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Running title: New species of *Australatya*

First occurrence of the genus *Australatya* (Crustacea: Decapoda: Atyidae) in Melanesia and Polynesia with description of a new species.

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Abstract: During specific inventories led by the Muséum national d'Histoire naturelle (MNHN, Paris), numerous specimens of Atyidae, particularly of *Atya*-like shrimps were collected in Melanesia (Vanuatu, Solomon Islands) and in Polynesia (Futuna, Samoa). These specimens were morphologically and genetically examined. Our study revealed that some specimens belonged to a new species in the genus *Australatya* Chace, 1983. The aim of this paper is to describe this new species, *Australatya keithi* sp. nov., and discuss the distribution of its genus in the studied area.

Introduction

Until recently, the taxonomy of Atyidae was mainly based on morphological characters. But, in the *Caridina* genus, some characters have been proven highly variable within a species (e.g. rostrum shape and indentation or coloration) and therefore taxonomically uninformative, making it difficult to establish boundaries between them (von Rintelen and Cai 2009, de Mazancourt et al. 2017). Thus, there is a need for an integrative and standardized approach to improve the group's systematics, focusing on informative morphological features and using molecular characters (Page et al. 2005, Page and Hughes 2011). To illustrate this problem, we focus here on the genus *Australatya* Chace, 1983. It has a wide but disjoint distribution in the Indo-Pacific region and includes until now only three species: *Australatya striolata* (McCulloch and McNeill 1923) and *Australatya hawkei* Choy, Page and Mos, 2019 from Australia and *Australatya obscura* Han and Klotz, 2015 from the Philippines, Taiwan (Han and Klotz 2015) and Ryukyu islands (Inui et al. 2019). This genus occurs in the higher course of tropical rivers like other *Atya*-like shrimps (*Atyoida pilipes* (Newport, 1847) or *Atyopsis spinipes* (Newport, 1847)). Only a few studies provided DNA data for species of *Australatya* (see Cook et al. 2012; Han and Klotz, 2015; Choy et al. 2019).

One of the aims of the Muséum national d'Histoire naturelle (MNHN, Paris) is to carry out faunistic inventories of rivers in tropical islands in order to establish better protection of these fragile ecosystems and, in this context, to clarify the taxonomy of poorly known organisms. For our study, several Pacific islands were surveyed: Futuna (Territory of Wallis and Futuna) in October 2004 (Mary et al. 2006), Upolu (Samoa) in July 2008 (Keith et al. 2013) and again in August 2014. Kolombangara and Vella Lavella islands (Solomon Islands) respectively in November 2015 and October 2016, and Santo and Aneityum (Vanuatu) respectively in July 2005 and June 2015. As we collected specimens from these different islands from the Pacific Ocean, we started to question the identity of some specimens previously identified as *Atyoida pilipes* or *Atyopsis spinipes* collected from these islands. The aim of this study is thus to

combine morphological data with a 16S rDNA analysis to investigate the “*Atya*-like” shrimps present in the sampled area.

Material and Methods

Collection of specimens

Specimens from Pacific islands were collected by electrofishing (portable Dekka 3,000 electric device, or SAMUS 1,000: <http://www.electro-fisher.net/>). All material was preserved in 75%-95% alcohol and has been deposited in the collections of the MNHN in Paris.

Morphological comparison

The rostrum, the general cephalon, the pereopods 1, 2, 3 and 5 and the abdomen were observed using a stereoscopic microscope. The proportions of the various joints of the appendages were measured using microphotographs and AnalySIS Works software (Olympus). Drawings were made using the ‘Digital Inking’ method (Coleman 2003, 2006) by tracing vectorial paths on stacks of high-resolution photographs using Adobe Illustrator (CS6).

Abbreviations for morphological analyses

The following abbreviations are used in the present text: cl, carapace length (mm): measured from the post-orbital margin to the posterior margin of the carapace. P1: first pereopod. P2: second pereopod. P3: third pereopod. P5: fifth pereopod. P11: first male pleopod. P12: second male pleopod.

DNA extraction, amplification, sequencing

Molecular analyses were conducted on mitochondrial DNA, on the 16S ribosomal RNA fragment, in order to differentiate each specimen by species and location. A total of 10 specimens of *Australatya* were genetically studied.

Total DNA was extracted from abdominal muscle samples using the NucleoSpin 96 Tissue Core (Macherey-Nagel) protocol. For each sample, PCR reactions contained: 15.44 µl of H₂O, 2 µl of Taq buffer (15 mM + MgCl₂), 1 µl of DMSO (1 ng/ml), 1 µl of BSA, 0.8 µl of dNTP (6.6 mM), 0.32 µl of Forward primer (16Sar-Lmod: TACTTCTGCCTGTTTATCAAAAA) and 0.32 µl of Reverse primer (16Sbmod: GGTCTGAACTCAAATCATGTAAA), both at 10 pM, 0.12 µl of Taq polymerase (Qiagen), and 3 µl of purified DNA from extraction. PCR program was: 4 min at 94°C, then 35 cycles in three steps with 30 sec at 94°C, 40 sec at 42°C and 1 min at 72°C. The program finished with 7 min at 72°C. PCR products were sequenced using Sanger method in both directions to minimize mistakes.

Molecular analysis

Analyses were performed using Geneious 7.1.8. A multiple alignment was realized between all sequences with the MUSCLE algorithm (Edgar 2004). Using Bayesian information criterion in jModelTest (Guindon and Gascuel 2003, Darriba et al. 2012) we retained the GTR + G + I model. From this alignment, a phylogenetic tree was produced by MrBayes 3.2.6, available on CIPRES Science Gateway V3.3 server (Miller et al. 2010, <https://www.phylo.org>), running for 10,000,000 generations, a sampling frequency of 1,000 and a burn in of 10%. Support for nodes was determined using posterior probabilities calculated by MrBayes. With MEGA X (Kumar et al. 2018), another phylogenetic tree was made by maximum likelihood using the same substitution model. Robustness of the nodes

was assessed using non-parametric bootstrapping (Felsenstein 1985) with 1,000 bootstrap replicates.

Species delimitation analyses were realized with the ABGD v. 07/12/18 method (Puillandre et al. 2011) to estimate intra and interspecific divergence in our data using JC69 distances. Priors were left as default (Pmin: 0.001; Pmax 0.1; 10 steps; relative gap width: 1.5; 20 bins).

Results and Discussion

Morphological analyses

Measures and observations made on the specimens caught allowed us to separate them into three genera, *i.e.* *Atyoida*, *Atyopsis* and *Australatya*. The general criteria to identify species of the genus *Atyoida* are P1 and P2 with chelae heteromorphic (with or without palm), P3 without meral spur in large males, 3rd maxilliped with uncinat terminal spine, P11 of male with endopod tapering sinuously but rather regularly to slender apex, for genus *Atyopsis* are P1 and P2 with chelae monomorphic (without palm), P3 with prominent spur on merus in large males, 3rd maxilliped not terminating in single apical spine, P11 of male with endopod rigid, rhomboidally oval, submarginally spinose, for *Australatya* are P1 and P2 with chelae monomorphic (without palm), P3 without meral spur in large males, interno-inferior margin of merus forming a carina with 4–9 strong teeth-like spiniform setae, third maxilliped dimorphic between sexes, with uncinat terminal spiniform seta (nail) partially concealed by dense serrate setae in males, tip rounded, without a nail in females, P11 of male with endopod tapering to slender apex. The species found in this last genus is new. The description of this species follows thereafter. 11 specimens of *Australatya* have been identified in our samples: 3 from the Solomon Islands, 2 from Futuna, 4 from Samoa and 2 from Vanuatu.

Phylogenetic analysis

A total of 34 sequences of 16S were used in the analysis, including 10 sequences of *Australatya* newly produced and 3 retrieved from GenBank. As outgroups, 8 sequences of *Atyopsis*, 12 of *Atyoida* and one of *Atya gabonensis* were retrieved from GenBank (Table 1). As the two phylogenetic trees obtained by Maximum Likelihood (ML) and Bayesian Inference (BI) were congruent, only the Bayesian tree is shown here. Support values above branches are BI posterior probabilities and below branches are ML bootstrap numbers (Fig. 1). These trees confirm the presence of the *Australatya* genus in our samples. Most of the nodes are highly supported ($PP > 0.98$ and $B > 95$) in both ML and BI methods. The ABGD method found 8 species in our sampling: *Atya gabonensis*, *Atyoida bisulcata*, *Atyoida pilipes*, *Atyopsis spinipes*, *Atyopsis moluccensis*, *Australatya obscura*, *Australatya striolata* and the new species we caught, *Australatya keithi* sp. nov.. This indicates that the latter is genetically distinct from the other species. The names of the taxa in the tree (Fig. 1) appear in accordance with the ABGD results, except for *Australatya striolata* and *Australatya hawkei* which are clustered together in a single species in the analysis. All the specimens identified as the new species described in the present study cluster in a same highly supported clade ($PP = 1$; $B = 100$). There seems to be some population structure within that species, with two clusters being distinctly separated from the specimens from Futuna and Samoa, one with specimens collected from Vanuatu and the other with specimens from the Solomon Islands.

<Table 1 here>

<Figure 1 here>

Taxonomy

150 Family Atyidae De Haan, 1849

151 Genus *Australatya* Chace, 1983

152 *Australatya keithi* sp. nov.

153 (Figure 2)

154

155 <Figure 2 here>

156

157 Material examined:

158 Holotype. VANUATU. ANEITYUM: Inwe Lengei River, 1♂, cl 5.5 mm (MNHN-IU-2018-3302;

159 DNA: CA1957), 20°12.409'S, 169°48.131'E, June 24, 2015, 200 m a.s.l., coll. D. Kalfatak, C.

160 Lord, G. Segura. Paratypes. VANUATU. ANEITYUM: 1♀ ovig., cl 6.8 mm (MNHN-IU-2018-

161 3303; DNA: CA1958), same data as holotype. SOLOMON ISLANDS. KOLOMBANGARA. Vage

162 River, 1♀ ovig., cl 4.0 mm (MNHN-IU-2018-3300; DNA: CA1934), 08°05.112'S,

163 156°59.867'E, November 10, 2015, coll. P. Keith, G. Marquet, C. Lord. – VELLA LAVELLA.

164 Maravari River, 1♀ ovig., cl 4.0 mm, (MNHN-IU-2018-3301; DNA: CA2359) 1 specimen

165 (MNHN-IU-2018-3308; DNA: CA1944), 07°51.703'S, 156°41.748'E, October 10, 2016, coll.

166 P. Keith and C. Lord. SAMOA. SAVAI. Ma'epu stream, 1♂ juvenile, cl 3.2 mm (MNHN-IU-

167 2018-3307), 13°51.919'S, 171°41.174'W, July 07, 2014, 20–50 m a.s.l., coll. P. Gerbeaux.

168 UPOLU. Tuafaleloa River, 1♀ ovig., cl 5.3 mm (MNHN-IU-2018-3304; DNA: CA1947) and

169 1♀ ovig., cl 5.7 mm (MNHN-IU-2018-3305; DNA: CA1948), 13°53.644'S, 171°30.922'W,

170 July 08, 2014, 100 m a.s.l., coll. P. Gerbeaux. Faleata River, 1♀ ovig., cl 5.0 mm (MNHN-IU-

171 2018-3306; DNA: CA2422), 13°43.741'S, 172°18.832'W, July 12, 2014, 195 m a.s.l., coll. P.

172 Gerbeaux. WALLIS AND FUTUNA. FUTUNA. Vainifao River, 1♀, cl 6.1 mm (MNHN-Na-15761;

173 DNA: CA2133) and 1♂ (MNHN-Na-15761; DNA: CA2433), 14°17.802'S, 178°8.423'W,

174 October 12, 2004, 151 m a.s.l., coll. P. Keith, G. Marquet, N. Mary.

175

176 Comparative material:

177 *Australatya hawkei* Choy, Page & Mos, 2019

178 AUSTRALIA. MNHN-Na-14383. Freshwater creek in Big Table Land, 1♀ ovig., cl 10.0 mm,
179 North-East Queensland, November 18, 1993, coll. K. McDonald.

180

181 Description

182 *Cephalothorax* (Fig. 2m): Carapace length 4.0–6.1 mm (N = 7). Carapace smooth, inferior
183 orbital angle fused with a distinct antennal tooth; pterygostomian margin rectangular rounded.
184 Rostrum short, 0.2–0.3 of cl, reaching near to end of basal segment of antennular peduncle,
185 with feebly marked lateral carina, dorsal ridge unarmed. The number of ventral teeth on the
186 rostrum varies from 0 to 4. Rostrum formula 0/0–4. Eyes well developed. Antennular
187 peduncle stout, 0.56 (♀) – 0.46 (♂) times as long as carapace; basal segment shorter than half
188 length of antennular peduncle, second segment longer than third segment. Stylocerite
189 reaching 0.86 length of the basal segment of antennular peduncle.

190 *Pereiopods*: P1 and P2 similar in size and shape. P1 chela (Fig. 2a) atyoid in shape, without
191 palm, 4.5–5.3 times as long as wide, without hooks; dactylus 4.9–5.8 times as long as wide,
192 with tufts of long setae distally; carpus short, cup-like 1.3–1.8 times as long as wide. P2 chela
193 (Fig. 2b) atyoid in shape without palm, 4.4–5.3 times as long as wide, tips of fingers rounded,
194 without hooks, dactylus 5.1–6.0 times as long as wide, with tufts of long setae distally; carpus
195 short, cup-like 1.2–1.7 times as long as wide. P3 (Fig. 2c) moderately strong, with a row of
196 small plumose setae on lateral margin from ischium to propodus; dactylus (Fig. 2e) 1.4–2.71
197 times as long as wide (terminal spiniform seta included), terminating in one large claw with
198 5–6 accessory spiniform setae on flexor margin, first spiniform setae distinctly smaller than
199 second; propodus with numerous small spiniform setae on ventral margin, distal pair of

200 spiniform setae not much prolonged, propodus 3.3–4.4 times as long as wide, 2.4–6.1 times as
201 long as dactylus; merus with an interno-inferior margin forming a very distinctive carina with
202 5–7 strong, teeth-like spiniform setae. P5 (Fig. 2d) slender, dactylus (Fig. 2f), 1.6–3.5 times as
203 long as wide (terminal spiniform seta included), terminating in one large claw, with 23–32
204 spiniform setae on flexor margin extending lateral to distal claw; propodus 6.3–8.6 times as
205 long as wide, 3.6–6.8 times as long as dactylus.

206 *Abdomen*: Sixth abdominal somite 0.43 length of carapace, 1.25 times as long as fifth somite,
207 0.87 times as long as telson.

208 Telson (Fig. 2j): slightly tapering distally, 2.4–3.5 times as long as proximally wide, distal
209 margin broadly rounded with a median projection, lateral angles not overreaching distal
210 margin, dorsal with 4–5 pairs of short spiniform setae and one pair of short spiniform setae
211 dorsolateral; distal margin with 2 strong spiniform setae lateral, in between 6–10 long,
212 plumose setae overreaching lateral spiniform setae.

213 P11 (Fig. 2k): Endopod of male subtriangular, 2.3 times as long as wide, reaching 0.29–0.41
214 times of exopod, with an appendix on the subdistal outer margin which reaches beyond distal
215 end of endopod with most of its length.

216 P12 (Fig. 2l): Appendix masculina on second pleopod reaching 0.54–0.56 times length of
217 endopod; appendix interna reaching 0.77 of appendix masculina.

218 Triangular preanal carina (Fig. 2i) with a spine.

219 Uropodal diaeresis (Fig. 2h) with 15–21 spinules.

220 Eggs (Fig. 2g): developed (visible eyes) $0.32\text{--}0.45 \times 0.52\text{--}0.71$ mm, undeveloped $0.33\text{--}0.34 \times$
221 $0.51\text{--}0.57$ mm.

222

223 Etymology

This new species is named *keithi* in honor of Philippe Keith, professor at the MNHN, who made extensive collections of both freshwater fish and crustaceans for more than 20 years in the Pacific islands in particular in Kolombangara, Vella Lavella (Solomon Islands), in Santo (Vanuatu archipelago) and Futuna island, where he collected ,with one of us, the new species here described,and photographed it (Figure 3) ; we appreciate his flawless friendship, his constant enthusiasm in the field and his dedication to his team.

Habitat

This species, largely rheophile, was collected in the uppermost sections of streams (Fig. 3B). It shared this habitat with other “*Atya*-like” shrimp (*Atyoida pilipes*, *Atyopsis spinipes*) and with medium sized palaemonids like *Macrobrachium latimanus* (von Martens, 1868).

Color pattern

Body overall dark with white dorsal stripes on the abdomen (Fig. 3A).

<Figure 3 here>

Distribution

This species occurs in Melanesia (Solomon Islands, Vanuatu) and in West Polynesia (Futuna and Samoa) (Fig. 4).

<Figure 4 here>

Comparison

249 Genus *Australatya* Chace, 1983 now includes four species: *Australatya keithi* sp. nov., *A.*
250 *striolata* (MacCulloch and McNeill, 1923) and *A. hawkei* Choy, Page and Mos, 2019, both
251 from Australia, and *A. obscura* Han and Klotz, 2015 from Taiwan, the Philippines and
252 Ryukyu islands. Morphologically, specimens of the new species differ from *A. striolata* by
253 their rostrum armed with fewer ventral teeth 0–4 (vs 4–8 in *A. striolata*) and their shorter P3
254 propodus, 3.3–4.4 times as long as wide (vs 5.1–6.3). They differ from *A. hawkei* by their
255 rostrum armed with fewer ventral teeth 0–4 (vs 5–8 in *A. hawkei*) and their shorter P3
256 propodus, 3.3–4.4 times as long as wide (vs 5.0–6.7). They differ from *A. obscura* by their
257 longer P1 carpus and P2 carpus 1.3–1.8 (vs 0.8–1.0 in *A. obscura*) and 1.2–1.7 (vs 0.9–1.0),
258 their P3 shorter propodus 3.3–4.4 times as long as wide (vs 5.3–6.9), and simple dactyli of the
259 fifth pereopod (vs. biunguiculate).

260

261 *Remarks.*

262 According to Han and Klotz (2015), the row of prominent, teeth-like spiniform setae on the
263 interno-inferior margin of the merus of the third pereopod, always present in adult specimens
264 of *Australatya*, with the sexual dimorphism of the distal segment of the third maxilliped
265 seems to be the best character to distinguish this genus from all other *Atya*-like genera of the
266 Indo-Pacific region. Our new species here described presents these same characteristics, thus
267 confirming its placement within *Australatya*.

268 Furthermore, *Australatya keithi* is differentiated from *Atyopsis spinipes* by its much smaller
269 body size; its merus of male specimens lacking a massive spur vs. having a massive spur in
270 large males; its endopod of males first pleopod tapering from proximal to distal vs. not
271 tapering from proximal to distal, rhomboidally oval, submarginally spinose; appendix
272 masculina on second pleopod of males with spinose area distal to tip of appendix interna vs.

273 spinose over more than half length; lateral angles of telson not overreaching distal margin vs.
274 overreaching.

275 The new species is distinguished from *Atyoida pilipes* by its chelae not sexually dimorphic vs.
276 dimorphic, with palm in male specimens, and its appendix masculina on second pleopod of
277 males with spinose area distal to tip of appendix interna vs. spinose area overlapping a part of
278 the appendix interna.

279

280 **Identification key**

281 1.1 Short P3 propodus 3.3-4.4 times as long as wide,***A. keithi* sp. nov.**

282 (Solomon Islands, Vanuatu, Samoa, Futuna)

283 1.2 Long P3 propodus 5.0-6.9 times as long as wide.....2

284

285 2.1 Short P1 carpus and P2 carpus 0.9-1.0 (Han and Klotz, 2015).....***A. obscura***

286 (Taiwan, Ryukyu, Philippines)

287 2.2 Long P1 carpus and P2 carpus 1.0-1.8 and 1.0-1.7 (Smith and Williams, 1982).....3

288

289 3.1 Rostrum length/carapace length 0.32-0.45 (Smith and Williams, 1982).....***A. striolata***

290 (Australia: New South Wales, South Queensland)

291 3.2 Rostrum length/carapace length 0.21-0.31 (Choy et al. 2019).....***A. hawkei*** (Australia:

292 North Queensland)

293

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295

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Litterature Cited

- Aznar-Cormano, L., J. Brisset, T. Y. Chan, L. Corbari, N. Puillandre, J. Utge, M. Zbinden, D. Zuccon and S. Samadi. 2015. An improved taxonomic sampling is a necessary but not sufficient condition for resolving inter-families relationships in Caridean decapods. *Genetica* 143:195–205.
- Bracken, H. D., S. De Grave and D. L. Felder. 2009. Phylogeny of the Infraorder Caridea Based on Mitochondrial and Nuclear Genes (Crustacea: Decapoda). In J. W. Martin, K. A. Crandall, and D. L. Felder (Eds.), *Decapod Crustacean Phylogenetics* (pp. 281–305). Chace, F. A. Jr. 1983. The *Atya*-like Shrimps of the Indo-Pacific Region (Decapoda: Atyidae). *Sm. C. Zool.* 384:1–54.
- Choy, S., T. J. Page, and B. Mos. 2019. Taxonomic revision of the Australian species of *Australatya* Chace, 1983 (Crustacea, Decapoda, Atyidae), and the description of a new species. *Zootaxa* 4711:366–378.
- Coleman, C. O. 2003. ‘Digital inking’: how to make perfect line drawings on computers. *Org. Divers. Evol.* 3 (Electronic Supplement 4):1–14.

347 ———. 2006. Substituting time-consuming pencil drawings in arthropod taxonomy using
 348 stacks of digital photographs. *Zootaxa* 1360:61–68.

349 Cook, B. D., T. J. Page and J. M. Hughes. 2012. Phylogeography of related diadromous
 350 species in continental and island settings, and a comparison of their potential and
 351 realized dispersal patterns. *J. Biogeo.* 39:421–430.

352 Darriba, D., G. L. Taboada, R. Doallo, and D. Posada. 2012. jModelTest 2: more models, new
 353 heuristics and parallel computing. *Nat. Methods*, 9:772–772.

354 De Grave, S., C. P. Li, L. M. Tsang, K. H. Chu and T.-Y Chan. 2014. Unweaving hippolytoid
 355 systematics (Crustacea, Decapoda, Hippolytidae): resurrection of several families.
 356 *Zool. Sci.* 43:496–507.

357 Edgar, R.C. 2004. MUSCLE: multiple sequence alignment with high accuracy and high
 358 throughput. *Nucleic Acids Res.* 32(5), 1792–1797.

359 Felsenstein, J. 1985. Confidence limits on phylogenies: an approach using the bootstrap.
 360 *Evolution* 39:783–791.

361 Guindon, S. and O. Gascuel. 2003. A simple, fast, and accurate algorithm to estimate large
 362 phylogenies by maximum likelihood. *Syst. Biol.* 52:696–704.

363 Lorang, C., V. de Mazancourt, G. Marquet and P. Keith. 2020. Taxonomic study of the
 364 freshwater shrimps genus *Atyoida* Randall, 1840 (Crustacea: Decapoda: Atyidae) in
 365 Polynesia with a revalidation of *A. tahitensis* Stimpson, 1860. *Zootaxa* 4751:55–74.

366 Mary, N., A. Dutartre, P. Keith, G. Marquet, and P. Sasal. 2006. Biodiversité des eaux douces
 367 de Wallis et Futuna, Mission d'octobre 2004. Rapport final, Ministère de l'Outre-Mer.
 368 84p + annexes.

369 de Mazancourt V., G. Marquet, and P. Keith. 2017. The "Pinocchio-shrimp effect": First
 370 evidence of rostrum length variation with the Environment in *Caridina* H. Milne
 371 Edwards, 1837 (Crustacea: Decapoda: Atyidae). *J. Crustacean Biol.* 37:249–257.

372 Miller, M. A., W. Pfeiffer, and T. Schwartz. 2010. Creating the CIPRES Science Gateway for
373 inference of large phylogenetic trees. In: Proceedings of the Gateway Computing
374 Environments Workshop (GCE), New Orleans, pp. 1–8.

375 Han, C. C., and W. Klotz. 2015. *Australatya obscura* sp. nov., a new filter-feeding shrimp
376 (Decapoda, Atyidae) from Taiwan and the Philippines, Crustaceana 88:66–81.

377 Inui, N., T. Maruyama, and K. Okamoto. 2019. First record of *Australatya obscura* Han &
378 Klotz, 2015 (Decapoda, Atyidae) from the Ryukyu Islands, Japan. Biodivers. Data J.
379 7:1–7.

380 Keith, P., G. Marquet, P. Gerbeaux, E. Vigneux and C. Lord. 2013. Poissons et Crustacés
381 d’eau douce de Polynésie : Taxonomie, écologie, biologie et gestion. Société
382 Française d’Ichtyologie. 1-282.

383 Kumar, S., G. Stecher, M. Li, C. Knyaz, and K. Tamura. 2018. MEGA X: molecular
384 evolutionary genetics analysis across computing platforms. Mol. Biol. Evol. 35:1547–
385 1549.

386 Page, T. J., S. Choy, and J. M. Hughes. 2005. The taxonomic feedback loop: symbiosis of
387 morphology and molecules. Biol. Letters 1:139–142.

388 Page, T. J., K. von Rintelen and J. M. Hughes. 2007. Phylogenetic and biogeographic
389 relationships of subterranean and surface genera of Australian Atyidae (Crustacea :
390 Decapoda : Caridea) inferred with mitochondrial DNA. Invert. Syst. 21:137–145.

391 Page, T. J., B. D. Cook, T. von Rintelen, K. von Rintelen and J. M. Hughes. 2008.
392 Evolutionary relationships of atyid shrimps imply both ancient Caribbean radiations
393 and common marine dispersals. J. N. Am. Benthol. Soc. 27:68–83.

394 Page, T. J., and J. M. Hughes. 2011. Neither molecular nor morphological data have all the
395 answers; with an example from *Macrobrachium* (Decapoda: Palaemonidae) from
396 Australia. Zootaxa 2874:65–68.

Porter, M. L., M. Perez-Losada and K. A. Crandall. 2005. Model-based multi-locus estimation of decapod phylogeny and divergence times. *Mol. Phyl. Evol.* 37:355–369.

Puillandre, N., A. Lambert, S. Brouillet, and G. Achaz. 2011. ABGD, Automatic Barcode Gap Discovery for primary species delimitation. *Mol. Ecol.* 21:1864–1877.

von Rintelen, K., and Y. Cai. 2009. Radiation of endemic species flocks in ancient lakes: systematic revision of the freshwater shrimp *Caridina* H. Milne Edwards, 1837 (Crustacea: Decapoda: Atyidae) from the ancient lakes of Sulawesi, Indonesia, with the description of eight new species. *Raffles B. Zool.* 57:343–452.

Smith, M. J., and W. D. Williams. 1982. Taxonomic revision of Australian species of *Atyoida* Randall (Crustacea: Decapoda: Atyidae), the genera *Atyoida* and *Atya* Leach. *Mar. Freshwater Res.* 33 :343–361.

Tables and Figure captions

Table 1: Sequences data.

Figure 1: Phylogenetic tree of *Australatya keithi* sp. nov. and other Indo-Pacific *Atya*-like species built using Bayesian Inference. Values above branches indicate posterior probabilities, those below are bootstrap values. Scale represents genetic distance.

Figure 2: *Australatya keithi* sp. nov.. a. first pereopod; b. second pereopod; c. third pereopod; d. fifth pereopod; e. dactylus of third pereopod; f. dactylus of fifth pereopod; g. developed eggs; h. uropodal diaeresis; i. pre-anal carina; j. telson; k. male first pleopod; l.

422 male second pleopod; m. cephalothorax. MNHN-IU-Na-15761: a, b, c, d, e, f, h, i, j, m;
423 MNHN-IU-2018-3301: g; MNHN-IU-2018-3306: k, l.

424

425 Figure 3: A: Live coloration of an ovigerous female of *Australatya keithi* sp. nov. caught on
426 Santo Island (Vanuatu), credit P. Keith. B: Vainifao River on Futuna Island (Wallis and
427 Futuna Territory, France), habitat of *Australatya keithi* sp. nov., credit A. Dutartre.

428

429 Figure 4: Current known geographical distribution of the four species of *Australatya*. Red
430 dots indicate sampling sites from the present study.