Sharov, 1961. PIN 1197/333, holotype, preserving a forewing.
2979	
2980	
	77.2. Phylogenetic justification
2981	77.2. Phylogenetic justification
2981 2982	77.2. Phylogenetic justification P. elegans is classified in the fossil family Palaeonemouridae, suborder Nemourina
2981 2982 2983	<ul> <li>77.2. Phylogenetic justification</li> <li><i>P. elegans</i> is classified in the fossil family Palaeonemouridae, suborder Nemourina</li> <li>(Sinitshenkova, 1987). At that time, Nemourina was one of only two suborders, the other being Perlina</li> </ul>
2981 2982 2983 2984	<ul> <li>77.2. Phylogenetic justification</li> <li><i>P. elegans</i> is classified in the fossil family Palaeonemouridae, suborder Nemourina</li> <li>(Sinitshenkova, 1987). At that time, Nemourina was one of only two suborders, the other being Perlina</li> <li>(Rasnitsyn and Quicke, 2002). Zwick (2000) summarized Nemourina as containing the (extant)</li> </ul>
2981 2982 2983 2984 2985	<ul> <li>77.2. Phylogenetic justification</li> <li><i>P. elegans</i> is classified in the fossil family Palaeonemouridae, suborder Nemourina</li> <li>(Sinitshenkova, 1987). At that time, Nemourina was one of only two suborders, the other being Perlina</li> <li>(Rasnitsyn and Quicke, 2002). Zwick (2000) summarized Nemourina as containing the (extant)</li> <li>families Notonemouridae, Nemouridae, Taeniopterygidae, Capniidae, and Leuctridae, therefore</li> </ul>
2981 2982 2983 2984 2985 2986	<ul> <li><i>P. elegans</i> is classified in the fossil family Palaeonemouridae, suborder Nemourina</li> <li>(Sinitshenkova, 1987). At that time, Nemourina was one of only two suborders, the other being Perlina</li> <li>(Rasnitsyn and Quicke, 2002). Zwick (2000) summarized Nemourina as containing the (extant)</li> <li>families Notonemouridae, Nemouridae, Taeniopterygidae, Capniidae, and Leuctridae, therefore</li> <li>equivalent to the new suborder Euholognatha. Grimaldi and Engel (2005; Fig. 7.6) prefer a placement</li> </ul>
2981 2982 2983 2984 2985 2986 2987	<ul> <li><i>P. elegans</i> is classified in the fossil family Palaeonemouridae, suborder Nemourina</li> <li>(Sinitshenkova, 1987). At that time, Nemourina was one of only two suborders, the other being Perlina</li> <li>(Rasnitsyn and Quicke, 2002). Zwick (2000) summarized Nemourina as containing the (extant)</li> <li>families Notonemouridae, Nemouridae, Taeniopterygidae, Capniidae, and Leuctridae, therefore</li> <li>equivalent to the new suborder Euholognatha. Grimaldi and Engel (2005; Fig. 7.6) prefer a placement</li> <li>of Palaeonemouridae outside the crown group of Plecoptera, on the basis that diagnostic characters</li> </ul>
2981 2982 2983 2984 2985 2986 2987 2988	<ul> <li><i>P. elegans</i> is classified in the fossil family Palaeonemouridae, suborder Nemourina</li> <li>(Sinitshenkova, 1987). At that time, Nemourina was one of only two suborders, the other being Perlina</li> <li>(Rasnitsyn and Quicke, 2002). Zwick (2000) summarized Nemourina as containing the (extant)</li> <li>families Notonemouridae, Nemouridae, Taeniopterygidae, Capniidae, and Leuctridae, therefore</li> <li>equivalent to the new suborder Euholognatha. Grimaldi and Engel (2005; Fig. 7.6) prefer a placement</li> <li>of Palaeonemouridae outside the crown group of Plecoptera, on the basis that diagnostic characters</li> <li>for crown group suborders within Plecoptera are rarely preserved (e.g. muscles, cellular structures).</li> </ul>
2981 2982 2983 2984 2985 2985 2986 2987 2988 2989	<ul> <li><i>P. elegans</i> is classified in the fossil family Palaeonemouridae, suborder Nemourina</li> <li>(Sinitshenkova, 1987). At that time, Nemourina was one of only two suborders, the other being Perlina</li> <li>(Rasnitsyn and Quicke, 2002). Zwick (2000) summarized Nemourina as containing the (extant)</li> <li>families Notonemouridae, Nemouridae, Taeniopterygidae, Capniidae, and Leuctridae, therefore</li> <li>equivalent to the new suborder Euholognatha. Grimaldi and Engel (2005; Fig. 7.6) prefer a placement</li> <li>of Palaeonemouridae outside the crown group of Plecoptera, on the basis that diagnostic characters</li> <li>for crown group suborders within Plecoptera are rarely preserved (e.g. muscles, cellular structures).</li> <li>While no formal phylogenetic hypothesis illustrates the relationship of Palaeonemouridae to other</li> </ul>

2991 (Béthoux, 2005, pers. comm.).

2992

2993 77.3. Age justification

2994

2995 The oldest specimen of *P. elegans* was discovered from the Mitino Horizon at the Kaltan 2996 locality in the Kuznetsk Basin, Kemerovo, Russia (Sharov, 1961; Shcherbakov, 2000). Correlation of 2997 insect faunas suggests the Kaltan locality is late early Kazanian (Lozovsky et al., 2009; Shcherbakov, 2998 2008). The Kazanian is a regional stage of the Russian Permian, which has been correlated to both 2999 the Wordian (Menning et al., 2006) and the Roadian global Stages (Lozovsky et al., 2009). Evidence 3000 for an age in the Roadian is stronger, demarcated by presence of ammonites such as Sverdrupites 3001 harkeri and S. amundseni (Lozovsky et al., 2009). These ammonites, and associated conodonts 3002 Kamagnathus khalimbadzhai and K. volgensis, correlate globally to the Roadian (Barskov et al., 2014; 3003 Leonova, 2007; Leonova and Shilovsky, 2007). The upper boundary of the Roadian is  $268.8 \text{ Ma} \pm 0.5$ 3004 Myr, so a minimum age is 268.3 Ma.

3005 Soft maximum as for 75.3.

3006

3007 77.4. Discussion

3008

3009 *Gulou carpenteri* Béthoux et al., 2011, from the Pennsylvanian Qilianshan entomofauna of 3010 China, is identified as a member of the stem group to Plecoptera (Béthoux et al., 2011), and thus 3011 cannot be used to calibrate a minimum age of the crown group. Moreover, other Permian plecopterans 3012 had terrestrial nymphs; an aquatic nymph is a symapomorphy uniting crown group Plecoptera (Zwick, 3013 2000), relegating any fossil without it to the stem group.

O. Béthoux (pers. comm.) cautioned that a Jurassic minimum age for crown Plecoptera, as
 used by Misof et al. (2014), would underestimate their age significantly. The calibrating fossil
 *Pronemoura angustithorax* Liu et al., 2011 used by Misof et al. (2014), from the Daohugou Beds, is

3017	likely a member of total group Euholognatha (Liu et al., 2011). Other crown Plecoptera groups are also
3018	known from the same locality (Liu et al., 2009b), suggesting diversification of the crown group was
3019	significantly earlier.
3020	
3021	78. Crown Orthoptera
3022	
3023	This clade comprises Ensifera (crickets, katydids) and Caelifera (grasshoppers), their last
3024	common ancestor and all of its descendants (Fig. 19). Monophyly is demonstrated by phylogenetic
3025	analysis of transcriptomes (Misof et al., 2014), mitochondrial genomes plus four nuclear genes (Song
3026	et al., 2015), morphology (Béthoux and Nel, 2002), and combined molecular and morphological data
3027	(Terry and Whiting, 2005).
3028	
3029	78.1. Fossil specimens
3030	
3031	Raphogla rubra Béthoux et al., 2002. Ld LAP 415 B, holotype, preserving the counterpart of a
3032	forewing ( <b>Fig. 20c</b> ).
3033	
3034	78.2. Phylogenetic justification
3035	
3036	Although no cladistic analysis exists combining extant and fossil Enserifa, R. rubra may be
3037	assigned to crown Enserifa based on forewing venation characters (Béthoux et al., 2002). It likely
3038	belongs to the stem group of the clade (Gryllidea + Tettigoniidea), based on the following characters:
3039	very broad area between anterior margin and Sc; RS moderately long basal of a short fusion with the
3040	anterior branch MA1a of MA; MP + CuA1 with only one simple anterior branch (Béthoux et al., 2002).
3041	As both Gryllidea and Tettigoniidea are crown clades within crown Enserifa, R. rubra is within crown
3042	group Orthoptera.

# 3044 78.3. Age justification

3046	R. rubra was found at the fossiliferous site F21 D, at "Le Moural D", in the basal Mérifrons
3047	Member of the Salagou Formation (Saxonian Group), near village Octon, Lodève Basin, Hérault,
3048	France (Béthoux et al., 2002; Nel et al., 1999; Schneider et al., 2006). U-Pb dates have been recently
3049	measured from zircons lying in tuff beds near the lower two-thirds of the Salagou Formation (Octon
3050	Member), in the Artinskian (Michel et al., 2015). The Mérifrons Member, overlying the Octon, is
3051	therefore inferred to be Artinskian at its base but continuing up through the Kungurian (Michel et al.,
3052	2015). As the exact stratum of the F21 site is not indicated within the Mérifrons member (Michel et al.,
3053	2015; Schneider et al., 2006), we apply a conservative minimum estimate from the upper boundary of
3054	the Kungurian (272.3 Ma $\pm$ 0.5 Myr), at 271.8 Ma.
3055	Soft maximum as for 75.3.
3056	
3057	78.4. Discussion
3058	
3059	An undescribed Namurian member of Archaeorthoptera was initially attributed to crown group
3060	Orthoptera (Prokop et al., 2005). However, an affinity with Archaeorthoptera is supported in the stem
3061	group of Orthoptera based on phylogenetic analysis (Béthoux and Nel, 2002), thus it cannot be used
3062	to calibrate the crown. Similarly, Oedischia williamsoni Brongniart, 1885, from the Pennsylvanian of
3063	France, is recognized as a stem group member of Orthoptera by cladistic analysis (Béthoux and Nel,
3064	2002). Together these fossils suggest a long stem branch for Orthoptera.
3065	The fossil Eolocustopsis primitiva Riek, 1976 from Natal, South Africa was listed as the oldest
3066	crown group member of Caelifera, and thus another Permian crown group member of Orthoptera
3067	(Song et al., 2015). However, the fossil comes from strata of the Normandien Formation,
3068	Changhsingian stage, latest Permian (due to the co-occurrence of the vertebrate fossil Dicynodon;

3069 e.g. Catuneanu et al., 2005), which is younger than the Kungurian.

3070 3071 79. Crown Notoptera 3072 3073 This clade comprises Mantophasmatodea (rock crawlers) and Grylloblattodea (ice crawlers), 3074 their last common ancestor and all of its descendants (Fig. 19). The monophyly of Notoptera is 3075 supported by phylogenetic analysis of transcriptomes (Misof et al., 2014), morphology (Wipfler et al., 3076 2011), and combined molecular and morphological data (Terry and Whiting, 2005). 3077 3078 79.1. Fossil specimens 3079 3080 Juramantophasma sinica D. Huang et al., 2008. NIGP 142171, holotype, preserving a nearly 3081 complete adult female (Fig. 20g). 3082 3083 79.2. Phylogenetic justification 3084 3085 J. sinica has several characters in common with crown Mantophasmatodea. These include: a 3086 third tarsomere with a sclerotized elongated dorsal process, enlarged and fanlike pretarsal arolia, last 3087 tarsomere at right angle to the others, female gonoplacs short and claw shaped, and egg with a 3088 circular ridge (D. Huang et al., 2008). As no morphological matrix exists for Mantophasmatodea, 3089 relationships to extant lineages are not possible to test (D. Huang et al., 2008). The fossil is excluded 3090 from the crown group of Grylloblattodea as it lacks segmented cerci. Thus, conservatively, a position 3091 on the stem lineage of Mantophasmatodea is likely (although J. sinica could be amended to within the 3092 crown of Mantophasmatodea). This would, in any case, mean it is a member of crown Notoptera. 3093

3094 **79.3**. Age justification

3096	This fossil was found in deposits of the Daohugou Beds, Ningcheng County, Inner Mongolia,
3097	China (D. Huang et al., 2008). There has been controversy about the accuracy and precise age and
3098	stratigraphic position of the Daohugou Beds (Gao and Ren, 2006; Wang et al., 2005; Zhang, 2015).
3099	The beds consist of 100–150 m thick succession of grey-white or locally reddish, thinly bedded
3100	claystones, shales, siltstones and sandy mudstones with intercalated ash-fall tuffs and ignimbrites.
3101	Ages have been proposed from Aalenian (Middle Jurassic) to Early Cretaceous (Liu et al., 2014; Wang
3102	et al., 2000), with several studies converging on Callovian-Oxfordian (Late Jurassic; Zhang, 2015).
3103	Radiometric dating of the ignimbrites with 40Ar/39Ar and SHRIMP U-Pb variously yields dates
3104	between 165 Ma $\pm$ 2.5 Myr and 158.7 Ma $\pm$ 0.6 Myr (Chang et al., 2009b; Gao and Ren, 2006; He et
3105	al., 2004; Peng et al., 2012). The fossiliferous shales overlay the volcanic deposits (Gao and Ren,
3106	2006), and are thus younger. The isotopic dates nonetheless provide a reasonable refutation of
3107	Cretaceous age estimates. Furthermore, the Daohugou Beds may be correlated to sediments from
3108	Oxfordian localities in China and Kazakhstan (Zhang, 2015). The most conservative (i.e. youngest) of
3109	the direct radiometric dates is 158.1 Ma (within the Oxfordian), giving a minimum age.
3110	Soft maximum as for 75.3.
3111	

3112 **79.4**. *Discussion* 

3113

3114 Stem group Grylloblattodea are uncommon, and extant grylloblattids (and mantophasmids) are 3115 wingless (Wipfler et al., 2014). A putative grylloblattid insect was described from the Pennsylvanian 3116 Montceau-les-Mines Lagerstatte, about 130 Myr older than *J. sinica* (Béthoux and Nel, 2010); 3117 however, the fossil preserved only the wings. We take the parsimonious view that there was a single 3118 loss of wings in the common ancestor of Grylloblattodea and Mantophasmatodea, i.e. in the crown 3119 group of Notoptera (Grimaldi and Engel, 2005). Therefore, any fossil bearing wings, such as the 3120 Pennyslvanian and Permian members, would be on the stem branch of Notoptera.
3121	
3122	80. Crown Eukinolabia
3123	
3124	This clade comprises Embioptera (webspinners) and Phasmatodea (stick and leaf insects),
3125	their last common ancestor and all of its descendants (Fig. 19). Monophyly of Eukinolabia is
3126	supported by phylogenetic analyses of transcriptomes (Letsch and Simon, 2013; Misof et al., 2014)
3127	and ribosomal and H3 sequences (Terry and Whiting, 2005).
3128	
3129	80.1. Fossil specimens
3130	
3131	Cretophasmomima melanogramma Wang et al., 2014. CNU-PHA-NN2012002, holotype,
3132	preserving a male (Fig. 20d).
3133	
3134	80.2. Phylogenetic justification
3135	
3136	C. melanogramma shares the 'shoulder pad' structure, and twig-like appearance (elongated
3137	meso- and metathorax) diagnostic of total group Phasmatodea (Wang et al., 2014). Crown
3138	membership within Phasmatodea is questionable, as important synapomorphies, the vomer and
3139	forceps-like extensions of the 10th abdominal tergum, are absent from C. melanogramma (Wang et
3140	al., 2014). The position of C. melanogramma on the stem lineage of Phasmatodea therefore places it
3141	within the crown group of Eukinolabia.
3142	
3143	80.3. Age justification
3144	
3145	As for 76.3.
3146	

3147	80.4. Discussion
3148	
3149	Renphasma sinica Nel and Delfosse, 2011 is of equal age, also from the Yixian Formation, and
3150	also a member of stem Phasmatodea, and thus crown Eukinolabia.
3151	
3152	81. Crown Phasmatodea
3153	
3154	This clade comprises Timematodea and Euphasmatodea, their last common ancestor and all
3155	of its descendants (Fig. 19). Monophyly of Phasmatodea is supported by phylogenetic analyses of
3156	transcriptomes (Misof et al., 2014), ribosomal and H3 sequences (Terry and Whiting, 2005), and
3157	morphology (Friedemann et al., 2012).
3158	
3159	81.1 Fossil specimens
3160	
3161	Echinosomiscus primoticus Engel et al., 2016c. NIGP 163536, holotype, preserving a male in
3162	amber ( <b>Fig. 20f</b> ).
3163	
3164	81.2 Phylogenetic justification
3165	
3166	Until recently, no Mesozoic fossil qualified for membership in the crown group of Phasmatodea
3167	(Bradler and Buckley, 2011). E. primoticus bears morphological characters shared with extant
3168	members of Euphasmatodea, in particular Heteropterygidae and Aschiphasmatidae, but lack the area
3169	apicalis on the tibiae (Engel et al., 2016c). It also shares characters with Lonchodinae, such as absent
3170	areole on all tibiae, comparatively long antennae, the absence of wings, and the division of the tenth
3171	abdominal tergum into moveable hemitergites (Engel et al., 2016c). Although a new family was
3172	erected to accommodate the unique character combination for <i>E. primoticus</i> , it is very clearly within

3173	Euphasmatodea (Phasmatidae s.l.), and thus a member of crown Phasmatodea (Engel et al., 2016c).
3174	
3175	81.3 Age justification
3176	
3177	Minimum as for 12.3. Soft maximum as for 75.3.
3178	
3179	82. Crown Dictyoptera
3180	
3181	This clade comprises Mantodea (praying mantids) and Blattodea (cockroaches, termites), their
3182	last common ancestor and all of its descendants (Fig. 19). Phylogenetic analysis of transcriptomes
3183	(Misof et al., 2014), mitochondrial genes (Legendre et al., 2015), and combined molecular and
3184	morphological data (Djernæs et al., 2015; Ware et al., 2008), support monophyly of Dictyoptera.
3185	
3186	82.1. Fossil specimens
3187	
3188	Valditermes brenanae Jarzembowski, 1981. BMNH In. 64588, holotype, preserving a forewing.
3189	
3190	82.2. Phylogenetic justification
3191	
3192	The position of V. brenanae was confirmed by morphological phylogenetic analysis (Engel et
3193	al., 2009). V. brenanae was resolved on the stem lineage of Mastotermitidae (Engel et al., 2009). This
3194	position was separately found for a congeneric species in the combined morphological and molecular
3195	phylogeny of Ware et al. (2010). Mastotermitidae is a monotypic family, sister to all other termites
3196	(Djernæs et al., 2015; Ware et al., 2010), so this phylogeny would also place V. brenanae in the
3197	crowns of Isoptera and Blattodea.
3198	

3199 82.3. Age justification

3200

3201 The fossil is from the Clockhouse Brickworks pit site, Surrey, England (Jarzembowski, 1981). 3202 The Clockhouse Brickworks belongs to the Lower Weald Clay, as indicated by the presence of the 3203 ostracods Cytheridea clavata, C. tuberculata, and C. valdensis (Anderson, 1985). Of these, C. 3204 tuberculata has the narrowest range, and is restricted to the middle portion of the Lower Weald Clay, 3205 at BGS Bed 3a (Anderson, 1985; Ross and Cook, 1995). This faunal Zone is now assigned to the 3206 lower portion of the C. pumila Subzone of the Theriosynoecum fittoni Zone (Horne, 1995). Based on 3207 palynomorph stratigraphy, the boundary between Lower and Upper Weald Clay at the base of BGS 3208 Bed 3a corresponds accurately to the boundary between the Hauterivian and Barremian Stages (Ross 3209 and Cook, 1995). The upper boundary of the Hauterivian is 130.8 Ma  $\pm$  0.5 Myr (Ogg et al., 2012a), 3210 therefore a minimum age of the Lower Weald Clay is 130.3 Ma. 3211 Soft maximum as for 75.3. 3212 3213 82.4. Discussion 3214 3215 There is ongoing debate over whether various Palaeozoic "roachoid" fossils, such as 3216 Qilianiblatta namurensis and Homocladus grandis Carpenter, 1966 (known only from wing venation 3217 characters), truly represent crown group members of Dictyoptera (e.g. Guan et al., 2016; Kjer et al., 3218 2015; Legendre et al., 2015; Tong et al., 2015). If roachoids are indeed within crown group 3219 Dictyoptera, their antiquity may push back the origins of crown Dictyoptera and crown Polyneoptera by 3220 80-88 Myr (Legendre et al., 2015; Tong et al., 2015). However, wing venation alone may be insufficient 3221 to place most fossils within the crown group of Blattodea or even Dictyoptera. Particularly in 3222 cockroaches, asymmetry at the individual level and convergence at higher taxonomic levels are 3223 impediments to wing venation taxonomy, as well as the paucity of comparative venation data for extant 3224 species (e.g. Béthoux et al., 2010; Béthoux and Wieland, 2009; Garwood and Sutton, 2010; Gorochov,

3225 2013; Guan et al., 2016).

3226 In the absence of detailed cladistic analysis of fossil roachoid wings together with extant 3227 Dictyoptera and other outgroups, we take the conservative view (Guan et al., 2016; Kier et al., 2015; 3228 Prokop et al., 2014) that roachoids (including the family Anthracoptilidae/Strephocladidae, containing 3229 H. grandis) likely represent a diverse and speciose fauna on the stem group of Dictyoptera, perhaps 3230 with some members on the stem group of Neoptera or Polyneoptera (Grimaldi and Engel, 2005). At 3231 least some such roachoids may be used to calibrate crown group Polyneoptera (as done herein by 3232 assigning Q. namurensis), but they cannot calibrate crown Dictyoptera. As a consequence, many 3233 recent analyses have begun to rewrite the traditional assumption of extremely old crown ages for 3234 Dictyoptera, with crown origins likely in the Jurassic (Misof et al., 2014). 3235 Morphological phylogenetic analyses have excluded all Cretaceous fossils from the crown

3236 group of Mantodea, although they remain as likely crown Dictyoptera (Delclòs et al., 2016; Grimaldi, 3237 2003). Given that the analysed morphological matrix has fewer characters than taxa and has substantial missing data, it is not definitive (Delclòs et al., 2016). A recently discovered fossil from Crato (Aptian of Brazil), *Cretophotina santanensis* Lee, 2014, may be a stem group Chaeteessidae, which may be the most basal crown family of Mantodea (Svenson and Whiting, 2009). The position of Chaeteessidae may be within polyphyletic Mantidae (Legendre et al., 2015), but we exercise caution and do not place *C. santanensis* in the crown group, as recommended by Lee (2014).

3243

#### 3244 83. Crown Blattodea

3245

This clade comprises Lamproblattidae, Blaberoidea, Blattidae, Nocticolidae, Polyphagidae, Cryptocercidae and Isoptera, their last common ancestor and all of its descendants (**Fig. 19**). The position of Isoptera (termites) within a paraphyletic Blattodea was first identified by Inward et al. (2007) with six molecular loci. Further support for the monophyly of the new concept of Blattodea comes from transcriptomes (Misof et al., 2014), mitochondrial genes (Legendre et al., 2015), housekeeping genes

3251	(Djernæs et al., 2012), and combined molecular and morphological data (Djernæs et al., 2015; Ware
3252	et al., 2008).
3253	
3254	83.1. Fossil specimens
3255	
3256	As for 82.1.
3257	
3258	83.2. Phylogenetic justification
3259	
3260	As for 82.2.
3261	
3262	83.3. Age justification
3263	
3264	As for 82.3.
3265	
3266	83.4. Discussion
3267	
3268	Baissatermes lapideus Engel et al., 2007 is a crown group member of Isoptera, and
3269	Mastotermes nepropadyom Vršanskỳ and Aristov, 2014 is crown Blattodea (Engel et al., 2016a); both
3270	have been used to calibrate Isoptera and Blattodea (Djernæs et al., 2015; Ware et al., 2010). Note that
3271	fossil Mastotermes are likely polyphyletic (Engel et al., 2016a). Although these are appropriate
3272	calibration fossils, they are not the oldest Blattodea. B. lapideus is from the Zaza Formation
3273	(Transbaikalian Russia), and <i>M. nepropadyom</i> is from Chernovskie Kopi, also in Transbaikalia and
3274	similar in age to the Turga Formation (Sukatsheva and Vassilenko, 2011; Vršanskỳ and Aristov, 2014).
3275	The Turga Formation has been correlated to the Baissa locality, Zaza Formation; this is based on
3276	shared presence of Asteropollis asteroides spores (Vakhrameev and Kotova, 1977). As discussed in

3277	section 86.3, the Zaza Formation may be much younger than initially described, with a minimum age
3278	of Campanian (71.9 Ma). Therefore both Russian fossils are younger than V. brenanae.

# 3280 84. Crown Eumetabola

3281

3282 This clade comprises Condylognatha, Psocodea and Holometabola, their last common 3283 ancestor and all of its descendants (Fig. 21). Monophyly of the clade is supported by transcriptomes 3284 (Letsch and Simon, 2013; Misof et al., 2014) and protein-coding genes (Ishiwata et al., 2011). Some 3285 morphological analyses do not support monophyly of Eumetabola (Kristensen, 1981; Wheeler et al., 3286 2001), although it is recovered (Kristensen, 1991; Kukalová-Peck, 1991) and assumed (Yoshizawa 3287 and Saigusa, 2001) in other analyses. Note also that support for Psocodea as the sister clade of 3288 Holometabola was statistically weak in analyses of transcriptomes (Misof et al., 2014), although 3289 monophyly of Eumetabola was well supported.

3290

3291 84.1. Fossil specimens

- 3292
- 3293 As for 74.1.
- 3294
- 3295 84.2. Phylogenetic justification
- 3296
- 3297 As for 74.2.
- 3298
- 3299 84.3. Age justification
- 3300
- 3301 Minimum as for 74.3. Soft maximum as for 75.3.
- 3302

3304	
3305	This clade comprises Hemiptera (true bugs) and Thysanoptera (thrips), their last common
3306	ancestor and all of its descendants (Fig. 21). Monophyly is determined by phylogenetic analysis of
3307	transcriptomes (Misof et al., 2014), nuclear protein-coding genes (Ishiwata et al., 2011), and wing
3308	morphology (Yoshizawa and Saigusa, 2001).
3309	
3310	85.1. Fossil specimens
3311	
3312	Aviorrhyncha magnifica Nel et al., 2013, holotype Avion No. 2 (provisionally stored in the
3313	collection of Entomological Laboratory, MNHN; to be deposited in the Musée Géologique Pierre Vetter,
3314	Decazeville, France), preserving a single forewing (Fig. 22a).
3315	
3316	85.2. Phylogenetic justification
3317	
3318	Nel et al. (2013) diagnose A. magnifica as stem Euhemiptera (the clade sister to
3319	Sternorrhyncha containing all other living Hemiptera; Cryan and Urban, 2012; Cui et al., 2013). At least
3320	two forewing characters in A. magnifica are synapomorphies of Euhemiptera, including presence of an
3321	ambient vein and a well-developed concave CP (its presence is a synapomorphy) (Nel et al., 2013).
3322	Unlike many extant Euhemiptera, the cua-cup vein is not zigzagged. Given that much of fossil insect
3323	taxonomy is conducted with only preserved wings, an assignment to the crown group of Hemiptera
3324	and thus Condylognatha is reasonable.
3325	
3326	85.4. Age justification
3327	
3328	A. magnifica was found in "Terril No. 7", a layer containing rocks from the slag heap of coal

3303 85. Crown Condylognatha

3329	mines 3 and 4 of Liévin, in the Avion outcrop of Pas-de-Calais, France (Nel et al., 2013). The coal
3330	mines are dated to the Westphalian C/D, or Bolsovian/Asturian, which has a youngest boundary
3331	equivalent to the latest Moscovian stage of the Pennsylvanian (Nel et al., 2013; Richards, 2013). As
3332	the upper boundary of the Moscovian is 307.0 Ma $\pm$ 0.1 Myr, this provides a minimum age of 306.9
3333	Ma.
3334	Soft maximum as for 75.3.
3335	
3336	86. Crown Thysanoptera
3337	
3338	This clade comprises Tubulifera and Terebrantia, their last common ancestor and all of its
3339	descendants (Fig. 21). Monophyly is established based on phylogenetic analysis of transcriptomes
3340	(Misof et al., 2014) and five nuclear protein-coding genes (Buckman et al., 2013). There is no
3341	adequate phylogenetic test of thysanopteran monophyly using morphology (reviewed by Mound and
3342	Morris, 2007).
3343	
3344	86.1. Fossil specimens
3345	
3346	Fusithrips crassipes Shmakov, 2009. PIN 3064/8547, holotype, preserving a female body (Fig.
3347	<b>22b</b> ).
3348	
3349	86.2. Phylogenetic justification
3350	
3351	F. crassipes has not been included in a phylogenetic analysis, however, Shmakov (2009)
3352	describes characters placing it in the crown of Thysanoptera. In particular, Rs1 and M2 as crossveins
3353	rather than oblique veins suggest membership in the family Aeolothripidae (Shmakov, 2009). Whether
3354	crown or stem Aeolothripidae, the family is a part of Terebrantia, indicating crown group membership in

3355 Thysanoptera.

3356

3357 86.3. Age justification

3358

3359 The fossil F. crassipes was found in Layer 31 on the left bank of the Vitim River, 3 km 3360 downstream from the mouth of the Baissa River, Buryatia, Transbaikalian Russia (Shmakov, 2009). 3361 The fossiliferous lacustrine deposits are part of the Zaza Formation, Baissa locality. The Zaza 3362 Formation was once assigned to the Valanginian, based on correlation of fossil insect species, 3363 however palynological data from the appearance of Asteropollis spores suggests a younger date 3364 (O'Reilly et al., 2015; Zherikhin et al., 1998). A. asteroides, one of the earliest angiosperms, has a 3365 worldwide distribution during the Early and mid Cretaceous (Friis et al., 2005), and has been 3366 biostratigraphically assigned to the Barremian-Aptian (Friis et al., 1999; Zherikhin et al., 1998). This 3367 range has since been completely revised to Albian-Campanian, on the basis of pollen morphology 3368 (Doyle and Endress, 2014) and younger appearances of Asteropollis (Dettmann and Thomson, 1987; Eklund et al., 2004; Martínez et al., 2013). A minimum age can thus be estimated by the upper 3369 3370 boundary of the Campanian, 72.1 Ma  $\pm$  0.2 Myr, or 71.9 Ma. 3371 Soft maximum as for 75.3. 3372 3373 86.4. Discussion 3374 3375 Triassothrips virginicus Grimaldi et al., 2004 was described from the Late Triassic of Virginia.

Although it was used as a calibration for Thysanoptera by Misof et al. (2014), *T. virginicus* is found in a basal polytomy outside of any crown group members in a morphological phylogeny (P. Nel et al., 2012). *Liassothrips crassipes* Martynov, 1927 is known from the Late Jurassic of Kazakhstan, but is classified in an extinct family, Liassothripidae (Shmakov, 2008). While Shmakov (2008) suggests Liassothripidae is the oldest family in the Tubulifera, making it crown Thysanoptera, characters are

3381	also listed linking it with Terebrantia; without a phylogenetic analysis it is difficult to assess their
3382	polarity and thus crown affinity.
3383	
3384	87. Crown Hemiptera
3385	
3386	This clade comprises Sternorrhyncha (aphids, scale insects), Fulgoromorpha (planthoppers),
3387	Cicadomorpha (cicadas, leafhoppers, treehoppers), Coleorrhyncha (moss bugs) and Heteroptera
3388	(typical bugs), their last common ancestor and all of its descendants (Fig. 21). Monophyly of
3389	Hemiptera is established by phylogenetic analysis of housekeeping genes (Cryan and Urban, 2012),
3390	whole mitochondrial genomes (Cui et al., 2013), transcriptomes (Misof et al., 2014; Simon et al.,
3391	2012), and wing morphology (Yoshizawa and Saigusa, 2001).
3392	
3393	87.1. Fossil specimens
3394	
3395	As for 85.1.
3396	
3397	87.2. Phylogenetic justification
3398	
3399	As for 85.2.
3400	
3401	87.3. Age justification
3402	
3403	As for 85.3.
3404	
3405	88. Crown Psocodea
3406	
	131

3407	This clade comprises Psocoptera (barklice) and Phthiraptera (true lice), their last common
3408	ancestor and all of its descendants (Fig. 21). Monophyly of this clade is supported by phylogenies of
3409	transcriptomes (Misof et al., 2014), nuclear protein-coding genes (Ishiwata et al., 2011), mitochondrial
3410	genes (Yoshizawa and Johnson, 2003), and morphology (Lyal, 1985).
3411	
3412	88.1. Fossil specimens
3413	
3414	Cretoscelis burmitica Grimaldi and Engel, 2006. AMNH Bu912, holotype, female in amber.
3415	
3416	88.2. Phylogenetic justification
3417	
3418	In a morphological phylogenetic analysis, C. burmitica was a stem group member of
3419	Liposcelididae (Grimaldi and Engel, 2006). Liposcelididae is an extant family of Psocoptera, thus
3420	within the crown group of Psocodea.
3421	
3422	88.3. Age justification
3423	
3424	As for 81.3.
3425	
3426	89. Crown Holometabola
3427	
3428	This clade comprises Hymenoptera (sawflies, ants, bees, wasps) and Aparaglossata, their last
3429	common ancestor and all of its descendants (Figs. 23 and 24). Support for monophyly comes from
3430	phylogenetic analysis of transcriptomes (Misof et al., 2014; Peters et al., 2014), morphology (Beutel et
3431	al., 2011), and morphology plus molecules (Oakley et al., 2013). This clade exists in GenBank, but as
3432	Endopterygota.

3434 89.1. Fossil specimens

3435

3436 *Westphalomerope maryvonneae* Nel et al., 2007. MNHN-LP-R.55181, holotype, preserving a 3437 hindwing. Pictured in Nel et al. (2007; Fig. 1a).

3438

3439 89.2. Phylogenetic justification

3440

3441 W. maryvonneae has not been included in a phylogenetic analysis, nor have any other 3442 members of its family, Protomeropidae. Mostly Permian members of Protomeropidae have been 3443 proposed to have affinities with a variety of holometabolan clades, including the total groups of 3444 Trichoptera, Mecoptera, and more generally Amphiesmenoptera or Antliophora (Grimaldi and Engel, 3445 2005; Kukalova-Peck and Willmann, 1990; Morse, 1997; Nel et al., 2013, 2007; Sukatsheva et al., 3446 2007). Crown amphiesmenopteran (and thus trichopteran) affinity may be unlikely, as Protomeropidae 3447 lack a key synapomorphy, a true 'double-Y loop' arrangement of the anal veins on the forewing 3448 (Labandeira, 2011; Minet et al., 2010). However, Permian Protomeropidae possess Carpenter's 3449 organs in the male, a probable apomorphy for total group Mecoptera (Minet et al., 2010). 3450 Protomeropidae (with a younger date) was subsequently used to calibrate the basal split of 3451 Mecopterida for divergence time estimation (Rehm et al., 2011). Pending phylogenetic analysis of 3452 wing morphology, it is difficult to assign a specific placement for Protomeropidae, however, even with a 3453 conservative view all these possibilities are within crown Aparaglossata, and therefore crown 3454 Holometabola. 3455

3456 89.3. Age justification

3457

3458 *W. maryvonneae* was collected from black shales in the "Terril no. 5" horizon at the "Faisceau

3459 de Modeste", "Veine Maroc" locality in Bruay-la-Bussière, Pas-de-Calais, France (Nel et al., 2007). 3460 The locality is dated as early Langsettian (Nel et al., 2007), equivalent to the Westphalian A stage 3461 (Pointon et al., 2012). There is a SHRIMP U-Pb date within the middle Langsettian estimated at 3462  $317.63 \text{ Ma} \pm 0.12 \text{ Myr}$ , however, the stratigraphy of Bruay-la-Bussière is not precise enough to 3463 determine when in the Westphalian A the fossil occurred (Nel et al., 2007; Pointon et al., 2012). 3464 Therefore, we use a date inclusive of the upper boundary of the Westphalian A, which is the upper boundary of Westphalian B. U-Pb dating of zircons constrains the upper boundary of the Westphalian 3465 3466 B to 313.78 Ma ± 0.08 Myr (Pointon et al., 2012), so a minimum age for W. maryvonneae is 313.70 3467 Ma. 3468 Soft maximum as for 75.3. 3469 3470 89.4. Discussion 3471 3472 Srokalarva berthei Haug et al., 2015 is a putative holometabolan larva, from the Mazon Creek 3473 and thus younger than W. maryvonneae. S. berthei has been interpreted as both an antliophoran (Labandeira, 2011) and a neuropterid (Haug et al., 2015), both positions within the crown group of 3474 3475 Holometabola. S. berthei, however, remains informative about the evolutionary timing of insect 3476 metamorphosis.

3477

## 3478 **90. Crown Hymenoptera**

3479

This clade comprises Symphyta (sawflies) and Apocrita (itself comprising Apoidea, Formicidae, and a paraphyletic group of wasps), their last common ancestor and all of its descendants (**Fig. 23**). Monophyly is supported by phylogenetic analysis of transcriptomes (Misof et al., 2014), morphology (Beutel et al., 2011), and morphology analysed together with molecular data (Ronquist et al., 2012).

3485	90.1. Fossil specimens
3486	
3487	<i>Triassoxyela foveolata</i> Rasnitsyn, 1964. PIN 2070/1, holotype ( <b>Fig. 25a</b> ).
3488	
3489	90.2. Phylogenetic justification
3490	
3491	In the total-evidence phylogenetic analysis of Ronquist et al. (2012), T. foveolata was found as
3492	a stem group member of the family Xyelidae. As Xyelidae is a crown group family of sawflies, it is thus
3493	crown Hymenoptera.
3494	
3495	90.3. Age justification
3496	
3497	T. foveolata was found in the Madygen Formation, south of the Fergana Valley, Kyrgyzstan.
3498	Key plant fossils Scytophyllum and Neocalamites correlate the Madygen to the Scytophyllum flora of
3499	the upper Keuper lithographic unit, of Ladinian-Carnian age (Dobruskina, 1995). The Scytophyllum
3500	flora is correlated with the Cortaderitian Stage of Gondwana due to the abundance of Scytophyllum
3501	(Morel et al., 2003). The Cortaderitian Stage is divided into 3 Biozones; a 40Ar/39Ar radiometric date
3502	for the middle biozone of the Cortaderitian Stage of 228.5 Ma $\pm$ 0.3 Myr was measured by Rogers et
3503	al. (1993), falling within the Carnian (O'Reilly et al., 2015). The Gondwanan Puesto Viejo Formation,
3504	part of the Barrealian Stage underlying the Cortaderitian Stage (and therefore the Scytophyllum flora)

3505 has been radiometrically dated to 232 Ma ± 4 Myr, also within the Carnian (Valencio et al., 1975).

3506 Recently calculated SHRIMP U-Pb dates dispute this age, instead constraining the Puesto Viejo

3507 Formation to 235.8 Ma ± 2.0 Myr (Ottone et al., 2014). This suggests the Cortaderitian Stage is no

3508 older than 237.8 Ma, and therefore the Scytophyllum flora and Madygen Formation can be no older

3509 than this age, still within the Carnian. Note that a GSSP for the Carnian-Norian boundary has not yet

3510 been identified; radioisotopic ages may suggest a younger boundary at ~220 Ma (Lucas et al., 2012).

3511	Nevertheless, a commonly accepted date for the Carnian upper boundary is estimated at 228.4 Ma $\pm$
3512	2 Myr based on cyclostratigraphy and a candidate GSSP (e.g. Ogg, 2012; Ogg et al., 2014), so this
3513	provides a minimum age at 226.4 Ma.
3514	Soft maximum as for 75.3.
3515	
3516	90.1 Discussion
3517	
3518	Previous work has suggested Archexyela ipswichensis Engel, 2005 from the Mt. Crosby
3519	Formation, Ipswich Coal Measures of Queensland, Australia may be the oldest hymenopteran (e.g.
3520	Nicholson et al., 2015). However, the stratigraphy of the Ipswich Basin also provides a minimum age
3521	of uppermost Carnian (Purdy and Cranfield, 2013), thus we calibrate crown Hymenoptera with the
3522	equally old T. foveolata, which has been included in landmark total-evidence phylogenies (O'Reilly et
3523	al., 2015; Ronquist et al., 2012).
3524	
3525	91. Crown Aparaglossata
3526	
3527	This clade comprises Neuropterida, Coleopterida and Mecopterida, their last common ancestor
3528	and all of its descendants (Fig. 23). The clade was first named by Peters et al. (2014) based on
3529	support from phylogenetic analysis of transcriptomes.
3530	
3531	91.1. Fossil specimens
3532	
3533	As for 89.1.
3534	
3535	91.2. Phylogenetic justification
3536	
	136

3537	As for 89.2.
3538	
3539	91.3. Age justification
3540	
3541	As for 89.3.
3542	
3543	92. Crown Neuropterida
3544	
3545	This clade comprises Raphidioptera (snakeflies), Megaloptera (fishflies), Neuroptera (net-
3546	winged insects), their last common ancestor and all of its descendants (Fig. 23). Monophyly is
3547	established by phylogenetic analysis of transcriptomes (Misof et al., 2014; Peters et al., 2014), protein-
3548	coding genes (Wiegmann et al., 2009), morphology (Beutel et al., 2011), and combined molecular and
3549	morphological data (Winterton et al., 2010).
3550	
3551	92.1. Fossil specimens
3552	
3553	Elmothone martynovae Carpenter, 1976. MCZ 5585, holotype, a forewing (Fig. 25b). Figured
3554	by Prokop et al. (2015; Fig. 7A).
3555	
3556	92.2. Phylogenetic justification
3557	
3558	A morphological phylogenetic analysis placed the Permithonidae sensu lato as a stem group to
3559	the extant Neuroptera (Ren et al., 2009; shown in supplementary information therein). A position on
3560	the stem lineage of Neuroptera is thus part of the crown group of Neuropterida. As the coding was
3561	done at a family level, we note with caution that monophyly of the Permithonidae and the exact
3562	relationships of its member species with Neuroptera has not been examined in a phylogenetic context
	137

3563 and remain obscure (Prokop et al., 2015). Nonetheless, most members of Permithonidae possess the 3564 character states coded by Ren et al. (2009), so we take the oldest well-described member, E. 3565 martynovae, as a calibration fossil. 3566 3567 92.3. Age justification 3568 3569 This fossil occurs in the Carlton Limestone Member of the Wellington Formation in the Sumner 3570 Group of Elmo, Dickinson County, central Kansas (Prokop et al., 2015; Zambito et al., 2012). The 3571 insect-bearing locality is correlated with the Leonardian regional Stage (Sawin et al., 2008; Zambito et 3572 al., 2012) on the basis of conchostracan biostratigraphy (Tasch, 1962). The Leonardian spans the 3573 Artinskian and the younger Kungurian Stage (Henderson et al., 2012). The upper boundary of the 3574 Kungurian is 272.3 Ma  $\pm$  0.5 Myr, thus providing a conservative minimum age estimate of 271.8 Ma. 3575 Soft maximum as for 75.3. 3576 3577 92.4. Discussion 3578 3579 A younger member of the Permithonidae, Permithone belmontensis Tillyard, 1922 3580 (Changhsingian or latest Permian of Belmont, Australia), was previously used as a calibration fossil for 3581 Neuropterida (Misof et al., 2014). 3582 3583 93. Crown Megaloptera 3584 3585 This clade comprises Sialidae and Corydalidae, their last common ancestor and all of its 3586 descendants (Fig. 23). Monophyly is established by phylogenetic analysis of full mitochondrial

3587 genomes (Wang et al., 2012), transcriptomes (Misof et al., 2014), and morphology of the wing base

3588 (Zhao et al., 2014).

3589	
3590	93.1. Fossil specimens
3591	
3592	Eochauliodes striolatus Liu et al., 2012. CNU-MEG-NN2011004 P/C, holotype part/counterpart,
3593	laterally preserving an adult including forewing and hindwing (Fig. 25c).
3594	
3595	93.2. Phylogenetic justification
3596	
3597	E. striolatus was included in a phylogenetic analysis of morphology, encompassing characters
3598	from wing venation, adult genitalia, and larval morphology where possible (Liu et al., 2012). E.
3599	striolatus was found within the crown Corydalidae, at the base of the 'Protochauliodes clade'
3600	(comprising extant species). This position is therefore within crown Megaloptera. The bifurcated
3601	anterior branch of the Rs vein is a relevant synapomorphy (Liu et al., 2012).
3602	
3603	93.3. Age justification
3604	
3605	As for 79.3.
3606	
3607	93.4. Discussion
3608	
3609	Another fossil from the Daohugou fauna, Jurochauliodes ponomarenkoi Wang and Zhang,
3610	2010 was found in a slightly more basal position within the Corydalidae (and thus Megaloptera) crown
3611	group (Liu et al., 2012). As it is of equal age to <i>E. striolatus</i> , it is also an acceptable calibration fossil
3612	for this clade.
3613	
3614	94. Crown Neuroptera

3616 This clade comprises Hemerobiiformia, Nevrorthiformia and Myrmeleontiformia, their last 3617 common ancestor and all of its descendants (Fig. 23). Monophyly is supported by phylogenetic 3618 analysis of ribosomal and mitochondrial genes (Haring and Aspöck, 2004), housekeeping genes 3619 (Wiegmann et al., 2009), and morphology (Beutel et al., 2011; Zhao et al., 2014). 3620 3621 94.1. Fossil specimens 3622 3623 Liassochrysa stigmatica Ansorge and Schlüter, 1990. MBA.I 5046 (formerly from the Ansorge 3624 collection, Dobbertin, Germany: No. LDA301), holotype, preserving a forewing. Imaged in (Wedmann 3625 and Makarkin, 2007: Fig. 5a). 3626 3627 94.2. Phylogenetic justification 3628 3629 L. stigmatica was coded in the morphological matrix for the total evidence phylogeny of Liu et 3630 al. (2015). In that tree, it was a member of crown group Mantispidae, a family within Hemerobiiformia, 3631 and therefore crown Neuroptera (Liu et al., 2015). This fossil was also the oldest calibration used for 3632 Neuroptera in the divergence time analysis of Winterton et al. (2010). 3633 3634 94.3. Age justification 3635 3636 The fossil was recovered from the former clay pit of Schwinz, near Dobbertin, Mecklenburg, 3637 northeast Germany (Ansorge and Schlüter, 1990). Multiple associated ammonites (Eleganticeras 3638 elegantulum, Lobolytoceras siemensi, Harpoceras capellatum) indicate that the locality is correlated to 3639 the lower part of the *H. falciferum* ammonite Zone, early Toarcian (Ansorge and Schlüter, 1990; 3640 O'Reilly et al., 2015; Pálfy et al., 2002, 2000). The Boreal falciferum Zone is equivalent to the Tethyan

140

3641	H. serpentinum ammonoid Zone (Macchioni, 2002), and succeeded by the Hildoceras bifrons
3642	ammonoid Zone. The base of the <i>bifrons</i> Zone has been dated to 180.36 Ma $\pm$ 0.7 Myr (Ogg et al.,
3643	2012b). From this, an upper boundary of the falciferum Zone can be derived, and thus a minimum age
3644	for Dobbertin, at 179.66 Ma.
3645	Soft maximum as for 75.3.
3646	
3647	95. Crown Coleopterida
3648	
3649	This clade comprises Strepsiptera (twisted wing parasites) and Coleoptera (beetles), their last
3650	common ancestor and all of its descendants (Fig. 23). Monophyly of this clade is an extremely well-
3651	examined question in systematics, often used to illustrate the principle of long branch attraction (e.g.
3652	Boussau et al., 2014; Carmean and Crespi, 1995; Huelsenbeck, 1998, 1997; Niehuis et al., 2012;
3653	Siddall and Whiting, 1999; Whiting et al., 1997; Wiegmann et al., 2009). However, recent analyses of
3654	genomes and transcriptomes have consistently converged on a sister group relationship between
3655	Strepsiptera and Coleoptera (Boussau et al., 2014; Misof et al., 2014; Niehuis et al., 2012).
3656	
3657	95.1. Fossil specimens
3658	
3659	Adiphlebia lacoana Scudder, 1885. USNM 38140, holotype, preserving a forewing. Imaged in
3660	Béthoux (2009: Fig. 1(3-5)).
3661	
3662	95.2. Phylogenetic justification
3663	
3664	A. lacoana has not been included in formal cladistic analysis to test its phylogenetic position.
3665	Variation in forewing venation within species provides a challenge to homology statements (Béthoux,
3666	2009; Garwood and Sutton, 2010). However, A. lacoana shares a forewing character with the crown
	141

3667 beetle suborder Archostemata, specifically: "the areas between ScP, RA, branches of RP, M, branches 3668 of CuA, and AA filled with a regular network of guadrangular to pentagonal cells forming intercalary 3669 longitudinal pseudo-veins" (Béthoux, 2009). Intercalary pseudo-veins are also observed in fossils 3670 throughout Pterygota, suggesting this is either a symplesiomorphic or homoplastic state. However, 3671 some of the wing regions exhibiting intercalary veins (ScP and RA) are restricted to fossil Coleoptera (Béthoux, 2009). A. lacoana has thus been designated as a sister group to all crown Coleoptera. i.e. a 3672 3673 member of its stem lineage (Béthoux, 2009), and thus a crown group member of Coleopterida. This 3674 assignment is also supported by putative larval material (Labandeira, 2011). 3675 There has been debate, however, about the taphonomy of the network of wing veins, 3676 suggesting they are clumps of clay instead of morphological characters (Kukalova-Peck and Beutel, 3677 2012). Alternative placements were on the stem lineage of Neuroptera or Neuropterida (Kukalova-3678 Peck and Beutel, 2012), or outside Holometabola altogether (Guan et al., 2016; Nel et al., 2013). 3679 3680 95.3. Age justification 3681 3682 Minimum as for 31.3. Soft maximum as for 75.3. 3683 3684 96. Crown Coleoptera 3685 3686 This clade comprises Archostemata, Myxophaga, Adephaga (ground beetles, tiger beetles, 3687 diving beetles, whirliging beetles) and Polyphaga (ladybugs, longhorn beetles, weevils, fireflies, 3688 scarabs, stag beetles, rove beetles), their last common ancestor and all of its descendants (Fig. 23). 3689 Monophyly is supported by phylogenetic analysis of nuclear protein-coding genes (McKenna et al., 3690 2015) and morphology (Beutel et al., 2011). 3691 3692 96.1. Fossil specimens

3693				
3694	Triadogyrus sternalis Ponomarenko, 1977. PIN 3320/13, holotype (Fig. 25d), an exoskeleton			
3695	without head, prothorax, or legs (Arnol'di et al., 1992).			
3696				
3697	96.2. Phylogenetic justification			
3698				
3699	In the morphological phylogenetic analysis of Beutel et al. (2013), T. sternalis is a stem group			
3700	member of the family Gyrinidae. As Gyrinidae is part of Adephaga, crown membership within both			
3701	Adephaga and Coleoptera is justified.			
3702				
3703	96.3. Age justification			
3704				
3705	T. sternalis was recovered from the mouth of Bereni River near Garazhokva settlement,			
3706	Khar'kov oblast, Izyum region, Ukraine (Arnol'di et al., 1992). Fossiliferous strata are lacustrine			
3707	claystone, part of the Protopivka Formation, estimated as Late Carnian-Early Norian age within the			
3708	late Triassic (Arnol'di et al., 1992; Rasnitsyn and Quicke, 2002; Shcherbakov, 2008). The upper Norian			
3709	boundary is estimated at ~208.5 Ma, so this provides a conservative minimum age.			
3710	Soft maximum as for 75.3.			
3711				
3712	96.4. Discussion			
3713				
3714	The Pennsylvanian (Mazon Creek) fossil A. lacoana is a member of the stem lineage of			
3715	Coleoptera (Béthoux, 2009). Recent divergence time analyses (McKenna et al., 2015; Misof et al.,			
3716	2014) have therefore elected not to calibrate the crown group of Coleoptera with A. lacoana. Resulting			
3717	age estimates for crown Coleoptera ranged from 250-280 Ma, substantially younger than A. lacoana			
3718	itself.			

The Permian *Coleopsis archaica* Kirejtshuk et al., 2014 was noted as a stem group fossil, potentially Protocoleoptera (stem Coleoptera) (McKenna et al., 2015). Thus it was not used as a calibration. However, using younger internal calibrations (the oldest from Madygen, 225 Ma in their dataset), the crown origin of Coleoptera was estimated around 250 Ma (McKenna et al., 2015). Accounting for error bars, the crown group may have originated shortly before (or shortly after) the end-Permian extinction, timing that is compatible with *C. archaica* as a very early representative.

3725

## 3726 **97. Crown Mecopterida**

3727

3728 This clade comprises Amphiesmenoptera and Antliophora, their last common ancestor and all 3729 of its descendants (Fig. 24). Phylogenetic support for monophyly of Mecopterida comes from 3730 genomes (Niehuis et al., 2012), transcriptomes (Misof et al., 2014) and morphology (Beutel et al., 3731 2011). Note that the clade we refer to as Mecopterida was called Panorpida by Grimaldi and Engel 3732 (2005), because they used Mecopterida to refer to paraphyletic Mecoptera containing Siphonaptera (and excluding Diptera). Our clade Mecopterida was also referred to as Panorpoidea by several 3733 3734 sources, including Ren et al. (2009). Analyses relying on molecular data alone do not support the 3735 paraphyly of Mecoptera (Misof et al., 2014; Peters et al., 2014; Wiegmann et al., 2009), and these 3736 tend to utilize our conception of Mecopterida.

3737

3738 97.1. Fossil specimens

3739

3740 *Permopanorpa inaequalis* Tillyard, 1926. YPM IP 005058, holotype, a wing (**Fig. 25e**).

3741

3742 97.2. Phylogenetic justification

3743

*P. inaequalis* is the oldest member of the family Permopanorpidae, which was coded (at the

family level) in the morphological matrix of Ren et al. (2009). In that tree, it was part of the total group of Antliophora (although the figure label indicated it was inside crown Antliophora, the topology clearly indicates it was on the stem lineage; Ren et al., 2009). As a stem group member of Antliophora, *P. inaequalis* is thus crown group Mecopterida.

3749

3750 97.3. Age justification

3751

3752 As for 92.3.

3753

3754 97.4. Discussion

3755

*W. maryvonneae* (family Protomeropidae), from the Bashkirian of France, has been proposed as an "amphiesmenopteran or antliophoran", which may mean it belongs on the stem lineage of one of those clades and thus in crown Mecopterida. It has also been drawn onto a phylogram as a stem member of Mecoptera (Nel et al., 2013). However, the evidence for any particular placement within Mecopterida is ambiguous, and thus it is possible the fossil is only stem Mecopterida. See 89.2 for greater detail.

Conversely, the early to middle Permian family Kaltanidae has been included in a phylogenetic analysis, and shown to fall on the stem lineage of Amphiesmenoptera (Ren et al., 2009). Although Kaltanidae have been previously discussed as calibration fossils for Mecopterida (e.g. Benton and Donoghue, 2007), their oldest members are from the Kungurian Stage of Russia, the same age as Elmo (Bashkuev, 2008). Additionally, the family Belmontiidae is within crown Mecopterida in a phylogenetic analysis (Ren et al., 2009), but its oldest fossil is from the late Permian (Changhsingian) of Australia (Grimaldi and Engel, 2005).

3769

#### 3770 **98. Crown Amphiesmenoptera**

3772 This clade comprises Trichoptera (caddisflies) and Lepidoptera (butterflies, moths), their last 3773 common ancestor and all of its descendants (Fig. 24). Monophyly is supported by phylogenetic 3774 analysis of transcriptomes (Misof et al., 2014), nuclear protein-coding genes (Wiegmann et al., 2009), 3775 and morphology (Beutel et al., 2011; Kristensen, 1991). 3776 3777 98.1. Fossil specimens 3778 3779 Archaeolepis mane Whalley, 1985. BMNH In. 59397, holotype, preserving a hindwing (Fig. 3780 25f). 3781 3782 98.2. Phylogenetic justification 3783 3784 A. mane has been used to calibrate the lepidopteran root in previous molecular dating analyses (e.g. Wahlberg et al., 2013), where this relationship is based on two lines of evidence: wing 3785 3786 scales and wing venation. The preservation of extremely rare scales completely covering the hindwing 3787 excludes A. mane from crown Trichoptera (Whalley, 1986, 1985) because Trichoptera only bear scales 3788 on the forewing. The presence of scales across the entirety of a wing with panorpoid venation can only 3789 signal amphiesmenopteran affinity. 3790 The Sc vein (with one visible branch) of A. mane is unlikely to represent the ancestral state for 3791 Lepidoptera, as the number of Sc vein branches varies in early-diverging moths, but is usually two 3792 branches, and this vein is multi-branched ancestrally in Amphiesmenoptera (Kukalova-Peck and 3793 Willmann, 1990; Minet et al., 2010; Sukatsheva and Vassilenko, 2011; Schachat and Brown, 2016). 3794 Although Trichoptera tend to have more wing veins than Lepidoptera, it is likely that fewer veins were

- 3795 lost by ancestral moths than is currently accepted in the literature, making distinctions between
- amphiesmenopteran branches difficult for Mesozoic fossils (Schachat and Brown, 2015, 2016). As
  - 146

3797 reconstructed by Whalley (1986), the wing venation of A. mane differs markedly from the venation of crown Lepidoptera: there is a single, branched Cubitus vein, with CuP apparently absent, and all three 3798 3799 branches of the anal vein reach the dorsum. In contrast, basal crown Lepidoptera nearly always have 3800 a CuP vein, and the anal vein becomes fused before reaching the dorsum (Common, 1973; Schachat 3801 and Brown, 2016). A position for A. mane within the crown group of Lepidoptera thus cannot be 3802 confirmed, but an identity as stem Lepidoptera is highly likely based on the wing scales in particular, in 3803 agreement with Whalley (1986). This fossil would therefore be within the crown group of 3804 Amphiesmenoptera. 3805 3806 98.3. Age justification 3807 3808 Whalley (1985) noted the locality as Black Ven, Charmouth, Dorset, on the Jurassic Coast of

England. This was further specified as calcareous flatstone, probably from Bed 75a, of the *Caenisites turneri* ammonoid Zone (Sohn et al., 2012), or *Microderoceras birchi* Nodular of the "Shales with Beef"
(Lang et al., 1923). Chemostratigraphy places the *C. turneri* (and *M. birchi*) Zones within the middle
Sinemurian (Jenkyns et al., 2002). The upper boundary of the *C. turneri* Zone is thus dated to 195.31
Ma (Ogg et al., 2012b), providing a minimum age.

3814 Soft maximum as for 75.3.

3815

# 3816 99. Crown Trichoptera

3817

3818This clade comprises 'Spicipalpia', Annulipalpia and Integripalpia their last common ancestor3819and all of its descendants (**Fig. 24**). Monophyly is supported by phylogenetic analysis of

transcriptomes (Misof et al., 2014), housekeeping genes (Kjer et al., 2002, 2001; Malm et al., 2013),

and morphology (Beutel et al., 2011).

3822

3823	99.1. Fossil specimens			
3824				
3825	Liadotaulius maior Handlirsch, 1906. Handlirsch (1906) did not designate a holotype, thus we			
3826	refer to three specimens figured by Ansorge (2002): (Ansorge collection, to be deposited at MBA: LGA			
3827	1995; Fig. 25g), female forewing, (LGA 672), male forewing, and (LGA 1710), hindwing.			
3828				
3829	99.2. Phylogenetic justification			
3830				
3831	Taxonomic placement of <i>L. maior</i> requires apomorphies from the male wings, as female wings			
3832	have many plesiomorphic venation characters (Ansorge, 2002). Further studies of a younger			
3833	congeneric, L. daohugouensis Wu and Huang, 2012, reveal new characters shared with crown group			
3834	Trichoptera. These include the apical part of Cu2 bending towards the wing margin, its			
3835	desclerotisation, and complete anal veins (Ansorge, 2002; Wu and Huang, 2012). These apomorphies			
3836	place the genus Liadotaulius in Philopotamidae, a family within crown group Annulipalpa, and thus			
3837	Trichoptera (Wu and Huang, 2012).			
3838				
3839	99.3. Age justification			
3840				
3841	The fossils were recovered from Grimmen, northeast Germany (Ansorge, 2002). Further age			
3842	information as for 94.3.			
3843				
3844	99.4. Discussion			
3845				
3846	Possible caddisfly larval cases were recently described from the early Permian of Brazil (Mouro			
3847	et al., 2016). The cases are tubular in form, and particulate matter is stuck to some of the cases			
3848	(Mouro et al., 2016). Of the two most basal extant trichopteran families that construct larval cases, the			
	148			

3849	Hydroptilidae construct tubular cases and the Glossosomatidae construct their cases from particulate
3850	matter (Malm et al., 2013). However, various types of larval cases, including tubular cases, are
3851	constructed by caddisflies belonging to distantly-related lineages (Malm et al., 2013); at present, it
3852	cannot be assumed that tubular larval cases have originated only once within the Trichoptera.
3853	Assuming the Permian fossils are indeed insect larval cases, therefore, does not confirm the
3854	phylogenetic position of their inhabitants within crown versus stem Trichoptera, as larval cases might
3855	have evolved in the stem group.
3856	
3857	100. Crown Lepidoptera
3858	
3859	This clade comprises Zeugloptera, Aglossata, Heterobathmiina and Glossata (itself comprising
3860	six infraorders, over 100 families, and over 160,000 species), their last common ancestor and all of its
3861	descendants (Fig. 24). The list of lepidopteran subclades comes from a recently published consensus
3862	(van Nieukerken et al., 2011), although some molecular analyses have not recovered these clades
3863	(Regier et al., 2013). Monophyly is supported by nuclear protein-coding genes (Regier et al., 2013),
3864	transcriptomes (Misof et al., 2014), and morphology (Beutel et al., 2011).
3865	
3866	100.1. Fossil specimens
3867	
3868	Parasabatinca aftimacrai Whalley, 1978. Although the holotype (the specimen to which we
3869	refer; Fig. 25h) and two paratypes were attributed to the NHMUK (Sohn et al., 2012), they are now
3870	housed as part of the Acra collection, curated by D. Azar, pending construction of a fossil museum at
3871	the Lebanese University in Fanar (Matn), Lebanon (D. Azar, pers. comm.).
3872	
3873	100.2. Phylogenetic justification
3874	

3875 Although not included in formal phylogenetic analysis, morphological characters (morphology 3876 of the antennae with ascoids, number and shape of tibial spurs, mouthpart and maxillary palp 3877 morphology) support the position of *P. aftimacrai* in what was formerly known as the 'Sabatinca' group 3878 of genera within Micropterigidae (Kristensen and Skalski, 1998; D. Azar, pers. comm.). As P. aftimacrai 3879 has an unbranched R vein and because Rs<sub>4</sub> terminates below the apex, the wing venation of P. 3880 aftimacrai most closely resembles that of the extant species Austromartyria porphyrodes, which 3881 belongs to what is now known as the 'Southern sabatincoid' lineage of Micropterigidae (Gibbs, 2010). 3882 Based on the above morphological characters, P. aftimacrai is supported as the oldest crown group 3883 member in multiple summaries of the fossil record of Lepidoptera (Grimaldi and Engel, 2005, Fig. 3884 13.13; Sohn et al., 2015, Fig. 2). Membership either within the crown or stem of Micropterigidae places 3885 the fossil within crown Zeugloptera and crown Lepidoptera. 3886 3887 100.3. Age justification 3888 3889 As for 76.3. 3890 3891 3892 100.4. Discussion 3893 3894 A number of older fossils have been assigned to Lepidoptera, but their position within the 3895 crown is ambiguous. A. mane, from the Early Jurassic of Dorset, England, has been used to calibrate 3896 the lepidopteran root in previous molecular dating analyses (e.g. Wahlberg et al., 2013). See 98.2 for 3897 exclusion of A. mane from the lepidopteran crown. 3898 Sohn et al. (2015) suggested that two undescribed fossil species are members of the 3899 Micropterigidae stem lineage (and thus crown Zeugloptera and crown Lepidoptera). These are from 3900 the Toarcian (Early Jurassic) Grüne Series of Grimmen, Germany (Ansorge, 2002), but they are too

3901 poorly characterized to be confidently used as calibration fossils.

# **101. Crown Antliophora**

3905	This clade comprises Siphonaptera (fleas), Mecoptera (scorpionflies) and Diptera (flies), their
3906	last common ancestor and all of its descendants (Fig. 24). Support for monophyly comes from
3907	phylogenetic analysis of transcriptomes (Misof et al., 2014; Peters et al., 2014) and morphology
3908	(Beutel et al., 2011). A recent analysis of mitochondrial genomes finds Amphiesmenoptera within
3909	Antliophora under some analytical conditions, potentially challenging antliophoran monophyly (Song et
3910	al., 2016).
3911	
3912	101.1. Fossil specimens
3913	
3914	Pseudonannochorista willmanni Novokshonov, 1994. PIN 966/21, holotype, preserving a
3915	forewing ( <b>Fig. 25i</b> ).
3916	
3917	101.2. Phylogenetic justification
3918	
3919	Pseudonannochoristinae is a subfamily of the Permochoristidae (Bashkuev, 2011;
3920	Novokshonov, 1994), however, a morphological phylogenetic analysis indicates polyphyly of this family
3921	(Ren et al., 2009). While the Permochoristinae (the other subfamily of Permochoristidae) fall on the
3922	stem lineage of Antliophora, Pseudonannochoristinae are part of the stem lineage of Mecoptera (Ren
3923	et al., 2009). Therefore, P. willmanni, as a member of Pseudonannochoristinae, is part of the crown
3924	group of Antliophora.
3925	
3926	101.3. Age justification

3928 Minimum as for 77.3. Soft maximum as for 75.3.

3929

3930 101.4. Discussion

3931

3932 Other fossils from the families Permotanyderidae, Permotipulidae, and Nannochoristinae are 3933 all demonstrably within crown group Antliophora (Ren et al., 2009). However, the localities from which 3934 they are known are younger, of Changhsingian age (Belmont, Australia and Mooi River, South Africa). 3935 Fossils of Siphonaptera from the Jurassic (Gao et al., 2012) and Cretaceous (Gao et al., 2014; 3936 Huang, 2015), suggested to parasitise dinosaurs, have been excluded from the crown group in a 3937 recent molecular phylogenetic analysis (Zhu et al., 2015). The molecular clock analysis (which was 3938 calibrated with better established fossils from Dominican and Baltic amber, of Miocene and Eocene 3939 age, respectively) estimated the origins of crown Siphonaptera in the Valanginian to Aptian stages of 3940 the Early Cretaceous (Zhu et al., 2015). Furthermore, none of the Mesozoic fossils possess a 3941 diagnostic character combination for the crown group (Dittmar et al., 2016). As siphonapteran 3942 parasites of dinosaurs would require a strong assumption that piercing mouthparts must be used for 3943 blood-feeding (Dittmar et al., 2016), we do not include any crown fossil calibrations.

3944

# 3945 **102. Crown Mecoptera**

3946

This clade comprises Apteropanorpidae, Bittacidae, Boreidae, Choristidae, Eomeropidae, Meropeidae, Nannochoristidae, Panorpidae, and Panorpodidae, their last common ancestor and all of its descendants (**Fig. 24**). Paraphyly of the traditional concept of Mecoptera (i.e. inclusion of Siphonaptera) was proposed by Whiting (2002) on the basis of four nuclear genes. This was, however, contradicted by analysis of six nuclear genes (Wiegmann et al., 2009), transcriptomes (Misof et al., 2014; Peters et al., 2014), and morphology (Beutel et al., 2011). Each of the latter studies recovered a

3953	monophyletic	Mecoptera a	as the sister	aroup o	f Siphonaptera.
				3	

3954	
3955	102.1. Fossil specimens
3956	
3957	Burmomerope eureka Grimaldi and Engel, 2013 (collection of James Zigras, available for study
3958	at AMNH: JZC Bu-84), holotype in amber.
3959	
3960	102.2. Phylogenetic justification
3961	
3962	B. eureka was assigned to the stem group of the extant family Meropeidae, based on several
3963	wing venation characters, including loss of slanted portion of CuA in forewing and R-Rs fork basal
3964	(Grimaldi and Engel, 2013). A position on the stem lineage of Meropeidae is therefore within the crown
3965	group of Mecoptera.
3966	
3967	102.3. Age justification
3968	
3969	As for 87.3.
3970	
3971	103. Crown Diptera
3972	
3973	This clade comprises Tipulomorpha (crane flies), Psychodomorpha (moth flies, sand flies),
3974	Culicomorpha (mosquitoes, black flies), Bibionomorpha (march flies, fungus gnats) and Brachycera
3975	(horse flies, robber flies, fruit flies, house flies, blow flies, etc.), their last common ancestor and all of
3976	its descendants (Fig. 24). Monophyly of Diptera has been supported in many phylogenetic analyses,
3977	including those based on transcriptomes (Misof et al., 2014), mitochondrial genomes and microRNA
3978	presence (Wiegmann et al., 2011), and morphology (Beutel et al., 2011; Wiegmann et al., 2011).

3979	
3980	103.1. Fossil specimens
3981	
3982	Grauvogelia arzvilleriana Krzeminski et al., 1994 (part of the private Louis Grauvogel collection,
3983	Ringendorf, Bas-Rhin, France, No. 5514), holotype (Fig. 25j).
3984	
3985	103.2. Phylogenetic justification
3986	
3987	G. arzvilleriana was included in the morphological cladistic analysis of Blagoderov et al. (2007).
3988	In that analysis, it was supported on the stem group of Psychodomorpha (Blagoderov et al., 2007).
3989	Although the original description assigned G. arzvilleriana to its own family, several wing venation
3990	characters were noted as similarities with families of Psychodomorpha (Krzeminski et al., 1994). The
3991	stem group of Psychodomorpha is within crown Diptera.
3992	
3993	103.3. Age justification
3994	
3995	Minimum as for 72.3. Soft maximum as for 75.3.
3996	
3997	103.4. Discussion
3998	
3999	A number of other dipteran fossils have been described from Grès à Voltzia; of special interest
4000	is Voltziapupa tentata Lukashevich et al., 2010, known only from well-preserved pupae, while G.
4001	arzvilleriana is known only from adult wings. The venation of the wing sheath in V. tentata is not well
4002	preserved, preventing a clear link of characters with G. arzvilleriana (Lukashevich et al., 2010).
4003	
4004	104. Conclusions

4006 Based on this compilation, qualitative trends in the fossil record of arthropod crown group 4007 members can be described. Patchiness in our taxonomic coverage results from differential 4008 preservation potential, with a notable scarcity of taxa living in habitats with poorly preserved facies 4009 (e.g. intertidal barnacles or pelagic copepods). More completely preserved fossils representing ancient 4010 divergences are well represented in our list of calibrations, perhaps owing to the attention devoted to 4011 phylogenetic analysis of deep fossil relationships within arthropods (e.g. Garwood and Dunlop, 2014; 4012 Lee et al., 2013; Legg et al., 2013; Oakley et al., 2013; Rota-Stabelli et al., 2011). However because 4013 our review is focused on crown groups, about half of our calibrations are from mid-Palaeozoic 4014 localities, making them much more numerous than those from Cambrian Burgess Shale-type biotas. 4015 Throughout the dataset, there is less of a relationship between 'hard part' preservation (calcified body 4016 parts, such as ostracod carapaces) and phylogenetic accuracy than might be expected.

4017 Particular Konservat-Lagerstätten, such as Herefordshire (Silurian), Rhynie Chert (Devonian), 4018 Mazon Creek (Carboniferous), Crato (Cretaceous) and Burmese amber (Cretaceous), provide several 4019 calibrations representing different arthropod clades, presumably owing to their preservation of non-4020 biomineralised tissues required to identify arthropods to the ordinal level. These sites are critically 4021 important for the arthropod fossil record because of their relatively low preservation potential of many 4022 groups, as is particularly the case for terrestrial arthropods, being less well mineralised than many of 4023 the marine groups. This is reflected in the low level of congruence between the order of appearance of 4024 lineages in the fossil record (stratigraphic appearance) and the order of phylogenetic branching (Wills, 4025 2001; O'Connor and Wills, 2016) in arthropods, as compared to more congruent datasets such as 4026 tetrapods (Benton et al., 1999, 2000; Norell and Novacek, 1992). Clustering of calibrations at 4027 Konservat-Lagerstätten localities may lead to highly variable lengths of ghost lineages for the different 4028 taxa that are preserved together at these sites, and indeed many of the clades in our database have 4029 soft maxima that are substantially older than their hard minimum date. Konservat-Lagerstätten 4030 localities are, however, fairly regularly spaced throughout the Middle to Late Palaeozoic and the

4031 Mesozoic, and interim periods of time are punctuated by numerous other fossil localities yielding fewer 4032 calibration points. This results in our database having good coverage throughout the Phanaerozoic 4033 with fossil localities occurring on average every 4-10 million years. A notable exception is the 43.2 4034 million year gap in the Ordovician, during which no definite earliest appearances of any crown-group 4035 orders have been identified in our study, despite this period being known as the Ordovician 4036 biodiversification event (Servais et al., 2008, 2010). Numerous arthropod stem lineage taxa were 4037 abundant during the Ordovician (e.g. trilobites), while the possible crown group taxa that have been 4038 described, e.g. ostracods (Siveter et al., 2014; Williams et al., 2008), barnacles (Van Roy et al., 2010), 4039 pycnogonids (Rudkin et al., 2013), xiphosurans (Lamsdell, 2013; Rudkin et al., 2008; Van Roy et al., 4040 2010), and acariform mites (Bernini et al., 2002) do not meet the rigorous standards employed herein 4041 for determining calibration points. From the Late Devonian through the Mississippian (382.7 to 323.2 4042 Ma) our dataset has another large gap during which we have only one calibration point, which 4043 interestingly corresponds with one of the largest mass extinctions events known in the fossil record 4044 (McGhee, 2013).

4045 The field of divergence time estimation itself is rapidly advancing. New methodologies to 4046 incorporate fossil morphology and stratigraphy into the model of diversification (Heath et al., 2014; 4047 Wilkinson et al., 2011) and the phylogenetic topology itself ('tip-dating'; Ronguist et al., 2012) are 4048 growing in popularity. Precision and accuracy of date estimates are improved with the inclusion of as 4049 many a priori justified fossils as possible in tip- (Lee et al., 2013; Ronquist et al., 2012; Zhang et al., 4050 2016) or node-dating studies (Heath et al., 2014; Ho and Phillips, 2009; Warnock et al., 2012, 2015; 4051 Yang and Rannala, 2006). When examined in the context of geological and evolutionary history, the 4052 distribution of fossil calibrations in our dataset are comprehensive, and have been rigorously vetted to 4053 ensure they meet a priori requirements (Parham et al., 2012; Warnock et al., 2015). Following their 4054 use in molecular clock analyses, a posteriori methods such as cross-validation could be employed to 4055 explore the impact of calibrations on the resulting divergence time estimates (e.g. Battistuzzi et al., 4056 2015; Dornburg et al., 2011; Marshall, 2008; Near et al., 2005), although these methods cannot justify
- 4057 removal of individual constraints (Warnock et al., 2015). Fossils mentioned in Discussion sections
- 4058 occupy key positions along clade stems, and should also be considered in divergence time
- 4059 applications. To this end, we have compiled a robust list of over 100 fossil calibrations covering much
- 4060 of the arthropod Tree of Life. We hope this summary will inspire further work clarifying the
- 4061 phylogenetic relationships of fossil arthropods, and morphological studies of characters linking them to
- 4062 their crown clades.
- 4063
- 4064

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5920 I	FIGURE	CAPTIONS
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5922 **Fig. 1.** Calibration diagram for Ecdysozoa (nodes 2-5, 22-23, 34, 41). Altocrust. = Altocrustacea.

5923 Numbers in this and all other calibration diagrams are ages in Ma.

5924

- 5925 **Fig. 2.** Major fossil calibrations for (A) nodes 2-3: *Rusophycus* trace fossils, GSC 85983, scale bar
- 5926 20mm, image credit M. Coyne; (B-C) nodes 4, 22, 34, 41: Yicaris dianensis, YKLP 10840, scale bars
- 5927 100µm, images credit X. Zhang; (B) whole specimen; (C) detail of epipodites; (D) node 5:
- 5928 Wisangocaris barbarahardyae, SAM P43679a, scale bar 5mm; (E) nodes 23-25, 27: Cowiedesmus
- 5929 eroticopodus, AMS F.64845, scale bar 2mm, image credit Y. Zhen; (F) nodes 64-65: Rhyniella
- 5930 *praecursor*, BMNH In.38228, scale bar 200µm, image credit NHMUK.

5931

5932 **Fig. 3.** Calibration diagram for non-arachnid Chelicerata (nodes 6-8).

5933

5934 Fig. 4. Calibration diagram for non-tetrapulmonate Arachnida (nodes 9-16). Pseudos. =

5935 Pseudoscorpiones.

5936

5937 Fig. 5. Chelicerate fossil calibrations for (A) node 6: Haliestes dasos, OUM C.29571, scale bar 500µm, 5938 image credit D. Siveter, M. Sutton, D. Briggs & D. Siveter; (B) node 7: Chasmataspis-like resting 5939 traces, MBA 1084, scale bar 20mm, image credit J. Dunlop; (C) node 13: Protofeaella peetersae, 5940 NHMII3115, scale bar 500µm, image credit H. Henderickx; (D) node 10: Eophalangium sheari, PBM 5941 3503, scale bar 1mm, image credit J. Dunlop; (E) node 14: Electrokoenenia yaksha, NIGP 163263, 5942 scale bar 500µm, image credit M. Engel; (F) node 15: Cratosolpuga wunderlichi, SMNK 1268PAL, 5943 scale bar 5mm, image credit P. Selden; (G) node 9: Eramoscorpius brucensis, holotype ROM 5324, 5944 scale bar 10mm, image credit D. Rudkin & J. Waddington; (H) node 9: Palaeophonus loudonensis, 5945 NMS 1897.122.196, scale bar 20mm, image credit: J. Lamsdell; (I-J) node 12: Cornupalpatum

5946 *burmanicum*, scale bars 100 μm, image credit G. Poinar; (I) Holotype A-10-160; (J) Paratype A-10-261;

5947 (K) node 11: *Protacarus crani*, BMNH In.24665, scale bar 100µm, image credit NHMUK.

5948

5949 **Fig. 6.** Calibration diagram for Tetrapulmonata (nodes 17-21).

5950

Fig. 7. Tetrapulmonata fossil calibrations for (A) nodes 17-19: *Parageralinura naufraga*, LWL Ar.K.1,
scale bar 5mm, image credit C. Brauckmann; (B) node 20: *Graeophonus anglicus*, BMNH In 31233,
scale bar 5mm, image credit J. Dunlop; (C, D) node 21: *Palaeothele montceauensis*, images credit P.
Selden; (C) Holotype MNHN 51961, scale bar 2mm; (D) Reconstructed specimen BMNH In.62050,
scale bar 0.2mm; (E) node 21: *Arthrolycosa* sp., PIN 5431/9, scale bar 1mm, image credit P. Selden.

Fig. 8. Calibration diagram for Myriapoda (nodes 24-33). Chilogn. = Chilognatha, Scutigerom. =
 Scutigeromorpha, Geophilom. = Geophilomorpha.

5959

5960 Fig. 9. Myriapod fossil calibrations for (A-B) node 26: Electroxenus jezzinensis, MNHN JS 231/1, scale 5961 bar 0.5mm, image credit D. Azar; (C-E) node 28: Crussolum sp., images credit L. Anderson; (C) 5962 Forcipular segment, slide AUGD 12308, scale bar 0.5mm; (D) Prefemur of a trunk leg, slide AUGD 5963 12307, scale bar 0.2mm; (E) Tibia of a trunk leg, slide AUGD 12307, scale bar 0.2mm; (F) node 29: 5964 Fulmenocursor tenax, SMNS 64275, scale bar 5mm, image credit G. Bechly; (G-H) node 30: 5965 Devonobius delta, scale bars 0.1mm, images credit W. Shear; (G) Head and anterior part of trunk, 5966 AMNH slide 411-15-AR18; (H) Forcipular segment, AMNH slide 4329-AR4; (I) nodes 31-32: 5967 Mazoscolopendra richardsoni, FMNH PE29002, scale bar 5mm, image credit J. Wittry; (J-K) node 33: Kachinophilus pereirai, AMNH Bu-Ba41a; (J) Head and anterior part of trunk, scale bar 0.3 mm; (K) 5968 5969 Posterior body segments, scale bar 0.1mm.

5970

5971 **Fig. 10.** Calibration diagram for Oligostraca (nodes 35-40).

Fig. 11. Oligostraca fossil calibrations for (A) nodes 35-36: *Boeckelericambria pelturae*, UB W116,
scale bar 50µm, image credit D. Waloszek; (B) nodes 37, 39-40: *Luprisca incuba*, YPM IP 307300,
scale bar 500µm, image credit D. Siveter, G. Tanaka, U. Farrell, M. Martin, D. Siveter & D. Briggs; (CE) node 38: *Cytherellina submagna*, ZPAL O.60/001, images credit E. Olempska; (C) steinkern left
lateral view, scale bar 200 µm; (D) soft anatomy of posterior region, scale bar 100µm; (E) walking legs
and presumed furca, scale bar 50µm.

5979

5980 **Fig. 12.** Calibration diagram for Copepoda and Thecostraca (nodes 42-47).

5981

5982 Fig. 13. Calibration diagram for Malacostraca (nodes 48-56). Verunip. = Verunipeltata, Tanaid =
5983 Tanaidacea.

5984

5985 Fig. 14. Multicrustacea fossil calibrations for (A) node 42: Arenosicaris inflata, PRI 10130, scale bar 5986 10mm, image credit J. Collette; (B) node 43: Kabatarina pattersoni, NHMUK 63466, scale bar 100µm, 5987 image credit G. Boxshall; (C-D) node 44: Rhamphoverritor reduncus, OUM C.29587, scale bars 5988 500µm, image credit D. Briggs, M. Sutton, D. Siveter & D. Siveter; (C) lateral views with (left) and 5989 without (right) head shield; (D) transverse section before serial grinding; (E) nodes 45-46: Illilepas 5990 damrowi, FMNH P32055, scale bar 5mm, image credit J. Wittry; (F-G) node 48: Cinerocaris magnifica. 5991 images credit D. Briggs, M. Sutton, S. Siveter & D. Siveter; (F) OUM C.29566, reconstruction in lateral 5992 view with (top) and without (bottom) head shield, scale bar 2mm; (G) holotype C.29565, sub-5993 transverse section, scale bar 1mm; (H-I) nodes 49, 55-56: Palaeopalaemon newberryi, KSU 3484, 5994 scale bars 5mm, image credit W. Jones; (H) left view; (I) right view; (J) nodes 52-53: Hesslerella 5995 shermani, FMNH PE 16527, latex cast whitened with ammonium chloride, scale bar image credit T. 5996 Hegna; (K) node 50: Anaspidites antiguus, AMS F64765, scale bar 5mm, image credit S. Ahyong; (L-5997 M) node 54: Alavatanais carabe, scale bars 500 µm, images credit A. Sánchez-Garcia; (L) holotype

5998 MCNA 9537; (M) MCNA 13888 lateral view.

5999

6000 **Fig. 15.** Calibration diagram for Allotriocarida (nodes 57-63).

6001

Fig. 16. Allotriocarida fossil calibrations for (A) node 57: *Rehbachiella kinnekullensis*, UB 611, scale
bar 200μm, image credit D. Waloszek; (B) node 58: *Lepidocaris rhyniensis*, NHMUK In. 24493, scale
bar 200μm, image credit NHMUK; (C) node 60: *Chenops yixianensis*, CNU-CAL-HP-2009001, scale
bar 10mm, image credit T. Hegna; (D) node 61: *Leaia chinensis*, NIGP 51786, scale bar 1mm, image
credit Y. Shen; (E) node 62: *Dundgobiestheria mandalgobiensis*, ED-A-14-1, scale bar 1 mm, image
credit G. Li; (F) node 63: *Smirnovidaphnia smirnovi*, PIN 1873/100, scale bar 200 μm, image credit A.

6009

Fig. 17. Calibration diagram for non-neopteran Hexapoda (nodes 64-73). Microc. = Microcoryphia,
 Zygent. = Zygentoma, Euplect. = Euplectoptera.

6012

6013 Fig. 18. Hexapoda fossil calibrations for (A) node 70: Delitzschala bitterfeldensis, BGR X 9216, scale 6014 bar 2mm, image credit C. Brauckmann; (B) node 68: Cretaceomachilis libanensis, Milki No. 194/35, 6015 scale bar 500µm, image credit G. Poinar; (C) node 69: Burmalepisma cretacicum, B-TH-1, scale bar 6016 500µm, image credit G. Poinar; (D) node 67: Rhyniognatha hirsti, BMNH IN. 38234, scale bar 200µm, 6017 image credit NHMUK; (E) node 72: Triassonurus doliiformis, Louis Grauvogel collection No. 9304, 6018 scale bar 10mm, image credit L. Grauvogel-Stamm. 6019 6020 Fig. 19. Calibration diagram for Polyneoptera (nodes 75-83). Dermap. = Dermaptera, Notop. = 6021 Notoptera, Phasm. = Phasmatodea. 6022

6023 Fig. 20. Polyneoptera fossil calibrations for (A) node 75: Qilianiblatta namurensis, CNU-NX1-303,

6024 scale bar 5mm, image credit D. Ren; (B) node 77: Palaeotaeniopteryx elegans, PIN 1197/333, scale 6025 bar 1mm, image credit N. Sinitshenkova; (C) node 78: Raphogla rubra, Ld LAP 415 B, scale bar 5 6026 mm, image credit S. Fouché; (D) node 80: Cretophasmomima melanogramma, CNU-PHA-6027 NN2012002, scale bar 10mm, image credit D. Ren; (E) node 76: Rhadinolabis phoenicica, Azar 6028 collection 1013, scale bar 500µm, image credit M. Engel;; (F) node 81: Echinosomiscus primoticus, 6029 NIGP 163536, scale bar 2mm, image credit M. Engel; (G) node 79: Juramantophasma sinica, NIGP 6030 142171, scale bar 10mm, image credit D. Huang. 6031 6032 Fig. 21. Calibration diagram for Condylognatha and Psocodea (nodes 74, 84-88). 6033 6034 Fig. 22. Condylognatha fossil calibrations for (A) nodes 85, 87: Aviorrhyncha magnifica, holotype 6035 MNHN Avion No. 2, scale bar 1mm, image credit A. Nel; (B) node 86: Fusithrips crassipes, PIN 6036 3064/8547, scale bar 200µm, image credit A. Rasnitsyn. 6037 6038 Fig. 23. Calibration diagram for Hymenoptera, Neuropterida, and Coleopterida (nodes 89-96). 6039 Hymenopt. = Hymenoptera, Mec. = Mecopterida, Megalopt. = Megaloptera. 6040 6041 **Fig. 24.** Calibration diagram for Mecopterida (nodes 97-103). Mecopt. = Mecoptera. 6042 6043 Fig. 25. Holometabola fossil calibrations for (A) node 90: Triassoxyela foveolata, PIN 2070/1, scale bar 6044 1mm, image credit A. Rasnitsyn; (B) node 92: Elmothone martynovae, MCZ 5585, scale bar 2mm, 6045 image credit Museum of Comparative Zoology, Harvard University (©President and Fellows of Harvard 6046 College); (C) node 93: Eochauliodes striolatus, CNU-MEG-NN2011004 P/C, scale bar 5mm, image 6047 credit D. Ren; (D) node 96: Triadogyrus sternalis, PIN 3320/13, scale bar 2mm, image credit A. 6048 Rasnitsyn; (E) node 97: Permopanorpa inaequalis, YPM IP 005058, scale bar 1mm, image credit J. 6049 Utrup; (F) node 98: Archaeolepis mane, BMNH In. 59397, scale bar 2mm, image credit NHMUK; (G)

- 6050 node 99: *Liadotaulius maior*, LGA 1995, scale bar 2mm, image credit J. Ansorge; (H) node 100:
- 6051 Parasabatinca aftimacrai, holotype, scale bar 2mm, image credit D. Azar; (I) node 101:
- 6052 *Pseudonannochorista willmanni,* PIN 966/21, scale bar 1mm, image credit A. Bashkuev; (J) node 103:
- 6053 Grauvogelia arzvilleriana, Louis Grauvogel collection No. 5514, scale bar 1mm, image credit L.
- 6054 Grauvogel-Stamm.

1	FOSSIL CALIBRATIONS FOR THE ARTHROPOD TREE OF LIFE
2	
3	AUTHORS
4	
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12	
13	ABSTRACT
14	
15	Fossil age data and molecular sequences are increasingly combined to establish a timescale for the
16	Tree of Life. Arthropods, as the most species-rich and morphologically disparate animal phylum, have
17	received substantial attention, particularly with regard to questions such as the timing of habitat shifts
18	(e.g. terrestrialisation), genome evolution (e.g. gene family duplication and functional evolution),
19	origins of novel characters and behaviours (e.g. wings and flight, venom, silk), biogeography, rate of
20	diversification (e.g. Cambrian explosion, insect coevolution with angiosperms, evolution of crab body
21	plans), and the evolution of arthropod microbiomes. We present herein a series of rigorously vetted
22	calibration fossils for arthropod evolutionary history, taking into account recently published guidelines
23	for best practice in fossil calibration. These are restricted to Palaeozoic and Mesozoic fossils, no
24	deeper than ordinal taxonomic level, nonetheless resulting in 80 fossil calibrations for 102 clades. This
25	work is especially timely owing to the rapid growth of molecular sequence data and the fact that many
26	included fossils have been described within the last five years. This contribution provides a resource
27	for systematists and other biologists interested in deep-time questions in arthropod evolution.

### 29 KEYWORDS

30

31 Arthropods; Fossils; Phylogeny; Divergence times

32

### 33 ABBREVIATIONS

34

35 AMNH, American Museum of Natural History; AMS, Australian Museum, Sydney; AUGD, University of 36 Aberdeen; BGR, Bundesanstalt für Geowissenschaften und Rohstoffe, Berlin; BMNH, The Natural 37 History Museum, London; CNU, Key Laboratory of Insect Evolutionary & Environmental Change, 38 Capital Normal University, Beijing: DE, Ulster Museum, Belfast: ED, Ibaraki University, Mito, Japan: 39 FMNH, Field Museum of Natural History; GMCB, Geological Museum of China, Beijing; GSC, 40 Geological Survey of Canada; IRNSB, Institut Royal des Sciences Naturelles de Belgique, Brussels; 41 KSU, Kent State University: Ld, Musée Fleury, Lodève, France; LWL, Landschaftsverband Westfalen-42 Lippe-Museum für Naturkunde, Münster; MACN, Museo Argentino de Ciencias Naturales, Buenos 43 Aires: MBA, Museum für Naturkunde, Berlin: MCNA, Museo de Ciencias Naturales de Álava, Vitoria-44 Gasteiz, Álava, Spain; MCZ, Museum of Comparative Zoology, Harvard University; MGSB, Museo 45 Geologico del Seminario de Barcelona; MN, Museu Nacional, Rio de Janeiro; MNHN, Muséum 46 national d'Histoire naturelle, Paris; NHMUK, The Natural History Museum, London; NIGP, Nanjing 47 Institute of Geology and Palaeontology; NMS, National Museum of Scotland; OUM, Oxford University 48 Museum of Natural History; PBM, Palaöbotanik Münster; PIN, Paleontological Institute, Moscow; PRI, 49 Paleontological Research Institution, Ithaca; ROM, Royal Ontario Museum; SAM, South Australian 50 Museum, Adelaide: SM, Sedgwick Museum, University of Cambridge: SMNK, Staatliches Museum für 51 Naturkunde, Karlsruhe; SMNS, Staatliches Museum für Naturkunde, Stuttgart; TsGM, F.N. Chernyshev 52 Central Geologic Prospecting Research Museum, St. Petersburg; UB, University of Bonn; USNM, US 53 National Museum of Natural History, Smithsonian Institution; UWGM, University of Wisconsin Geology 54 Museum; YKLP, Yunnan Key Laboratory for Palaeobiology, Yunnan University; YPM, Yale Peabody

55 Museum; ZPAL, Institute of Paleobiology, Polish Academy of Sciences, Warsaw.











### PANTOPODA

CHELICERATA

PARASITIFORMES

PSEUDOS.

PALPIGRADI

SOLIFUGA

SCORPIONES







Schizomida Thelyphonida Parageralinura other Ambylpygi Paracharontidae Graeophonus Mesothelae Palaeothele Mygalomorphae Araneomorphae



ARANEAE







# **TETRAPULMONATA**

























**JCERA** 

CLADO



## BRANCHIOPODA

# ALLOTRIOCARIDA

### Figure 16 Click here to download high resolution image











NEOPTERA

DICTYOPTERA





1 LOGNATHA 7 ABOLA TERA	CONDY	
ABOLA	EUMET	
<b>LOGNATHA</b>	CONDY	
THYSANOPTERA	HEMIPTERA	PSOCODEA







## HOLOMETABOLA



## MECOPTERIDA


Table A.1Click here to download Background dataset for online publication only: Table A.1.xls