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► **To cite this version:**

Arnaud Meng, Camille Marchet, Erwan Corre, Pierre Peterlongo, Adriana A. Alberti, et al.. A de novo approach to disentangle partner identity and function in holobiont systems. 2017. hal-01643153v1

HAL Id: hal-01643153

<https://hal.science/hal-01643153v1>

Preprint submitted on 21 Nov 2017 (v1), last revised 13 Sep 2018 (v2)

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A *de novo* approach to disentangle partner identity and function in holobiont systems

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Abstract

Background

Study of meta-transcriptomic datasets involving non-model organisms represents bioinformatic challenges. The production of chimeric sequences and our inability to distinguish the taxonomic origins of the sequences produced are inherent and recurrent difficulties in *de novo* assembly analyses. The study of holobiont transcriptomes shares similarities with meta-transcriptomic, and hence, is also affected by challenges invoked above. Here we propose an innovative approach to tackle such difficulties which was applied to the study of marine holobiont models as a proof of concept.

Results

We considered three holobionts models, of which two transcriptomes were previously assembled and published, and a yet unpublished transcriptome, to analyze their raw reads and assign them to the host and/or to the symbiont(s) using Short Read Connector, a k-mer based similarity method. We were able to define four distinct categories of reads for each holobiont transcriptome: host reads, symbiont reads, shared reads and unassigned reads. The result of the independent assemblies for each category within a transcriptome led to a significant diminution of *de novo* assembled chimeras compared to classical assembly methods. Combining independent functional and taxonomic annotations of each partner's transcriptome is particularly convenient to explore the functional diversity of an holobiont. Finally, our strategy allowed to propose new functional annotations for two well-studied holobionts and a first transcriptome from a planktonic Radiolaria-Dinophyta system forming widespread symbiotic association for which our knowledge is limited.

Conclusions

In contrast to classical assembly approaches, our bioinformatic strategy not only allows biologists to studying separately host and symbiont data from a holobiont mixture, but also generates improved transcriptome assemblies. The use of Short Read Connector has proven to be an effective way to tackle meta-transcriptomic challenges to study holobiont systems composed of either well-studied or poorly characterized symbiotic lineages such as the newly sequenced marine plankton Radiolaria-Dinophyta symbiosis and ultimately expand our knowledge about these marine symbiotic associations.

Keywords

holobiont; transcriptomic; *de novo* assembly; marine; plankton; k-mer based similarity

Background

1 In its scientific acceptance, symbiosis is defined as the living together of unlike organisms
2 whatever the nature of their relationship [1], ranging from parasitism to mutualism. Symbiosis is a
3 widespread phenomenon in the biosphere and plays crucial roles in evolution and ecology. One of
4 the most popular examples of mutualism is the interaction between fungi and land plants, where
5 fungi form mycorrhizae that help land plants to retrieve nutrients from soil [2]. In the ocean, benthic
6 coastal ecosystems are structured and supported by symbiotic associations involving
7 multipartners such as corals (Cnidaria, i.e. multicellular eukaryotes), microalgae (Dinophyceae,
8 *Symbiodinium* spp., i.e. unicellular eukaryotes), and Bacteria. Breakdown of this symbiosis
9 ultimately leads to coral bleaching (the loss of photosynthetic symbionts), dramatically affecting
10 the whole reef ecosystems [3]. While coral bleaching has been largely studied, there is a growing
11 evidence that other partners are involved in the holobiont system, and contribute to make coral
12 reef persisting in oligotrophic seas. For instance, symbiotic association between sponges
13 (Porifera, i.e. multicellular eukaryotes) and Bacteria (prokaryotes) allows Bacteria to grow within
14 the mesohyl matrix of the sponge where they can be metabolically active and persist in a highly
15 oligotrophic habitat. The symbiotic interactions between sponges and bacteria are currently poorly
16 understood from the genomic point of view [4]. Symbiotic associations involving two unicellular
17 eukaryotes are also widespread in the oceanic plankton [5–7,9]. For instance, the cosmopolitan
18 mutualistic associations between heterotroph Radiolaria (host) and endosymbiotic microalgae play
19 significant ecological and biogeochemical roles in the oceans [8] but the underlying genomic basis
20 of such associations remains uncharacterized. Although not cultivable *in vitro*, nucleic acids
21 extraction is nevertheless possible on such symbiotic partnerships, and this recently allowed
22 shedding light on the identity of the partners and their co-evolutionary history [6, 7]. Several
23 symbiotic microalgae have been identified using such molecular approaches, and many of them
24 belong to the eukaryote Dinophyta [9]. Mainly because of their highly complex and large genomes,
25 the lack of reference genomes for both Dinophyta and Radiolaria make their study challenging for
26 *de novo* assembly and functional annotation [10, 11]. The study of the RNA mixture from a

27 holobiont system, being composed of the host and its symbiotic microbial communities offers the
28 opportunity to characterized functional aspects through their expressed genes, and so in different
29 abiotic conditions/decoupling the functional/metabolic role of each partner.

30 Currently, RNA-seq approaches are the best available tools to obtain large amount of genomic
31 information from uncultured organisms isolated in the environment [12, 13]. RNA sequencing for a
32 holobiont is now possible [14–16] and has promoted the development of sequencing projects [17]
33 for non-model organisms. Non-model holobiont RNA-seq datasets corresponds to a mixture of
34 data coming simultaneously from the host and from the symbiont(s). Studying such datasets share
35 similarities with meta-transcriptomics and requires *de novo* assembly of transcripts sequences,
36 which implies large computational resources and has the potential to introduce biases such as
37 generating numerous chimeric sequences resulting from the mis-assembly of RNA fragments from
38 the host and from the symbiont(s) [18, 19]. A variety of analysis strategies has been developed to
39 address meta-transcriptomic challenges. Some of these strategies avoid the assembly step to
40 focus on identifying abundant species and significant functional differences between meta-
41 transcriptomes directly from raw data [20, 21]. Other strategies use statistical tools and machine
42 learning algorithms to improve the quality of *de novo* assembly of meta-transcriptome by learning
43 from their abundance information [22].

44 Here we developed an original strategy aiming at improving *de novo* assembly for newly
45 generated holobiont sequence dataset. We chose to use the Short Read Connector software in its
46 Counter version (SRC_c) [23]. SRC_c is a fast kmer-based method initially developed to estimate
47 the similarity between numerous (meta)genomic datasets by extracting their common sequences.
48 We focused on holobiont transcriptomes for which *a priori* no or little genomic knowledge has been
49 previously produced for host and symbionts, and we used SRC_c to compare these holobiont
50 sequences to publicly available databases. Our strategy is to use SRC_c to assign at best
51 holobiont sequences either to the host or to the symbionts before the *de novo* assembly step (Fig.

52 1). It allows then independent assembly of the datasets and prevents the potential mis-assemblies
53 of reads from diverse origin.

54 We applied our strategy to disentangle the sequences and then *de novo* assemble the
55 transcriptome of three distinct marine holobiont systems (Fig 2). Two of them were already
56 assembled and published. The first model (M1) involves a Cnidaria host (*Orbicella faveolata*,
57 belonging to the Metazoa) and Dinophyta symbionts (*Symbiodinium* spp., a unicellular eukaryote
58 belonging to the Alveolata) forming a mutualistic association [24, 25]. This symbiotic association
59 represents the best-known example of symbiosis in marine ecosystems, and many studies have
60 been made trying to understand coral bleaching events (*i.e.* the loss of symbionts) [26, 27]. The
61 coral holobiont also encompass other microorganisms consisting of bacteria, archaea, fungi,
62 viruses [28, 29]. In the second holobiont model (M2) the marine sponge *Xestospongia muta*
63 (Porifera) harbors a dense (~40% of its volume) and diverse microbial community including marine
64 protists (*e.g.* fungi), archaea and mainly bacteria [30–32]. The symbiotic associations between
65 sponges and bacteria (suggested to be commensalism [33]) have become a major research focus
66 to understand how sponges and their microbial communities can perform a variety of functional
67 roles such as nutrition, cycling of metabolites and host defense allowing them to proliferate in
68 oligotrophic conditions [34, 35]. We chose a third, yet unpublished, holobiont dataset (M3)
69 involving two distinct lineages of protists (unicellular eukaryotes): the radiolarian *Collozoum* sp. as
70 host and Dinophyta symbionts belonging to the *Brandtodinium nutricula* species [6]). In this
71 association, the radiolarian host forms a gelatinous matrix of several centimeters, which contains
72 hundreds of host cells and thousands of symbiotic microalgae (refer to image). Recent studies
73 showed that this symbiosis is widely distributed in the ocean and significantly contribute to
74 biomass and carbon export in the open ocean [36, 37]. As a proof of concept, we these holobiont
75 transcriptomes datasets, and we compared quantitatively and qualitatively results obtained when
76 involving SRC_c or not.

Figure 1 Theoretical overview on the application of SRC_c on holobiont transcriptome. The comparisons to (1) host and (2) symbiont reads/sequences library are done against the entire holobiont dataset to retrieve host and symbiont similar reads. The 4 resulting subsets (host, symbiont, shared and unassigned reads) are then processed independently (de novo assembly and downstream analyses)

Results

Choice of holobiont models and building of host and symbiont reference libraries

77 For each of the three holobiont models (Fig. 2), we built reference sequences libraries
78 representing host and symbiont(s) by selecting the taxonomically closest organisms available in
79 public datasets (see Methods, Additional files 1). The M1 host reference library encompasses 22
80 assembled transcriptomes from Cnidaria (including data from the host species *Orbicella faveolata*
81 itself) and the M1 symbiont reference library encompasses 123 RNA-seq reads datasets (including
82 the presumed major symbiont *Symbiodinium* spp. [38]). The M2 host reference library involves 4
83 RNA-seq reads datasets from distinct Porifera genera (and differ from the *Xestospongia* genus)
84 whereas the M2 symbiont reference library corresponds to the *Tara Oceans* metagenomic gene
85 catalogue (OM-RGC) assembled from the pico-planktonic fractions (< 3 µm) including bacteria or
86 Archaea [39]. For M3, we used the four Rhizaria transcriptomes published so far to create the
87 reference host library whereas the same library as for M2 has been used for symbiont references.
88 All reference libraries described above include assembled transcriptomes, genomes or RNA-seq
89 raw reads datasets for eukaryotic or prokaryotic holobiont partners (Additional files 1). Their sizes
90 vary from 4.5 Mbp to 25 Gbp with sequences length from 100 bp to 84 Kbp (Additional files 1).

Figure 2 Pictures of the 3 holobiont models. (A) the *Orbicella faveolata* holobiont in symbiosis (unbleached) in 2010 at reefs of La Parguera, Puerto Rico (credits: [24]). (B) A *Xestospongia muta* specimen in symbiosis on a coral reef near Little Cayman in the Caribbean (credits: Cara Fiore, january 14, 2015 <http://feedthedatamonster.com>). (C) A Collodaria colony with symbionts sampled in South Pacific Ocean at station 112.01 of the *Tara Pacific* expedition in 2011 (credits: Johan Decelle).

Disentangling the holobiont sequences

91 Disentangling the holobiont sequences for all three models (M1, M2 and M3), the SRC_c memory
92 footprint was far lower than our cluster's capacity (Tab. 1), even for the biggest data set to index
93 (M2 symbiont library of 25 Gbp has been built with 58.9G of RAM). This induces that any addition
94 of data can be considered.

Table 1 Performances of SRC_c

		Time(hh:mm:ss)	Memory (Gb)
Cnidaria-Dinophyta holobiont (M1)	all symbionts library (M1a)	15:40:42	34,2
	<i>Symbiodinium</i> spp. library (M1b)	01:34:57	6,96
	other symbionts library (M1c)	15:08:45	33,7
	host library	01:06:56	3,9
Porifera-Bacteria holobiont (M2)	symbionts library	21:04:47	58,9
	host library	02:46:06	9,60
Radiolaria-Dinophyta holobiont (M3)	symbionts library	07:05:28	4,10
	host library	00:05:57	3,9

Memory peak and wallclock time of SRC_c indexing and query steps on the several data sets for models M1, M2 and M3.

95 The comparison of holobiont reads to reference host and symbiont sequence libraries enabled to
96 identify and classify them into four categories (Fig. 1): (1) reads specific to the host, (2) reads
97 specific to the symbionts (including microalgae, bacteria...), (3) reads which can be assigned to
98 both reference libraries and (4) reads which do not match any reference library (referred as to
99 'unassigned'). For the three holobiont models, the distribution within the four categories is reported
100 in Tab. 2.

101 With M1, SRC_c assigned 64.3% of the holobiont reads to the cnidarian host and 7.2% to the
102 Dinophyta symbiont full library (analysis M1a, Tab. 2). Restricting the symbiont library to the genus
103 *Symbiodinium* spp. sequences allowed obtaining similar results with 64.5% of the reads identified
104 as specific to the host library and 7.1% as specific to the symbiont library (analysis M1b, Tab. 2).
105 On the contrary, when *Symbiodinium* spp. is removed from the library, only 0.6% of the holobiont
106 reads could be assigned to the symbionts and the proportion of reads assigned to the host
107 increases up to 67.3% (analysis M1c, Tab. 2). Our tests on the symbionts library showed that the

108 library content impacted drastically the reads retrieval by SRC_c and demonstrated the sensitivity
 109 of the strategy. Considering these results, we focused on the M1a dataset for downstream
 110 analyses. We also noticed that shared reads (i.e. found in both host and symbiont libraries) always
 111 represent the lowest proportion of holobiont reads (M1a, M2 and M3).

Table 2 SRC_c assignment results for the holobiont models M1, M2 and M3

		# reads	% reads from holobiont
<i>Orbicella faveolata</i> holobiont (M1a)	total	775 025 024	
	assigned to host library	498 008 661	64.26%
	assigned to symbiont library	56 011 798	7.23%
	shared	32 133 818	4.15%
	unassigned	188 870 747	24.37%
<i>Orbicella faveolata</i> holobiont (M1b)	assigned to host library	500 145 229	64.53%
	assigned to symbiont library	54 850 148	7.08%
	shared	29 997 250	3.87%
	unassigned	190 032 397	24.52%
<i>Orbicella faveolata</i> holobiont (M1c)	assigned to host library	521 591 231	67.30%
	assigned to symbiont library	4 817 450	0.62%
	shared	8 551 248	1.10%
	unassigned	240 065 095	30.98%
<i>Xestospongia muta</i> holobiont (M2)	total	33 220 038	
	assigned to host library	6 193 678	19.04%
	assigned to symbiont library	825 154	10.64%
	shared	5 112 031	8.63%
	unassigned	21 090 174	61.69%
<i>Collozoum</i> sp. holobiont (M3)	total	97 957 794	
	assigned to host library	3 188 944	3.26%
	assigned to symbiont library	23 234 402	23.72%
	shared	531 432	0.54%
	unassigned	71 003 016	72.48%

SRC_c assignment results for the Cnidaria-Dinophyta holobiont model (M1) against the complete Dinophyta library (M1a), the *Symbiodinium* spp. exclusive library (M1b) and the Dinophyta library excluding *Symbiodinium* spp. (M1c), the Porifera-Bacteria holobiont model (M2) and the Radiolaria-Dinophyta holobiont model (M3).

De novo assembly, contigs evaluation and downstream analyses for M1 and M2

112 For each holobiont transcriptome, four subsets of reads were independently *de novo* assembled,
113 producing contigs from which protein domains were then predicted and functionally annotated
114 (Fig. 1). For holobiont models M1a and M2, the assembly metrics, statistics and functional
115 annotations from our contigs are summarized in Tab. 3, and comparison with previous studies are
116 shown in Fig. 3.

117 Compared to the studies where these datasets were initially published, our strategy allows
118 considering more reads (16,818,599 reads for M2) in the assembly step as well as obtaining more
119 assembled contigs (136,039 contigs for M1a and 78,567 contigs for M2) (Fig. 3). The contigs
120 metrics show shorter lengths of N50 (580 bp shorter for M1a and 219 bp shorter for M2) (Fig. 3)
121 compared to the original publication analyses. The M1a contigs display high remapping rates
122 (>80%) while M2 contigs show mixed results (25% < x < 86%) (Tab. 3). With M1a, a total of
123 255,223 protein coding domains were predicted for 44.1% of the assembled contigs and functional
124 annotations were found for nearly 30% of these protein coding domains (Tab. 3). With M2, protein
125 coding domains were predicted for 39.6% of the contigs, and 54.9% of the domains were
126 functionally annotated (Tab. 3). In comparison with statistics available in previous studies, we
127 obtained 1.6 times more functionally annotated contigs for M1a (Fig. 3). This comparison for M2
128 could not be made since the exact number of annotated contigs in the holobiont assembly has not
129 been reported by the authors.

Figure 3 Overview and comparison to previous studies. The total assembled contigs for holobiont model M1a and M2 compared to the assembled meta-transcriptomes from (A) Pinzon et al. 2015 [24] and (B) Fiore et al. 2015 [30] respectively are shown. General details about *de novo* assembly and functional annotation (termed FA) features are presented in corresponding tables for (A) holobiont model M1a versus Pinzon et al. 2015 [24] meta-transcriptome, and (B) holobiont model M2 versus Fiore et al. 2015 [30]. NC means that exact number is not communicated.

130 To further test the usefulness of the reads sorting before the *de novo* assembly step, we
131 compared the contigs assignment of M1a and M2 (column 1 in Tab. 3) with a taxonomic

132 assignment performed with MEGAN6 [40]. For M1a, MEGAN6 assigned 71,143 contigs to the host
133 *Orbicella faveolata* and 148,409 contigs to the symbiont *Symbiodinium* spp. (Additional files 2). All
134 the contigs assigned to *Orbicella faveolata* with MEGAN6 were also found with the SRC_c
135 strategy (Tab. 3) but we assigned 19,415 more contigs to the host category. On the contrary,
136 MEGAN6 assigned 21,197 additional contigs to *Symbiodinium* spp. compared to our
137 categorization strategy (Tab. 3, Additional files 2). With M2, MEGAN6 assigned 11 contigs to the
138 host *Xestospongia muta* (Additional files 2) which is far less than the 2,654 contigs defined with
139 the SRC_c strategy (Tab. 3). However, MEGAN6 assigned also 33,810 contigs to *Amphimedon*
140 *queenslandica*, a distinct sponge species which is not supposed to be the host in this holobiont
141 system. MEGAN6 also succeeded to assign more contigs to Bacteria (21,318 contigs) than the
142 SRC_c strategy (2,431 contigs) (Tab. 3).

143 Our functional annotations were compared to initial studies having generated these datasets. As
144 previous publications do not provide exhaustive lists of the functional annotations and their
145 corresponding abundance, these comparisons are essentially qualitative. For the *O. faveolata* host
146 (M1), we only found similarities in the most abundant annotations (Additional file 3). At biological
147 processes level, both our study and Pinzón et al. 2015 found abundant metabolic process GO
148 term (GO:0008152; 819 CDs (coding sequences) and 5,278 genes respectively). At the molecular
149 function level, our host contigs mainly corresponded to binding protein (GO:0005515; 36,349 CDs)
150 while Pinzón et al. 2015 mainly found catalytic activity functions (GO:0003824; 3,361 genes). For
151 M2, rare overlaps are found between Fiore et al. 2015 and our annotations (Additional file 3): at
152 the biological processes level, 1 of the top 15 host annotations is identical (signal transduction
153 (GO:0007165)) and 3 of the top 15 symbiont annotations are in common (metabolic process
154 (GO:0008152); proton transport (GO:0015992) and protein folding (GO:0006457)).

Table 3 *De novo* assembly metrics and downstream analysis of SRC_c resulting subsets for holobiont models M1a, M2 and M3. (upload as additional files)

Benchmark comparisons on M3: what difference does it make to use SRC_c?

155 For the holobiont model M3, assembly metrics, abundance of chimera and functional contents
156 were compared between the SRC_c contig sets (host, symbiont, shared and unassigned) and a
157 direct *de novo* assembled transcriptome obtained from holobiont reads considered all together
158 (this strategy is hereafter called *noSRC*).

159 The assembly metrics appear very similar between SRC and noSCR (Tab. 4). A comparable
160 number of reads were used for the assembly step and a comparable number of assembled contigs
161 were obtained. The N50 value for the *noSRC* strategy is slightly longer while the remapping rates
162 are 5% better with the SRC strategy. Calculation times performed on the same bioinformatic
163 cluster revealed that the SRC strategy was 40 hours longer. The SRC strategy showed 50% less
164 chimeras (418 contigs) than the *noSRC* strategy (777 contigs) with most chimeras contained in the
165 unassigned set (Tab. 4). We noticed slightly less annotated CDs with the SRC strategy (45,768
166 against 47,260), however the number and the composition in GO annotations were very similar
167 (Fig 1 from Additional files 4). We found 253 different biological processes with SRC against 255
168 with the *noSRC* strategy, and the top 5 functional annotations in the 3 Gene Ontology levels
169 (Molecular Function, Biological Process and Cellular Component) are strictly identical (Fig 2 from
170 Additional files 4). Considering all GO annotations, 686 are common to both strategies while 52
171 are exclusive to the SRC strategy and 42 to the *noSRC* strategy (Fig 3 from Additional files 4).

172 To test the usefulness of the categorization step, all M3 contigs from the SRC strategy were
173 taxonomically assigned using MEGAN6 (Additional files 5). MEGAN6 assigned 10 contigs to
174 Collodaria whereas the SRC strategy assigned 683 contigs to the host category. MEGAN6
175 assigned 1,383 contigs to Dinophyceae compared to the 5,207 contigs categorized as symbionts.
176 The leftover MEGAN6 contigs were assigned to Bacteria and Archeae (3,799 contigs), Viruses (76
177 contigs), other-eukaryotes (29,524 contigs) and 127,447 contigs remained unassigned (162,947
178 unassigned contigs with the categorization strategy).

Table 4 SRC_c impact on Radiolaria-Dinophyta holobiont model (M3)

		no SRC	SRC
# reads used in assembly		48 733 956	48 660 697
# assembled contigs		167 023	168 899
# predicted cds		75 450	74 017
# annotated cds		47 260	45 768
N50 (bp)	total	818	702
	host		277
	symbiont		324
	shared		298
	unassigned		714
remapping rates (%)	total	85,6	90,5
	host		65,2
	symbiont		76,2
	shared		81,3
	unassigned		89,7
# chimera	total	777	418
	host		4
	symbiont		47
	shared		0
	unassigned		367
Calculation time (min)	total	330	2 783
	SRC		2 460
	assembly	330	323

SRC_c impact on assembled contigs quality and calculation times of Radiolaria-Dinophyta holobiont model (M3) compared to a direct meta-transcriptome assembly strategy. In grey are displayed the details for SRC_c holobiont categories (host, symbiont, shared and unassigned). The “total” values for N50 and remapping rates of the SRC_c strategy were re-calculated on pooled contigs from host, symbiont, shared and unassigned subsets.

Discussion

The use of SRC_c to tackle meta-transcriptomic challenges

179 The strategy proposed here is a practical and scalable solution for transcriptomic assembly of non-
 180 model holobiont organisms, from which no or limited genomic information is available. The present
 181 implementation of SRC_c [23] based on reference databases of putative partners involved in the
 182 holobiont consortium, and our analysis strategy, enabled the categorization of holobiont reads into

183 4 subsets. Then, these subsets have been independently assembled, limiting potential creation of
184 chimeras while generating more assembled contigs (Fig. 1). The newly defined shared reads
185 category represents an added value compared to other holobiont transcriptomic studies and has
186 been later processed with the same methodology than other categories (Fig. 1).

187 With respect to the reference libraries, as exemplified in M1, when the expected symbiotic partner
188 (i.e. *Symbiodinium* spp.) is missing from the reference library, the number of reads assigned to the
189 symbiont category decreases drastically from 50M reads to nearly 5M reads (Tab. 2). The M2 and
190 M3 libraries do not contain reference data for the expected host partner, and consequently only a
191 low proportion of the holobiont reads are assigned to the host (19% and 3%, respectively).
192 Accordingly, the proportion of unassigned reads is directly linked to both host and symbiont
193 libraries content with respect to the studied holobiont. Overall, less unassigned reads were
194 observed when the “correct” actors are involved (M1a: 24.4%) compared to the poorly studied
195 models (M2: 61.6% and M3: 72.5%). These results highlight the sensitivity and specificity of the
196 SRC_c requests that relies on the completeness of the database to accurately sort the reads of
197 the holobiont. The SRC_c assignation step could be further improved by adding more sequences
198 (i.e. reads, assembled genes or transcripts) from taxonomically close species to the host and
199 symbiont reference libraries, but also from parasites and viruses that are common in multicellular
200 and unicellular host cells.

201 We also compared the metrics of our SRC_c contigs to those from previous studies (M1a and M2)
202 [24, 30]. With the SRC_c strategy, the amount of reads used for *de novo* assembly of M2 was
203 higher than for previous studies (Fig. 3). We found that, not only our strategy allowed defining a
204 new category of contigs (the “shared” contigs), but also allowed assembling more contigs than
205 previous studies (Fig. 3). Our contigs metrics showed lower N50 for both models compared to
206 previous studies, but showed higher remapping rates overall for M1a (up to 90%, (Tab. 3)).
207 Differences in the number of contigs as well as contigs metrics could be the results of the use of

208 distinct *de novo* assembly software: e.g. M2 data were processed with the CLC workbench [CLC
209 bio, Boston, MA, USA; (<https://www.qiagenbioinformatics.com/>)] in the original publication while we
210 choose the Trinity software [41] otherwise we suggest that SRC_c do not significantly impact
211 transcriptome assembly. In fact, previous studies had shown that Trinity is able to generate more
212 assembled contigs than the CLC assembler when applied on the same dataset. It is also known
213 that assembled contigs from Trinity are shorter than those assembled by CLC but provided similar
214 proportion of significant hits to the nr database [42].

215 With M1a, our strategy produced 1.5 times more CDs with a functional annotation (Fig. 3). At that
216 point we are unable to tell whether this observation can be the consequence of a better suited
217 assembly strategy (SRC_c treatment and / or assembly software), and / or the use of a different
218 annotation pipeline, and / or the supplementation of reference annotation databases between 2015
219 [24] and 2017.

220 With M3 analyses we can estimate how SRC_c impacts the *de novo* assembly step and
221 downstream analyses compared to a more conventional protocol (here called the *noSRC* strategy)
222 (Tab. 4). The calculation time for the two protocols showed that the SRC_c strategy increases the
223 total time with nearly 40 additional hours compared to a classic assembly strategy (Tab. 4).
224 However, compared to classic strategies, the SRC_c strategy has the tremendous benefit to create
225 directly 4 independent subsets (two of which are directly assigned to holobionts partners).
226 Otherwise, minimal differences were found between the two protocols concerning the number of
227 assembled contigs and, as for M1a and M2, the SRC_c strategy produces shorter contigs
228 sequences with higher remapping rates but a significant diminution of the number of potential
229 chimeras was observed. We conclude that the read assignment performed before the assembly
230 step largely contributes to limit the production of chimeras. This shows that the use of SRC_c
231 impacts the *de novo* assembled transcriptome quality and contributes to address one of the most
232 delicate *de novo* assembly challenge [43]. The MEGAN6 contigs assignment from M2 shows more
233 contigs than SRC_c could assign to host and symbiont (Tab. 3 and Additional files 2). In contrast,

234 MEGAN6 assigned less contigs to host and symbiont than SRC_c for the M3. We suggest that
235 SRC_c performs well in non-model organisms context with libraries containing taxonomically close
236 organisms reference sequences.

SRC_c helps us to make new biological assumptions

237 For all models, the SRC_c strategy led to a higher number of annotated contigs, however as only
238 partial information on the annotation content were provided separately for the host or the
239 symbionts in previous publications [24, 30], we were mainly restricted to qualitative comparisons.

240 Comparing the M1a host transcriptomes to the previous study transcriptome, very few similarities
241 were found for the most occurring functions, even if the most annotated function is common (i.e.
242 metabolic process GO). Our 20 most occurring functions include signal transduction functions
243 (14% of the total annotations) and molecule transport functions (8% of the total annotations) that
244 do not appear in the most occurring function from [24]. These newly highlighted functions could
245 help better understanding the *Orbicella faveolata* host with respect to communication and cellular
246 exchanges with its partners. We were not able to perform a similar analysis for the symbiont
247 transcriptome since authors of previous studies focused on the host transcriptome. For M2, only
248 1/15 and 3/15 common annotations were found for host and symbiont respectively. We suggest
249 that the divergences in the analytical pipeline used, here Trinity versus CLC for *de novo* assembly
250 followed by InterProScan versus FastAnnotator for functional annotation, make the functional
251 annotations contents hardly comparable between studies. Despite these discrepancies, results
252 from both analyses must be considered as potentially valuable and have to be checked with
253 genome alignment when available or through *in vitro* validation when considering restricted group
254 of functions (e.g. PCR).

255 Symbioses involving single cell heterotrophic hosts and photosynthetic symbionts have been
256 described in the oceanic plankton using morphological and molecular data [5–7, 15]. Radiolarians
257 and their symbiotic microalgae (e.g. Haptophytes, Dinoflagellates) have an ecological and

258 biogeochemical significance [44–47], but little is known about symbiosis establishment and
259 maintenance. If most microalgal symbionts can be grown in the laboratory as free-living stage
260 [Meng et al. *submitted*], the study of radiolarian host only relies on single-cell isolation from the
261 field [36, 48]. In this study, the radiolarian host belongs to the Collodaria order which is ubiquitous
262 and abundant in the open ocean [36, 49]. Our knowledge about their ecology and evolution is
263 limited and hence our analyses represent an opportunity to learn more about the genetic repertoire
264 of such uncultivable, non-model lineage. Regarding functional annotations, the SRC and the
265 *noSRC* strategies provided very similar results but the SRC strategy categorized the GO
266 annotations among 4 subsets (host, symbiont, shared and unassigned) (Additional files 5), which
267 can be explored independently, allowing group specific interpretations and biological hypothesis
268 building for each partner from the holobiont. For instance, symbiont CDs linked to the photosystem
269 I and II were detected, confirming that SRC_c succeeded to assign reads to photosynthetic actors,
270 as expected here for the symbiotic partner (Additional files 4).

Strategies regarding the use of SRC_c and future perspectives

271 SRC_c successfully compared different holobiont read sets to large reference libraries in less than
272 24h, with reasonable computational resources (*i.e.* 10 CPUs and less than 20Go of RAM). By
273 setting parameters (*i.e.* solidity threshold, k-mer size, similarity threshold), we adapted SRC_c to
274 heterogeneous nature of sequences in libraries (*i.e.* length, raw reads or assembled
275 genes/transcripts, data volume, k-mers distribution) and to poorly studied systems. When studying
276 meta-transcriptome reads, selecting abundant k-mers helps to remove the one corresponding
277 potentially to sequencing errors; however rare sequence k-mers are consequently lost. On the
278 contrary, when indexing already assembled sequences from genomes or transcriptomes, we do
279 not expect a redundancy of the k-mers such as in high-throughput sequencing experiments, and
280 we thus assume that any k-mer is relevant when it comes from a reference sequence.
281 Accordingly, in this study, we kept the default k-mer solidity threshold value that was appropriate

282 when indexing reads (*i.e.* sequences shorter than 300 bp, with a relatively high coverage), and
283 lowered it to 1 when indexing longer sequences as ESTs or assembled genes. Due to the
284 presence of small reads (50 bp) in our holobiont datasets, we also modified the default k-mer size
285 value of 31 to a value of 25, so that any read contains at least a few k-mers. Usually the k-mer
286 size is higher [50], however 25 base pairs corresponds to a decent value to ensure the uniqueness
287 of the read [51]. During the query phase of SRC_c, a query sequence (from a dataset Q) must
288 contain at least $s\%$ positions covered by at least one indexed k-mers (from a dataset B), to be
289 considered similar to data from the set B [23]. As the s default value is set to 50%, it means that a
290 read of size l should have at least $l \times s$ positions covered by (overlapping or nonoverlapping)
291 indexed k-mers. Consequently, when a large majority of the reads could not be assigned, our
292 strategy was to decrease the s parameter from 50 to 40 in order to increase the quantity of
293 recalled reads. SRC_c implements a heuristic computing a k-mer based similarity. Contrary to
294 BLAST-like methods, SRC_c relies uniquely on shared k-mers for its similarity computation. It
295 means that a certain amount of error-free k-mers (*i.e.* k-mers that do not contain sequencing
296 errors) must be found in common in order to output sequences, which can make SRC_c less
297 sensitive compared to alignment methods which authorize mismatches. However contrary to
298 alignment methods, SRC_c was tailored to scale to very high-volume datasets and comparisons
299 presented in [23] showed that SRC_c could handle sets of orders of magnitudes higher volumes
300 than BLAST (Additional files 7). SRC_c's efficiency relies on its particular probabilistic data
301 structure. The lightweight indexing and query of k-mers is made at the price of rare false positives.
302 In our case, false positives correspond to k-mers that are not contained in the original indexed
303 library. Such a false positive rate is controlled and low (Additional files 7). As in this work, the k-
304 mer size was relatively low (*i.e.* 25), the default value for this parameter was kept ensuring a low
305 false positives rate. For longer k-mers (*i.e.* size > 31), we recommend to increase the size of the
306 fingerprint if more precision is needed. SRC_c can also be used in a no-false positive mode that
307 requires more memory, but that is still less costly than a hash table as demonstrated in [23].

308 In our tests, SRC_c helps to retrieve holobiont reads similar to host or symbiont close species.
309 Previous tools like COMMET [50] already proposed such computation, although their data
310 structure makes difficult the use of k-mers of small size, as computation time would be drastically
311 impacted. SRC_c was chosen for its simple output and its adaptability to the heterogeneous
312 nature of the libraries studied. This is simply made by adapting the k-mer lowest occurrence and
313 size parameters.

314 Future works on SRC_c parameters settings could include more extensive exploration of the
315 impact of the similarity threshold parameter on the sensitivity of our approach. In this regard, if the
316 reads similarity rate to the libraries could be relaxed, it may decrease the number of unassigned
317 reads in particular for poorly studied models. A second strategy would be to implement an iterative
318 enriching strategy to maximize the proportion of holobiont reads assigned to the host or to the
319 symbiont. This strategy can allow to assign more sequences in the case of non-model organisms.

320 After a first assignment round with SRC_c, holobiont reads linked to an identified group
321 (host/symbiont) can be added to the reference libraries. Then, based on these new enriched
322 libraries, a second run of SRC_c can be performed on the holobiont reads. This can be
323 implemented as an iterative pipeline: at each round, more reads will be assigned to the host or
324 symbiont categories and will then be used as reference libraries. Finally, the approach proposed
325 here has been applied to holobiont systems (between 2 partners) but it could be used to address
326 larger metatranscriptomic datasets composed of more complex assemblages. Depending on the
327 SRC_c library content, the user can choose to target either one or more specific species among
328 the variety that composed such metatranscriptomic datasets. Coupled to our assembly and
329 downstream analysis strategy, the subsets resulting of the used of SRC_c are processed *de novo*
330 allowing the potential discovery of newly assembled transcripts and the exploration of the
331 functional their functional feature contents without reference genome.

Conclusions

332 SRC_c successfully processed a variety of large-scale datasets and offered a pragmatic way to
333 classify sequences from different holobiont partners before assembly. We showed that our strategy
334 allows improving assembly metrics, and also helped to reduce drastically the proportion of
335 chimeras in the newly *de novo* assembled sequences. Our approach offers an efficient, large
336 scale, comparison strategy to assemble and study holobionts involving non-model organisms.
337 Overall, this *de novo* approach, allowing a taxonomic categorization of functionalities, can reveal
338 the link between identity and function, which is necessary to better understand the functioning and
339 contribution of each partner in holobiont systems.

Methods

Radiolaria-Dinophyta holobiont model (M3) sampling, RNA-seq library and sequencing

340 The Collodaria colony was sampled in the South Pacific Ocean at the station 112.01 (coordinates
341 in decimal degrees: latitude -23.3, longitude -133.9) during the *Tara* Oceans expedition in 2011
342 [52]. The radiolarian colony of few centimeters diameter was collected *in situ* at the subsurface
343 (1m deep) with a plastic jar, preventing disruption of the colony and aggregation of other
344 planktonic organisms. Live observations through the binocular were performed to verify that no
345 organisms were accidentally attached to the colony before preservation. The collected colony was
346 directly isolated in 15 mL of RNeasy (ThermoFisher Scientific, Waltham, MA) and preserved at -
347 20°C. Total RNA extraction was performed using NucleoSpin RNA kit (Macherey-Nagel, Düren,
348 Germany) starting from a slice (about 1 cm diameter) of Collodaria PAC 37 colony. Briefly, frozen
349 cells were transferred in a 1.5 mL tube containing 100 μ L RA1 lysis buffer and grinded for 1 min
350 with a motor driven pellet pestle previously refrigerated in liquid nitrogen. Then 250 μ L RA1 lysis
351 buffer, previously mixed with 3,5 μ L β -mercaptoethanol (1% of total RA1 volume), were added to
352 the lysed cells and the total volume was transferred to a Nucleospin filter. After centrifugation and
353 addition of an equal volume of 70% ethanol, the RNA was purified following the manufacturer's
354 instructions and finally eluted in 40 μ L nuclease-free water. Quantity and quality of extracted RNA

355 were assessed by capillary electrophoresis on an Agilent Bioanalyzer (Agilent Technologies,
356 Santa Clara, CA).

357 Finally, in order to reduce as far as possible the risk of residual genomic DNA, a further DNase
358 treatment was applied on the total RNA using Turbo DNA-free kit (Thermo Fisher Scientific),
359 according to the manufacturer's protocol. After purification with the RNA Clean and Concentrator-5
360 kit (ZymoResearch, Irvine, CA), RNA was eluted in 10 μ L nuclease-free water and used to
361 synthesize cDNA with the Ovation RNA-seq System Version 2 (NuGEN, San Carlos, CA), following
362 the manufacturer's protocol. After cDNA shearing by Covaris E210 instrument (Covaris, Woburn,
363 MA), Illumina library was prepared using the SPRIWorks Library Preparation System on a SPRI
364 TE instrument (Beckmann Coulter Genomics, Danvers, MA), according to the manufacturer's
365 protocol without size selection. Ligation products were PCR-amplified using Illumina adapter-
366 specific primers and Platinum Pfx DNA polymerase (ThermoFisher Scientific). After library profile
367 analysis by Agilent 2100 Bioanalyzer and qPCR quantification (MxPro, Agilent Technologies), the
368 library was sequenced using 101 base-length read chemistry in a paired-end flow cell on
369 HiSeq2000 Illumina sequencer (Illumina, San Diego, CA), in order to obtain nearly 50 million
370 paired end reads.

Data retrieval and sequence libraries construction

371 For each holobiont model, sequence libraries were created based on published data from
372 taxonomically close organisms to host and symbiont species. Detailed statistics of these reference
373 libraries can be found in Additional files 1.

374 For the Cnidaria-Dinophyta holobiont model (M1), the host library includes 20 assembled
375 transcriptomes (466,582 contigs) of cnidarian organisms [53] and 2 genome-derived ESTs
376 (201,677 ESTs) of *Nematostella vectensis* and *Orbicella faveolata* [54]. The symbiont library is
377 composed of 123 RNA-seq reads datasets (a total of 5,563,498,607 reads) of Dinophyta from the
378 MMETSP project [55]. We built 3 versions of the symbiont reference library, one composed of all

379 Dinophyta (M1 a), the second exclusively composed of *Symbiodinium* spp. (15 RNA-seq datasets,
380 a total of 123,122,726 reads) (M1 b) and the third composed of all Dinophyta except
381 *Symbiodinium* spp. (108 RNA-seq datasets, a total of 5,440,375,881 reads) (M1 c).

382 For the Porifera-Bacteria holobiont model (M2), 4 RNA-seq datasets of poriferan species were
383 included in the host library (642,229,924 total reads): *Amphimedon queenslandica* [56] *Crella*
384 *elegans* [57] and both *Haliclona amboinensis* and *Haliclona tubifera* [58]. The complete bacterial
385 gene catalog (40,154,822 assembled gene sequences) derived from the first stations from the
386 *Tara* Oceans expedition [39] has been downloaded to constitute the symbiont reference library
387 (OM-RGC).

388 For the Radiolaria-Dinophyta holobiont model (M3), we gathered Rhizaria sequences from 4 *de*
389 *nov*o assembled holobionts: 7,215 presumed host transcripts were extracted among a total 15,404
390 *de novo* assembled transcripts [15]. Host specific sequences were extracted from holobionts
391 assemblies removing first sequences from prokaryotic origin with a blastn (e-value 1e-3) against
392 the OM-RGC database, and second, removing symbionts sequences with a blastx (e-value 1e-3)
393 against Dinophyta *de novo* assembled transcriptomes [Meng et al. *submitted*]. The exhaustive
394 Dinophyta library created for the M1a was used for the reference symbiont library.

Comparing meta-transcriptomes (i.e. holobiont reads) to reference libraries using Short Read Counter (SRC_c)

> Presentation of SRC_c

395 Short Read Connector Counter (SRC_c) [23] relies on a very lightweight data structure called a
396 quasi-dictionary that enables to work with voluminous sequence sets. The quasi-dictionary
397 enables to associate a piece of information to any element from a static set composed of N distinct
398 elements. It is composed of two parts: a minimal perfect hash function (MPHF) [59] and a
399 fingerprint table. The MPHF allows to index very efficiently the elements of the set in memory,
400 such that each element can be associated to any piece of information (*i.e.* k-mer coverage,

401 location in reads, ...). The fingerprint table is used to verify the membership of an element to the
402 indexed set of elements using the MPHf. This way, stranger elements to the MPHf can be filtered
403 out. The quasi-dictionary is a probabilistic structure with a controlled false positive rate that
404 depends on the size of the fingerprint. SRC_c needs as input two sets of sequences (that can be
405 identical). To compare sequences from a query set Q to those from a target set T, the set indexed
406 in the quasi-dictionary is a set of k-mers from T. Finally, for each sequence S from Q, the number
407 of k-mers of S shared with T provides a similarity measure of S with the set T. This implies that the
408 similarity measure given is asymmetrical: it depends on the placement of the k-mers on the reads
409 of Q, not of those of T. SRC_c is available at <https://github.com/GATB/short-read-connector>, the
410 commit 94aa6a65b5ddf61eba95108069fae29c41e51fb0 was used for this study.

> Application on data

411 In this study, SRC_c is used to assign reads from an holobiont transcriptome either to the host or
412 to the symbionts. We divided the query of the holobiont data set Q in two parts, one that consists
413 in the comparison of Q reads to a bank (i.e. reference library) of host sequences, and another that
414 performs the comparison to a bank of symbiont sequences. The sets to index are composed of k-
415 mers from the sequences. In each comparison, two sequence sets are considered. The whole
416 holobiont set Q and the target bank set B. First, the set B, which contains reads or assembled
417 sequences and represents sequences close to the host (resp. symbiont), is indexed. During the
418 indexation phase, the solid set of k-mers (i.e. the set composed of any k-mer which occurrence is
419 above a user-fixed threshold (the solidity threshold) in the data set) from T is computed using the
420 DSK [60] method. This set is next indexed in the quasi-dictionary previously described. Then the
421 reads from the holobiont data set (Q) are queried. For each read, the query phase reports the
422 abundance of its indexed k-mers. In the meantime, reads are checked to have enough positions
423 (i.e. more than a given threshold which can be parameterized) for which an indexed k-mer starts
424 over their length. This enables to add stringency to the query: a read that shares only a few k-mers
425 with the index is considered not enough similar to the index. Finally, each read from Q (the

426 holobiont) which was found similar to T (the host or the symbionts) during the query are returned
427 in a binary vector and can be extracted to a FASTA format.

> Parameters choice

428 Parameters from SRC_c must be carefully chosen. First, the solidity threshold is adapted
429 according to the nature of the sequences in the bank data set. For libraries which sequences are
430 reads (symbiont libraries for model 1) the default value for the solidity threshold (= 2) was kept. For
431 longer sequences (host libraries for model 1, sequences of models 2 and 3) the threshold was
432 adapted and set to 1 when using libraries of assembled sequences or EST (host libraries for
433 model 1, sequences of models 2 and 3). We chose a k-mer length of 25 according to the smaller
434 input read length. We set the similarity value s to 50% for models 1 and 3, and decreased it to
435 40% for model 2. Both query and indexation phases are parallelized in SRC_c. For this study
436 analyses were performed on a Linux system with 40 cores, with the option -t 0 (maximal number of
437 available threads is used) and 250 GB of memory.

Read filtering, de novo assembly and downstream analysis

438 All read subsets resulting from the SRC_c step were first filtered (sequences trimming and
439 cleaning) with the Trimmomatic program [61] (v0.36) and custom parameter
440 SLIDINGWINDOW:10:20. Filtered reads were assembled using the *de novo* transcriptome
441 assembly program Trinity [41] (v2.4.0) with default parameters. The newly assembled contigs
442 metrics were calculated with the Transrate program [62] (v1.0.3). Additional downstream analyses
443 include protein coding domain prediction using Transdecoder [63] (v3.0.1) and functional
444 annotation with InterProScan 5 [64] (v5.24-63), both with default parameters. The pipeline used for
445 the steps described above is publicly available on a GitHub repository
446 <https://github.com/arnaudmeng/dntap> [53, Meng et al. *submitted*].

Taxonomic assignment with MEGAN6

447 The contigs sequences were compared to the nr database (August 2017 version) with the
448 DIAMOND software [66] (v0.28.22.84) using default parameters for BLASTx comparison and a e-
449 value of $1e^{-3}$. The resulting alignments were processed with the *daa2rma* tool script provided with
450 MEGAN6 and GeneInfo Identifier (GI) were mapped to alignments using the *gi_taxid.bin* file
451 (version of May 2017). Finally, taxonomic assignment has been calculated with default parameters
452 using the MEGAN LCA (Last Common Ancestor) algorithm and were visualized through the
453 MEGAN6 software.

Chimeras identification

454 We followed the protocol described in [67]. 50,000 randomly sampled *de novo* assembled contigs
455 for the M3 (with the SRC strategy and without SRC strategy) were compared to the 7,215 Rhizaria
456 presumed contigs from [15] and 3,494,295 coding domains from *de novo* assembled contigs of 54
457 dinoflagellates transcriptomes [Meng et al. *submitted*]. The comparison was made using the
458 BLASTx program [68] (e-value $1e^{-3}$). The tools scripts *detect_chimera_from_blastx.py* from [67]
459 was applied to resulting alignments to detect potential chimeras.

Declarations

Acknowledgements

We thank the RCC staff for providing the dinoflagellates cultures as well as ABIMS staff for the help on computational facilities. This work was supported by a 3-year Ph.D. grant from the "Interface pour le Vivant" (IPV) program at the University of Pierre et Marie Curie (UPMC), Paris, France. This project was supported by Région Ile-de-France and benefited from the support of the project IMPEKAB ANR-15-CE02-0011.

Competing interests

The authors declare that they have no competing interests.

Author's contributions:

LB and AM designed the analysis, and LB guided the study. IP, JD and FN performed sampling and culture steps. AA and CDS optimized the molecular protocols and performed the sequencing analysis. AM and CM performed the computational analyses, with the help of PP and EC. AM, CM, PP, SLC, FN and LB wrote the manuscript. EP and PW provided critical discussions. All authors read and approved the final manuscript.

Data Accessibility:

Link to data: <http://application.sb-roscoff.fr/project/radiolaria/>

Additional Files

Additional file 1 SRC_c library content information and data sources. Table with detailed information of SRC_c libraries contents. The type of data and the total library sizes are displayed. It includes taxonomic contents and links to data repositories for holobiont models M1, M2 and M3 and data that constitute SRC_c reads/sequences libraries.

Additional file 2 Taxonomic assignment of SRC assembled contigs with MEGAN6 for the holobiont models M1 and M2.

Additional file 3 details of common GO annotations M1 and M2 our contigs versus previous studies

Additional file 4 Comparison of functional annotations between SRC assembled transcriptomes and a *de novo* assembled transcriptome without the use of SRC_c in the case of holobiont model M3. Details of the functional annotations results for the SRC strategy applied to M3, the tables displayed correspond to the top 15 GO annotations found in host, symbiont, shared and unassigned transcriptomes for the three levels of annotations (MF: Molecular Functions, BP: Biological Process and CC: Cellular Component).

Additional file 5 Radiolaria-Dinophyta meta-transcriptome taxonomic assignment with MEGAN6. Table of taxonomic assignation of the 167,023 *de novo* assembled contigs from the assembly without SRC reads sorting of the holobiont model M3.

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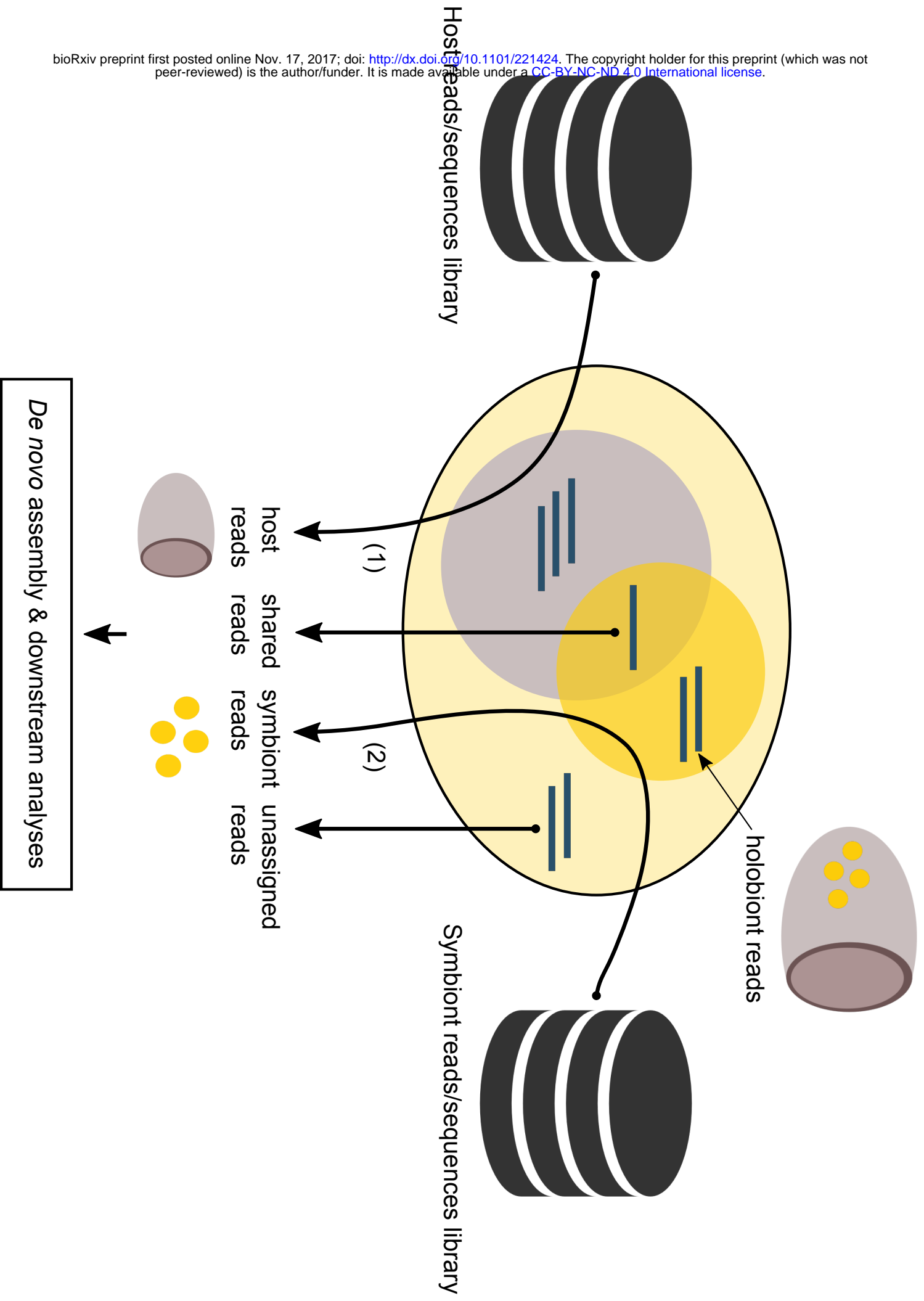
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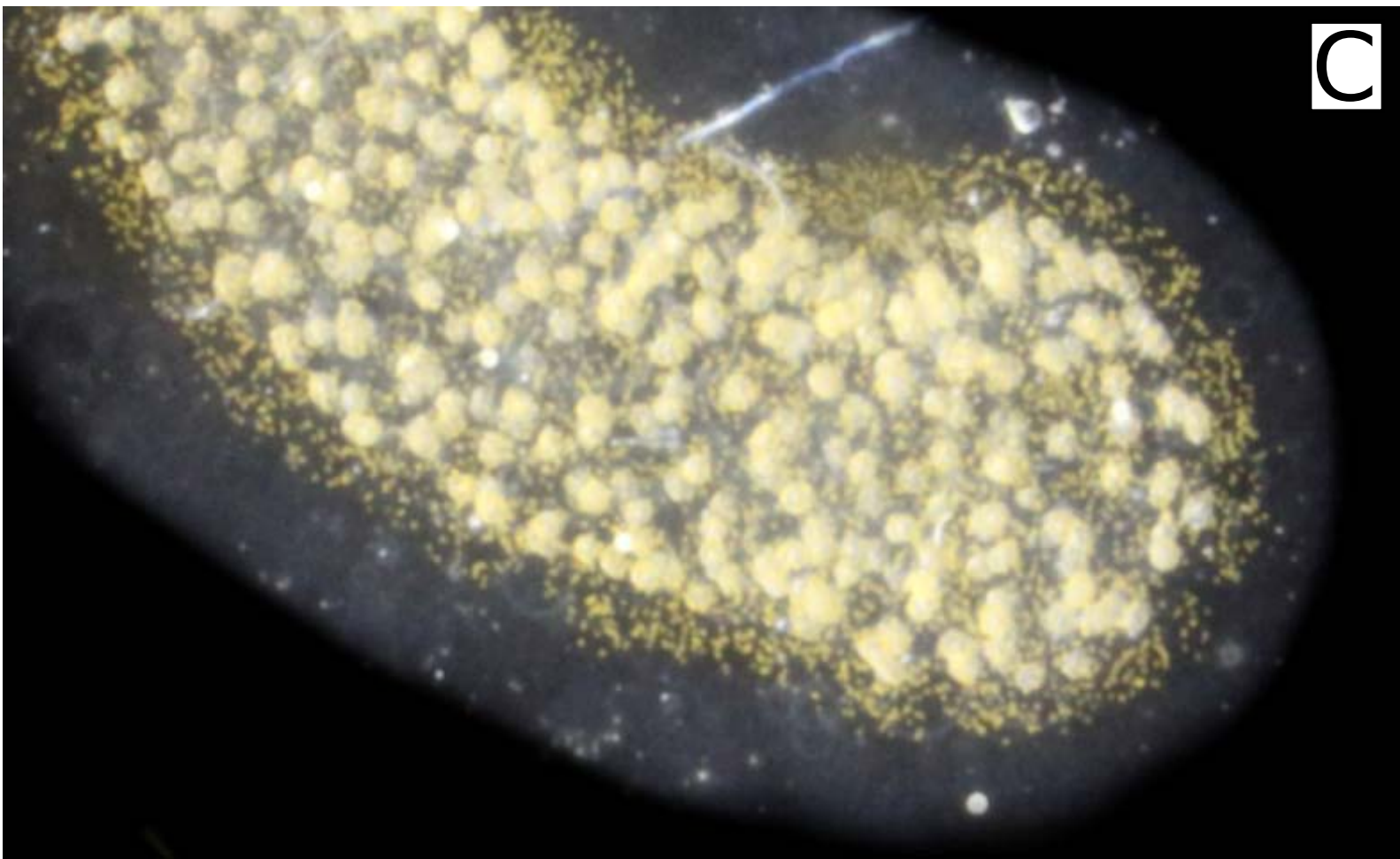
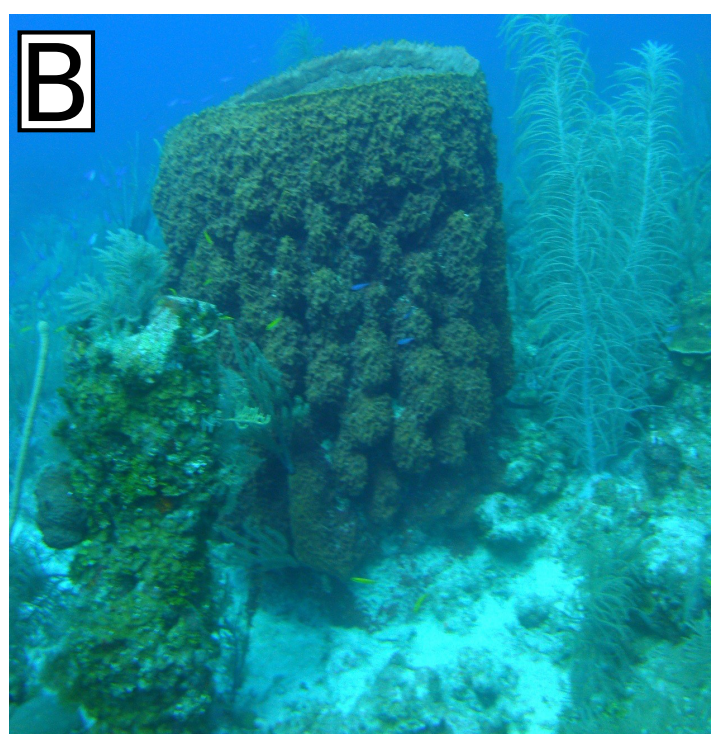
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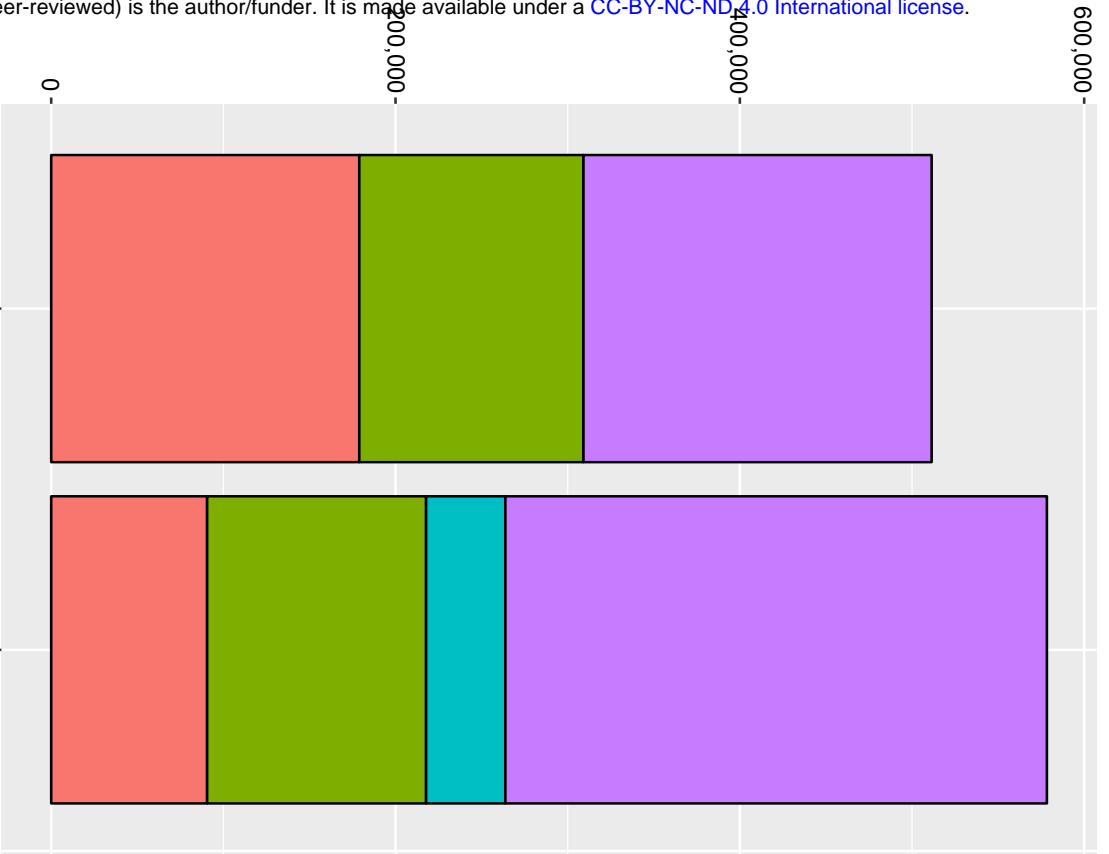




Number of assembled contigs

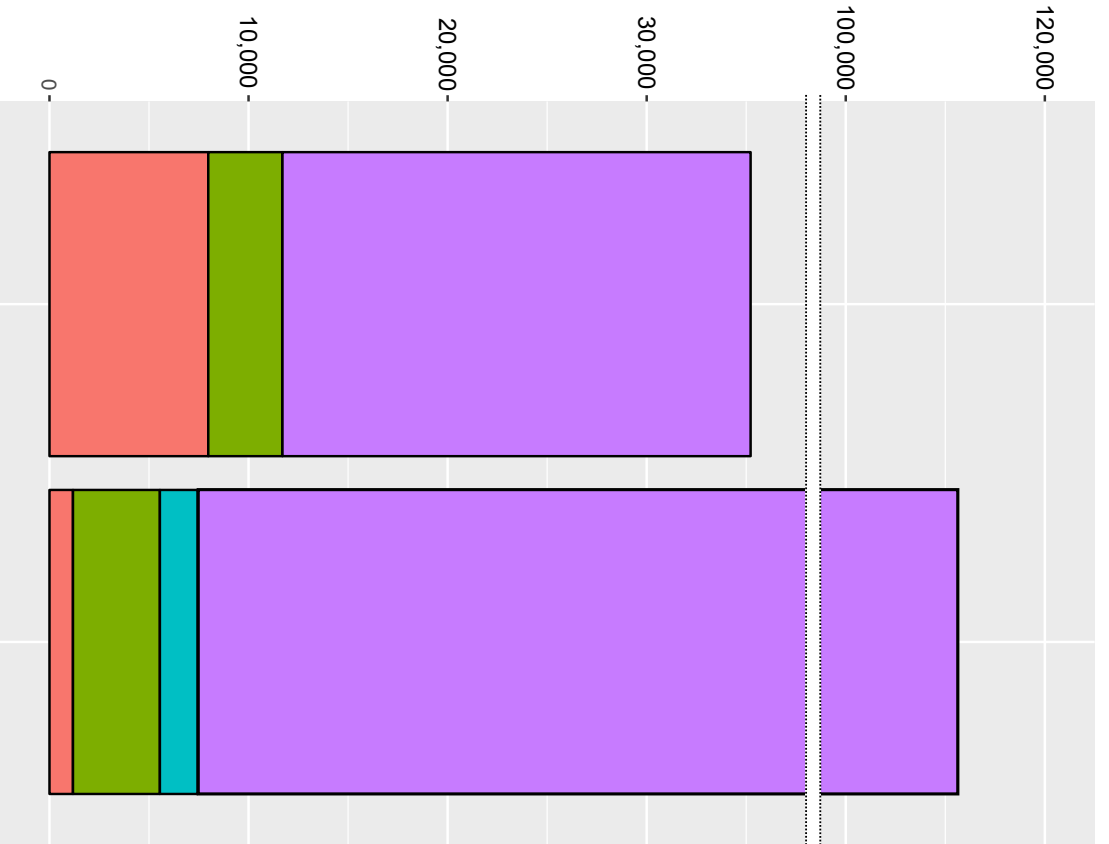
bioRxiv preprint first posted online Nov. 17, 2017; doi: <http://dx.doi.org/10.1101/221424>. The copyright holder for this preprint (which was not peer-reviewed) is the author/funder. It is made available under a [CC-BY-NC-ND 4.0 International license](https://creativecommons.org/licenses/by-nc-nd/4.0/).

A

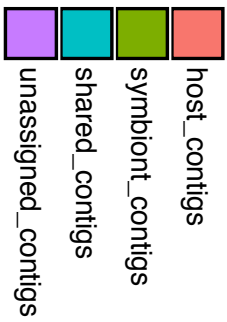


	Pinzón et al. 2015	M1a
# reads for assembly	775,025,024	775,025,024
# assembled contigs	442,294	578,333
N50 (bp)	1551	971
# cds with FA	108,409	171,931

B



	Fiore et al. 2015	M2
# reads for assembly	13,723,211	30,541,810
# assembled contigs	35,219	113,786
N50 (bp)	1010	719
# cds with FA	NC	24,738



		# contigs	% contigs in holobiont	smallest	longest	N50	mean length	%GC	remapping rate (%)	# with ORFs	% of contigs with ORFs	remapping rate of holobiont reads (%)	# predicted cds	% contigs with predicted cds	# annotated cds	% cds with functional annotations
Cnidaria-Dinophyta holobiont (M1a)	host	90 558	15.66%	201	29 214	1 840	949	42%	97.8%	31 105	34.3%	71.6%	42 992	47.5%	35 358	39%
	symbiont	127 212	22%	201	13 093	1 091	719	57%	90.4%	58 286	45.8%	72.3%	84 151	66.2%	53 011	41.7%
	shared	46 017	7.96%	201	7 727	1 067	796	55%	82.3%	28 075	61%	41.4%	38 547	83.8%	25 382	55.2%
	unassigned	314 546	54.39%	201	19 174	732	558	46%	83.6%	67 509	21.5%	25.9%	89 533	28.5%	58 188	18.5%
	total	578 333								184 975			255 223		171 939	
Porifera-Bacteria holobiont (M2)	host	2 654	2.33%	201	1 921	299	311	42%	44.4%	215	8.1%	17.6%	707	26.6%	593	83.9%
	symbiont	2 431	2.14%	201	5 001	406	396	46%	25%	411	16.9%	4.7%	1 072	44.1%	988	92.2%
	shared	2 324	2.04%	201	751	301	299	54%	86.4%	8	0.3%	22.3%	163	7%	30	18.4%
	unassigned	106 377	93.49%	201	8 811	748	572	39%	73.2%	29 520	27.8%	59.1%	43 150	40.6%	23 127	53.6%
	total	113 786								30 154			45 092		24 738	54.9%
Radiolaria-Dinophyta holobiont (M3)	host	693	0.41%	201	1 209	277	303	42%	65.2%	44	6.3%	10.6%	123	17.7%	49	7.1%
	symbiont	5 207	3.08%	201	1 777	324	328	54%	76.2%	618	11.9%	32%	1 468	28.2%	942	18.1%
	shared	52	0.03%	201	639	298	308	39%	81.3%	0	0%	18.6%	6	11.5%	5	9.6%
	unassigned	162 947	96.48%	201	10 569	714	580	41%	89.7%	49 032	30.1%	73.2%	72 420	44.4%	44 772	27.5%
	total	168 899								49 694			74 017		45 768	