

1 **Phylogeny and revision of the ‘*Cubitermes* complex’ termites (Termitidae:**
2 **Cubitermitinae)**

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4 **Working title:** Phylogeny of *Cubitermes*

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26

27 **Abstract**

28 The phylogeny of the genus *Cubitermes* Wasmann was reconstructed using two mitochondrial
29 genes (*COI* and *COII*) and a fragment of the nuclear *28S rDNA*, including samples of
30 *Apilitermes* Holmgren, *Crenetermes* Silvestri, *Megagnathotermes* Silvestri, and *Thoracotermes*
31 Wasmann. Based on our analyses, we recovered these genera within a paraphyletic *Cubitermes*
32 clade. *Cubitermes* species are distributed between five main clades, highly reflective of their
33 enteric valve armatures (EVAs). Consequently, *Cubitermes* is here divided into five
34 monophyletic genera based on phylogenetic analyses and EVAs: *Cubitermes* (*sensu stricto*),
35 *Isognathotermes* Sjöstedt, *Nitiditermes* Emerson, *Polyspathotermes* Josens & Deligne, **gen.n.**,
36 and *Ternicubitermes* Josens & Deligne, **gen.n.** Moreover, the two species of
37 *Megagnathotermes* included in this study, exhibiting different EVAs, are phylogenetically
38 distant: *M. katangensis* Sjöstedt belongs in the genus *Polyspathotermes*, while *M. notandus*
39 Silvestri remains as a monotypic genus. During the evolution of the *Cubitermes* complex,
40 sclerotized EVA spatulae appeared twice independently: three or six spatulae in
41 *Polyspathotermes* (*sulcifrons* and *oblectatus* patterns) and two jaw-like spatulae in *Nitiditermes*
42 (*sankurensis* pattern), which is absent in some species (*oculatus* pattern).

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44 Zoobank registration: [http://zoobank.org/urn:lsid:zoobank.org:pub:576A AFF8-63C6-4962-](http://zoobank.org/urn:lsid:zoobank.org:pub:576A AFF8-63C6-4962-A8F5-75C9317AEA7B)
45 [A8F5-75C9317AEA7B](http://zoobank.org/urn:lsid:zoobank.org:pub:576A AFF8-63C6-4962-A8F5-75C9317AEA7B).

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47 **Key words:** Blattodea; Dictyoptera; Ethiopian Region; Enteric valve; Mitochondrial DNA.

48 **Introduction**

49 *Cubitermitinae* is one of the eight subfamilies of the termite family *Termitidae* (Engel *et al.*,
50 2009) and contains 25 genera restricted to sub-Saharan Africa. Their gut anatomy is
51 characterized by (i) a mixed segment separated from the ileum (P1) by a faint constriction; (ii)
52 the enteric valve (P2) is funnel-shaped, not separated from P1, and bearing a characteristic
53 armature; and (iii) a blind diverticulum, or caecum, occurring on the paunch (P3) (Noirot, 2001;
54 Krishna *et al.*, 2013a). Within this subfamily, the soldiers of the genus *Cubitermes* Wasmann
55 are characterized by sabre-like mandibles, a bifurcated labrum and presence of soil in the gut
56 (Fig. 1 A). *Cubitermes* is one of the most diverse and abundant genera of African termites, and
57 have successfully colonized various ecosystems from evergreen forests to rather dry savannahs
58 (Williams, 1966). Some species build epigeal mushroom-shaped nests, which are typical of
59 certain landscapes (Fig. 1 B-D). They play important ecological roles mainly through their
60 action on the soil (Wood *et al.*, 1983; Okwakol, 1987; Donovan *et al.*, 2001b) and may be
61 locally abundant (Wango & Josens, 2011). Krishna *et al.* (2013b) listed 67 valid species-group
62 names, while Josens & Deligne (2019) proposed some new species and some invalid synonyms
63 among the species that were synonymized by Ruelle (1975) and by Krishna *et al.* (2013b),
64 bringing the number of species to 81. This figure might further increase if the genera
65 *Megagnathotermes* Silvestri and *Nitiditermes* Emerson are found to be synonymous with
66 *Cubitermes*, as suggested by Sands (1998).

67 As in the soldierless *Apicotermatinae* (Sands, 1972), the *Cubitermes* enteric valve
68 armature (EVA), mainly of the worker caste, can be used for differentiating species groups
69 (Josens & Deligne, 2019). In the subfamily *Cubitermitinae*, the basic enteric valve is a funnel
70 bearing six elongated primary, prominent cushions of the valve (PC) alternating with non-
71 prominent, secondary cushions of the valve (SCs) (Noirot, 2001). The cushions are armed with

72 cuticular outgrowths of different sizes and shapes: spines and bristles can be straight, bent, or
73 even hooked.

74 *Cubitermes* workers feed on crude soil and display different types of fully developed
75 enteric valves. Bouillon & Vincke (1971) mentioned the existence of at least three main kinds
76 of EVA in the genus *Cubitermes*, with or without sclerotized spatulae. Josens & Deligne (2019)
77 distinguished nine species groups on the basis of their EVA. Six of them are variations on the
78 basic EVA, but three of them, namely the *sankurensis*, *oblectatus*, and *sulcifrons* groups are
79 characterized by the presence of two, three, and six sclerotized spatulae on the PC, which
80 project from the valve into the paunch (P3). Note that *Nitiditermes berghei* Emerson and
81 *Megagnathotermes katangensis* Sjöstedt respectively possess two and three such spatulae as
82 well (Sands, 1998; plate 10: fig. 6; plate 11: fig. 5). One of the main conclusions from Josens
83 & Deligne (2019) is that several species may have soldiers with similar external morphologies,
84 which used to make *Cubitermes* so difficult to identify, but may possess different types of EVA.
85 A brief overview of EVA is given in Table 1 (modified from Josens & Deligne, 2019: table 4).

86 Bouillon & Vincke (1971) suggested that EVAs might reflect different diets, although
87 all *Cubitermes* species are basically soil feeders and considered to belong to the feeding group
88 IV of Donovan *et al.* (2001a). A link between diet differentiation and EVA is indeed supported
89 by the fact that two or three species can occupy the same niche habitat at high densities
90 (Williams, 1966; Wango & Josens, 2011), and when this happens, the coexisting species display
91 different EVA. Moreover, two coexisting *Cubitermes* species with different EVA display
92 different isotopic signatures, probably reflecting the consumption of soil at different levels
93 (Josens & Wango, 2019).

94 Few species of *Cubitermes* have hitherto been sequenced for molecular phylogenetic
95 studies. In a limited area around the Lopé reserve in Gabon, Roy *et al.* (2006) found that
96 *Cubitermes* sp. aff. *subarquatus* Sjöstedt represented four cryptic species. Inward *et al.* (2007)

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97 included two unidentified *Cubitermes* species in their phylogenetic study. They considered the
98 *Cubitermes* group (= Cubitermitinae) to be monophyletic (based on 13 sampled genera). They
99 also recovered *Cubitermes*, *Crenetermes* Silvestri, and *Thoracotermes* Wasmann in an
100 unresolved clade with *Apilitermes* Holmgren as the sister group. Bourguignon *et al.* (2017)
101 examined the historical biogeography of 11 Cubitermitinae genera, including seven *Cubitermes*
102 species. They concluded that Cubitermitinae evolved around 30 Mya during the early Oligocene
103 and are endemic to Africa, and that *Thoracotermes macrothorax* (Sjöstedt), *Apilitermes*
104 *longiceps* (Sjöstedt) and *Crenetermes albotarsalis* (Sjöstedt) were included within the
105 *Cubitermes* clade. Here, we consider that the *Cubitermes* complex comprises the genera
106 *Cubitermes*, *Apilitermes*, *Crenetermes*, *Megagnathotermes*, *Nitiditermes* and *Thoracotermes*.

107 The taxonomy of *Cubitermes* complex genera has been obscured by many inadequately
108 detailed historical descriptions. A first step in modernising the taxonomic concepts of this genus
109 was to split it into nine species groups according to their EVA (Josens & Deligne, 2019).
110 Whether or not these groups should be raised to generic rank remains subjective although
111 genetic data helps discriminate groups of related taxa. In the context of this limited
112 morphological and genetic background, the objectives of this paper are to (i) establish a
113 comprehensive phylogeny of the *Cubitermes* complex, (ii) investigate whether the nine species
114 groups based on EVA (*sensu* Josens & Deligne, 2019) are consistent with their phylogeny and
115 thus predicating any robust species level revision; (iii) organize the present genus *Cubitermes*
116 accordingly into natural groups (e.g., genera); and (iv) assess the monophyly of
117 *Megagnathotermes* and *Nitiditermes* relative to *Cubitermes* as suggested by Sands (1998).

118 **Materials and Methods**

119 *Biological samples*

120 Termites were collected either into pure ethanol or RNA-later® from various localities across
121 West and Central Africa, including Benin, Burkina Faso, Burundi, Cameroon, Central African
122 Republic, Congo, Côte d'Ivoire, DRC (Haut-Katanga, Kinshasa and Tshopo provinces), Gabon
123 and Senegal. Termites were identified to species using Sjöstedt (1926) and Williams (1966)
124 and by comparison with type specimens. A total of 56 samples of the *Cubitermes* complex were
125 selected for molecular analyses so as to maximize the number of species and their geographic
126 distribution, including samples of *Apilitermes longiceps*, *Crenetermes albotarsalis*,
127 *Megagnathotermes notandus* Silvestri, *M. katangensis*, and *Thoracotermes macrothorax*. Five
128 species were added as outgroups for phylogenetic reconstructions: (i) Macrotermitinae:
129 *Macrotermes amplus* (Sjöstedt) —replacement name for *M. muelleri* (Sjöstedt) (see Krishna *et*
130 *al.*, 2013b: 1024), (ii) Cubitermitinae: *Furculitermes parviceps* Emerson and *Procubitermes*
131 *aburiensis* Sjöstedt, as well as (iii) Neotropical Termitinae: *Cavitermes tuberosus* (Emerson)
132 and *Palmitermes impostor* Hellemans & Roisin (Table S1).

133 Enteric valves (Fig. 2) were dissected and mounted on microscope slides. Images of
134 slide preparations were obtained with a Zeiss Discovery V12 stereomicroscope equipped with
135 an AxioCam ICc3 camera and controlled by AxioVision software. Images are each
136 compilations of a series of successive stepwise-focussed photographs.

137

138 *Phylogenetic reconstruction*

139 We reconstructed the phylogeny of the termite genus *Cubitermes* using two mitochondrial
140 genes, cytochrome oxidase I (*COI*) and II (*COII*), and a fragment of the nuclear ribosomal gene
141 *28S rDNA*. Details of molecular procedures are provided in Supplementary Methods (Section
142 SM-1), with cycling conditions in Table S2. From the initial 61 samples, all were successfully

143 amplified for *COII* and *28S rDNA*, and 54 for *COI*. All sequences have been deposited in
144 GenBank under accessions MN646697 to MN646750 for *COI*, MN685897 to MN685956 for
145 *COII*, and MN685957 to MN686017 for *28S rDNA* (see Supplementary Table S1 for details).

146 Bayesian Inferences (BI) were performed on the combined data in order to infer the
147 species tree from two separate datasets: (i) 61 samples for which we obtained both *COII* and
148 *28S rDNA*, and (ii) 54 samples for which all genes were obtained. For both analyses, each gene
149 was aligned individually using the MUSCLE algorithm (Edgar, 2004) implemented in
150 CodonCode Aligner. In the first analysis, alignments consisted in 61 sequences of 685 and 894
151 bp, with 278 and 160 polymorphic sites respectively for *COII* and *28S rDNA*. In the second
152 analysis, alignments consisted in 54 sequences of 657, 685, and 894 bp, with 294, 277, and 154
153 polymorphic sites respectively for *COI*, *COII*, and *28S rDNA*. The best nucleotide-substitution
154 models with the lowest Bayesian Information Criterion (BIC) were determined as TPM2uf+G
155 for *COI*, TrN+I+G for *COII*, and TVM+I+G for *28S rDNA* for both analyses using jModelTest
156 v2.1.10 (Darriba *et al.*, 2012). Phylogenetic analyses with BI were performed using the software
157 BEAST v2.5.1 (Bouckaert *et al.*, 2014) with the method StarBEAST2 (Ogilvie *et al.*, 2017).
158 Gene trees were modelled under strict molecular clocks with nucleotide-substitution models
159 determined above. For the three-gene analysis, *COI* and *COII* trees were linked to account for
160 the transmission of the mitochondrial sequences as one single locus. A Yule speciation process
161 was modelled by setting the population mean to $1/X$ with a uniform speciation rate. Markov
162 Chain Monte Carlo (MCMC) analyses were run for 30 million generations, sampling every
163 10,000 generations, and a burn-in of 10%, leaving a total of 5,400 trees. We followed traces
164 with Tracer v1.7.1 (Rambaut *et al.*, 2014) to ensure that all effective sample sizes (ESS) of
165 estimated parameters were above 200. Resulting ultrametric phylogenetic trees were
166 reconstructed as maximum clade credibility trees with mean node heights using TreeAnnotator
167 v2.5.1 (Bouckaert *et al.*, 2014) and visualized using FigTree v1.4.3 (Rambaut, 2017).

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168 Mitochondrial and nuclear trees were mirrored using the ‘cophyloplot’ function from the ape
169 package (Paradis *et al.*, 2004) in R v3.5.1 (R Development Core Team, 2018).

170 We also carried out BI on *COII* using the 61 sequences obtained in this study, as well
171 as 13 previously published sequences retrieved from GenBank (see Table S3; Roy *et al.*, 2006;
172 Bourguignon *et al.*, 2015; Bourguignon *et al.*, 2017). Taxonomic identity of *Cubitermes*
173 samples, from which published sequences originated, was re-evaluated following Josens &
174 Deligne (2019) (Table S3). The 75 sequences were aligned using the MUSCLE algorithm
175 (Edgar, 2004) implemented in CodonCode Aligner, resulting in an alignment of 685 bp with
176 281 polymorphic sites. The best nucleotide-substitution model was HKY+I+G according to the
177 BIC using jModelTest v2.1.10 (Darriba *et al.*, 2012). BI was undertaken with MrBayes v3.2.7
178 (Ronquist *et al.*, 2012), using two parallel runs, each consisting in four simultaneous MCMC
179 of 10 million generations, sampling every 5,000 generations and discarding the first 20%
180 samples from the cold chain as a burn-in. Convergence was ensured by checking that average
181 standard deviation of split frequencies between the two runs was below 0.01, and all ESS were
182 above 200. The resulting non-ultrametric consensus tree was visualized using FigTree v1.4.3
183 (Rambaut, 2017).

184

185 *Phylogenetic analyses and reconstruction of trait states*

186 The following analyses were conducted on the three-gene analysis, excluding distant outgroups
187 (*i.e.*, *Macrotermes amplus*, *Cavitermes tuberosus*, and *Palmitermes impostor*). We performed
188 a Mantel test (Mantel, 1967) between genetic and geographic distance to test for the presence
189 of recent gene flow; a positive correlation would indicate the absence of gene flow, contrary to
190 a near-zero correlation. Matrices of pairwise genetic distances of both mitochondrial (*COI* and
191 *COII*) and nuclear (*28S rDNA*) DNA were obtained using the Kimura 2-parameter model
192 (Kimura, 1980) implemented in MEGA X (Kumar *et al.*, 2018). Geographic distances were

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193 computed as spherical (Vincenty, 1975) using the geosphere package in *R* (Hijmans, 2019).
194 Mantel tests were performed using 9,999 permutations with the *ade4* package in *R* (Dray &
195 Dufour, 2007).

196 Mesquite v3.6 (build 917) (Maddison & Maddison, 2019) was used in order to better
197 understand the evolution of morphological traits, using the best resolved BI tree. Traits used for
198 reconstruction were: (i) the nine worker EVA types (see Table 1 A) *sensu* Josens & Deligne
199 (2019), and (ii) soldier labrum shape. Ancestral states were reconstructed under a parsimony
200 model with unordered characters for each trait, minimizing the switches along the tree.

201 **Results**

202 *Phylogenetic analyses*

203 Overall, the topologies of phylogenetic trees were consistent among outgroups in both the two
204 and three-gene StarBEAST2 analyses (61 and 54 sequences respectively). However, the
205 topology was better resolved amongst internal nodes (*i.e.*, supported by higher Bayesian
206 Posterior Probabilities (BPP) values) in the three-gene analysis. Therefore, only phylogenetic
207 trees of the three-gene analyses are considered in the following sections (Figs 3, S1 A-C; see
208 Fig. S2 A-D for trees from the two-gene analyses). Mantel tests on samples from the subfamily
209 Cubitermitinae (three-gene dataset, *i.e.* 51 samples) revealed some structure of the genetic
210 diversity for the mitochondrial loci ($r = 0.161$, $p < 0.01$) but none for the nuclear one ($r = 0.003$,
211 $p = 0.47$).

212 Topologies of mitochondrial (1,342 bp; linked *COI* and *COII*; Fig. 3) and nuclear (894
213 bp; *28S rDNA*; Fig. S1 A) trees were not congruent (Fig. S1 B; see Fig. S2 C for the two-gene
214 analysis) with the latter not recovering prior species-level concepts. This was notably the case
215 for *C. proximatus* (Fig. S1 A) and *C. sankurensis* (Fig. S2 B) which were split into several
216 clades. Furthermore, most internal nodes of the mitochondrial tree were highly resolved (BPP
217 > 0.95), while those of the nuclear tree were characterized by lower BPP. The total evidence
218 tree (Fig. S1 C) exhibited the same topology (although with lower BPP support values) as the
219 mitochondrial one, except for the position of *Megagnathotermes notandus* and *Th.*
220 *macrothorax*. Consequently, the results below are mainly described with respect to the highly
221 resolved mitochondrial tree (Fig. 3).

222 Based on the results of the mitochondrial and nuclear trees, as well as the total evidence
223 tree, *A. longiceps*, *Cr. albotarsalis*, *M. notandus*, and *Th. macrothorax* were included within
224 the *Cubitermes* clade (Figs 3; S1A-C; S2A-D). Considering both the mitochondrial and the total
225 evidence trees, *Cubitermes* species were distributed between five main clades, highly reflective

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226 of EVA groups, described hereafter according to separation events. (i) The first clade was
227 composed of two species with a *bilobatus* EVA (*C. exiguus* Mathot and *C. tenuiceps* (Sjöstedt))
228 with *Apilitermes* as sister group. (ii) The second consisted of seven species, six with a
229 *sankurensis* EVA (*C. orthognathus* (Emerson), *C. proximatus* Silvestri, *C. sankurensis*
230 Wasmann, *C. schereri* (Rosen), and two undescribed species), within which an undetermined
231 species with an *oculatus* EVA was nested. (iii) The third combined species with either a
232 *fungifaber* EVA (*C. fungifaber* (Sjöstedt), *C. severus* Silvestri, and *C. ugandensis* Fuller) or a
233 *finitimus* EVA (*C. finitimus* Schmitz, *C. planifrons* Sjöstedt, and two undescribed species) into
234 a sister group to *Crenetermes*. (iv) The fourth comprised five species with either a *sulcifrons*
235 EVA (*C. bugeserae* Bouillon & Vincke, *C. inclitus* Silvestri, *C. sulcifrons* Wasmann, and an
236 undescribed species) or an *oblectatus* EVA (*M. katangensis*). (v) The fifth was constituted of
237 three species with a *bilobatodes* EVA (*C. bilobatodes* Silvestri, *C. weissii* Silvestri, and an
238 undetermined species, see Fig. S2 A,D) within which two species with a *muneris* EVA (*C.*
239 *muneris* (Sjöstedt) and *C. pallidiceps* (Sjöstedt)) were nested.

240 Finally, it is to be highlighted that the two species of *Megagnathotermes* included in this
241 study, exhibiting different EVAs, were separated within the *Cubitermes* clade: *M. katangensis*
242 was grouped with *sulcifrons* EVA species, while *M. notandus*, showing affinities with *Th.*
243 *macrothorax* (BPP = 0.98; Fig. 3), was established as the sister group of clades III-IV-V
244 detailed above (BPP = 0.97; Fig. 3).

245

246 *Classification*

247 After EVA and morphology examination, it appeared that the four cryptic species assigned to
248 ‘*Cubitermes* sp. aff. *subarquatus*’ in Roy *et al.* (2006) belonged to two groups. (i) ‘*Cubitermes*
249 spA’ and ‘*Cubitermes* spD’ (GenBank accessions DQ127302 and DQ246541, respectively;
250 Table S3) displayed the *fungifaber* EVA and matched the morphology of *C. fungifaber*. (ii)

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251 ‘*Cubitermes* spB’ and ‘*Cubitermes* spC’ (DQ127312 and DQ127306, respectively) possessed
252 a *finitimus* EVA; *C. subarquatus* is probably a junior synonym of *C. finitimus* (Emerson in
253 Krishna *et al.*, 2013b: 1938). While ‘spB’ matched well the *C. planifrons* morphology, ‘spC’
254 was very close to the *C. finitimus* morphology but was definitely different on a genetic basis
255 (this is truly a cryptic species). Phylogenetic reconstruction on the *COII* alignment with
256 MrBayes confirmed the assignment of ‘spA’ and ‘spD’ to *C. fungifaber* and ‘spB’ to *C.*
257 *planifrons*, while ‘spC’ was established as a sister group of *C. fungifaber* (Fig. 4; Table S3).

258 Additionally, seven *Cubitermes* samples for which entire mitogenomes were sequenced
259 previously (Bourguignon *et al.*, 2015, 2017), were morphologically re-examined (for details,
260 see Table S3). The taxonomic assignment of DJ 0091 (KY224661) and DJ 0676 (KY224606)
261 to *C. ugandensis* and *C. sulcifrons*, respectively, was confirmed, as their *COII* sequences
262 clustered with other conspecific samples (Fig. 4). DJ 0183 (KY224600), identified nominally
263 as *C. nr. fulvus*, was confirmed as *C. fulvus* Williams and also grouped with the other species
264 with a *sankurensis* EVA based on *COII* (Fig. 4). Contrary to Bourguignon *et al.* (2017) who
265 identified DJ 0186 (KY224421) as *C. fulvus* Williams, we identified it here as *C. bugeserae*
266 (Fig. 4). The sample CA1 with accession KP026265, assigned to *C. fungifaber* by Bourguignon
267 *et al.* (2015), was re-identified as a species belonging to the *finitimus* EVA group based on
268 photographs; based on its *COII* sequence it formed a clade with the sample ‘spC’ from Roy *et*
269 *al.* (2006), as the sister group to *C. fungifaber* (Fig. 4). DJ 0620 (KY224569), labelled as
270 ‘*Cubitermes* sp. A’, was identified as *C. finitimus*; we similarly recovered it clustered with the
271 other members of this species on the *COII* tree (Fig. 4). Finally, DJ 0093 (KY224475) was
272 identified as *C. oblectatus* by Bourguignon *et al.* (2017) but was here re-assigned to *C. sp. aff.*
273 *katangensis*.

274

275 *Taxonomic status of the ‘Cubitermes complex’*

Phylogeny of *Cubitermes*

276 Our results showed that enteric valve armature patterns (or EVAs), as defined in Josens &
277 Deligne (2019), were supported as five major clades and that the genera *Apilitermes*,
278 *Crenetermes*, *Megagnathotermes*, and *Thoracotermes* were nested within a paraphyletic
279 *Cubitermes*. It follows that the genus *Cubitermes* is here split into five monophyletic genera,
280 defined according to the major clades and EVAs. These five genera share these same
281 morphological characters in soldiers: presence of a diverticulum on the paunch, presence of soil
282 in their gut (dark abdomen), cubic to cuboid head capsule bearing a dense bunch of bristles
283 around and above fontanelle, bifurcated labrum, reaping mandibles from almost straight to
284 evenly curved or even more or less hooked, each one bearing a small marginal tooth near the
285 molar tooth, and fore, mid and hind tibiae bearing 3, 2, 2 apical spurs and 0, 2, 0 subapical spurs
286 respectively. Full descriptions of these genera will be provided in the ongoing revisions,
287 together with identification keys to the species level. Here, we provide diagnostic characters at
288 the genus level, *i.e.* the characteristics of the workers' EVAs (see Table 1 A). Species to be
289 included in the various genera are designated according to combinations recently in use (as in
290 Krishna *et al.*, 2013b). A list of described taxa considered as currently valid (following Josens
291 & Deligne, 2019; this work) is given below for each genus as well as in Supplementary Table
292 S4 with their authority.

293

294 *Taxonomy*

295 **Genus *Cubitermes* Wasmann**

296 **Type species:** *Termes bilobatus* Haviland, 1898: 411-412; by original designation.

297 **Diagnosis.** The workers within this genus have basic *bilobatus* EVAs, with nearly triangular
298 primary cushions (see Table 1 and Fig. 2 A).

299 **Species included (9).** *C. bilobatus* (Haviland) (synonym: *C. bilobatus curtus* Sjöstedt), *C.*
300 *conjenii* (Fuller), *C. exiguus* Mathot, *C. pretorianus* Silvestri, *C. pretorianus heidelbergi* Fuller,

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301 *C. sanctaeluciae* (Fuller), *C. tenuiceps* (Sjöstedt), *C. transvaalensis* (Fuller), *C. zulucola*
302 Sjöstedt (synonym: *C. pseudoduplex* (Fuller)).

303 **Etymology.** From Latin *cubus*, cube; and *termes*, termite. Refers to the cubic or cuboid shape
304 of the soldiers' heads.

305 **Comments.** This genus corresponds to the clade I in this work and to the *bilobatus* pattern in
306 Josens & Deligne (2019).

307

308 **Genus *Isognathotermes* Sjöstedt**

309 **Type species:** *Eutermes (Cubitermes) minitabundus* Sjöstedt, 1913: 368-369; by original
310 designation.

311 **Diagnosis.** The odd-numbered PCs of worker's enteric valve bear either crests or bulges in their
312 downstream part (see Table 1 and Fig. 2 D,E).

313 **Species included (15).** *I. bulbifrons* (Sjöstedt) (synonym: *I. heghi* (Sjöstedt)), *I. congoensis*
314 (Emerson), *I. finitimus* (Schmitz) (synonyms: *I. loubetsiensis* (Sjöstedt), *I. subarquatus*
315 (Sjöstedt)), *I. fungifaber* (Sjöstedt) (synonyms: *I. banksi* (Emerson), *I. comstocki* (Emerson), *I.*
316 *schmidti* (Emerson)), *I. gaigei* (Emerson), *I. gibbifrons* (Sjöstedt), *I. kemneri* (Emerson), *I.*
317 *minitabundus* (Sjöstedt), *I. modestior* (Silvestri), *I. planifrons* (Sjöstedt) (suspected synonym:
318 *I. fungifaber elongatus* (Sjöstedt)), *I. severus* (Silvestri), *I. silvestrii* (Sjöstedt), *I. speciosus*
319 (Sjöstedt), *I. ugandensis* (Fuller) (synonym: *I. antennalis* (Sjöstedt)), *I. zenkeri* (Desneux).

320 **Etymology.** From Greek *ισος*, *isos*, equal, even; *γναθος*, *gnathos*, mandible; and Latin *termes*,
321 termite. Probably refers either to the resemblance between both mandibles, or to the fact that
322 their diameter varies little between both ends, as it is the case in the type species *I.*
323 *minitabundus*.

324 **Comments.** This genus was considered a junior synonym of *Cubitermes* since Snyder's catalog
325 (1949); here, we restore it as valid. It corresponds to the clade III in this work and to the
326 *fungifaber* and *finitimus* patterns in Josens & Deligne (2019).

327

328 **Genus *Nitiditermes* Emerson**

329 **Type species:** *Nitiditermes berghei* Emerson, 1960: 10-12; by original designation.

330 **Diagnosis.** In most of the species (grouping the *sankurensis* EVA), the worker has an enteric
331 valve with two PCs (PC3 and PC4) ending downstream in two yellow to brown sclerotized
332 spatulae which look like two jaws (“*valvule à mâchoires*” in Bouillon & Vincke, 1971; see
333 Table 1 and Fig. 2 G). However, in two species (of the *oculatus* pattern), the workers have basic
334 enteric valves i.e. without any spatulae (see Table 1 and Fig. 2 F).

335 **Species included (15).** *N. aemulus* (Silvestri), *N. anatruncatus* (Fuller), *N. berghei* Emerson,
336 *N. curtatus* (Silvestri), *N. fulvus* (Williams), *N. niokoloensis* (Roy-Noël), *N. oculatus* (Silvestri),
337 *N. orthognathus* (Emerson), *N. proximatus* (Silvestri), *N. sankurensis* (Wasmann) (synonyms:
338 *N. cubicephalus* (Sjöstedt), *N. sankurensis elongatus* (Sjöstedt), *N. sibitiensis* (Sjöstedt)), *N.*
339 *schერი* (von Rosen), *N. sierraleonicus* (Sjöstedt), *N. testaceus* (Williams), *N. truncatoides*
340 (Fuller) (synonym: *N. truncatoides sordwana* (Fuller)), *N. truncatus* (Holmgren) (synonym: *N.*
341 *duplex nduma* (Fuller)).

342 **Etymology.** From Latin *nitidus*, shiny; and *termes*, termite. Clearly refers to the shiny
343 appearance of the imago's tegument and soldier's mandibles pointed out by Emerson in the
344 specific case of the type species *N. berghei*.

345 **Comments.** This genus corresponds to the clade II in this work and to the *oculatus* and
346 *sankurensis* patterns in Josens & Deligne (2019).

347

348 **Genus *Polyspathotermes* Josens & Deligne, gen.n.**

349 <http://zoobank.org/urn:lsid:zoobank.org:act:563784CA-7CA6-4923-BAE2-0634A186436F>

350 **Type species:** *Cubitermes sulcifrons* Wasmann, 1911: 156-158.

351 **Diagnosis.** Two worker enteric valve patterns are found within this group: either with three PCs
352 (PC3, PC4, and PC5) ending downstream in yellow to brown sclerotized spatulae or with all
353 six PCs ending in sclerotized spatulae (see Table 1 and Fig. 2 H,I).

354 **Species included (8).** *P. bugeserae* (Bouillon & Vincke), *P. inclitus* (Silvestri) (synonym: *P.*
355 *domifaber* (Sjöstedt)), *P. intercalatus* (Silvestri) (synonym: *P. hamatus* (Sjöstedt)), *P.*
356 *katangensis* (Sjöstedt), *P. montanus* (Williams), *P. oblectatus* (Harris), *P. sulcifrons*
357 (Wasmann), *P. umbratus* (Williams).

358 **Etymology.** From Greek *πολυς*, *polus*, many; and *σπαθος*, *spathos*, spatula. Refers to the
359 morphology of EVAs, in which more than two cushions bear sclerotized spatulae. Gender:
360 masculine.

361 **Comments.** This genus corresponds to the clade IV in this work and to the *oblectatus* and
362 *sulfifrons* patterns in Josens & Deligne (2019); it includes *Megagnathotermes katangensis*.

363

364 **Genus *Ternicubitermes* Josens & Deligne, gen.n.**

365 <http://zoobank.org/urn:lsid:zoobank.org:act:D3850221-F28D-4527-8345-D5E2477C41BF>

366 **Type species:** *Cubitermes bilobatodes* Silvestri, 1912: 247-249.

367 **Diagnosis.** The workers within this genus have basic EVAs, with fusiform or roughly
368 rectangular primary cushions (see Table 1 and Fig. 2 B,C).

369 **Species included (13).** *T. bilobatodes* (Silvestri), *T. breviceps* (Sjöstedt), *T. duplex* (Holmgren),
370 *T. falcifer* (Williams), *T. glebae* (Sjöstedt), *T. latens* (Williams), *T. microduplex* (Fuller), *T.*
371 *muneris* (Sjöstedt) (synonym: *T. bisulcatus* (Sjöstedt)), *T. pallidiceps* (Sjöstedt), *T.*
372 *subcrenulatus* (Silvestri), *T. undulatus* (Fuller), *T. weissii* (Silvestri), *T. zavattarii* (Ghidini).

373 **Etymology.** From Latin *terni*, triple; *cubus*, cube; and *termes*, termite. Refers to *Cubitermes*-
374 like species with triradial symmetry of the EVAs. Gender: masculine.

375 **Comments.** This genus corresponds to the clade V in this work and to the *muneris* and
376 *bilobatodes* patterns in Josens & Deligne (2019).

377

378 *Phylogenetic reconstruction of trait states*

379 Ancestral reconstruction of traits was based on the three-gene dataset for Cubitermitinae (*i.e.*
380 31 species). Parsimony analyses indicated that 11 and 16 state shifts in worker EVA types and
381 soldier labral lobes, respectively, were involved along the evolution of the *Cubitermes* complex.
382 As detailed in the previous section, worker EVA types highly matched the phylogenetic
383 relationships (Fig. 5 A); notably, sclerotized EVA spatulae appeared independently in
384 *Polyspathotermes* and *Nitiditermes*. However, soldier labral lobes were found to be highly
385 plastic and disappeared three times independently (Fig. 5 B; in *A. longiceps*, *Cr. albotarsalis*,
386 and *Th. macrothorax*).

387

388 **Discussion**

389 *Evolutionary trends in the Cubitermes complex*

390 In the subfamily Cubitermitinae, the basic enteric valve is a funnel bearing six primary
391 elongated prominent cushions alternating with non-prominent, secondary cushions (Noirot,
392 2001). The functioning of these enteric valves is still poorly understood. Globally, they act as
393 filters, slowing down the fine soil particles and directing them towards the periphery of the
394 second paunch (Bignell, 2000; Donovan, 2002). The EVAs are well developed in workers,
395 which directly feed on crude soil. In the soldiers, they are either a little less developed than in
396 workers or dramatically reduced, to the point of disappearing totally in the so-called ‘white-

397 gutted soldiers' (Scheffrahn *et al.*, 2017). In the imago caste, they are present but noticeably
398 reduced (Josens & Deligne, 2019).

399 The ancestral EVA of Cubitermitinae matches well with Noirot's (2001) definition but
400 has undergone various changes along the phylogeny: the subfamily Cubitermitinae is divided
401 into three main clades (Bourguignon *et al.*, 2017), as follows:
402 (i) the *Furculitermes* complex (*Furculitermes* and *Ophioterme*s) that has EVAs characterized
403 by PCs not elongated but more or less shaped like dumbbells (see Sands, 1998; Fig. 2 L); the
404 genus *Euchiloterme*s has a similar digestive anatomy (Sands, 1998) and probably belongs in
405 this clade as well; (ii) the *Basidentiterme*s complex (five genera: *Basidentiterme*s, *Noditerme*s,
406 *Orthoterme*s, *Probosciterme*s, and *Procubiterme*s) has maintained rather basic valves in
407 workers (see Sands, 1998; Fig. 2 N), whereas soldiers are all white-gutted with vanishing EVA
408 or no EVA at all (Scheffrahn *et al.*, 2017); some other genera (*Fastigiterme*s, *Lepidoterme*s,
409 *Mucrotermes*, *Pilotermes*, *Profastigiterme*s, *Unguiterme*s, and *Unicorniterme*s) also have
410 white-gutted soldiers and might therefore join the *Basidentiterme*s complex; and (iii) the
411 *Cubiterme*s complex (four genera in Bourguignon *et al.* (2017), now nine genera: *Apiliterme*s,
412 *Creneterme*s, *Cubiterme*s (*sensu stricto*), *Isognathoterme*s, *Megagnathoterme*s, *Nitiditerme*s,
413 *Ternicubiterme*s, *Polyspathoterme*s, and *Thoracoterme*s) that show various EVAs; the four
414 remaining Cubitermitinae genera, with basic EVAs and dark-gutted soldiers (*Batilliterme*s,
415 *Okavangoterme*s, *Ovamboterme*s, and *Trapelliterme*s; see Sands, 1998) might join the
416 *Cubiterme*s complex.

417

418 *Enteric valve evolution (Fig. 5A)*

419 *Cubiterme*s (*sensu stricto* = the *bilobatus* pattern) is at the base of the *Cubiterme*s complex; the
420 species (of small size) remaining in this genus have small PCs with very few lateral supporting
421 bristles and few distal strong setae (Fig. 2 A), and wide SCs. Their architecture is similar to the

422 ancestral EVA. Its sister species, *A. longiceps*, has also a basic EVA with clearly more lateral
423 supporting bristles in accordance with its larger size (Fig. 2 J). *Cubitermes* and *A. longiceps*
424 together make the sister clade to the other species of the *Cubitermes* complex.

425 *Nitiditermes* diverges next and it is also the first with two spatulae, on PC3 and 4;
426 moreover, PC1 is clearly longer and frequently also wider than the other PCs without spatulae,
427 making the whole EVA asymmetrical. The SCs are as narrow as the PCs. This genus, however,
428 unexpectedly merges the *sankurensis* pattern (with spatulae; Fig. 2 G) and the *oculatus* pattern
429 (without spatulae; Fig. 2 F). Beside the absence of spatulae, the *oculatus* EVA looks like the
430 *sankurensis* EVA; the similarity was strongly suggested by a long and wide PC1 and also by
431 narrow SCs. *Nitiditermes* therefore first evolved spatulae which were later lost in one lineage,
432 probably rather recently in dry West African savannahs (Josens & Deligne, 2019). Although
433 *Nitiditermes berghei* could not be sequenced, it was incorporated into the *Cubitermes* complex
434 (as expected by Sands, 1998) and now in the *sankurensis* pattern because of its bi-spatulated
435 EVA. Unfortunately, *N. berghei* is only known from its type series collected near Lubumbashi,
436 DRC. Another sample labelled *N. berghei* in the NHMUK collection, collected near Mbala,
437 Zambia, clearly belongs to *N. orthognathus*.

438 The clade made by *Th. macrothorax* and *M. notandus* stemmed after *Nitiditermes*,
439 followed by *Ternicubitermes* and *Polyspathotermes*. *Thoracotermes macrothorax* displays a
440 basic EVA (Fig. 2 O) whereas *M. notandus* developed long soft dorsal ridges and lateral comb-
441 like supporting setae on every PC (Fig. 2 M); both have rather narrow SCs tending toward a
442 spearhead shape.

443 *Ternicubitermes* merges the *muneris* and *bilobatodes* patterns (Fig. 2 B,C): their EVAs
444 are aligned with the ancestral EVA; they are provided with more numerous and longer bristles
445 in their downstream part than in *Cubitermes* species. They have triradial symmetry, the odd-
446 numbered PCs being clearly longer than the even-numbered PCs. Both have wide SCs with

447 either homogeneous or tending toward a spearhead-shaped spine scattering. Grouping these two
448 patterns could be expected since several samples displayed intermediate EVAs.

449 *Polyspathotermes* is the second genus that developed spatulae, independently from
450 *Nitiditermes*. This genus, however, merges the *sulcifrons* pattern (with six spatulae and
451 hexaradial EVA symmetry; Fig. 2 I) and the *oblectatus* pattern (three spatulae on PC 3-5, with
452 bilateral symmetry; Fig. 2 H). The latter shows unsclerotized sketches of spatulae on PC1, 2,
453 and 6. *Megagnathotermes katangensis* was transferred to *Polyspathotermes* because of its tri-
454 spatulated EVA (*oblectatus* pattern), a change confirmed by molecular data. However, the type
455 species *M. notandus* has distinctive EVA (Fig. 2 M) and sequences, which justify retaining
456 *Megagnathotermes* as a monospecific genus, close to *Thoracotermes*.

457 *Isognathotermes* and *Crenetermes* are among the last genera to appear in the *Cubitermes*
458 complex. *Isognathotermes* merges the *fungifaber* and *finitimus* patterns: their PCs differ from
459 the ancestral EVA by the presence of bristly crests or globular protrusions, respectively, on the
460 downstream part of the odd-numbered PCs (Fig. 2 D,E). If present on the even-numbered PCs,
461 those crests or globular protrusions are weakly developed; the EVAs therefore have triradial
462 symmetry. SCs are very wide with a homogeneous spine scattering. Merging these two patterns
463 could be expected since some samples showed intermediate EVAs. The sister genus
464 *Crenetermes*, as represented by *C. albotarsalis*, has tiny crests that are sketched on the odd-
465 numbered PCs (Fig. 2 K); it also has narrower SCs.

466

467 *Variation in Soldier labrum lobe*

468 The soldier's labrum (Fig. 5B) in *Cubitermes* (*sensu lato*) and *Megagnathotermes* is always
469 more or less deeply bifurcated, but this is not the case in other members of the *Cubitermes*
470 complex: *A. longiceps*, *Cr. albotarsalis*, and *Th. macrothorax* have not developed any lobe on
471 the labrum (Bouillon & Mathot, 1965). On the other hand, many genera of the *Furculitermes*

Phylogeny of *Cubitermes*

472 and *Basidentitermes* complexes (*Euchilotermes*, *Furculitermes*, *Mucrotermes*, *Noditermes*,
473 *Ophiotermes*, *Pilotermes*, *Procubitermes*, and *Unguitermes*) also have soldiers with a
474 bifurcated or at least indented labrum (Bouillon & Mathot, 1965). Moreover, the soldier's
475 labrum is very flexible. Its precise shape can vary within a species and even within a single
476 individual, the left lobe being different from the right one (pers. obs.).

477

478 *Conclusions*

479 This work provides valuable insights for the ongoing revision of *Cubitermes*. It is clear that the
480 genus *Cubitermes sensu lato* is paraphyletic and required splitting into five monophyletic
481 genera. The EVA of workers is the morphological trait best correlated with genetic data and is
482 therefore the most efficient diagnostic trait. Along the *Cubitermes* complex phylogeny,
483 sclerotized EVA spatulae appeared twice independently: as three or six spatulae in
484 *Polyspathotermes* (*sulcifrons* and *oblectatus* patterns) and as two jaw-like spatulae in
485 *Nitiditermes* (*sankurensis* pattern), which later disappeared in species with the *oculatus* pattern.
486 Other morphological traits, mainly in soldiers, used in Sjöstedt's (1926) and Williams's (1966)
487 keys (labrum shape, fore head projection, mandible curvature) are useful at the species level,
488 but not genus. Our data confirm the hypothesis of Sands (1998), that the genera *Nitiditermes*
489 and *Megagnathotermes* presents affinities to *Cubitermes*, and *M. notandus* remains the sole
490 species of the latter genus. Further sequencing, especially of complete mitochondrial genomes
491 (see Bourguignon *et al.*, 2017) or a multitude of orthologous genes generated by transcriptomic
492 data (Bucek *et al.*, 2019) as well as the incorporation of more taxa, will enable to fully resolve
493 the evolutionary history of the *Cubitermes* complex.

494

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527

528 **Data Archiving**

529 Sequences produced for this study have been deposited in GenBank under accessions
530 MN646697 to MN646750 for *COI*, MN685897 to MN685956 for *COII*, and MN685957 to
531 MN686017 for *28S rDNA* (see Supplementary Table S1 for details).

532

533 **Supporting Information**

534 Additional Supporting Information may be found in the online version of this manuscript.

535 **Supplementary Methods SM-1:** Molecular procedures used in this study.

536 **Figure S1:** Nuclear tree (A), cophyloplot (B), and total evidence tree (C) resulting from the
537 StarBEAST2 three-genes analysis.

538 **Figure S2:** Mitochondrial (A) and nuclear (B) trees, cophyloplot (C), and total evidence tree
539 (D) resulting from the StarBEAST2 two-gene analysis.

540 **Table S1:** Samples used in this study.

541 **Table S2:** Primers and cycling conditions used in this study.

542 **Table S3:** *COII* sequences retrieved from GenBank.

543 **Table S4:** List of valid names of the taxa formerly included (as in Krishna *et al.* 2013c) in the
544 genera *Cubitermes*, *Megagnathotermes* and *Nitiditermes*.

545 **References**

- 546 Bignell, D. E. (2000). Introduction to symbiosis. In ‘Termites: Evolution, Sociality, Symbioses,
547 Ecology’. (Eds T. Abe, D. E. Bignell, and M. Higashi.) pp. 189–208. (Kluwer Academic
548 Publishers: Dordrecht, The Netherlands.). doi:10.1007/978-94-017-3223-9_9
- 549 Bouckaert, R., Heled, J., Kühnert, D., Vaughan, T., Wu, C. H., Xie, D., Suchard, M. A.,
550 Rambaut, A., and Drummond, A. J. (2014). BEAST 2: a software platform for bayesian
551 evolutionary analysis. *PLoS Computational Biology* **10**, e1003537.
552 doi:10.1371/journal.pcbi.1003537
- 553 Bouillon, A., and Mathot, G. (1965). Quel est ce termite africain? *Zooleo (Léopoldville)* **1**, 1–
554 115.
- 555 Bouillon, A., and Vincke, P. P. (1971). Valvule entérique et révision du genre *Cubitermes*
556 Wasmann. *Cubitermes bugeserae* sp. nov. (Isoptera, Termitidae). *Revue de Zoologie et de*
557 *Botanique Africaines* **84**, 269–280.
- 558 Bourguignon, T., Lo, N., Cameron, S. L., Šobotník, J., Hayashi, Y., Shigenobu, S., Watanabe,
559 D., Roisin, Y., Miura, T., and Evans, T. A. (2015). The evolutionary history of termites as
560 inferred from 66 mitochondrial genomes. *Molecular Biology and Evolution* **32**, 406–421.
561 doi:10.1093/molbev/msu308
- 562 Bourguignon, T., Lo, N., Šobotník, J., Ho, S. Y. W., Iqbal, N., Coissac, É., Lee, M., Jendryka,
563 M. M., Sillam-Dussès, D., Křížková, B., Roisin, Y., and Evans, T. A. (2017).
564 Mitochondrial phylogenomics resolves the global spread of higher termites, ecosystem
565 engineers of the tropics. *Molecular Biology and Evolution* **34**, 589–597.
566 doi:10.1093/molbev/msw253
- 567 Bucek, A., Šobotník, J., He, S., Shi, M., McMahon, D. P., Holmes, E. C., Roisin, Y., Lo, N.,
568 and Bourguignon, T. (2019). Evolution of termite symbiosis informed by transcriptome-
569 based phylogenies. *Current Biology* **29**, 3728–3734.e4. doi:10.1016/j.cub.2019.08.076
- 570 Darriba, D., Taboada, G. L., Doallo, R., and Posada, D. (2012). jModelTest 2: more models,
571 new heuristics and parallel computing. *Nature Methods* **9**, 772. doi:10.1038/nmeth.2109
- 572 Donovan, S. E. (2002). A morphological study of the enteric valves of the Afrotropical
573 Apicotermitinae (Isoptera: Termitidae). *Journal of Natural History* **36**, 1823–1840.
574 doi:10.1080/00222930110062309
- 575 Donovan, S. E., Eggleton, P., and Bignell, D. E. (2001a). Gut content analysis and a new
576 feeding group classification of termites. *Ecological Entomology* **26**, 356–366.
577 doi:10.1046/j.1365-2311.2001.00342.x
- 578 Donovan, S. E., Eggleton, P., Dubbin, W. E., Batchelder, M., and Dibog, L. (2001b). The effect
579 of a soil-feeding termite, *Cubitermes fungifaber* (Isoptera: Termitidae) on soil properties:
580 termites may be an important source of soil microhabitat heterogeneity in tropical forests.
581 *Pedobiologia* **45**, 1–11. doi:10.1078/0031-4056-00063
- 582 Dray, S., and Dufour, A. B. (2007). The ade4 package: implementing the duality diagram for
583 ecologists. *Journal of Statistical Software* **22**, 1–20. doi:10.1.1.177.8850
- 584 Edgar, R. C. (2004). MUSCLE: a multiple sequence alignment method with reduced time and
585 space complexity. *BMC Bioinformatics* **5**, 1–19. doi:10.1186/1471-2105-5-113
- 586 Emerson, A. E. (1960). Six new genera of Termitinae from the Belgian Congo (Isoptera,
587 Termitidae). *American Museum Novitates* **1988**, 1–49.
- 588 Engel, M. S., Grimaldi, D. A., and Krishna, K. (2009). Termites (Isoptera): their phylogeny,
589 classification, and rise to ecological dominance. *American Museum Novitates* **3650**, 1–27.
- 590 Haviland, G. D. (1898). Observations on termites; with descriptions of new species. *Journal of*
591 *the Linnean Society of London, Zoology* **26**, 358–442, pl. 22–25.
- 592 Hijmans, R. J. (2019). geosphere: spherical trigonometry. Version 1.5-10. Available at:
593 <https://cran.r-project.org/package=geosphere>

- 594 Inward, D. J. G., Vogler, A. P., and Eggleton, P. (2007). A comprehensive phylogenetic
595 analysis of termites (Isoptera) illuminates key aspects of their evolutionary biology.
596 *Molecular Phylogenetics and Evolution* **44**, 953–967. doi:10.1016/j.ympev.2007.05.014
- 597 Josens, G., and Deligne, J. (2019). Species groups in the genus *Cubitermes* (Isoptera:
598 Termitidae) defined on the basis of enteric valve morphology. *European Journal of*
599 *Taxonomy*, 1–72. doi:10.5852/ejt.2019.515
- 600 Josens, G., and Wango, S. P. M. (2019). Niche differentiation between two sympatric
601 *Cubitermes* species (Isoptera, Termitidae, Cubitermitinae) revealed by stable C and N
602 isotopes. *Insects* **10**, 38. doi:10.3390/insects10020038
- 603 Kimura, M. (1980). A simple method for estimating evolutionary rate of base substitutions
604 through comparative studies of nucleotide sequences. *Journal of Molecular Evolution* **16**,
605 111–120. doi:10.1007/BF01731581
- 606 Krishna, K., Grimaldi, D. A., Krishna, V., and Engel, M. S. (2013a). Treatise on the Isoptera
607 of the World. 1. Introduction. *Bulletin of the American Museum of Natural History* **377**,
608 1–200. doi:10.1206/377.1
- 609 Krishna, K., Grimaldi, D. A., Krishna, V., and Engel, M. S. (2013b). Treatise on the Isoptera
610 of the World. 4. Termitidae (Part One). *Bulletin of the American Museum of Natural*
611 *History* **377**, 973–1494. doi:10.1206/377.4
- 612 Krishna, K., Grimaldi, D. A., Krishna, V., and Engel, M. S. (2013c). Treatise on the Isoptera
613 of the World. 5. Termitidae (Part Two). *Bulletin of the American Museum of Natural*
614 *History* **377**, 1495–1988. doi:10.1206/377.5
- 615 Kumar, S., Stecher, G., Li, M., Knyaz, C., and Tamura, K. (2018). MEGA X: molecular
616 evolutionary genetics analysis across computing platforms. *Molecular Biology and*
617 *Evolution* **35**, 1547–1549. doi:10.1093/molbev/msy096
- 618 Maddison, W. P., and Maddison, D. R. (2019). Mesquite: a modular system for evolutionary
619 analysis. Version 3.6. Available at: <http://mesquiteproject.org>
- 620 Mantel, N. (1967). The detection of disease clustering and a generalized regression approach.
621 *Cancer Research* **27**, 209–220.
- 622 Noirot, C. (2001). The gut of termites (Isoptera): comparative anatomy, systematics, phylogeny.
623 II. - Higher termites (Termitidae). *Annales de la Société Entomologique de France*
624 (*Nouvelle Série*) **37**, 431–471.
- 625 Ogilvie, H. A., Bouckaert, R. R., and Drummond, A. J. (2017). StarBEAST2 brings faster
626 species tree inference and accurate estimates of substitution rates. *Molecular Biology and*
627 *Evolution* **34**, 2101–2114. doi:10.1093/molbev/msx126
- 628 Okwakol, M. J. N. (1987). Effects of *Cubitermes testaceus* (Williams) on some physical and
629 chemical properties of soil in a grassland area of Uganda. *African Journal of Ecology* **25**,
630 147–153. doi:10.1111/j.1365-2028.1987.tb01101.x
- 631 Paradis, E., Claude, J., and Strimmer, K. (2004). APE: analyses of phylogenetics and evolution
632 in R language. *Bioinformatics* **20**, 289–290. doi:10.1093/bioinformatics/btg412
- 633 R Development Core Team (2018). R: A Language and Environment for Statistical Computing.
- 634 Rambaut, A. (2017). FigTree v1.4.3. Available at: <https://github.com/rambaut/figtree/releases>
- 635 Rambaut, A., Suchard, M., Xie, W., and Drummond, A. J. (2014). Tracer v1.6.
- 636 Ronquist, F., Teslenko, M., van der Mark, P., Ayres, D. L., Darling, A., Höhna, S., Larget, B.,
637 Liu, L., Suchard, M. A., and Huelsenbeck, J. P. (2012). MrBayes 3.2: Efficient Bayesian
638 phylogenetic inference and model choice across a large model space. *Systematic Biology*
639 **61**, 539–542. doi:10.1093/sysbio/sys029
- 640 Roy, V., Demanche, C., Livet, A., and Harry, M. (2006). Genetic differentiation in the soil-
641 feeding termite *Cubitermes* sp. *affinis subarquatus*: occurrence of cryptic species revealed
642 by nuclear and mitochondrial markers. *BMC Evolutionary Biology* **6**, 102.
643 doi:10.1186/1471-2148-6-102

- 644 Ruelle, J. E. (1975). Type specimens of Isoptera in the National Collection of Insects, Pretoria.
 645 *Entomology Memoir, Department of Agricultural and Technical Services, Republic of*
 646 *South Africa* **45**, 1–22.
- 647 Sands, W. A. (1998). ‘The identification of worker castes of termite genera from soils of Africa
 648 and the Middle East’. (CABI Publishing.)
- 649 Sands, W. A. (1972). The soldierless termites of Africa (Isoptera, Termitidae). *Bulletin of the*
 650 *British Museum (Natural History) Entomology Supplement* **18**, 1–244.
- 651 Scheffrahn, R. H., Bourguignon, T., Bordereau, C., Hernandez-Aguilar, R. A., Oelze, V. M.,
 652 Dieguez, P., Šobotnik, J., and Pascual-Garrido, A. (2017). White-gutted soldiers:
 653 simplification of the digestive tube for a non-particulate diet in higher Old World termites
 654 (Isoptera: Termitidae). *Insectes Sociaux* **64**, 525–533. doi:10.1007/s00040-017-0572-9
- 655 Silvestri, F. (1912). Termiti raccolte da L. Fea alla Guinea Portoghese e alle isole S. Thomè,
 656 Annobon, Principe e Fernando Poo. *Annali del Museo Civico di Storia Naturale di Genova*
 657 (Ser. 3) **5**, 211–255.
- 658 Sjöstedt, Y. (1913). Über Termiten aus dem inneren Kongo, Rhodesia, und Deutsch-Ostafrika.
 659 *Revue Zoologique Africaine (Bruxelles)* **2**, 354–391, pl. VIII–X.
- 660 Sjöstedt, Y. (1926). Revision der Termiten Afrikas. 3. Monographie. *Kungliga Svenska*
 661 *Vetenskapsakademiens Handlingar (3)* **3**, 1–419, 16pl.
- 662 Snyder, T. E. (1949). Catalog of the Termites (Isoptera) of the World. *Smithsonian*
 663 *Miscellaneous Collections* **112**, 1–490.
- 664 Vincenty, T. (1975). Direct and inverse solutions of geodesics on ellipsoid with applications of
 665 nested equations. *Survey Review* **23**, 88–93.
- 666 Wango, S. P., and Josens, G. (2011). Comparison of nest shapes and densities of two sympatric
 667 species of *Cubitermes* (Isoptera: Termitidae: Termitinae) as clues for the study of their
 668 population dynamics. *African Zoology* **46**, 156–168. doi:10.3377/004.046.0106
- 669 Wasmann, E. (1906). Beispiele rezenter artenbildung bei ameisengästen und termitengästen.
 670 *Biologisches Centralblatt* **26**, 565–580.
- 671 Wasmann, S. J. (1911). Zur Kenntnis der Termiten und Termitengäste von Belgischen Congo
 672 (Schluss, mit 2 Tafeln.). *Revue Zoologique Africaine (Bruxelles)* **1**, 145–176.
- 673 Williams, R. M. C. (1966). The East African termites of the genus *Cubitermes* (Isoptera:
 674 Termitidae). *Transactions of the Royal Entomological Society of London* **118**, 73–118.
- 675 Wood, T. G., Johnson, R. A., and Anderson, J. M. (1983). Modification of soils in Nigerian
 676 savanna by soil-feeding *Cubitermes* (Isoptera, termitidae). *Soil Biology and Biochemistry*
 677 **15**, 575–579. doi:10.1016/0038-0717(83)90052-4
 678

679 **Figure captions**

680 **Fig. 1.** Pictures of (A) living soldier and workers of *Isognathotermes planifrons*
 681 (Sjöstedt) (Cameroon; scale bar, 0.5 cm), young (B) and old (C) nests of *Isognathotermes*
 682 *severus* (Silvestri) (Central African Republic; scale bars, 10 cm), and (D) landscape
 683 characterized by mounds of *Nitiditermes* sp. NS22 (Côte d'Ivoire). Credits: Y. Roisin (A, D),
 684 and G. Josens (B, C). This figure is available in colour in the online version.

685 **Fig. 2.** Enteric valve armature patterns from workers of studied taxa (described in Table 1): (A)
 686 *Cubitermes exiguus* Mathot; (B) *Ternicubitermes weissi* (Silvestri); (C) *Ternicubitermes*
 687 *muneris* (Sjöstedt); (D) *Isognathotermes fungifaber* (Sjöstedt); (E) *Isognathotermes finitimus*
 688 (Schmitz); (F) *Nitiditermes oculatus* (Silvestri); (G) *Nitiditermes sankurensis* (Wasmann); (H)
 689 *Polyspathotermes oblectatus* (Harris); (I) *Polyspathotermes sulcifrons* (Wasmann); (J)
 690 *Apilitermes longiceps* (Sjöstedt); (K) *Crenetermes albotarsalis* (Sjöstedt); (L) *Furculitermes*
 691 *parviceps* Emerson; (M) *Megagnathotermes notandus* Silvestri; (N) *Procubitermes aburiensis*
 692 Sjöstedt; (O) *Thoracotermes macrothorax* (Sjöstedt). Scale bars, 0.5 mm. This figure is
 693 available in colour in the online version.

694 **Fig. 3.** Maximum clade credibility ultrametric mitochondrial (linked *COI* and *COII*) tree
 695 resulting from Bayesian inference using the StarBEAST2 method on the three-gene dataset (for
 696 the nuclear tree, cophyloplot and total evidence trees, see Supplementary Fig. S1). Node support
 697 values are Bayesian posterior probabilities (BPP). Scale bar indicates the mean number of
 698 substitutions per site. Genera which previously made *Cubitermes* Wasmann paraphyletic are
 699 indicated in bold.

700 **Fig. 4.** Non-ultrametric 50% majority rule consensus Bayesian phylogenetic tree generated by
 701 MrBayes using the *COII* alignment of sequences produced in this study and retrieved from
 702 GenBank (for details, see Tables S1 and S3). Node support values are Bayesian posterior
 703 probabilities (BPP). Scale bar indicates the mean number of substitutions per site. Genera which
 704 previously made *Cubitermes* Wasmann paraphyletic are indicated in bold.

705 **Fig. 5.** Ancestral reconstruction of (A) workers' EVA types (see Table 1 A), and (B) soldiers'
 706 labral lobes (Absence of lobes; Digitiform; Subtruncated; Truncated; Triangular), on the
 707 mitochondrial (*COI* and *COII*) BI tree. Ancestral states were reconstructed using Mesquite v3.6
 708 under a parsimony model with unordered characters for each trait. Genera which previously
 709 made *Cubitermes* Wasmann paraphyletic are indicated in bold. This figure is available in colour
 710 in the online version.

Phylogeny of *Cubitermes*

711 **Table 1:** Overview of enteric valve armatures (EVAs) among (A) groups of species described within the genus *Cubitermes* (*sensu lato*) and derived
 712 monophyletic genera, as well as (B) non *Cubitermes* species, with details on primary cushions (PCs) and secondary cushions (SCs). Asterisks
 713 denote observations made on two to seven individuals. In (A), the last three columns refer to genus assignment based on molecular data (see
 714 Results).

	EVA type	Valve symmetry	Shape (pairs of supporting bristles)	PCs		SCs	Comments	Genus revision (genetic clade) Type species
				Sclerotized spatulae	Crests			
(A) <i>Cubitermes</i> species (<i>sensu lato</i>)	<i>bilobatus</i> See Fig. 2 A	triradial to bilateral	nearly triangular (2-6)	none	none	wider than PCs; generally heterogeneous		<i>Cubitermes</i> Wasmann, 1906: 573 (clade I) <i>Termes bilobatus</i> Haviland, 1898: 411-412
	<i>bilobatodes</i> See Fig. 2 B	triradial	fusiform (10-30)	none	none	wider than PCs; spearhead shaped	sometimes intermediate with <i>sulcifrons</i> EVA	<i>Ternicubitermes</i> Josens & Deligne gen.n. (clade V) <i>Cubitermes bilobatodes</i> Silvestri, 1912: 247-249
	<i>muneris</i> See Fig. 2 C	triradial	roughly rectangular (10-19)	none	none	wider than PCs; homogeneous	sometimes intermediate with <i>bilobatodes</i> EVA	
	<i>fungifaber</i> See Fig. 2 D	triradial	triangular or fusiform (13-30)	none	high, on PC1, 3 & 5	wider than PCs; homogeneous	sometimes intermediate with <i>finitimus</i> EVA	<i>Isognathotermes</i> Sjöstedt, 1926: 216 (clade III) <i>Eutermes (Cubitermes) minitabundus</i> Sjöstedt, 1913: 368-369
	<i>finitimus</i> See Fig. 2 E	triradial	roughly rectangular (17-37)	none	wide, on PC1, 3 & 5	wider than PCs; homogeneous	sometimes intermediate with <i>fungifaber</i> EVA	
	<i>oculatus</i> See Fig. 2 F	bilateral	nearly triangular (3-8)	none	none	not wider than PCs; SCs surrounding PC1 faint or lacking		<i>Nitiditermes</i> Emerson, 1960: 3-10 (clade II) <i>Nitiditermes berghei</i> Emerson, 1960: 10-12
	<i>sankurensis</i> See Fig. 2 G	none	roughly triangular (8-24)	2 (PC3 & 4)	none	not wider than 120% of PCs; SCs surrounding PC1 weakly developed		
	<i>oblectatus</i> See Fig. 2 H	bilateral	roughly rectangular to fusiform (14-23)	3 (PC3, 4 & 5)	high, on PC1, 3 & 5	2-3 times wider than PCs; homogeneous	spatulae sketched on PC1, 2 & 6, not sclerotized	<i>Polyspathotermes</i> Josens & Deligne gen.n. (clade IV) <i>Cubitermes sulcifrons</i> Wasmann, 1911: 156-158
	<i>sulcifrons</i> See Fig. 2 I	hexaradial	more or less fusiform (13-23)	6 (all PCs)	high, on all PCs	spearhead shaped or wider than PCs and homogeneous		

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716

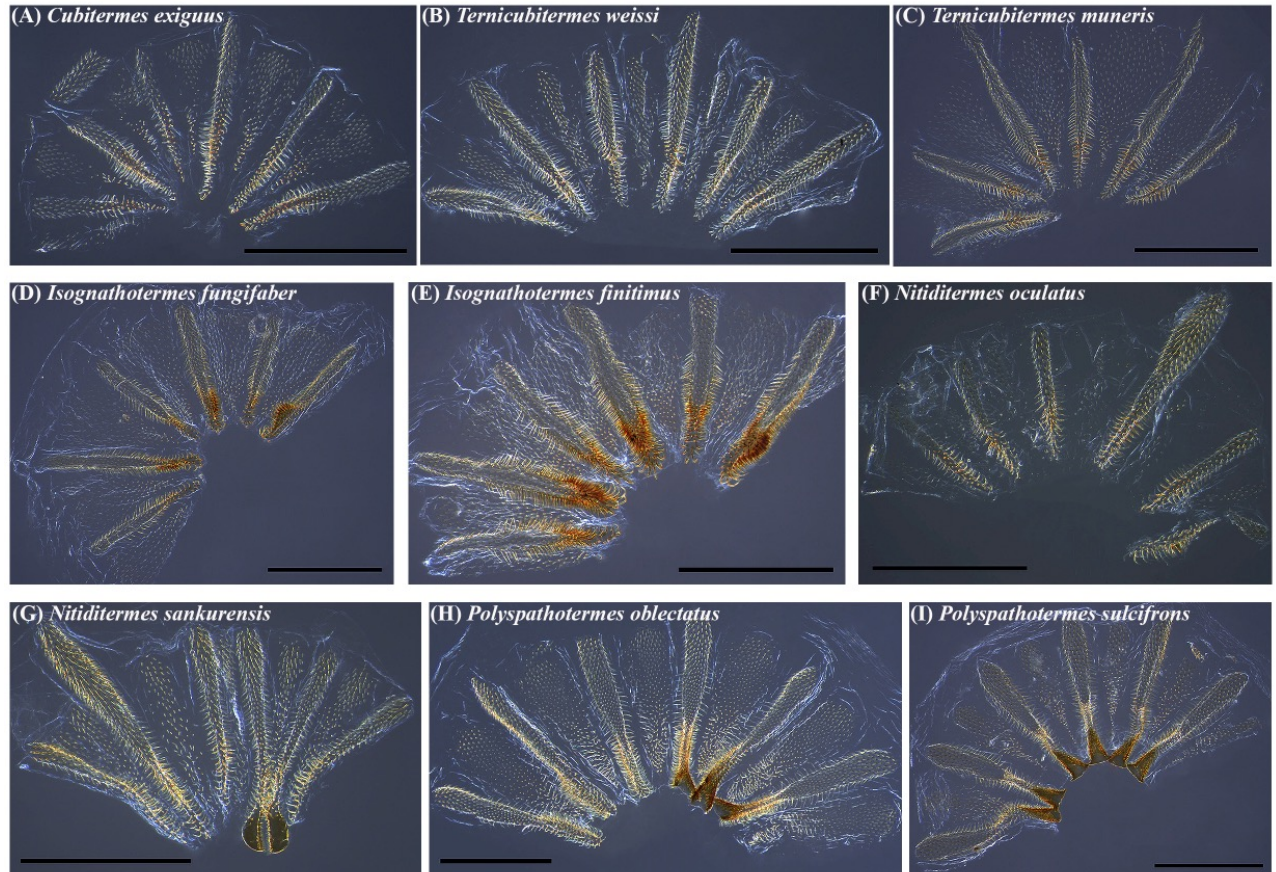
717 **Table 1. Continued (B).**

	EVA type	Valve symmetry	Shape (pairs of supporting bristles)	PCs		SCs Size and spine scattering	Comments	Genus
				Sclerotized spatulae	Crests			
(B) Other Cubitermitinae species	<i>Apilitermes longiceps</i> (Sjöstedt) * See Fig. 2 J	hexaradial to triradial	nearly triangular (15-18)	none	none	as wide as PCs; homogeneous or spearhead shaped		<i>Apilitermes</i> Holmgren
	<i>Crenetermes albotarsalis</i> (Sjöstedt) * See Fig. 2 K	triradial	nearly triangular to fusiform (15-18)	none	on PC1, 3 & 5	as wide as PCs; homogeneous	hairy appearance	<i>Crenetermes</i> Silvestri
	<i>Furculitermes parviceps</i> Emerson * See Fig. 2 L	triradial to bilateral	asymmetric dumbbell shaped (10-15)	none	none	as wide as PCs; homogeneous	hairy oval SCs	<i>Furculitermes</i> Emerson
	<i>Megagnathotermes notandus</i> Silvestri * See Fig. 2 M	triradial	nearly triangular plus fusiform pectinate sides (16-19)	none	long, on all PCs	not wider than PCs; tendency towards two groups	comb-like supporting bristles	<i>Megagnathotermes</i> Silvestri
	<i>Procubitermes aburiensis</i> Sjöstedt * See Fig. 2 N	triradial	nearly triangular to fusiform (17-20)	none	none	not wider than PCs; tendency towards spearhead shaped	close to <i>bilobatodes</i> EVA but with narrow SCs	<i>Procubitermes</i> Silvestri
	<i>Thoracotermes macrothorax</i> (Sjöstedt) * See Fig. 2 O	hexaradial	nearly triangular (17-23)	none	none	not wider than PCs; tendency towards two groups		<i>Thoracotermes</i> Wasmann

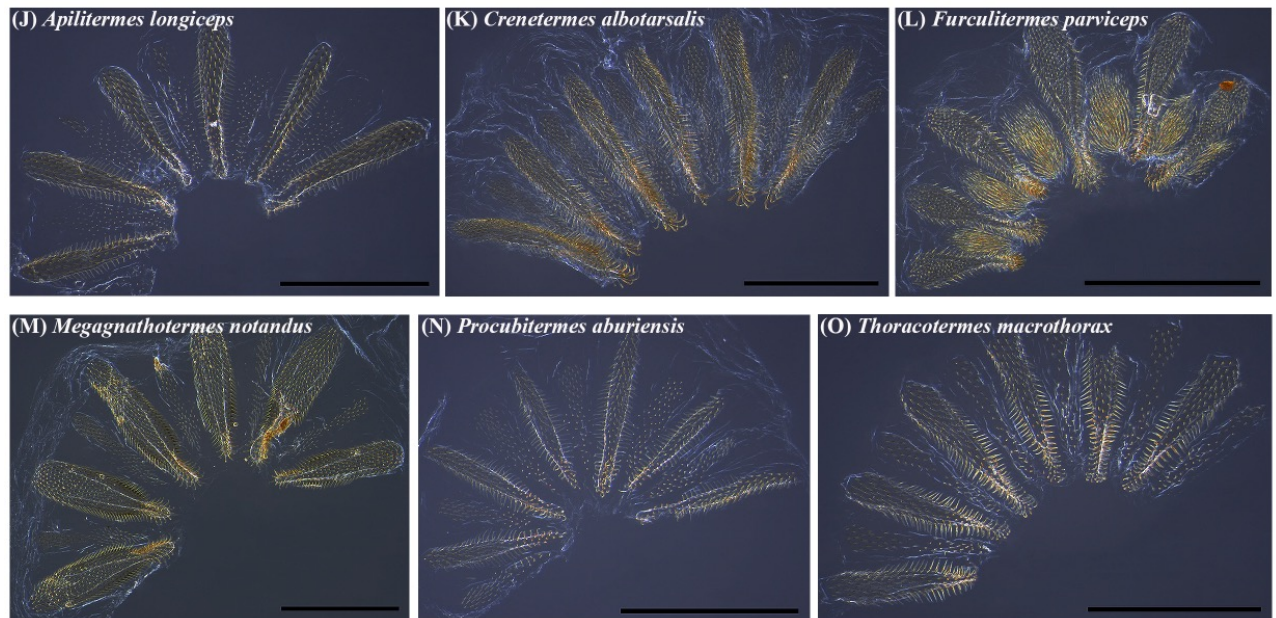


719
720 **FIGURE 1.**

Cubitermes (sensu lato) EVAs



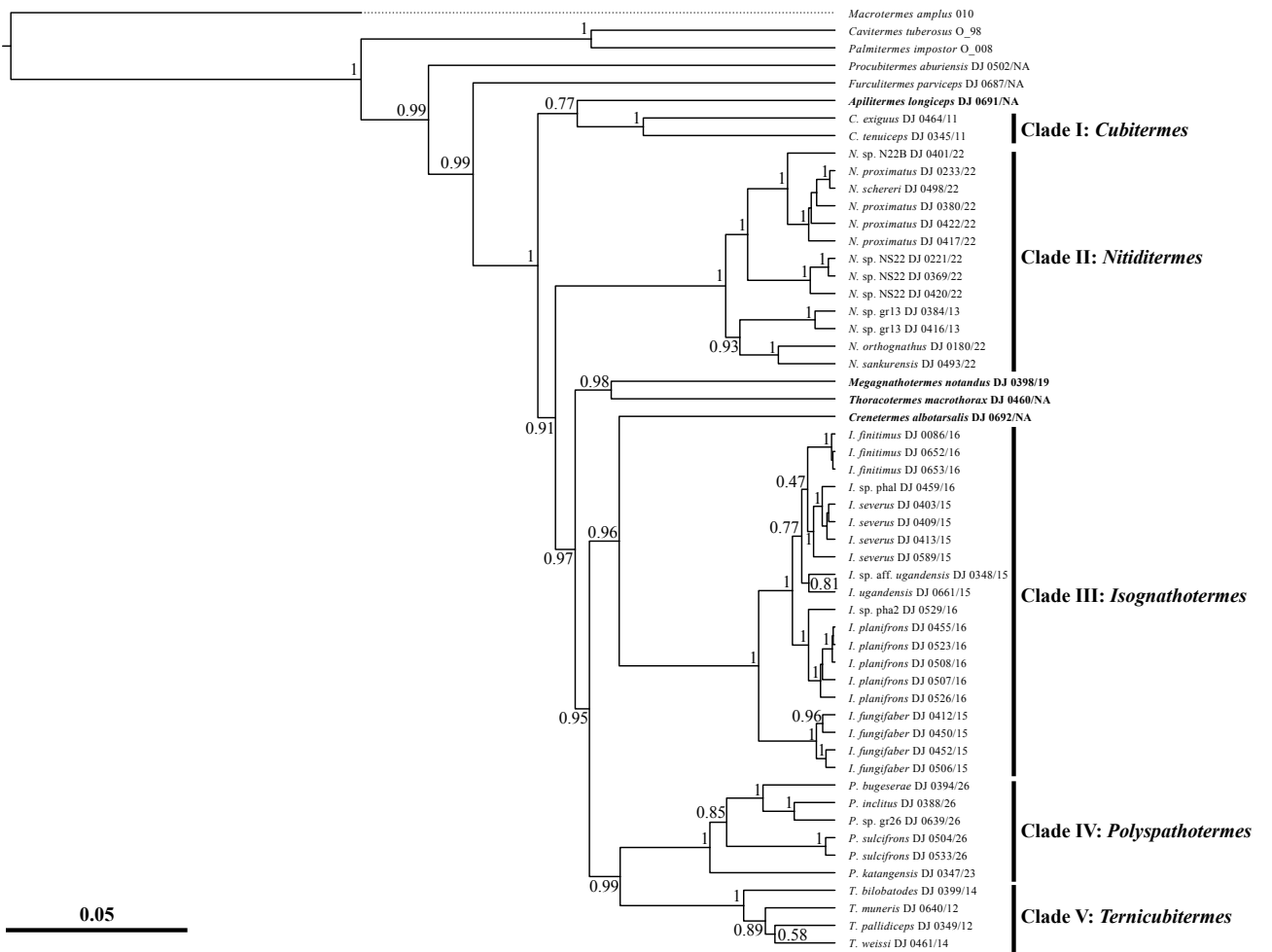
Other *Cubitermitinae* EVAs



721

722 **FIGURE 2.**

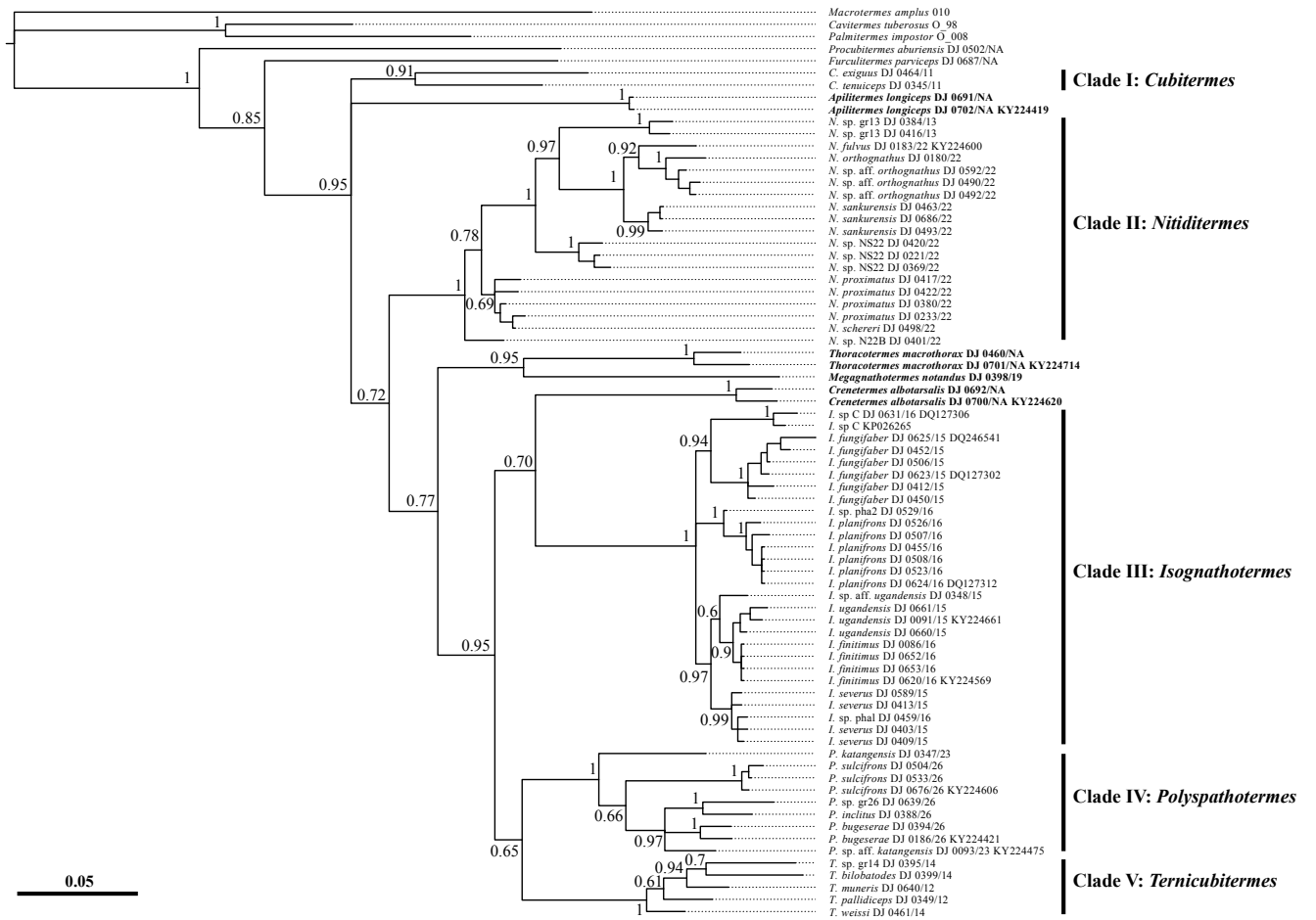
Phylogeny of *Cubitermes*



723

724 **FIGURE 3.**

Phylogeny of *Cubitermes*

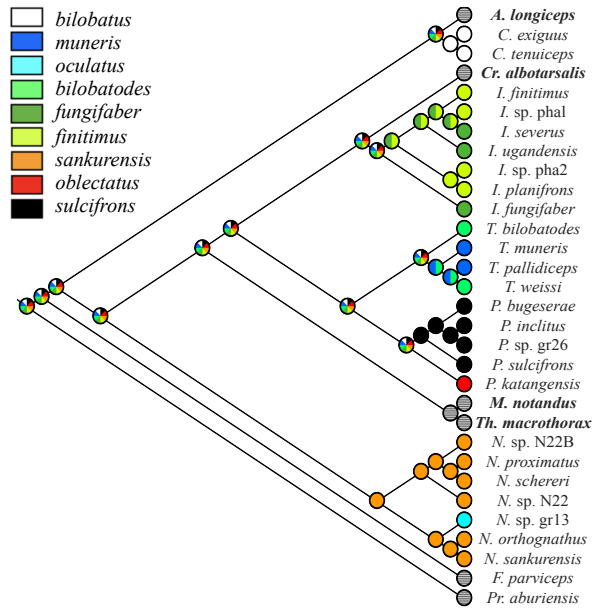


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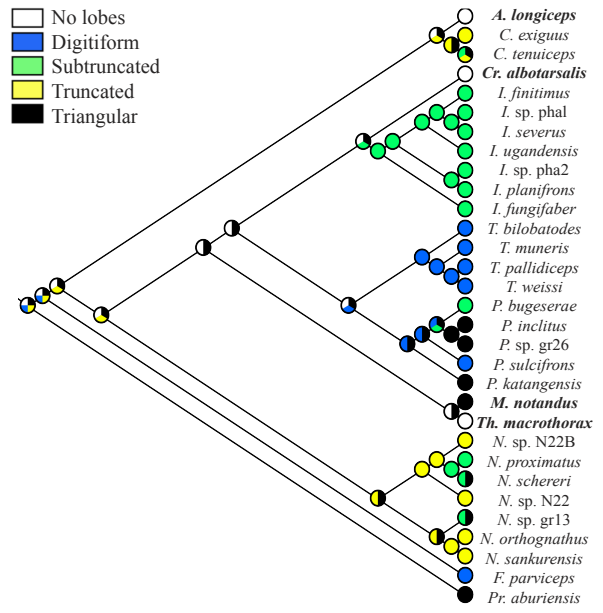
726 **FIGURE 4.**

Phylogeny of *Cubitermes*

(A) Workers' EVA types



(B) Soldiers' labral lobes



727

728 **FIGURE 5.**

**Phylogeny and revision of the ‘*Cubitermes* complex’ termites (Termitidae:
Cubitermitinae)**

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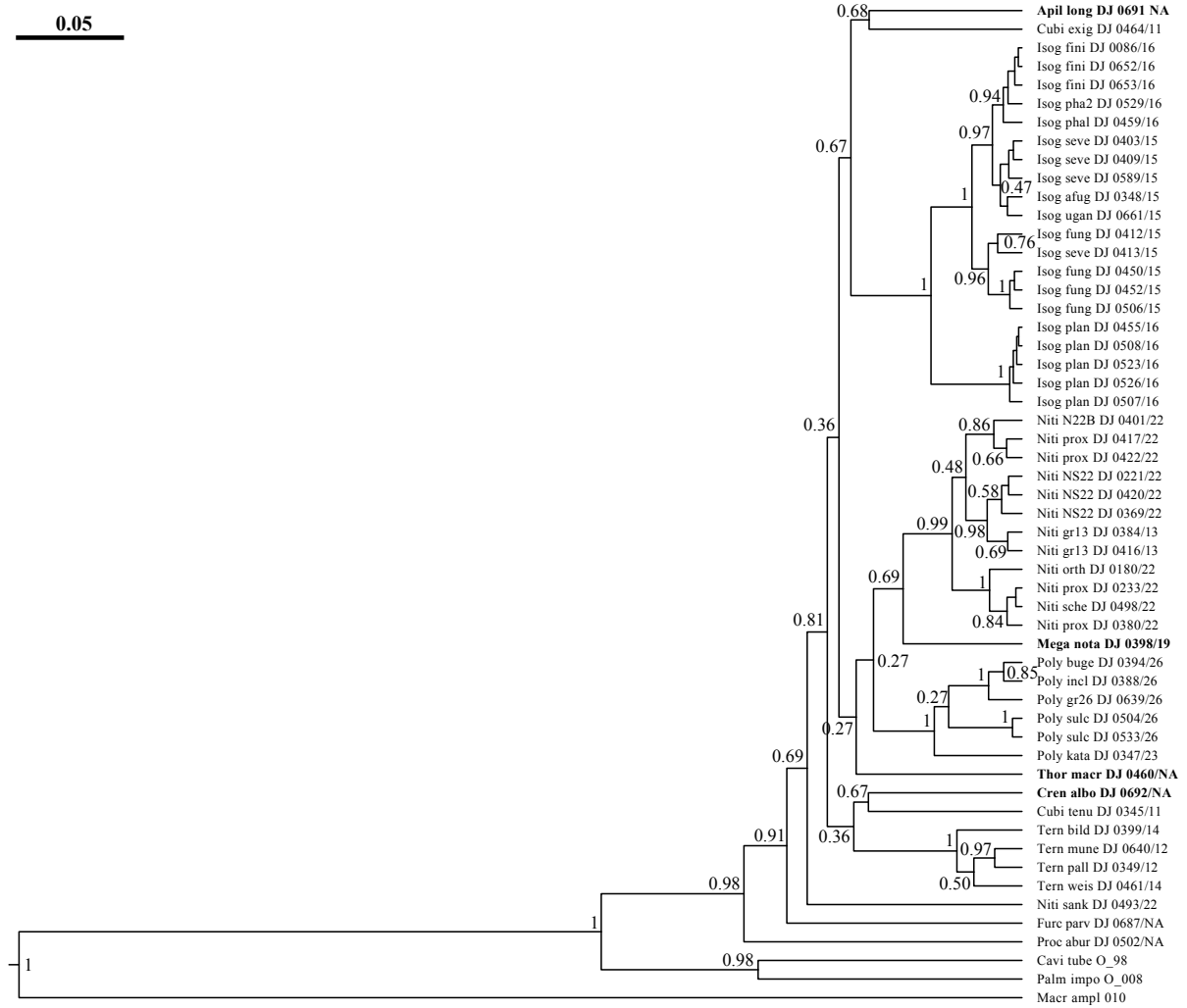
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A. Supplementary Figures

(S1A) Three-gene analysis: nuclear tree (28S rDNA)

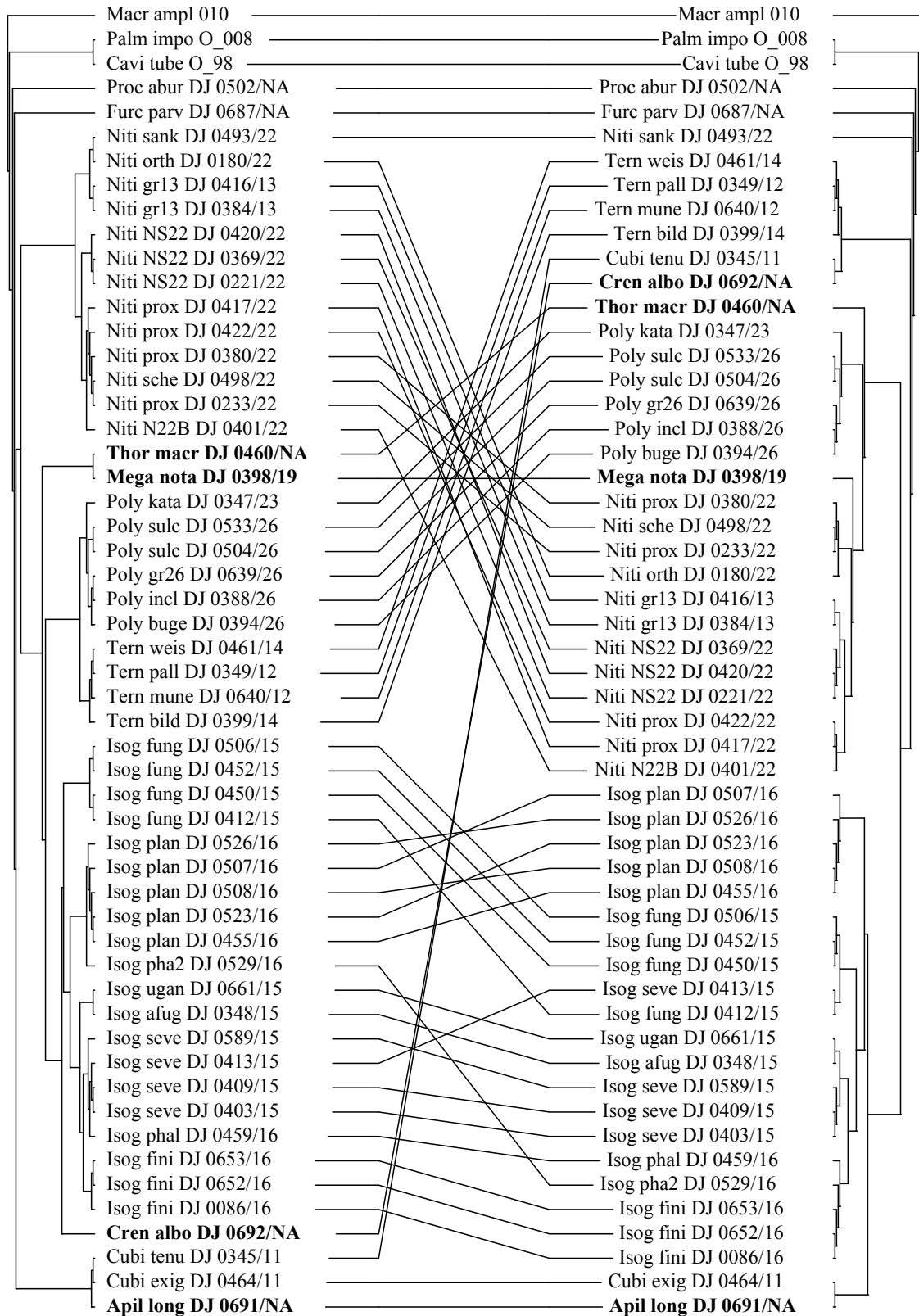


ELECTRONIC SUPPLEMENTARY MATERIALS

(S1B) Three-gene analysis: cophyloplot

Mitochondrial (*COI+COII*)

Nuclear (*28S rDNA*)



ELECTRONIC SUPPLEMENTARY MATERIALS

(S1C) Three-gene analysis: species tree

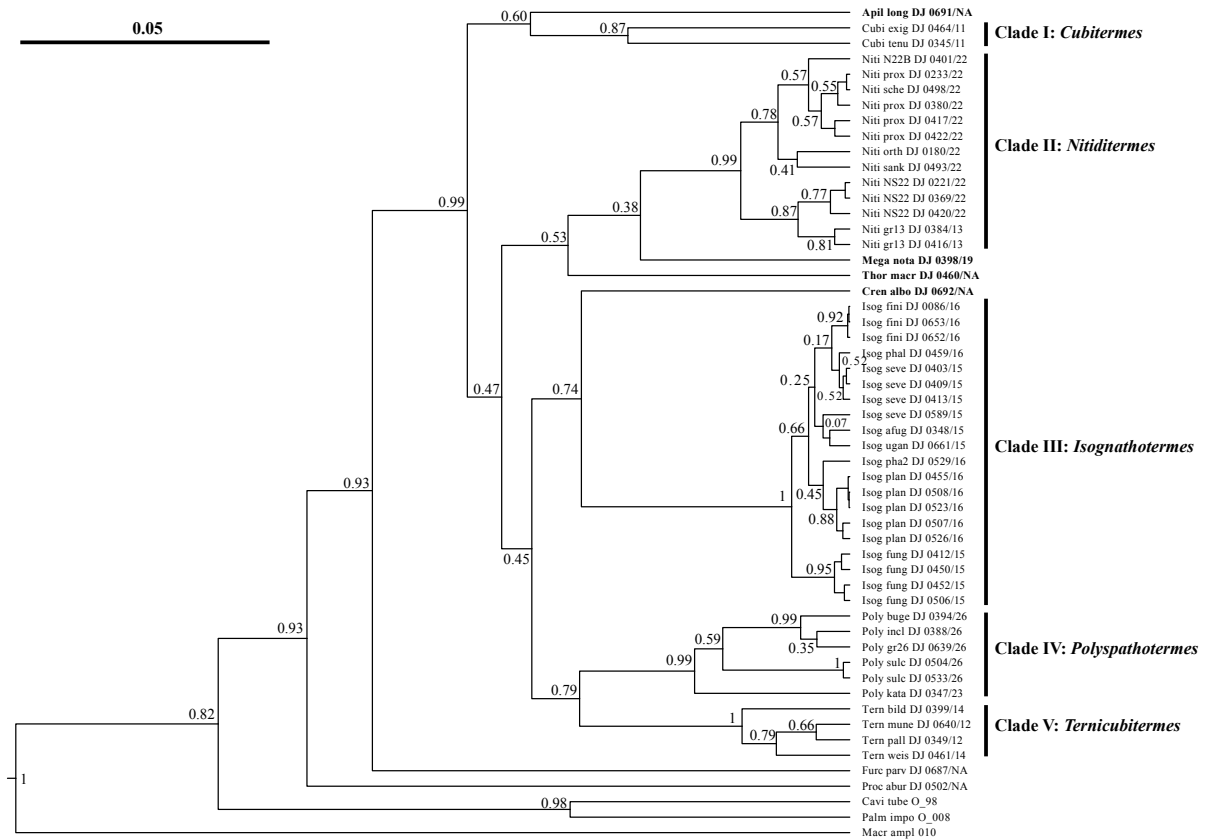
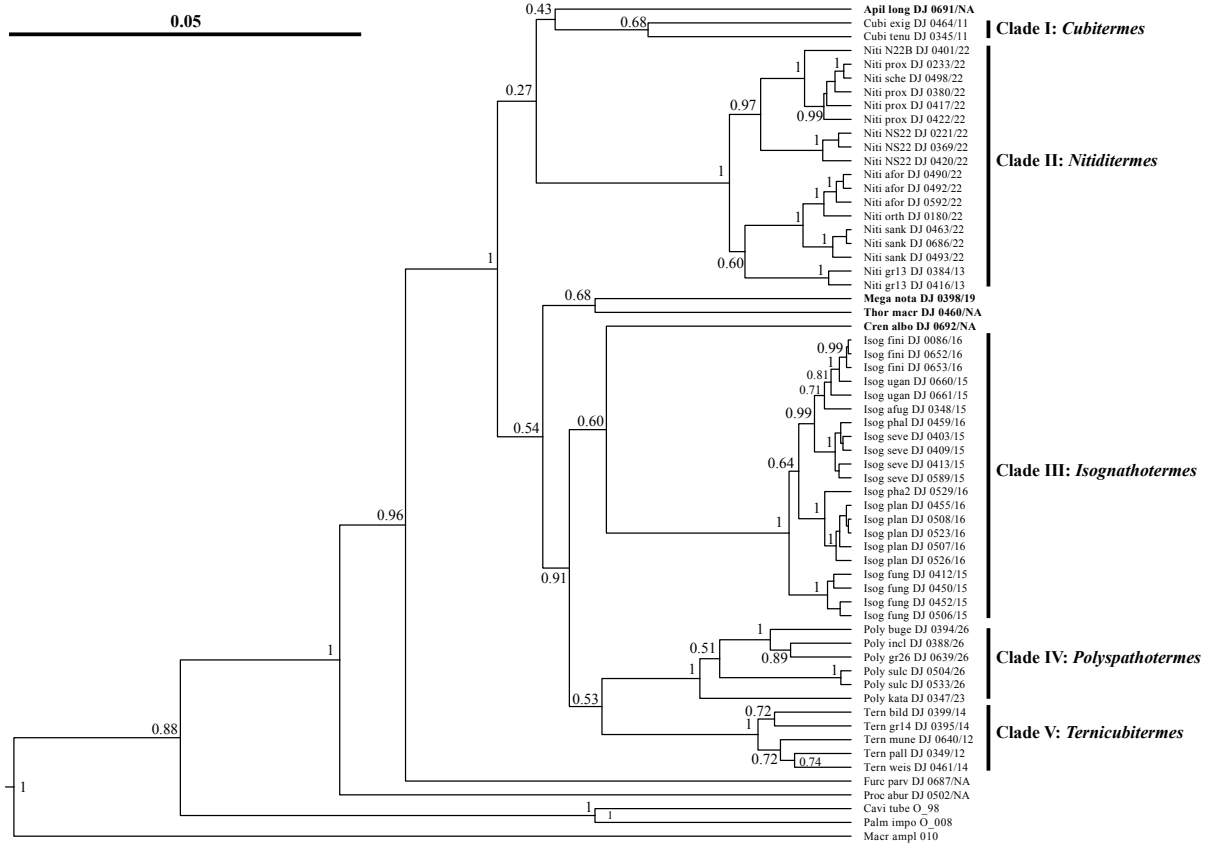


Fig. S1. Maximum clade credibility ultrametric gene and species trees resulting from Bayesian inference using the StarBEAST2 method for the three-gene dataset (mitochondrial linked *COI+COII* and nuclear *28S rDNA*; 54 sequences): (A) nuclear tree, (B) a cophyloplot showing the incongruence between the mitochondrial and nuclear trees, and (C) the total evidence tree. Node support values are Bayesian posterior probabilities (BPP). Scale bar indicates the mean number of substitutions per site. Genera which previously made *Cubitermes* paraphyletic are indicated in bold.

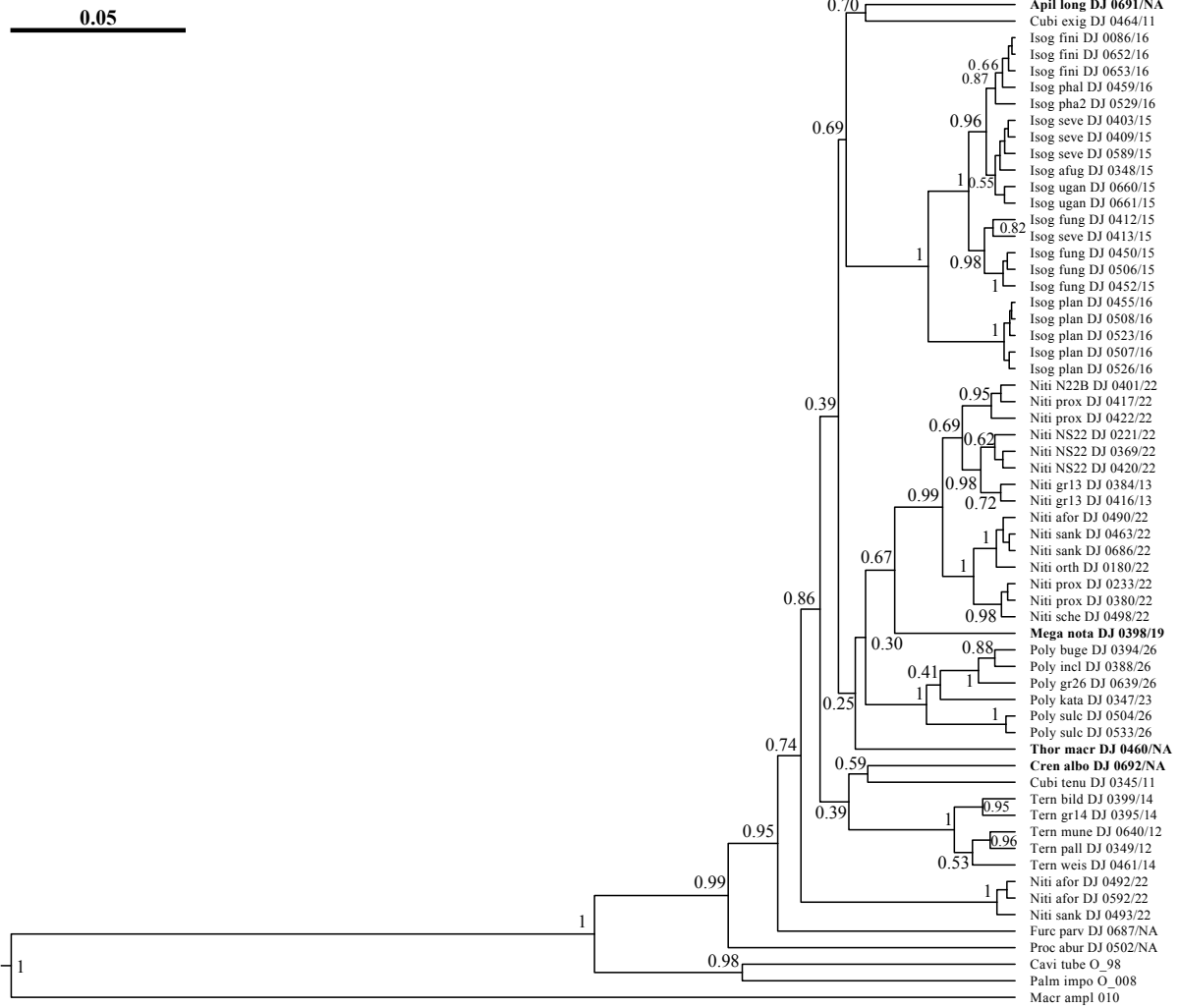
ELECTRONIC SUPPLEMENTARY MATERIALS

(S2A) Two-gene analysis: mitochondrial tree (*COII*)



ELECTRONIC SUPPLEMENTARY MATERIALS

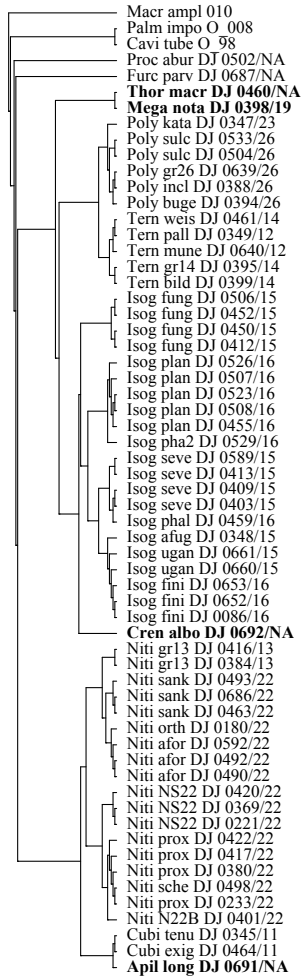
(S2B) Two-gene analysis: nuclear tree (*28S rDNA*)



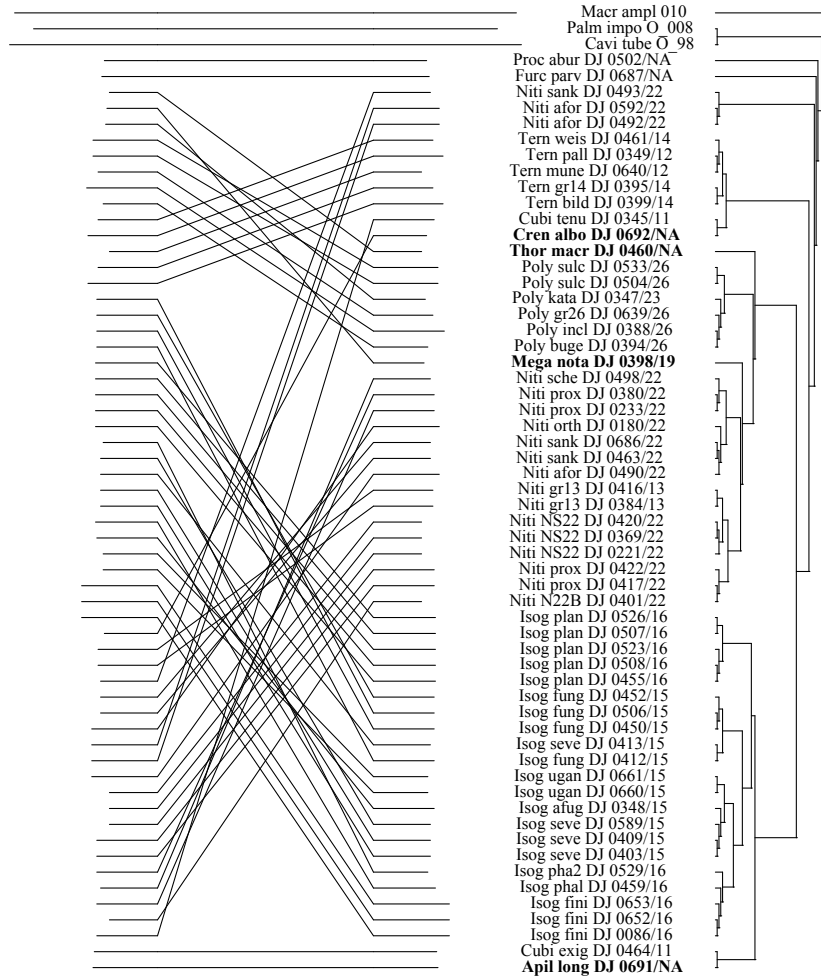
ELECTRONIC SUPPLEMENTARY MATERIALS

(S2C) Two-gene analysis: cophyloplot

Mitochondrial tree (*COII*)



Nuclear tree (*28S rDNA*)



ELECTRONIC SUPPLEMENTARY MATERIALS

(S2D) Two-gene analysis: species tree

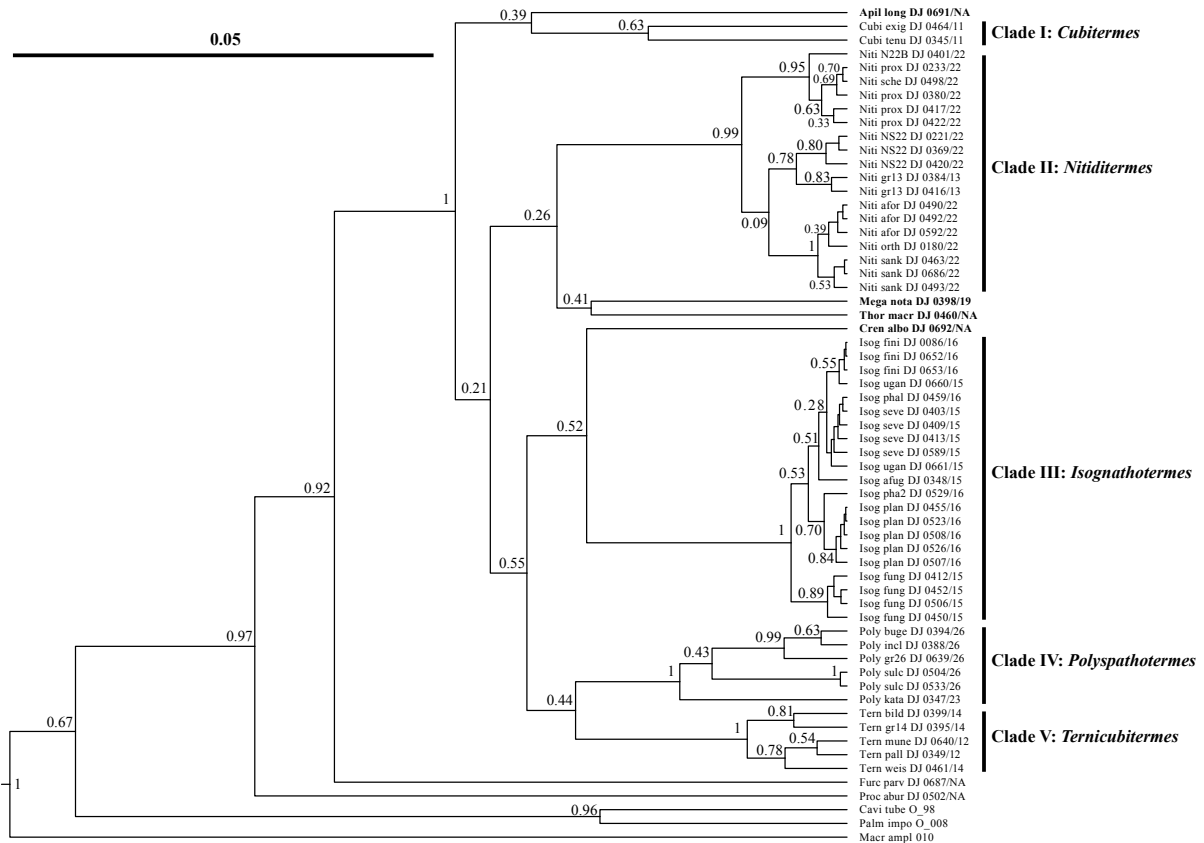


Fig. S2. Maximum clade credibility ultrametric gene and species trees resulting from Bayesian inference using the StarBEAST2 method for the two-gene dataset (mitochondrial *COII* and nuclear *28S rDNA*; 61 sequences): (A) mitochondrial and (B) nuclear trees, (C) a cophyloplot showing the incongruence between the two trees, and (D) the total evidence tree. Node support values are Bayesian posterior probabilities (BPP). Scale bar indicates the mean number of substitutions per site. Genera which previously made *Cubitermes* paraphyletic are indicated in bold.

B. Supplementary Methods SM-1: Molecular procedures

Total DNA was extracted from termite heads using a NucleoSpin Tissue kit (Macherey-Nagel). A fragment of ~650 bp of the *COI* was amplified using the universal forward LCO (LCO1490) and the reverse HCO (HCO2198) primers (Folmer *et al.* 1994), a fragment of ~680 bp of the *COII* with the modified forward primer A-tLeu (Miura *et al.* 2000) and the reverse primer B-tLys (Simon *et al.* 1994), and a fragment of ~840 bp of the *28S rDNA* with the forward Rd1.2a and reverse Rd4.2b primers (Whiting 2002). Amplification of each fragment was carried in 25 μ L reactions containing 0.5 μ L (1 U) MyTaq DNA polymerase (Bioline GmbH, Germany), 5 μ L 5x MyTaq Reaction Buffer, 0.5 μ L of each forward and reverse primer (20 μ M of each), 1.5 μ L of template DNA and PCR-grade water (q.s.). Cycling conditions used in this study are given in Table S2. A fraction of the amplification products was screened by electrophoresis on a 1% agarose gel and another fraction was purified with the Nucleofast PCR purification kit (Macherey-Nagel). Purified amplicons were sequenced with BigDye Terminator Cycle Sequencing kit v3.1. (Applied Biosystems) in 11.2 μ L reactions containing 1.0 μ L BigDye, 2.1 μ L 5x Sequencing Buffer, 0.1 μ L of forward or reverse primer (20 μ M of each), 3-8 μ L of amplicon and PCR-grade water (q.s.). Cycling conditions were as follow: an initial denaturing step at 96°C for 1 min, 25 cycles of denaturing at 96°C for 10 s, annealing at 50°C for 5 s, and extension at 60°C for 4 min. Sequencing products were purified with an ethanol/EDTA/sodium acetate method. Sequence data were obtained with an ABI 3730 Genetic Analyzer (Applied Biosystems) and were visualized and edited using the software CodonCode Aligner v8.0.2 (CodonCode Corporation, Dedham, MA.).

Hellemans *et al.* – Phylogeny of *Cubitermes*
ELECTRONIC SUPPLEMENTARY MATERIALS

C. Supplementary Tables

Table S1: Samples used in this study with corresponding GenBank accessions of amplified genes.

Collection code	Code in this study	Species	Country; Locality	Latitude; Longitude (°)	Elevation (m.)	Collecting date	Collector	<i>COI</i>	<i>COII</i>	<i>28S rDNA</i>
CGO_073	Apil long DJ 0691/NA	<i>Apilitermes longiceps</i>	Rep. of the Congo; Mokabi	3.15 N; 16.97 E	528	3-Dec-17	Y. Roisin	MN646697	MN685897	MN685957
O_98	Cavi tube O98	<i>Cavitermes tuberosus</i>	French Guiana; Petit Saut	5.07 N; 52.98 W	75	19-Oct-14	S. Hellemans	MN646698	MF953242	MN685958
CMRT 176	Cren albo DJ 0692/NA	<i>Crenetermes albotarsalis</i>	Cameroon; Nyong river-left bank	3.41 N; 11.46 E	652	31-May-17	Y. Roisin	MN646699	MN685898	MN685959
9 RNAL Kin	Cubi exig DJ 0464/11	<i>Cubitermes exiguus</i>	Dem. Rep. of the Congo; Kinshasa, Unikin campus	4.43 S; 15.31 E	450	24-Apr-17	C. Kifukieto	MN646707	MN685909	MN685970
10 RNA K	Cubi tenu DJ 0345/11	<i>Cubitermes tenuiceps</i>	Dem. Rep. of the Congo; Mikembo-Kisangwe	11.49 S; 27.66 E	1200	1-Jun-16	P. Kasangij	MN646741	MN685946	MN686007
8 RNAL Bip	Furc parv DJ 0687/NA	<i>Furculitermes parviceps</i>	Cameroon; Bipindi	3.05 N; 10.47 E	100	23-Nov-16	P. Akama	MN646744	MN685950	MN686011
8 RNA K	Isog afug DJ 0348/15	<i>Isognathotermes</i> sp. aff. <i>ugandensis</i>	Dem. Rep. of the Congo; Mikembo-Kisangwe	11.49 S; 27.66 E	1200	1-Jun-16	P. Kasangij	MN646704	MN685906	MN685967
RDCT 17	Isog fini DJ 0086/16	<i>Isognathotermes finitimus</i>	Dem. Rep. of the Congo; Yangambi	0.88 N; 24.33 E	470	7-Jul-13	Y. Roisin	MN646708	MN685910	MN685971
RDCT 1	Isog fini DJ 0652/16	<i>Isognathotermes finitimus</i>	Dem. Rep. of the Congo; Yangambi	0.79 N; 24.52 E	470	5-Jul-13	Y. Roisin	MN646709	MN685911	MN685972
RDCT 143	Isog fini DJ 0653/16	<i>Isognathotermes finitimus</i>	Dem. Rep. of the Congo; Yangambi	0.80 N; 24.49 E	470	15-Jul-13	Y. Roisin	MN646710	MN685912	MN685973
RNAL 30	Isog fung DJ 0412/15	<i>Isognathotermes fungifaber</i>	Côte d'Ivoire; Banco forest	5.38 N; 4.06 W	70	17-Feb-15	G. Josens	MN646711	MN685913	MN685974
1 RNAL Mbo	Isog fung DJ 0450/15	<i>Isognathotermes fungifaber</i>	Cameroon; Mbongé	4.54 N; 9.11 E	40	30-Nov-16	P. Akama	MN646712	MN685914	MN685975
5 RNAL Bip	Isog fung DJ 0452/15	<i>Isognathotermes fungifaber</i>	Cameroon; Bipindi	3.05 N; 10.47 E	100	23-Nov-16	P. Akama	MN646713	MN685915	MN685976
CMRT 026	Isog fung DJ 0506/15	<i>Isognathotermes fungifaber</i>	Cameroon; Ebogo	3.38 N; 11.46 E	660	23-May-17	Y. Roisin	MN646714	MN685916	MN685977
CGO_036	Isog pha2 DJ 0529/16	<i>Isognathotermes</i> sp. pha2	Rep. of the Congo; Loundougou	2.38 N; 17.07 E	490	4-Dec-17	Y. Roisin	MN646722	MN685925	MN685986
2 RNAL Kin	Isog phal DJ 0459/16	<i>Isognathotermes</i> sp. phal	Dem. Rep. of the Congo; Luméné gallery on Batéké Plateau	4.43 S; 16.05 E	550	22-Apr-17	C. Kifukieto	MN646723	MN685926	MN685987
4 RNAL GA	Isog plan DJ 0455/16	<i>Isognathotermes planifrons</i>	Gabon; Nkobissimo	2.24 N; 11.49 E	600	15-Apr-17	G. Trembleau	MN646724	MN685927	MN685988
CMRT 154	Isog plan DJ 0507/16	<i>Isognathotermes planifrons</i>	Cameroon; Akometa	3.47 N; 11.55 E	675	6-Jun-17	Y. Roisin	MN646725	MN685928	MN685989
CMRT 100	Isog plan DJ 0508/16	<i>Isognathotermes planifrons</i>	Cameroon; Yolo-Chimpa	5.59 N; 10.89 E	1200	30-May-17	Y. Roisin	MN646726	MN685929	MN685990

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Collection code	Code in this study	Species	Country; Locality	Latitude; Longitude (°)	Elevation (m.)	Collecting date	Collector	COI	COII	28S rDNA
CGO_059	Isog plan DJ 0523/16	<i>Isognathotermes planifrons</i>	Rep. of the Congo; Mokabi	3.15 N; 16.96 E	530	6-Dec-17	Y. Roisin	MN646727	MN685930	MN685991
CGO_008	Isog plan DJ 0526/16	<i>Isognathotermes planifrons</i>	Rep. of the Congo; Loundoungou	2.38 N; 17.07 E	455	3-Dec-17	Y. Roisin	MN646728	MN685931	MN685992
7 RNAL BE	Isog seve DJ 0403/15	<i>Isognathotermes severus</i>	Benin; Birni forest	10.02 N; 1.53 E	200	1-Nov-16	L.E. Loko	MN646735	MN685940	MN686001
7 RCI	Isog seve DJ 0409/15	<i>Isognathotermes severus</i>	Côte d'Ivoire; Taabo	6.30 N; 5.00 W	140	21-Feb-15	G. Josens	MN646736	MN685941	MN686002
50 RCI	Isog seve DJ 0413/15	<i>Isognathotermes severus</i>	Côte d'Ivoire; Man- Duékoué road	6.83 N; 7.41 W	250	1-Mar-15	G. Josens	MN646737	MN685942	MN686003
6 RNAL CA	Isog seve DJ 0589/15	<i>Isognathotermes severus</i>	Central African Rep.; Bondoé	5.17 N; 17.74 E	700	26-Apr-18	S.P. Wango	MN646738	MN685943	MN686004
BDIT 105	Isog ugan DJ 0660/15	<i>Isognathotermes ugandensis</i>	Burundi; Ruvubu N.P.	2.95 S; 30.43 E	1500	29-Nov-13	Y. Roisin	NA	MN685947	MN686008
BDIT 88	Isog ugan DJ 0661/15	<i>Isognathotermes ugandensis</i>	Burundi; Gihofi-Giharo road pk 75	3.99 S; 30.15 E	1200	27-Nov-13	Y. Roisin	MN646742	MN685948	MN686009
CGO_010	Macr ampl 010	<i>Macrotermes amplus</i>	Rep. of the Congo; Loundoungou	2.38 N; 17.07 E	462	3-Dec-17	Y. Roisin	MN646745	MN685951	MN686012
RNAL 57	Mega nota DJ 0398/19	<i>Megagnathotermes notandus</i>	Côte d'Ivoire; Torogo	9.38 N; 5.63 W	330	26-Feb-15	G. Josens	MN646747	MN685953	MN686014
CMRT 082	Niti afor DJ 0490/22	<i>Nitiditermes</i> sp. aff. <i>orthognathus</i>	Cameroon; Koutaba	5.62 N; 10.75 E	1200	29-May-17	Y. Roisin	NA	MN685903	MN685964
CMRT 113	Niti afor DJ 0492/22	<i>Nitiditermes</i> sp. aff. <i>orthognathus</i>	Cameroon; Koutaba- Manchi road	5.60 N; 10.75 E	1150	31-May-17	Y. Roisin	NA	MN685904	MN685965
3 RNAL CA	Niti afor DJ 0592/22	<i>Nitiditermes</i> sp. aff. <i>orthognathus</i>	Central African Rep.; Bondoé	5.17 N; 17.74 E	700	26-Apr-18	S.P. Wango	NA	MN685905	MN685966
11 RNAL BF	Niti gr13 DJ 0384/13	<i>Nitiditermes</i> sp. gr13	Burkina Faso; Tiogo	12.19 N; 2.71 W	280	1-Aug-16	S. Traoré	MN646715	MN685917	MN685978
01 SE	Niti gr13 DJ 0416/13	<i>Nitiditermes</i> sp. gr13	Senegal; Diouroup	14.38 N; 16.54 W	10	19-Nov-16	A. Ndiaye	MN646716	MN685918	MN685979
4 RNAL BE	Niti N22B DJ 0401/22	<i>Nitiditermes</i> sp. N22B	Benin; Birni forest	10.02 N; 1.53 E	400	1-Nov-16	L.E. Loko	MN646700	MN685899	MN685960
70 RCI	Niti NS22 DJ 0221/22	<i>Nitiditermes</i> sp. NS22	Côte d'Ivoire; Toumodi	6.60 N; 5.08 W	195	25-Feb-15	G. Josens	MN646701	MN685900	MN685961
3 RNAL BF	Niti NS22 DJ 0369/22	<i>Nitiditermes</i> sp. NS22	Burkina Faso; Bekuy	11.61 N; 3.91 W	300	1-Aug-16	S. Traoré	MN646702	MN685901	MN685962
05 SE	Niti NS22 DJ 0420/22	<i>Nitiditermes</i> sp. NS22	Senegal; Indiga, on Tambacounda road	12.60 N; 12.22 W	150	22-Nov-16	A. Ndiaye	MN646703	MN685902	MN685963
BDIT 91	Niti orth DJ 0180/22	<i>Nitiditermes orthognathus</i>	Burundi; Gihofi-Giharo road pk 76	3.98 S; 30.16 E	1200	27-Nov-13	Y. Roisin	MN646720	MN685923	MN685984
RNAL 59	Niti prox DJ 0233/22	<i>Nitiditermes proximatus</i>	Côte d'Ivoire; Danané- Man road	7.28 N; 7.77 W	330	28-Feb-15	G. Josens	MN646729	MN685932	MN685993

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Collection code	Code in this study	Species	Country; Locality	Latitude; Longitude (°)	Elevation (m.)	Collecting date	Collector	COI	COII	28S rDNA
6 RNAL BF	Niti prox DJ 0380/22	<i>Nitiditermes proximatus</i>	Burkina Faso; Bobo Dioulasso	11.21 N; 4.39 W	400	1-Aug-16	S. Traoré	MN646730	MN685933	MN685994
02 SE	Niti prox DJ 0417/22	<i>Nitiditermes proximatus</i>	Senegal; Dienoudiala	13.19 N; 13.05 W	80	22-Nov-16	A. Ndiaye	MN646731	MN685934	MN685995
07 SE	Niti prox DJ 0422/22	<i>Nitiditermes proximatus</i>	Senegal; Samékouta-Kédougou	12.61 N; 12.11 W	130	22-Nov-16	A. Ndiaye	MN646732	MN685935	MN685996
5 RNAL Kin	Niti sank DJ 0463/22	<i>Nitiditermes sankurensis</i>	Dem. Rep. of the Congo; Batéké Plateau	4.39 S; 16.07 E	660	23-Apr-17	C. Kifukieto	NA	MN685936	MN685997
CMRT 117	Niti sank DJ 0493/22	<i>Nitiditermes sankurensis</i>	Cameroon; Koutaba-Manchi road	5.61 N; 10.75 E	1150	31-May-17	Y. Roisin	MN646733	MN685937	MN685998
6 RNAL Kin	Niti sank DJ 0686/22	<i>Nitiditermes sankurensis</i>	Dem. Rep. of the Congo; Batéké Plateau	4.39 S; 16.08 E	660	23-Apr-17	C. Kifukieto	NA	MN685938	MN685999
71 RCI	Niti sche DJ 0498/22	<i>Nitiditermes schereri</i>	Côte d'Ivoire; Man	7.41 N; 7.59 W	450	27-Feb-15	G. Josens	MN646734	MN685939	MN686000
O_008	Palm impo O008	<i>Palmitermes impostor</i>	French Guiana; Petit Saut	5.07 N; 52.98 W	82	15-Nov-15	S. Hellemans	MN646748	MN685954	MN686015
BH353	Poly buge DJ 0394/26	<i>Polyspathotermes bugeserae</i>	Burundi; Ruvubu N.P.	2.95 S; 30.48 E	1500	30-Sep-14	B. Host	MN646706	MN685908	MN685969
2 RNAL ZA	Poly gr26 DJ 0639/26	<i>Polyspathotermes</i> sp. gr26	Dem. Rep. of the Congo; South of Moero Lake	9.68 S; 28.58 E	930	23-Nov-18	P. Kasangij	MN646717	MN685920	MN685981
6 RNA K	Poly incl DJ 0388/26	<i>Polyspathotermes inclitus</i>	Dem. Rep. of the Congo; Mikembo-Kisangwe	11.49 S; 27.66 E	1200	1-Jun-16	P. Kasangij	MN646718	MN685921	MN685982
4 RNA K	Poly kata DJ 0347/23	<i>Polyspathotermes katangensis</i>	Dem. Rep. of the Congo; Mikembo-Kisangwe	11.49 S; 27.66 E	1200	1-Jun-16	P. Kasangij	MN646746	MN685952	MN686013
CMRT 015	Poly sulc DJ 0504/26	<i>Polyspathotermes sulcifrons</i>	Cameroon; Ebogo	3.38 N; 11.46 E	660	22-May-17	Y. Roisin	MN646739	MN685944	MN686005
CGO_075	Poly sulc DJ 0533/26	<i>Polyspathotermes sulcifrons</i>	Rep. of the Congo; Mokabi	3.15 N; 16.96 E	530	9-Dec-17	Y. Roisin	MN646740	MN685945	MN686006
29 RCI	Proc abur DJ 0502/NA	<i>Procutitermes aburiensis</i>	Côte d'Ivoire; Lamto-Pakobo	6.22 N; 5.03 W	120	21-Feb-15	G. Josens	MN646749	MN685955	MN686016
RNAL 39	Tern bild DJ 0399/14	<i>Ternicubitermes bilobatodes</i>	Côte d'Ivoire; Youhouli	5.44 N; 4.49 W	100	18-Feb-15	G. Josens	MN646705	MN685907	MN685968
BH343	Tern gr14 DJ 0395/14	<i>Ternicubitermes</i> sp. gr14	Burundi; Ruvubu N.P.	2.95 S; 30.44 E	1500	30-Sep-14	B. Host	NA	MN685919	MN685980
3 RNAL ZA	Tern mune DJ 0640/12	<i>Ternicubitermes muneris</i>	Dem. Rep. of the Congo; South of Moero Lake	9.68 S; 28.54 E	930	23-Nov-18	P. Kasangij	MN646719	MN685922	MN685983
1 RNA K	Tern pall DJ 0349/12	<i>Ternicubitermes pallidiceps</i>	Dem. Rep. of the Congo; Mikembo-Kisangwe	11.49 S; 27.66 E	1200	1-Jun-16	P. Kasangij	MN646721	MN685924	MN685985
3 RNAL Kin	Tern weis DJ 0461/14	<i>Ternicubitermes weissii</i>	Dem. Rep. of the Congo; Batéké Plateau	4.39 S; 16.08 E	660	22-Apr-17	C. Kifukieto	MN646743	MN685949	MN686010
1 RNAL Kin	Thor macr DJ 0460/NA	<i>Thoracotermes macrothorax</i>	Dem. Rep. of the Congo; Luméné gallery on Batéké Plateau	4.43 S; 16.05 E	550	23-Apr-17	C. Kifukieto	MN646750	MN685956	MN686017

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Table S2: Primers and cycling conditions used in this study.

Gene	Primer name	Sequence (5'-3')	Reference	Cycling conditions	Initial denaturation	Denaturation	Annealing	Extension	Final extension	Number of cycles
COI	LCO1490	GGT CAA CAA ATC ATA AAG ATA TTG G	Folmer <i>et al.</i> , 1994	T (°C)	94	94	47	72	72	40
	HCO2198	TAA ACT TCA GGG TGA CCA AAA AAT CA	Folmer <i>et al.</i> , 1994	t (s)	120	60	60	75	420	
COII	Mod A-tLeu	CAG ATA AGT GCA TTG GAT TT	Miura <i>et al.</i> , 2000	T (°C)	94	94	45	72	72	35
	B-tLys	GTT TAA GAG ACC AGT ACT TG	Simon <i>et al.</i> , 1994	t (s)	180	30	30	60	600	
28S rDNA	Rd1.2a	CCC SSG TAA TTT AAG CAT ATT A	Whiting, 2002	T (°C)	94	94	44	72	72	40
	Rd4.2b	CCT TGG TCC GTG TTT CAA GAC GG	Whiting, 2002	t (s)	120	60	60	75	420	

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Table S3: *COII* sequences retrieved from GenBank for the construction of the MrBayes non-ultrametric tree, and re-identification of species prior to the splitting of *Cubitermes* into new genera. Abbreviations: DRC, Democratic Republic of the Congo; N. P., National Park.

Collection code	Code in this study	Identification in original publication	Identification revised	Locality	Accession	Original publication
RDCT183	Apil long DJ 0702/NA KY224419	<i>Apilitermes longiceps</i>	<i>Apilitermes longiceps</i>	DRC Yangambi	KY224419	Bourguignon <i>et al.</i> (2017)
O_98	Cavi tube O_98	<i>Cavitermes tuberosus</i>	<i>Cavitermes tuberosus</i>	French Guiana Petit Saut	MF953242	Hellemans <i>et al.</i> (2019)
RDCT129	Cren albo DJ 0700/NA KY224620	<i>Crenetermes albotarsalis</i>	<i>Crenetermes albotarsalis</i>	DRC Yangambi	KY224620	Bourguignon <i>et al.</i> (2017)
CA1	Isog sp_C KP026265	<i>Cubitermes fungifaber</i>	<i>Isognathotermes "spC"</i>	Cameroon, Mbal Mayo	KP026265	Bourguignon <i>et al.</i> (2015)
ROCT46	Isog sp_C DJ 0631/16 DQ127306	<i>Cubitermes sp. affinis subarquatus "spC"</i>	<i>Isognathotermes "spC"</i>	Gabon Rocher (Lopé N. P.)	DQ127306	Roy <i>et al.</i> (2006)
RDCT220	Isog fini DJ 0620/16 KY224569	<i>Cubitermes sp A</i>	<i>Isognathotermes finitimus</i>	DRC Yangambi	KY224569	Bourguignon <i>et al.</i> (2017)
ROCT16	Isog fung DJ 0623/15 DQ127302	<i>Cubitermes sp. affinis subarquatus "spA"</i>	<i>Isognathotermes fungifaber</i>	Gabon Rocher (Lopé N. P.)	DQ127302	Roy <i>et al.</i> (2006)
DODTD2	Isog fung DJ 0625/15 DQ246541	<i>Cubitermes sp. affinis subarquatus "spD"</i>	<i>Isognathotermes fungifaber</i>	Gabon Doda (Lopé N. P.)	DQ246541	Roy <i>et al.</i> (2006)
OKOT26	Isog plan DJ 0624/16 DQ127312	<i>Cubitermes sp. affinis subarquatus "spB"</i>	<i>Isognathotermes planifrons</i>	Gabon Okoumé (Lopé N. P.)	DQ127312	Roy <i>et al.</i> (2006)
BDIT078	Isog ugan DJ 0091/15 KY224661	<i>Cubitermes ugandensis</i>	<i>Isognathotermes ugandensis</i>	Burundi Mahanga	KY224661	Bourguignon <i>et al.</i> (2017)
BDIT069	Niti fulv DJ 0183/22 KY224600	<i>Cubitermes nr. fulvus</i>	<i>Nitiditermes fulvus</i>	Burundi Buga	KY224600	Bourguignon <i>et al.</i> (2017)
BDIT106	Poly katb DJ 0093/23 KY224475	<i>Cubitermes oblectatus</i>	<i>Polyspathotermes sp. aff. katangensis</i>	Burundi Ruvubu N. P.	KY224475	Bourguignon <i>et al.</i> (2017)
BDIT075	Poly buge DJ 0186/26 KY224421	<i>Cubitermes fulvus</i>	<i>Polyspathotermes bugeserae</i>	Burundi Mahanga	KY224421	Bourguignon <i>et al.</i> (2017)
RDCT130	Poly sulc DJ 0676/26 KY224606	<i>Cubitermes sulcifrons</i>	<i>Polyspathotermes sulcifrons</i>	DRC Yangambi	KY224606	Bourguignon <i>et al.</i> (2017)
RDCT128	Thor macr DJ 0701/NA KY224714	<i>Thoracotermes macrothorax</i>	<i>Thoracotermes macrothorax</i>	DRC Yangambi	KY224714	Bourguignon <i>et al.</i> (2017)

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Table S4: List of valid names of the taxa formerly included (as in Krishna *et al.* 2013c) in the genera *Cubitermes*, *Megagnathotermes* and *Nitiditermes*. Asterisks indicate type species. Indented names are synonyms. With the exception of *Polyspathotermes katangensis* (transferred from *Megagnathotermes*) and the type species of *Megagnathotermes* and *Nitiditermes* (unchanged), all species were formerly in the genus *Cubitermes*.

***Cubitermes* Wasmann, 1906**

- **Cubitermes bilobatus* (Haviland, 1898)
 - C. bilobatus curtus* Sjöstedt, 1926
- Cubitermes conjenii* (Fuller, 1925)
- Cubitermes exiguus* Mathot, 1964
- Cubitermes pretorianus* Silvestri, 1914
- Cubitermes pretorianus heidelbergi* Fuller, 1925
- Cubitermes sanctaeluciae* (Fuller, 1925)
- Cubitermes tenuiceps* (Sjöstedt, 1913)
- Cubitermes transvaalensis* (Fuller, 1925)
- Cubitermes zulucola* Sjöstedt, 1924
 - C. pseudoduplex* (Fuller, 1925)

***Isognathotermes* Sjöstedt, 1926**

- Isognathotermes bulbifrons* (Sjöstedt, 1924)
 - I. heghi* (Sjöstedt, 1924)
- Isognathotermes congoensis* (Emerson, 1928)
- Isognathotermes finitimus* (Schmitz, 1915)
 - I. loubetsiensis* (Sjöstedt, 1924)
 - I. subarquatus* (Sjöstedt, 1926)
- Isognathotermes fungifaber* (Sjöstedt, 1896)
 - I. banksi* (Emerson, 1928)
 - I. comstocki* (Emerson, 1928)
 - I. schmidti* (Emerson, 1928)
- Isognathotermes gagei* (Emerson, 1928)
- Isognathotermes gibbifrons* (Sjöstedt, 1924)
- Isognathotermes kemneri* (Emerson, 1928)
- **Isognathotermes minitabundus* (Sjöstedt, 1913)
- Isognathotermes modestior* (Silvestri, 1914)
- Isognathotermes planifrons* (Sjöstedt, 1924)
 - ? *I. fungifaber elongatus* (Sjöstedt, 1924)
- Isognathotermes severus* (Silvestri, 1914)
- Isognathotermes silvestrii* (Sjöstedt, 1925)
- Isognathotermes speciosus* (Sjöstedt, 1924)
- Isognathotermes ugandensis* (Fuller, 1923)
 - I. antennalis* (Sjöstedt, 1924)
- Isognathotermes zenkeri* (Desneux, 1904)

***Megagnathotermes* Silvestri, 1914**

- **Megagnathotermes notandus* Silvestri, 1914

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***Nitiditermes* Emerson, 1960**

- Nitiditermes aemulus* (Silvestri, 1914)
- Nitiditermes anatruncatus* (Fuller, 1925)
- **Nitiditermes berghei* Emerson, 1960
- Nitiditermes curtatus* (Silvestri, 1914)
- Nitiditermes fulvus* (Williams, 1966)
- Nitiditermes niokoloensis* (Roy-Noël, 1969)
- Nitiditermes oculatus* (Silvestri, 1914)
- Nitiditermes orthognathus* (Emerson, 1928)
- Nitiditermes proximatus* (Silvestri, 1914)
- Nitiditermes sankurensis* (Wasmann, 1911)
 - N. cubicephalus* (Sjöstedt, 1913)
 - N. sankurensis elongatus* (Sjöstedt, 1926)
 - N. sibitiensis* (Sjöstedt, 1925)
- Nitiditermes schereri* (von Rosen, 1912)
- Nitiditermes sierraleonicus* (Sjöstedt, 1911)
- Nitiditermes testaceus* (Williams, 1966)
- Nitiditermes truncatoides* (Fuller, 1925)
 - N. truncatoides sordwana* (Fuller, 1925)
- Nitiditermes truncatus* (Holmgren, 1913)
 - N. duplex nduma* (Fuller, 1925)

***Polyspathotermes* Josens & Deligne, gen. nov.**

- Polyspathotermes bugeserae* (Bouillon & Vincke, 1971)
- Polyspathotermes inclitus* (Silvestri, 1912)
 - P. domifaber* (Sjöstedt, 1913)
- Polyspathotermes intercalatus* (Silvestri, 1914)
 - P. hamatus* (Sjöstedt, 1926)
- Polyspathotermes katangensis* (Sjöstedt, 1927)
- Polyspathotermes montanus* (Williams, 1966)
- Polyspathotermes oblectatus* (Harris, 1958)
- **Polyspathotermes sulcifrons* (Wasmann, 1911)
- Polyspathotermes umbratus* (Williams, 1954)

***Ternicubitermes* Josens & Deligne, gen. nov.**

- **Ternicubitermes bilobatodes* (Silvestri, 1912)
- Ternicubitermes breviceps* (Sjöstedt, 1913)
- Ternicubitermes duplex* (Holmgren, 1913)
- Ternicubitermes falcifer* (Williams, 1966)
- Ternicubitermes glebae* (Sjöstedt, 1913)
- Ternicubitermes latens* (Williams, 1966)
- Ternicubitermes microduplex* (Fuller, 1925)
- Ternicubitermes muneris* (Sjöstedt, 1913)
 - T. bisulcatus* (Sjöstedt, 1914)
- Ternicubitermes pallidiceps* (Sjöstedt, 1913)
- Ternicubitermes subcrenulatus* (Silvestri, 1914)
- Ternicubitermes undulatus* (Fuller, 1925)
- Ternicubitermes weissi* (Silvestri, 1912)
- Ternicubitermes zavattarii* (Ghidini, 1937)

D. Supplementary References

- Folmer, O., Black, M., Hoeh, W., Lutz, R., and Vrijenhoek, R. (1994). DNA primers for amplification of mitochondrial cytochrome c oxidase subunit I from diverse metazoan invertebrates. *Molecular Marine Biology and Biotechnology* **3**, 294–299. doi:10.1371/journal.pone.0013102
- Hellemans, S., Kaczmarek, N., Marynowska, M., Calusinska, M., Roisin, Y., Fournier, D. (2019). Bacteriome-associated *Wolbachia* of the parthenogenetic termite *Cavitermes tuberosus*. *FEMS Microbiology Ecology* **95**, fiy235. doi:10.1093/femsec/fiy235
- Miura, T., Roisin, Y., and Matsumoto, T. (2000). Molecular phylogeny and biogeography of the nasute termite genus *Nasutitermes* (Isoptera: Termitidae) in the Pacific tropics. *Molecular Phylogenetics and Evolution* **17**, 1–10. doi:10.1006/mpev.2000.0790
- Simon, C., Frati, F., Beckenbach, A., Crespi, B., Liu, H., and Flook, P. (1994). Evolution, weighting, and phylogenetic utility of mitochondrial gene sequences and a compilation of conserved polymerase chain reaction primers. *Annals of the Entomological Society of America* **87**, 651–701. doi:10.1080/17470210902990829
- Whiting, M. F. (2002). Mecoptera is paraphyletic: multiple genes and phylogeny of Mecoptera and Siphonaptera. *Zoologica Scripta* **31**, 93–104. doi:10.1046/j.0300-3256.2001.00095.x