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► To cite this version:

Paul Zaharias, Eric Pante, Delphine Gey, Alexander E Fedosov, Nicolas Puillandre. Data, time and money: evaluating the best compromise for inferring molecular phylogenies of non-model animal taxa. *Molecular Phylogenetics and Evolution*, 2020, 142, pp.106660. 10.1016/j.ympev.2019.106660 . hal-02458233

HAL Id: hal-02458233

<https://hal.science/hal-02458233>

Submitted on 28 Jan 2020

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1 **Data, Time and Money: Evaluating the Best Compromise for Inferring Molecular**
2 **Phylogenies of Non-Model Animal Taxa**

3

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24 *Abstract.* — For over a decade now, High Throughput sequencing (HTS) approaches
25 have revolutionized phylogenetics, both in terms of data production and methodology.
26 While transcriptomes and (reduced) genomes are increasingly used, generating and
27 analyzing HTS datasets remains expensive, time consuming and complex for most non-
28 model taxa. Indeed, a literature survey revealed that 74% of the molecular phylogenetics
29 trees published in 2018 are based on data obtained through Sanger sequencing. In this
30 context, our goal was to identify the strategy that would represent the best compromise
31 among costs, time and robustness of the resulting tree. We sequenced and assembled 32
32 transcriptomes of the marine mollusk family Turridae, considered as a typical non-
33 model animal taxon. From these data, we extracted the loci most commonly used in
34 gastropod phylogenies (*cox1*, 12S, 16S, 28S, *h3* and 18S), full mitogenomes, and a
35 reduced nuclear transcriptome representation. With each dataset, we reconstructed
36 phylogenies and compared their robustness and accuracy. We discuss the impact of
37 missing data and the use of statistical tests, tree metrics, and supertree and supermatrix
38 methods to further improve the phylogenetic data acquisition pipelines. We evaluated
39 the overall costs (time and money) in order to identify the best compromise for
40 phylogenetic data sampling in non-model animal taxa. Although sequencing full
41 mitogenomes seems to constitute the best compromise both in terms of costs and node
42 support, they are known to induce biases in phylogenetic reconstructions. Rather, we
43 recommend to systematically include loci commonly used for phylogenetics and
44 taxonomy (i.e. DNA barcodes, rRNA genes, full mitogenomes, etc.) among the other
45 loci when designing baits for capture.

46

- 47 [phylogenomics, transcriptomics, high throughput sequencing, Sanger sequencing, non-
48 model taxa, Turridae]

49 **1. Introduction**

50 For over a decade now, high throughput sequencing (HTS) data has allowed not only
51 the production of a substantial amount of DNA sequences relevant for phylogenetics,
52 but also triggered many discussions on phylogenetic reconstruction methods (e.g.
53 Edwards 2009; Lemmon & Lemmon 2013; Leaché et al. 2015a; Leaché & Oak 2017).
54 Most authors concluded in the superiority of HTS approaches for reconstructing trees at
55 all phylogenetic scales, especially in terms of robustness of the tree but also in the
56 context of studying biological processes (e.g. introgression or horizontal transfer).
57 Nevertheless, there is still a considerable amount of recent studies presenting trees
58 obtained using first generation sequencing (chain-termination sequencing based on the
59 incorporation of dideoxynucleotides, herein referred to as “Sanger sequencing” – e.g.
60 Heather & Chain 2016). This technique has typically been used to sequence a few loci
61 amplified by PCR. Although the first commercial HTS technology was introduced in
62 2004 (Mardis 2008), phylogenetic studies using this technology were not exceeding
63 12% of the total molecular phylogenetic studies up until 2016 (Fig. 1). In 2018, only
64 26% of molecular phylogenetic studies were based on HTS data. The simple, rapid, and
65 stable standard protocols for producing and analyzing datasets based on Sanger
66 sequencing data may explain why they are still primarily used in phylogenetic studies,
67 while HTS-based studies remain costlier and more complex (both in terms of library
68 preparation and data analysis). Thus, the sustained attractiveness of the Sanger
69 sequencing approach to phylogenetics, indisputable in terms of number of published
70 studies to date, contrasts with the premise that HTS data will allow us to “achieve
71 phylogenomic Nirvana” (Faircloth 2013).

72 Multiple studies have explored tree robustness through the dissection of a particular
73 HTS dataset – the recently defined practice of “phylogenomic subsampling” (reviewed
74 in Edwards 2016). This practice mostly focuses on “the study of the information content
75 of phylogenomic matrices of different sizes,” implying an *in silico* subsampling of loci
76 (Edwards 2016). One way of extending the practice of phylogenomic subsampling
77 beyond its quantitative aspects would be to take into account the nature of particular
78 loci. This approach would evaluate the phylogenetic significance of the use of particular
79 genome regions (e.g. coding vs. non-coding sequences; Chen et al. 2017). The
80 development of orthology assessment pipelines (e.g. UPhO; Ballesteros & Hormiga
81 2016) also enabled their comparison with the same dataset, usually of transcriptomic
82 nature (Washburn et al. 2017; Cuhna & Giribet 2019). Other studies also focused on the
83 sequencing method used to extract a particular set of loci, mostly leading to studies
84 comparing HTS vs. Sanger sequencing methods to recover phylogenetic datasets and
85 draw conclusions on the superiority of one dataset type over another (e.g. Ruane et al.
86 2015; Lee et al. 2018).

87 In addition to data exploration alone, the computational time needed to analyze various
88 datasets - including the phylogenetic reconstruction - can be calculated (e.g. Leaché et
89 al. 2015b). The time for sample preparation and sequencing can also be estimated (e.g.
90 Lemmon et al. 2012), but this information is more often reported in HTS method
91 description articles, and rarely compared among methods of data acquisition. Even
92 fewer studies evaluated monetary costs (reagents, library preparation and sequencing)
93 for a particular phylogenetic dataset (e.g. Moreau & Wray 2017) or more generally for a
94 taxonomic group (e.g. McKain et al. 2018). Finally, we only found two studies that
95 evaluated both time and money in relation with the preparation of a specific

96 phylogenetic dataset (Lemmon et al. 2012; Cruaud et al. 2014). These studies led to the
97 conclusion that HTS data will produce more data and more robust trees, justifying the
98 higher costs.

99 However, such studies are often conducted on so-called “model taxa” (e.g. Primates in
100 Collins & Hbrek 2018), for which genomic data is already abundant and the range of
101 possible data acquisition methods is not limited by the absence of annotated genomes.
102 However, more than 99% of the biodiversity is constituted on non-model taxa, i.e. taxa
103 for which no or little genomic and/or transcriptomic data are available, and for which
104 orthologous loci databases are information-poor. For those taxa, alternative strategies
105 have been developed such as exon-capture (Bi et al. 2012), Anchored hybrid
106 Enrichment (Lemmon et al., 2012) or Ultraconserved elements (McCormack et al.,
107 2012), referred herein as “sequence capture”. These strategies allowed
108 phylogenomicists to utilize very distant genomic resources for specific non-model
109 groups (e.g. Haddad et al., 2017). Still, lacking whole genome data limit the possibilities
110 to a handful of loci (the highly conserved ones), exclude non-coding material from
111 potential markers, and complexify the task of sorting orthology from paralogy.

112

113 Thus, most available studies focus on model taxa only, are generally limited to the
114 comparison of datasets of either different quantity or different nature of data, but rarely
115 both, using criteria related to tree robustness or time and money needed, but rarely both.

116 To provide arguments to choose one strategy over another in phylogenetic
117 reconstruction in non-model taxa, we here provide a comparison of several sequencing
118 and tree-reconstruction strategies in terms of robustness of resulting trees, and time and
119 money needed to produce and analyze the datasets. To do so, we used the family

120 Turridae (Conoidea, Gastropoda), a group of marine molluscs, as an example. The
121 Turridae constitute a good example of non-model animal taxon because of the lack of
122 genomic resources (e.g. no assembled and annotated genome, less than ten nuclear
123 markers represented in public databases, no karyotypes available), even in closely
124 related groups. The closest reference would be the recently published genome of
125 *Pomacea canaliculata* (Liu et al. 2018) and its divergence time with the family Turridae
126 is estimated at 283 Ma (Zapata et al. 2014). The family comprises 216 species
127 (WoRMS, checked on May 2019) but this number is largely underestimated (Puillandre
128 et al. 2012). Most of the molecular phylogenies published for this group used the same
129 classical mitochondrial (*cox1*, 12S and 16S rRNA) and/or nuclear (28S rRNA) markers
130 (Heralde et al. 2007, 2010; Olivera et al. 2008; Puillandre et al. 2012; Fedosov et al.
131 2011; Todd & Rawlings 2014; Puillandre et al. 2017). Two venom-gland transcriptomes
132 are published (Gonzales and Saloma 2014) that were not used primarily for
133 phylogenetic purposes but for toxin research, because the Turridae are venomous and
134 constitute a group of interest for bioactive compound discovery (Puillandre & Holford
135 2010). Finally, only one phylogenomic (RAD-seq) study (Abdelkrim et al. 2018a) was
136 published for species-delimitation purposes on eight species in the *Xenuroturris/Iotyrris*
137 complex.

138 We analyzed 32 transcriptomes (29 Turridae + 3 outgroups), corresponding to 18
139 species, from different tissues (venom gland, salivary gland or foot), from which we
140 extracted *in silico* five datasets: (i) the barcode fragment (658bp) of the *cox1* gene, the
141 most frequently sequenced marker in gastropod systematics; (ii) a multilocus dataset
142 that is typically produced using Sanger sequencing to conduct phylogenetic studies in
143 gastropods, corresponding to fragments of the mitochondrial *cox1*, 16S rRNA and 12S

144 rRNA genes, and the nuclear 28S rRNA, 18S rRNA and histone *h3* genes (e.g. Fedosov
145 et al. 2018; Johnson et al 2010); (iii) complete mitochondrial genomes (e.g. Uribe et al.
146 2018); (iv) a sequence capture approach, targeting a selection of nuclear loci (e. g.
147 Abdelkrim et al. 2018b); (v) an RNA-seq dataset (e.g. Cunha et Giribet 2019). Because
148 this dataset include only a limited number of Turridae lineages, the goal is not to resolve
149 the Turridae phylogeny, but to compare those five datasets. We empirically evaluated
150 the capacity of each dataset to resolve relationships among the 32 samples, within
151 which divergence ranges between 0 (intra-specimen divergence) and 79.4 Ma
152 (estimated age of origin of the family Turridae; Abdelkrim et al. 2018b). We also
153 evaluated the time necessary for sample preparation, sequencing and data analysis,
154 along with the monetary costs of each step to estimate the overall cost of producing
155 each dataset.

156

157 **2. Material and Methods**

158 **2.1 Sampling**

159 Twenty-eight specimens, representing six genera of Turridae and related outgroups
160 (Conidae and Mitridae) were collected during several field expeditions organized by the
161 Muséum national d'Histoire naturelle (MNHN; “KAVIENG” in Papua New Guinea,
162 “KANACONO” in South New Caledonia), by joined Russian-Vietnamese Tropical
163 Center (Vietnam), and by the University of Utah in collaboration with the University of
164 the Philippines (Philippines). Specimens were photographed and the shells were broken
165 to access the animal. For twenty-seven specimens, only one tissue type was sampled
166 (venom gland, salivary gland or foot) depending on the project they were associated
167 with; for one specimen, both venom gland and salivary gland tissue were sampled,

168 resulting in a total of 29 tissues (Supplementary Table 1). Remains of vouchers, when
169 available, were kept and are deposited in the MNHN collections.

170 In addition, we used publicly available transcriptomes from three species:

171 *Unedogemmula bisaya*, *Gemmula speciosa* (Turridae) and *Terebra subulata* from a
172 closely related family Terebridae (NCBI Sequence Read Archive (SRA) accession no.'s
173 SRR1574923, SRR1574907 and SRR2060989, respectively; Gonzales and Saloma
174 2014; Gorson et al. 2015).

175

176 **2.2 RNA Extraction, Library Preparation and Sequencing**

177 RNA was extracted using a Trizol protocol or the Qiagen RNeasy Micro kit, following
178 the manufacturer's recommendations. Bioanalyzer traces were used to assess total RNA
179 quality and determine suitability for sequencing. The cDNA libraries were prepared and
180 sequenced either at the New York Genome Center or at the Evolutionary Genetics Lab
181 at UC Berkeley (Supplementary Table 1). In New York, libraries were prepared using
182 the automated polyA RNAseq library prep protocol and sequenced with Illumina HiSeq
183 4000 with 150-bp paired-end reads. In Berkeley, the KAPA Stranded mRNA-Seq kit
184 was used to synthesize cDNA, ligate adapters using TruSeq HT adapters and barcode
185 samples. Samples were then sequenced with Illumina HiSeq 2000 or 4000 (see
186 Supplementary Table 1) with 100-bp paired-end.

187

188 **2.3 Transcriptome Assembly and Quality Assessment**

189 All the transcriptomes, including the ones downloaded from GenBank, were assembled
190 following the same procedure. Trimmomatic v.0.36 (Bolger et al. 2014) was used to
191 remove adapters and filter low quality reads (ILLUMINACLIP option enabled, seed

192 mismatch threshold = 2, palindrome clip threshold = 40, simple clip threshold of 15;
193 SLIDING WINDOW option enabled, window size = 4, quality threshold = 20;
194 MINLEN = 36; LEADING = 3; TRAILING = 3). Reads were merged using FLASH
195 v1.2.8 (Magoc and Salzberg 2011) with a min. overlap parameter of 5, a maximum
196 overlap parameter of 100 and a mismatch ratio of 0.05. FastQC (Andrews 2010) was
197 used for raw reads quality control. Transcripts were assembled using Trinity v2.4 with
198 default parameter (Grabherr et al. 2011). Cap3 (Huang and Madan 1999) with default
199 parameters and cd-hit v4.6 (percent identity = 99%; Li and Godzik 2006) were finally
200 applied to reduce redundancy in the assemblies.
201 BMap (Bushnell 2014) was used to generate basic assembly statistics and BUSCO
202 (Simão et al. 2015) to evaluate transcriptome completeness. Finally, bowtie2 v2.2.6
203 (Langmead and Salzberg 2012) and samtools v1.3 (Li et al. 2009) were used to evaluate
204 read representation in each assembled transcriptome, as recommended in the Trinity
205 manual.

206

207 **2.4 Transcriptome Orthology Inference**

208 Two approaches were used to assess orthology among transcripts, from here onwards
209 referred to as “reference-based” approach and “graph-based” (without a reference
210 genome) approach (Fig. 2).

211 For the reference-based approach, the *Pomacea canaliculata* genome (ASM307304v1;
212 Liu et al. 2018) was used as a reference. Following the pipeline described in Phuong
213 and Mahardika (2018) and Phuong et al. (2019), blastx was used to associate transcripts
214 to peptide sequences of *P. canaliculata* and tblastn to associate peptides of
215 *P. canaliculata* to transcripts from the BLAST + v2.2.31 suite (Altschul et al. 1990) with

216 an e-value threshold of $1e10^{-10}$ and a word size value of 11. For each sample, bowtie2
217 v2.3.4.1 was used with the very sensitive-local alignment option and not allowing for
218 discordant pair mapping (unexpected paired read orientation during mapping) to map
219 reads to the selected transcripts from the reciprocal blast step. Duplicates were marked
220 using picard-tools v2.0.1 (<http://broadinstitute.github.io/picard>) using default
221 parameters. All positions with a coverage $< 5X$ were masked and the entire sequence
222 was removed if $>30\%$ of the sequence was masked. To fix assembly errors, single
223 nucleotide polymorphisms (SNPs) were called using samtools v1.3 (default parameters)
224 and bcftools v1.3 (Li et al. 2009) using the call command. Transcripts for each locus
225 were aligned as nucleotides using MAFFT v7.222 (Katoh et al. 2005) option -auto. To
226 limit misalignments and paralogs inclusion, uncorrected pairwise distances were
227 calculated at each locus for all possible pairwise comparisons and sequences were
228 removed if the uncorrected pairwise distance was greater than the 90th percentile
229 (threshold was set empirically) of pairwise distances across all loci for that pair of
230 species.

231 For the graph-based approach, we used UPhO (Unrooted Phylogenetic Orthology;
232 Ballesteros and Hormiga 2016), a method that uses the topology of individual gene trees
233 to identify clades corresponding to orthologous groups. Following the workflow
234 established by the authors, all transcripts in open reading frame (ORF) were extracted
235 from the transcriptome assemblies with custom Python scripts, and all ORFs that were
236 less than 100 amino-acid long were eliminated. An all-versus-all blastp search was then
237 performed, using a relaxed expectation value threshold of $e = 1 \times 10^{-5}$.

238 To reduce missing data, only the clusters that contained the maximum number of
239 samples (32) were selected. The gene-family amino-acid sequence clusters were aligned

240 and cleaned using mafft (option ‘-auto’), trimAL (option ‘-gappyout’) and Al2phylo (-m
241 32 -t 300 -p 0.80). After alignments, the sequences were converted from amino acids
242 back to nucleotides to increase the number of informative sites and improve the
243 phylogenetic pipeline accuracy. Gene-family trees (GFTs) were estimated using IQ-tree
244 (Nguyen et al. 2014). The best substitution model for each GFT was estimated with
245 ModelFinder (Kalyaanamoorthy et al. 2017) following the BIC criterion. Subsequently,
246 1,000 ultrafast bootstraps (UFBoot) (Hoang et al. 2017) were performed on each GFT to
247 obtain branch support. The branches representing putative orthogroups were finally
248 extracted with UPhO (-m 4 -S 0.80). The orthogroup alignments obtained were cleaned
249 and analyzed using MAFFT, trimAL, Al2phylo and IQ-tree with the same parameters as
250 above (except for the -m parameter in Al2phylo, set to 4).

251

252 **2.5 Transcriptome Phylogeny**

253 Ten datasets were generated. For the reference-based approach three subsets were
254 defined with a minimum of 4, 16 and 32 samples / locus. These subsets were analyzed
255 using a supermatrix - concatenated alignment of all the loci - and a supertree approach,
256 resulting in six datasets referred as follows: Ref-IQ4, Ref-IQ16, Ref-IQ32, Ref-AS4,
257 Ref-AS16 and Ref-AS32 (IQ referring to IQ-tree and AS to ASTRAL – see below).
258 Similar subsets were constructed for the graph-based approach with 16 and 4 samples /
259 locus (the 32 sample/locus dataset was not analyzed here because only one locus was
260 retrieved). The resulting four datasets are referred to as follows: Uph-IQ4, Uph-IQ16,
261 Uph-AS4 and Uph-AS16.

262 Best substitution models were estimated for each partition (locus) in each concatenated
263 dataset with ModelFinder following the BIC criterion. Supermatrix trees were

264 reconstructed using IQ-tree and 1,000 UFBoot were performed on each dataset. An
265 individual tree for each locus was also generated with IQ-tree, using the associated best
266 substitution model for datasets Ref-AS4, Ref-AS16, Ref-AS32, Uph-AS4 and Uph-
267 AS16. The supertree approach implemented in the program ASTRAL-III (Zhang,
268 Sayyari and Mirarab 2017) was then applied to combine the single-locus trees into a
269 single supertree for each of these datasets.

270

271 **2.6 Sequence Capture**

272 We used the Ref-AS4 dataset and selected the 3,000 shortest loci (ranging from 96 to
273 839 bp) to simulate a sequence capture datasets (Bi et al. 2012; Jiang et al. 2017;
274 Abdelkrim et al. 2018b). Three subsets were generated, with a minimum of 4, 16 and 32
275 samples / locus for which both supermatrix and supertree approaches were applied, as
276 explained above. These datasets will be referred as follow: Cap-IQ4, Cap-IQ16, Cap-
277 IQ32, Cap-AS4, Cap-AS16 and Cap-AS32.

278

279 **2.7 Mitogenomes and Nuclear Markers**

280 The *Pinguicemula* sp. (Turridae) mitogenome (MH308408.1; Uribe et al. 2018) was
281 used as a reference to extract partial (up to 20% missing data) to complete mitogenomes
282 (including tRNAs) from the transcriptomes and create the dataset “MT.” Several
283 sequences of 28S rRNA, 18S rRNA and histone 3 (*h3*) of Turridae from GenBank were
284 used as references to extract the corresponding loci from the 32 transcriptomes by
285 BLAST. Along with the mitochondrial *cox1*, 12S and 16S fragments, they constitute the
286 Sanger multilocus dataset “SAN.” Finally, the *cox1* alone constitutes the Sanger
287 barcode dataset “BC.” The same protocol as for the reference-based approach was

288 applied for mapping, filtering and alignment. For the MT, SAN and BC datasets, each
289 codon position of the protein coding genes was treated as an independent partition, as
290 well as each non-protein coding gene. The best substitution model was estimated for
291 each partition in each concatenated dataset with ModelFinder following the BIC
292 criterion and 1,000 UFBoot were performed on each dataset to obtain branch support
293 for the trees reconstructed with IQ-tree.

294

295 **2.8 Tree Topology Evaluation**

296 The Turridae trees published so far suffer from both incomplete sampling and lack of
297 resolution (e.g. Heralde et al. 2007; Puillandre et al. 2012). Thus, these published trees
298 can hardly be used as a reference tree for the Turridae. Consequently, two approaches
299 were used to evaluate tree topology decisiveness and informativeness.

300 For the matrix and supermatrix datasets (BC, SAN, MT, Cap-IQ, Ref-IQ, Uph-IQ), the
301 log-likelihood of multiple constrained tree searches for each dataset was compared and
302 the results were statistically tested with IQ-TREE using the Shimodaira-Hasegawa
303 (1999) (SH) test. The trees were constrained respectively following all the different
304 topologies retrieved with the different datasets, except for the intra-specific and
305 outgroup nodes, resulting in a total of eight unique constrained topologies (the same
306 topologies found for Cap-IQ32 and CapIQ16, Cap-IQ4 and Ref-IQ32, Ref-IQ16 and
307 Ref-IQ4).

308 For the supertree datasets (Cap-AS, Ref-AS and Uph-AS), tree metrics were used to
309 evaluate loci quality. The normalized quartet distance of each locus was calculated
310 using TreeCmp (Bogdanowicz et al. 2012) with reference to the corresponding supertree
311 with collapsed intraspecies nodes. Additionally, the quartet distance metric score

312 distribution of BUSCO (single-copy + fragmented) loci trees versus all other single-
313 locus trees for Ref-AS16 and Ref-AS32 were compared to evaluate the quality of the
314 reference-based approach. The quartet score (proportion of quartets satisfying the
315 supertree) was also used to evaluate the overall support of supertree analysis using
316 ASTRAL-III's log.

317

318 **2.9 Data, Time and Money Evaluation**

319 *Data* – The AMAS python program (Borowiec 2016) was used to calculate alignment
320 statistics for each dataset, including the number of loci, the alignment length (in the case
321 of ASTRAL-III, the median length of all loci), the total number of matrix cells and
322 undetermined cells (to evaluate missing data) and the proportion of variable and
323 parsimony-informative sites.

324 *Time and money* – Comparisons of costs (time and money) were measured respectively
325 in number of days and euros but did not take into account specimen collection and
326 salary costs, both varying too much depending respectively on the taxon, the country
327 where research is carried out, or the academic level of the person employed (e.g.
328 graduate or engineer). Costs were evaluated by the Service de Systématique Moléculaire
329 (SSM) platform at the MNHN (UMS 2700). The time estimates were based on a
330 realistic best-case scenario, meaning that each step of lab preparation and data analysis
331 are supposed to work on the first try with the methods used at the SSM.

332

333 **3. Results**

334 **3.1 Transcriptome Sequencing, Assembly and Quality Assessment**

335 The total number of raw reads used for transcriptome assembly ranged from 42,770,212
336 to 138,181,918 and the number of assembled contigs ranged from 46,027 to 283,318.
337 The mean value of N50 is 539. At least 80% of input reads mapped back to the
338 transcriptome assemblies. The mean BUSCO completeness value is 49.1%, ranging
339 from 36% to 83.7% (Supplementary Table 1). Pearson's r showed a strong correlation
340 between assembly size and BUSCO completeness ($\rho=0.78$, p -value = $1.54E-07$) but no
341 correlation between the number of raw reads and BUSCO completeness ($\rho=-0.01$, p -
342 value= 0.98) (Supplementary Table 2). Transcriptomes produced from foot tissue
343 (*Gemmula* sp. and *M. mitra*) showed a greater BUSCO completeness than
344 transcriptomes produced from venom or salivary glands, suggesting transcript
345 abundance variation among tissues and/or overrepresentation of some transcripts in
346 glands (e.g. highly expressed toxins – Dutertre et al. 2014). However, more
347 transcriptomes assembled based on different tissues from the same specimen are needed
348 to properly test this hypothesis.

349

350 **3.2 Phylogenetic Results**

351 The monophyly of the ingroup Turridae is always confirmed, except with two datasets
352 (Uph-AS16 and Uph-AS4), where the outgroup *Terebra* is found in the ingroup
353 (Supplementary Fig. 1). The genera *Gemmula* and *Turris* are systematically retrieved
354 polyphyletic (Fig. 3), as shown in previous studies (Puillandre et al. 2012; Fedosov et
355 al. 2011). The species represented by several specimens (*X. legitima*, *I. cingulifera*, *I.*
356 *musivum* and *I. olangoensis*) are always recovered as monophyletic groups except for
357 one dataset (Uph-IQ4), in which a specimen of *I. cingulifera* is placed as a sister group
358 of the other members of *Iotyrris*. Apart from the Uph-IQ4 dataset, the relationships

359 inferred among *X. legitima* and all three *Iotyrris* species are always identical. The long
360 branches *Turris* and *Lophiotoma* are found as sister groups only in the “Ref” and “Cap”
361 datasets. Finally, the relationships among *Gemmula* sp., *T. nadaensis*, *Unedogemmula* –
362 the earliest offshoots in the ingroup – and the rest of the Turridae appear to be the most
363 problematical (Fig. 3). The phylogenetic results are globally congruent with previous
364 studies (e.g. Puillandre et al. 2012), despite the heterogeneity in the number of species
365 per lineage and several missing lineages. Overall, the graph-based approach (UPhO)
366 shows very low taxon occupancy (see also Fernandez et al., 2018) and fewer
367 parsimony-informative sites, and hence results in shortest branches and incongruent
368 results with the reference-based approach. An extreme case is the specimen of *I.*
369 *cingulifera* not retrieved within the *I. cingulifera* species node in the UPh-IQ4 dataset.
370 This specimen’s transcriptomes shows poorer results in terms of assembly size
371 (38,931,364 bp, compared to the 56,711,565 mean) and BUSCO completeness (23.8%
372 of complete single loci). Nevertheless, the reference-based reconstructions do not suffer
373 from this low-quality transcriptome.

374 Except for the BC and SAN datasets, support for specific to supra-specific nodes ranged
375 between 75% and 100% (Table 1), and shows no correlation with the dataset size.
376 Interestingly, in the mitogenome dataset (MT), bootstrap supports were similar or
377 superior to those of larger datasets, but those values were negatively affected by the
378 removal of some regions such as tRNAs (Supplementary Fig. 1).

379

380 **3.3 Topology Evaluation**

381 Except for UPh-IQ4, all the datasets had at least one alternative constrained topology
382 credible under the SH test (Table 2). The credible sets of trees for the smallest datasets

383 (BC, SAN and MT) contained more constrained trees than the credible sets of trees for
384 the larger datasets (Cap, Ref & Uph).
385 Not a single-locus tree with 16 or more terminal entities fully matches its corresponding
386 supertree (Figure 4). This is also true for the UPhO-AS16 single-locus tree distribution
387 (Supplementary Fig. 2). The student's t test results of quartet distance metric score
388 distribution of BUSCO (single-copy + fragmented) loci trees versus all other loci trees
389 for Ref-AS16 showed a significant difference between the two distributions (p-value
390 $<2.2e-16$; Fig. 4b). The quartet score decreases when reducing taxon occupancy: for
391 Ref-AS32, Ref-AS16 and Ref-AS4 the normalized quartet scores were respectively
392 0.730, 0.709 and 0.707 (Supplementary Table 3).

393

394 **3.4 Data, Time and Money**

395 All Sanger markers were extracted from the transcriptomes except for *h3*, lacking in 25
396 of the transcriptomes. The largest dataset (DS5aIQ4) is a concatenated alignment of
397 14,586,607bp (71.7% of missing data), corresponding to 9,232 loci (DS5aAS4), of
398 which all other datasets were constructed, except for the graph-based approach ones.
399 The graph-based approach generated too few loci with no missing data (32
400 terminals/locus), therefore only four datasets were retained (Table 1). As shown on the
401 Figure 5, the reference-based and graph-based approach used respectively 285,660 and
402 35,595 transcripts for each pipeline, but only 19,008 (6.8%) of the total transcripts are
403 in common between the two pipelines.
404 Unsurprisingly, the larger datasets are also more costly (Table 1), ranging from an
405 estimated 226€ for the CO1 dataset to 8,828€ for transcriptomes, for the production of a
406 32 terminal entity phylogeny (as for this study). But, while the Sanger datasets (BC,

407 SAN) costs increase proportionally with the number of specimens and number of loci
408 targeted, the mitochondrial and sequence capture datasets costs will dramatically reduce
409 when pooling a lot of specimens. This is particularly the case for the sequence capture
410 dataset, especially when considering the price of custom baits. By pooling 100 post-
411 capture libraries on a single sequencing lane (instead of the 32 in this study), the cost
412 per specimen goes down from 196€ to 81€ (273€ to 105€ if including the transcriptome
413 sequencing and the design of the probes). Finally, the transcriptomes dataset is the only
414 HTS dataset not following the rule of decreasing costs when pooling more specimens,
415 simply because there is a limit on the number of transcriptomes that can be sequenced
416 on a single lane.

417

418 **4. Discussion**

419 **4.1 Comparison of the Five Sequencing Strategies**

420 In the present study, we compare datasets that are representative of the outputs of the
421 pipelines used in most empirical phylogenetic studies in non-model animal taxa, and
422 evaluate them in terms of costs (money and time) and robustness of the resulting tree. It
423 should be noted that the conclusions on the cost evaluations rely on the assumption that
424 the overall costs and timeframes of analyzed methodologies will be similar in other
425 labs. Furthermore, another cost, the environmental cost (the impact of each pipeline on
426 the environment), was not calculated due to the multicity of parameters to take in
427 account. However, library preparations and the use of data centers (Jones, 2018) would
428 surely represent a substantial environmental cost for HTS-based trees. If this cost is
429 rarely considered, in the future scientists might be encouraged to lower their ecological
430 footprint.

431 Our results show that traditional Sanger sequencing of one to six loci will retrieve trees
432 with robust nodes for more than half of the clades, quickly and at very affordable costs.
433 Indeed, the *cox1* barcode tree alone retrieved both monophyletic species and most nodes
434 well supported. This particular result might partially explain why, despite 15 years of
435 HTS development and democratization, the vast majority of articles is still presenting
436 trees produced with such datasets (Fig. 1). Surely, the “Sanger era” has not yet arrived
437 to its end, and many more phylogenies with such datasets will be published in the years
438 to come.

439 Nevertheless, some nodes remain unsupported, in particular the deeper nodes. We found
440 that the best compromise for retrieving a fully resolved and highly supported tree is the
441 mitogenome dataset, for which all nodes have >80% bootstrap and the costs are less
442 than half the price of a sequence capture. However, previous studies have already
443 shown that mitogenomic trees are subject to artifacts, such as long-branch attraction
444 generated because of the high rates of mutation of the mitochondrial genome, especially
445 in the third codon positions (Bergsten 2005, Arabi et al. 2010). Moreover, a
446 mitogenome can be considered as a single locus and thus cannot be subjected to
447 congruence tests. The use of nuclear HTS data becomes even more indispensable when
448 investigating biological processes such as introgression (e.g. Eaton et al. 2015; Zhang et
449 al. 2015), where analysis of unlinked markers is necessary.

450 The sequence capture and RNA-seq datasets (based on a reference genome) yielded
451 similar results in terms of phylogenetic reconstruction accuracy, number of credible sets
452 of trees passing the SH test and single-loci tree metrics distribution. However, the costs
453 of sequence capture are by far more affordable than costs of producing and analyzing
454 transcriptomes. Furthermore, RNA-seq requires high-quality, fresh RNA samples, not

455 often available for a representative set of taxa. These considerations led to the
456 conclusion that sequence capture might be the best method to produce a complete, high
457 resolution tree for a non-model taxon, with a cost per specimen estimated at 80-100€(if
458 at least 100 specimens are sequenced on one lane) and a processing time of a few weeks
459 to a few months (Supplementary Table 4). Nevertheless, transcriptomic data remains
460 necessary to identify suitable markers that will be targeted by sequence-capture,
461 especially when there is no available genome. Furthermore, transcriptomic data might
462 be more suitable for backbone phylogenetic trees, including very deep relationships (i.e.
463 several hundreds of millions of years; Cunha & Giribet 2019; Kocot et al. 2011). But
464 very deep relationships also imply that it will be harder to distinguish orthology from
465 paralogy. In summary, the Sanger approach still remains relevant to resolve
466 phylogenetic relationships at a low price (both time and money), and can provide a
467 preliminary outline of the taxon diversity, useful to select a subset of samples that can
468 be analyzed with a more costly approach. However, some gene markers might not be as
469 useful as thought, depending on the taxon (e.g. 18S, see Fig. 4), and 12S and 16S will
470 generally only confirm the *cox1* results. We thus recommend starting with DNA
471 barcoding but from there going directly to sequence capture (if there is a strong need to
472 clarify the remaining challenging nodes). Mitogenomes indeed provide the best
473 compromise between tree quality and costs, but are subject to potential biases. Finally,
474 RNA-seq appears only appropriate for constructing phylogenies in the case of very deep
475 relationships or simply to identify suitable markers for sequence capture.
476
477 Another class of HTS datasets that has not been explored is the reduced-representation
478 approaches such as RAD-seq (e.g. Baird et al 2008). RAD-seq has already been

479 established as a suitable tool for phylogenetic inference (e.g., Cariou et al. 2013; Cruaud
480 et al. 2014). In a recent *in silico* study (Collins & Hbrek 2018), the authors even found
481 that RAD and sequence capture datasets gave highly congruent results. However, RAD-
482 seq datasets are reduced-representation of genomes, and extracting an *in silico* RAD-seq
483 dataset from our transcriptomes may have produced biased results, not equivalent to
484 other RAD-seq datasets. Nonetheless, it could be argued that sequence capture methods
485 are more promising for phylogenetic studies, because markers are not anonymous, and
486 their sets can be tailored with more versatility according to the needs, samples with
487 fragmented DNA can be sequenced more efficiently, information content per locus is
488 higher (allowing the use of supertree approaches) and larger evolutionary time scales
489 are covered (Harvey et al. 2016).

490

491 **4.2 A Note on Topology Accuracy Assessment**

492 As shown in Table 1, the majority of the concatenated datasets show >80% or even
493 100% bootstrap values for all nodes – the same applies for ASTRAL support values –
494 even though the amount of data can vary by a factor of 100 between datasets. Despite
495 high node support, several topologies are in conflict, especially for the earliest
496 relationships of the Turridae (*Gemmula* sp., *Unedogemmula* and *T. nadaensis*). Even if
497 the true tree is unknown, we know that, at best, only one of these topologies is correct.
498 It has already been showed that the bootstrap support value can rapidly saturate when
499 increasing the number of sites (especially invariant ones), proportion of missing data, or
500 both (Simmons & Freudenstein 2011). Furthermore, when using supermatrix
501 approaches, log-likelihood ratio tests have been used to statistically test if a given
502 dataset can accommodate several topologies (e.g. McFadden et al. 2006). In our case, all

503 datasets (except the particular case of Uph-AS4) tolerated at least one, but not all,
504 different (constrained) topologies, suggesting that the unconstrained topology is equal to
505 or only slightly better than alternative one(s). The high-bootstrap values and non-
506 conclusive log-likelihood ratio tests for each phylogenomic datasets called for
507 alternative methods to measure tree robustness.

508 The normalized quartet score (Bayzid et al. 2015) is the proportion of quartets from the
509 input single-locus trees that agree with the resulting supertree. We used it to measure
510 the relevance of datasets with low taxon occupancy (e.g. Ref-AS4) when considering a
511 supertree approach. Our results show that the normalized quartet scores for Cap-AS,
512 Ref-AS and UPh-AS datasets are systematically lower with low taxon occupancy. Such
513 results would imply that, as for supermatrix (Philippe et al. 2017), datasets with low
514 taxon occupancy should be avoided (but see e.g. Kallal et al. 2018). Graphical
515 representations of single-loci tree distribution, sometimes referred to tree space
516 visualization in its extended version (Hillis et al. 2005) show promising results for
517 understanding inconsistency among the datasets. The distribution of single-loci tree
518 distance to a reference tree (Fig. 4a) has already been used to compare the quality of
519 different datasets (Simmons 2017), but also within-dataset informativeness (e.g. intron
520 vs. exon; Chen et al. 2017). In the case of non-model taxa, such distribution patterns can
521 be used to compare loci with high reliability of orthologous relationships (e.g. BUSCO
522 single-copies) versus shallow orthologous loci (e.g. from a reference-based or a graph-
523 based approaches) and thus evaluate the quality of a pipeline (Fig. 4b). In our case, we
524 show that a simple blast and downstream filtering approach against a reference genome,
525 even a very distant one, gives satisfactory results, although not sufficient to obtain
526 orthologous loci of similar confidence to BUSCO single-copy loci.

527

528 **4.3 Improving Sequence Capture: Challenges and Perspectives**

529 An important challenge of HTS in phylogenetic reconstruction is to *a priori* identify
530 loci that better reflect evolutionary relationships among taxa. Our reference-based and
531 graph-based approaches implemented herein correspond to the two alternative
532 strategies, widely used to infer orthologous loci from *de novo* assembled transcriptomes
533 (as reviewed in Laumer 2018). In our case, the graph-based approach with UPhO
534 yielded poor results in comparison to the reference-based approach, but more empirical
535 and *in silico* generated datasets need to be analyzed to properly compare them. The
536 UphO approach was especially sensitive to missing data (specimen of *I. cingulifera* not
537 found with other *I. cingulifera* specimens in DS Uph-IQ4) and the tree reconstruction
538 method (*Terebra* found in the ingroup for DS Uph-AS16 and Uph-AS4). One of the
539 reasons that *Terebra* was found in the ingroup for the Uph-AS16 and Uph-AS4 datasets
540 could be that the orthologs found with the graph-based approach were generally poorly
541 informative (~7% parsimony-informative sites on average), thus resulting in poorly
542 resolved single-locus trees. Conversely, the reference-based approach showed satisfying
543 results, both in terms of pipeline celerity (avoiding “all-vs-all” blast use), tree
544 robustness and congruency between subsamples. Furthermore, it retrieved far more loci
545 than the BUSCO database. However, single-loci tree evaluation (Fig. 4) showed that the
546 loci retrieved with our reference-based approach are not all informative and/or accurate,
547 and the loci selection could be improved. The use of other alignment statistics, such as
548 the proportion of parsimony-informative sites, could allow for a more precise *a priori*
549 selection of loci (e.g. HaMStR; Ebersberger et al. 2009). Nonetheless, in our dataset,
550 and quite paradoxically, there is a slight negative correlation between the number of

551 parsimony-informative sites in the single-locus alignments and the single-locus-tree
552 distances to the supertree (e. g. for Ref-AS32 $\rho=0.40$, p-value = 9.93E-20 –
553 Supplementary Table 5), suggesting that most of the phylogenetic signal retrieved in the
554 single-locus trees would not be conveyed by the parsimony-informative sites. Finding
555 true, orthologous, informative loci still needs development, especially when no close
556 reference genome is available. This relies on finding a better combination of filtering
557 thresholds, alignments statistics and tree metrics to reduce the costs and increase the tree
558 robustness, generating a solid framework to test evolutionary hypotheses.

559 Finally, one particular advantage of the Sanger approach to reconstructing phylogenies
560 is its routine application. A phylogenetic dataset can be completed regularly, by adding
561 additional sequences on a day-to-day basis, with little doubt on the loci sequenced (but
562 see Mutanen et al. 2016). This is less true for HTS based approaches, which usually
563 provide a large amount of data requiring significant investment and staff trained in
564 bioinformatics to eventually combine several datasets, produced in several batches
565 and/or by different research teams. To combine the advantage of both approaches, i.e. a
566 small set of well identified loci that can easily be incremented and a larger, more
567 informative dataset, we propose the following strategy: together with the loci that will
568 be identified as targets in the exon capture approach, the mitochondrial and nuclear loci
569 traditionally used in Sanger sequencing (typically, the *cox1*, 16S, 12S, 28S, 18S and *h3*
570 for the mollusks), and even full mitogenomes, could also be captured (e.g. Espeland et
571 al. 2018 with the *cox1* only). Hence, the backbone phylogeny obtained with a sequence
572 capture dataset can further be completed with additional nuclear core markers or
573 mitochondrial genomes, using a multilevel dataset approach.

574

575 **Fundings**

576 This work was supported by the CONOTAX project funded by the French Agence
577 Nationale pour la Recherche (ANR-13-JSV7-0013-01).

578

579 **Acknowledgments**

580 Material was collected during several expeditions: the Kavieng Lagoon Biodiversity
581 Survey in Papua New Guinea (June 2014, MoU with the University of Papua New
582 Guinea, PIs: Philippe Bouchet, Jeff Kinch), as part of the Our Planet Reviewed
583 expeditions organized jointly by Muséum national d'Histoire naturelle (MNHN), Pro-
584 Natura International (PNI) and Institut de Recherche pour le Développement (IRD),
585 with support from Papua New Guinea's National Fisheries Authority, the Total
586 Foundation, the Laboratoire d'Excellence Diversités Biologiques et Culturelles (LabEx
587 BCDiv, ANR-10-LABX-0003-BCDiv), the Programme Investissement d'Avenir (ANR-
588 11-IDEX-0004-02), the Fonds Pacifique, and CNRS' Institut Ecologie et
589 Environnement (INEE); the KANACONO expedition in New Caledonia (August 2016,
590 convention MNHN-Province Sud, APA_NCPS_2016_012; PI N. Puillandre and S.
591 Samadi), as part of the Our Planet Reviewed expeditions and the Tropical Deep-Sea
592 Benthos program (expedition.mnhn.fr), with support from the LabEx BCDiv; the Nha-
593 Trang expedition in Vietnam, supported by the Russian–Vietnamese Tropical Center,
594 with support from the staff of the Tropical Center for assistance in organization of the
595 field sampling and loan of some laboratory equipment; and a collection trip supported
596 by the 'Conus-Turrid' project (principal investigator B. M. Olivera, University of Utah,
597 USA). These expeditions were operated under the regulations then in force in the
598 country in question and satisfy the conditions set by the Nagoya Protocol for access to

599 genetic resources. This project was partly supported by the Service de Systématique
600 Moléculaire (UMS 2700 CNRS-MNHN). The authors also thank Laetitia Aznar-
601 Cormano, Juliette Gorson and Mandë Holford for their help in the lab work, Yuri
602 Kantor for his help in Turridae dissections, Barbara Buge for her help in curating the
603 specimens, Mark Phuong, Lou Mary and Jérémie Bardin for their help with
604 bioinformatics scripts.

605

606 **Declaration of interest**

607 The authors declare no competing interests that could inappropriately influence (bias)
608 their work.

609

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843 **Figure legends**

844 **Figure 1.** Proportion of articles over time that used Sanger sequencing (dark grey) or
845 HTS (light grey) to reconstruct a phylogeny. Articles were extracted using the Web of
846 Science “Basic Search”, every two years from 2006 to 2018, and using the keyword
847 “Phylogen*” in TITLE only. Only the first 50 articles of the list with newly produced
848 genetic data with one of the two methods were screened and categorized as “Sanger” or
849 “HTS”.

850 **Figure 2.** Flowchart summarizing the in-silico approach used to generate all the
851 datasets. Data are framed by parallelograms, tasks by rectangles and datasets by
852 rounded rectangles.

853 **Figure 3.** From top to down and left to right: phylogenetic trees corresponding to the
854 BC, SAN, MT, Cap-IQ16, Ref-IQ16 and UPh-IQ4 datasets. Outgroups are not shown.
855 Bootstrap values for the fully supported and intraspecies nodes are not shown. Colors
856 represent genera or genera-level groups. Scale: average number of substitutions per site.

857 **Figure 4.** Distribution of quartet distance of single-locus trees of the Ref-AS16 dataset
858 against the Ref-AS16 supertree, for the BUSCO loci (dark grey) and the other loci (light
859 grey). (a) Total number of counts, with indication of some specific loci (e.g. 28S)
860 distance to supertree (arrows). (b) Scaled density plot, with dotted lines representing the
861 mean values.

862 **Figure 5.** Number of unique and shared transcripts for the Ref, UPh and BUSCO sets of
863 loci recovered after the first blast step of each pipeline. Total number of transcripts for
864 all transcriptomes is 3,634,333 (supplementary Table 1).

865

866 **Tables**

867 **Table 1.** Description of the datasets analyzed. Me = median loci length. For the
868 robustness evaluation, only the nodes between the ingroup to the species nodes were
869 taken into account. More details on time and money evaluation is available in
870 Supplementary Table 4.

871 **Table 2.** Summary table of the Shimodaira-Hasegawa tests for each dataset constrained
872 with each topology, with 1,000 resamplings using the RELL method. The topologies are
873 on the top (as column headers) and the datasets on the side (as row headers). “+”: the
874 corresponding topology is not rejected; “-”: vice-versa.

875

876 **Supplementary Material**

877 **Supplementary Table 1.** Description of the specimens and transcriptomes.

878 **Supplementary Table 2.** Correlation table between different sequencing and assembly
879 results

880 **Supplementary Table 3.** Quartet scores for ASTRAL-III datasets

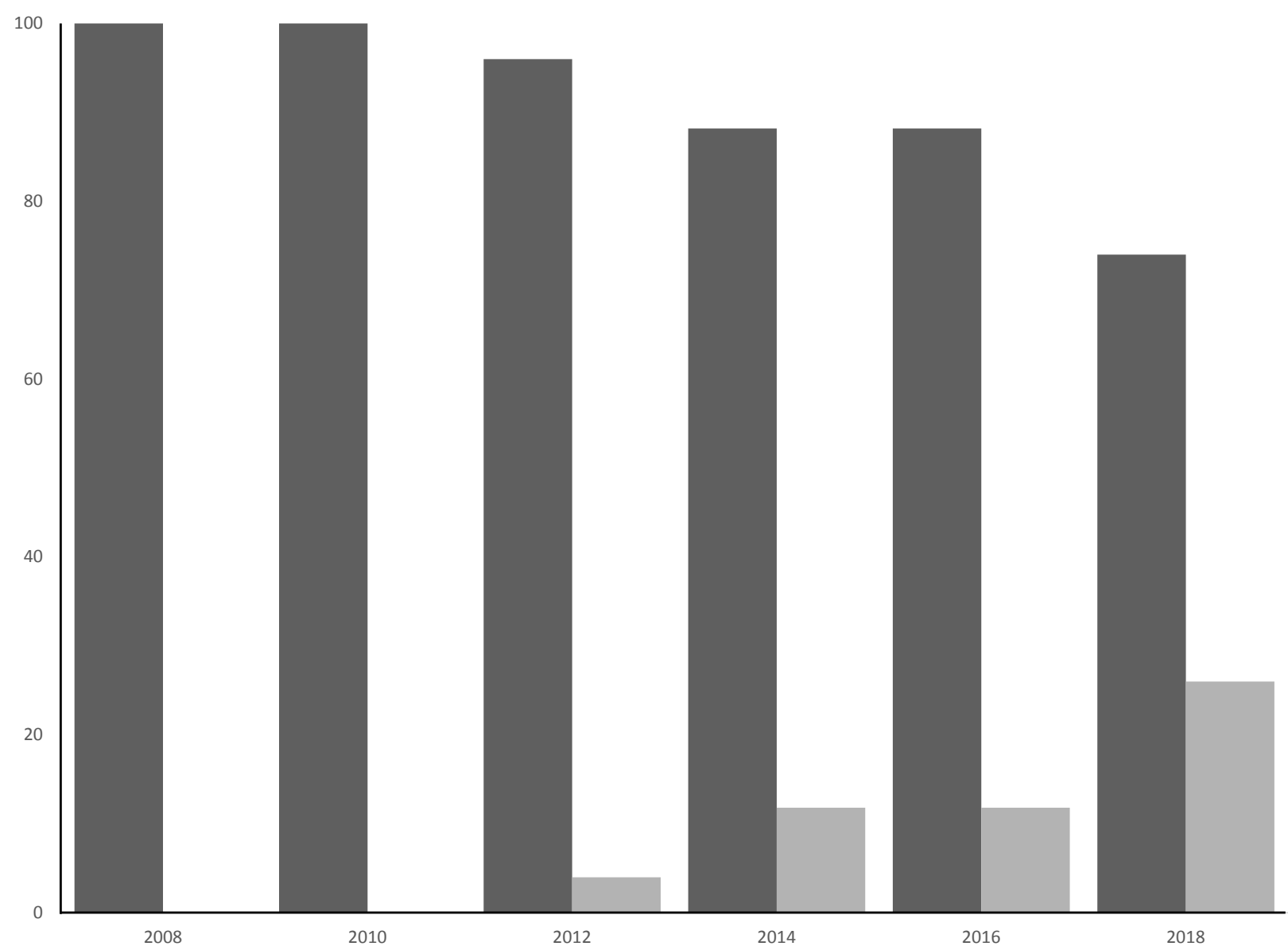
881 **Supplementary Table 4.** Evaluation of the costs (time and money) for each dataset.

882 **Supplementary Table 5.** Correlation coefficient of single-loci's quartet distance
883 against several alignment statistics.

884 **Supplementary Figure 1.** 20 species tree produced for this study.

885 **Supplementary Figure 2.** Distribution of quartet distance of single-locus trees of the
886 UPh-AS16 dataset against the UPh-AS16 supertree

		DATA						TIME (days)			MONEY (euros)			ROBUSTNESS	
dataset type	orthology assesment	Phylogenetic method	Dataset name	No of loci	Alignment length	Missing data	Variable sites	Parsimony informative sites	Lab work	Data analysis	Cost per specimen	Cost per base (per specimen)	Cost per variable site (per specimen)	% nodes > 80% BS or 95 PP*	% nodes = 1*
Sanger - DNA barcoding gene		ML (IQ-TREE)	BC	1	658	76 (0.4%)	258 (39.2%)	165 (29%)	2	-	7	0,011	0,027	61.1	16.6
Sanger - multilocus		ML (IQ-TREE)	SAN	6	4,787	12,820 (8.4%)	889 (18.6%)	565 (11.8%)	2	-	40	0,01	0,045	77.7	55.5
mitogenome		ML (IQ-TREE)	MT	1	14,927	27,562 (5.8%)	6,491 (43.5%)	4,922 (33%)	5	1	54	0,0036	0,0085	100	77.7
sequence capture	Genome reference	ML (IQ-TREE)	Cap-IQ32	274	136,799	249,086 (5.7%)	46,491 (34%)	28,083 (20.5%)	10	6 to 10	196	0,001432759	0,00445	100	83.3
		Supertree (ASTRAL-III)	Cap-AS32	274	Me = 498	Me = 402.5 (2.6%)	Me = 165.5 (32.6%)	Me = 95.5 (18.6%)						77.7	77.7
		ML (IQ-TREE)	Cap-IQ16	1373	743,778	8,009,019 (33.6%)	266,325 (35.8%)	148,171 (19.9%)						100	88.8
		Supertree (ASTRAL-III)	Cap-AS16	1373	Me = 548	Me = 1,901 (15.2%)	Me = 182 (34%)	Me = 92 (17.5%)						94.4	83.3
		ML (IQ-TREE)	Cap-IQ4	3000	1,623,052	31,758,137 (61.1%)	499,798 (30.8%)	218,629 (13.5%)						94.4	94.4
		Supertree (ASTRAL-III)	Cap-AS4	2999	Me = 555	Me = 1,491 (26.4%)	Me = 154 (29.9%)	Me = 56 (11.8%)						94.4	88.8
transcriptomes	Genome reference	ML (IQ-TREE)	Ref-IQ32	473	480,293	2,533,447 (16.5%)	158,798 (33.1%)	91,619 (19.1%)	8	20 to 40	275	0,000572567	0,00071	94.4	94.4
		Supertree (ASTRAL-III)	Ref-AS32	473	Me = 698	Me = 1,046 (4.2%)	Me = 239 (31.8%)	Me = 139 (17.8%)						88.8	88.8
		ML (IQ-TREE)	Ref-IQ16	4663	8,187,363	153,998,814 (58.8%)	2,450,395 (29.9%)	1,147,534 (14%)						94.4	94.4
		Supertree (ASTRAL-III)	Ref-AS16	4663	Me = 1,276	Me = 9,438 (34.6%)	Me = 409 (31.2%)	Me = 183 (14.8%)						94.4	94.4
		ML (IQ-TREE)	Ref-IQ4	9232	14,586,607	334,525,406 (71.7%)	3,832,278 (26.3%)	1,465,372 (10%)						94.4	94.4
		Supertree (ASTRAL-III)	Ref-AS4	9232	Me = 1,173	Me = 5,877.5 (42.9%)	Me = 314 (27.7%)	Me = 100 (9.6%)						94.4	94.4
	UPhO	ML (IQ-TREE)	Uph-IQ16	347	245,095	2,812,587 (35.9%)	43,022 (17.6%)	20,211 (8.2%)	30 to 50			0,001122014	0,0026	88.8	88.8
		Supertree (ASTRAL-III)	Uph-AS16	345	Me = 618	Me = 0 (0%)	Me = 88 (14.3%)	Me = 41 (6.7%)						NA (84.2)	NA(78.9)
		ML (IQ-TREE)	Uph-IQ4	7313	6,681,038	170,796,960 (79.9%)	1,165,551 (17.4%)	368,737 (5.5%)						88.8	88.8
		Supertree (ASTRAL-III)	Uph-AS4	7058	Me = 645	Me = 2 (0%)	Me = 82 (11.6%)	Me = 16 (2.2%)				0,000041161	0,000097	NA (73.7)	NA (73.7)



Assembled
transcriptome
contigs

REFERENCE-BASED PIPELINE

GRAPH-BASED PIPELINE

BLAST
Ref. genome
P. canaliculata

BLAST
Ref. mitoch. & nucl. mark.
Pinguicemula, GenBank

ORF EXTRACTION
AND FILTERING
Python

MAPPING + FILTERING
Bowtie 2, Samtools,
Bcftools, Picard, Python

Transcriptome
reads

UPhO PIPELINE
Ballesteros & Hormiga, 2016

MULTIPLE SEQUENCE
ALIGNMENT + FILTERING
Mafft, Python

Graph-based
orthologs

Reference-based
orthologs

Mitochondrial &
nuclear markers

TAXON FILTERING
min. 4-16 samples / locus

TAXON FILTERING
min. 4-16-32 samples / locus

BC
cox1 barcode fragment

SAN
mitoch. + nucl. markers

MT
mitoch. genomes

UPh-IQ4 | **UPh-AS4**
Supermatrix | Supertree
IQ-Tree | Astral-III

UPh-IQ16 | **UPh-AS16**
Supermatrix | Supertree
IQ-Tree | Astral-III

Cap-IQ4 | **Cap-AS4**
Supermatrix | Supertree
IQ-Tree | Astral-III

Cap-IQ16 | **Cap-AS16**
Supermatrix | Supertree
IQ-Tree | Astral-III

Ref-IQ4 | **Ref-AS4**
Supermatrix | Supertree
IQ-Tree | Astral-III

Ref-IQ16 | **Ref-AS16**
Supermatrix | Supertree
IQ-Tree | Astral-III

Ref-IQ32 | **Ref-AS32**
Supermatrix | Supertree
IQ-Tree | Astral-III

LOCUS FILTERING
3,000 short loci
(96-839 nt)

Cap-IQ32 | **Cap-AS32**
Supermatrix | Supertree
IQ-Tree | Astral-III

