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3 **Free-living Bacterial Communities Are Mostly Dominated by Oligotrophs**

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10 **Abstract**

11 In response to resource availability, bacteria have evolved two distinct ecological strategies.  
12 Copiotrophic bacteria grow fast and are heavily favored by selection where the resource is  
13 abundant. In contrast, oligotrophic bacteria grow slowly but more efficiently and are highly  
14 adaptive in nutrient-poor environments (Koch, 2001). Although oligotrophs and copiotrophs  
15 are ubiquitous, except for a few well-characterized environments like the open ocean and  
16 animal gut, the relative abundance of oligotrophic and copiotrophic bacteria and their  
17 importance in the global ecosystem are still unclear. In addition, although several studies  
18 have demonstrated the impact of nutrient availability on the bacterial community structure  
19 under experimental conditions (Klappenbach et al., 2000, Nemergut et al., 2016), the role of  
20 nutrients in shaping the structures of bacterial communities in their natural habitats remains  
21 largely unknown. Using the ribosomal RNA operon (*rrn*) copy number to capture the  
22 bacterial ecological strategy, we analyzed 44,045 samples from two large bacterial  
23 community repositories that cover 78 environmental types. Here we show that animal-  
24 associated microbiota are dominated by copiotrophs while plant-associated and free-living  
25 bacterial communities are mostly dominated by oligotrophs. Our results suggest that nutrient  
26 availability plays an important role in determining the structure and ecological strategy of  
27 bacterial communities in nature. We demonstrate that the average and distribution of *rrn*  
28 copy number are simple yet robust predictors of the ecological strategy of bacterial  
29 communities that can be applied to all sequence-based microbial surveys to link the  
30 community structure and function.

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## 34 **Introduction**

35 The fundamental trade-off between the growth rate and efficiency in bacteria leads to  
36 genomic features that distinguish between copiotrophs and oligotrophs (Lauro et al., 2009;  
37 Roller et al., 2016). These features include genome size (Roller et al., 2016), codon usage  
38 bias (Vieira-Silva & Rocha, 2010), transporter gene diversity (Lauro et al., 2009), motility  
39 (Lauro et al., 2009; Roller et al., 2016) and etc. Among them, the copy number of ribosomal  
40 RNA operon (*rrn*) is the best studied genomic trait that predicts the ecological strategy of  
41 bacterial species. The *rrn* copy number positively correlates with cellular ribosomal content  
42 and the maximum growth rate (Roller et al., 2016; Vieira-Silva & Rocha, 2010), and deletion  
43 of *rrn* reduces the maximum growth rate of *Escherichia coli* and *Bacillus subtilis* (Nanamiya  
44 et al., 2010; Stevenson & Schmidt, 2004; Yano et al., 2013). On the other hand, the *rrn* copy  
45 number negatively correlates with the growth efficiency. One study has shown that the  
46 carbon use efficiency and protein yield (protein synthesized per unit O<sub>2</sub> consumed)  
47 decreases when the *rrn* copy number increases in several strains of bacteria (Roller et al.,  
48 2016). As such, high *rrn* copy number indicates a copiotrophic strategy while low *rrn* copy  
49 number predicts an oligotrophic one.

50 As bacteria adopt different ecological strategies, the *rrn* copy number in their genomes  
51 varies from 1 to as many as 15 (Klappenbach et al., 2000). Bacteria have the potential to  
52 rapidly change their *rrn* copy numbers in adaptation to the growth condition, as mutant  
53 strains of *B. subtilis* with only one copy of *rrn* increased their *rrn* copies through operon  
54 duplication within generations (Yano et al., 2013). Despite the potential for rapid change,  
55 there is clearly phylogenetic signal in bacterial *rrn* copy number, as closely related species  
56 tend to have similar *rrn* copy numbers (Kembel et al., 2012). The existence of such  
57 phylogenetic signal suggests that *rrn* copy number, albeit labile, is under strong natural  
58 selection. Although *rrn* copy number cannot be directly measured for environmental bacteria,  
59 the phylogenetic signal in *rrn* copy number makes it possible to estimate the copy number  
60 from the 16S rRNA gene sequence alone (Kembel et al., 2012). And such method is

61 applicable to both 16S rRNA amplicon and shotgun metagenomic sequence data, making  
62 prediction of ecological strategies of individual bacterial species and the whole community  
63 relatively simple and straightforward.

## 64 **Results**

65 First we set out to identify an optimal *rrn* copy number that can be used to classify  
66 oligotrophs and copiotrophs. We used 63 representatives of oligotrophs and copiotrophs  
67 classified by Lauro *et al* (Lauro et al., 2009) as our training set. As expected, oligotrophs and  
68 copiotrophs are well separated in their *rrn* copy number distribution (Figure 1A). The area  
69 under the curve (AUC) of the receiver operating characteristic (ROC) curve is 0.86 (Figure  
70 1B), indicating that classification by *rrn* copy number has high accuracy (Šimundić, 2008).  
71 Maximizing Youden's J statistic, we found that 2 was the optimal cutoff to distinguish  
72 oligotrophs and copiotrophs, with a true positive rate of 0.789 and a false positive rate 0.200  
73 for identifying oligotroph. Using this cutoff, we classified bacterial species (Operational  
74 Taxonomic Units or OTUs) as oligotrophs if they had 1 or 2 *rrn* copies or as copiotrophs if  
75 they had 3 or more *rrn* copies.

76 The free-living bacterial community in open ocean is known to be dominated by oligotrophic  
77 bacteria (Lauro et al., 2009; Yooseph et al., 2010). Therefore, we tested whether the  
78 average copy number (ACN) and distribution of *rrn* captured the ecological strategy of  
79 marine bacteria in the open ocean using the shotgun metagenomic sequencing data from  
80 the Tara Oceans Expedition (TARA) (Pesant et al., 2015). The ACN in surface water  
81 samples from TARA ranged from 1.3 to 1.9, with a median of 1.4 (Supplementary Figure  
82 1A). As expected, the community is dominated by oligotrophic bacteria with 1 or 2 *rrn* copies.  
83 Overall, 93% of the bacterial cells in the community were oligotrophic, with 66% of the  
84 bacteria cells had only one copy of *rrn* and 27% of them had 2 copies (Supplementary  
85 Figure 1B).

86 Next we examined the ACN of bacterial communities from a broader range of environments  
87 present in the EBI Metagenomics dataset (Mitchell et al., 2018). In total, we analyzed 2,528  
88 whole genome shotgun (WGS) metagenomic samples that covered 6 environmental  
89 categories (freshwater, marine, non-marine saline, soil, animal and human-associated) and  
90 21 environmental types (Supplementary Table 1). We observed that ACN varied  
91 substantially between environmental categories (Figure 2A). Animal and human-associated  
92 bacterial communities had the highest ACN (median 4.4 and 4.8 respectively), while those  
93 from marine, non-marine saline and soil environments had the lowest ACN (median 1.8, 2.0  
94 and 2.0, respectively). Freshwater bacteria communities had intermediate ACN (median  
95 3.1).

96 As the majority of microbial surveys are based on 16S rRNA amplicon sequencing, we  
97 investigated whether the ACNs estimated from amplicon sequencing were consistent with  
98 those estimated from WGS sequence data, out of concern that PCR bias associated with  
99 amplicon sequencing (Acinas et al., 2005) can potentially skew the ACN. From the EBI  
100 Metagenomics database, we identified 275 animal and human-associated microbiomes that  
101 were surveyed by both methods. We compared the ACNs estimated from the WGS and  
102 amplicon sequences of these 275 samples and found that they were highly correlated  
103 (Figure 3). The r-squared of the one-to-one fit between the two ACNs was 0.708 and the  
104 difference in ACNs estimated by the two methods was negligible (1.2% difference on  
105 average).

106 Because ACN estimated from 16S rRNA amplicon data was reliable, we examined the ACN  
107 of bacterial communities surveyed by amplicon sequencing in both the EBI Metagenomics  
108 and Earth Microbiome Project (EMP) database (Thompson et al., 2017). In total, we  
109 analyzed 41,517 amplicon-sequenced samples from the two databases, which were 16  
110 times larger than the WGS metagenomic data and together covered 11 environmental  
111 categories and 74 environmental types (Supplementary Table 1). ACN from the amplicon  
112 data varied between environment categories and showed a distribution pattern similar to

113 what had been observed in the EBI WGS metagenomic data (Figure 2B) and a previous  
114 report (Thompson et al., 2017). Animal and human-associated bacterial communities had  
115 highest ACN (median 4.5 and 4.6 respectively), followed by air and indoor surface  
116 communities with intermediate ACN (median 3.7 and 3.1 respectively). Bacterial  
117 communities in the other environments (freshwater, marine, non-marine saline, soil,  
118 sediment, biofilm and plant-associated) all had low ACN (median less than 2.5).

119 We then examined the distribution of the *rrn* copy number within each of the 74  
120 environmental types to directly assess the relative abundance of oligotrophs and copiotrophs  
121 in each type of environment. Figure 2C shows that animal and human-associated bacterial  
122 communities are dominated by copiotrophs (with 3 or more *rrn* copies) while free-living  
123 bacterial communities are dominated by oligotrophs (with 1 or 2 *rrn* copies). Plant-associated  
124 bacterial communities show a distribution of *rrn* copy number similar to those of the free-  
125 living ones, dominated by oligotrophs. We classified bacterial communities in which the  
126 relative abundance of oligotrophs was greater than 60% as oligotrophic, and communities in  
127 which the relative abundance of copiotrophs was greater than 60% as copiotrophic, and the  
128 rest of communities as intermediate. We found that 91.5% of 31,835 animal and human-  
129 associated bacterial communities were copiotrophic, while 72.6% of 6,215 free-living and  
130 71.2% of 3,467 plant-associated microbiomes were oligotrophic (Figure 4).

## 131 **Discussion**

132 The *rrn* copy number has been shown to be a useful predictor of the ecological strategy of  
133 individual bacterial species (Klappenbach et al., 2000; Lauro et al., 2009; Roller et al., 2016)  
134 and bacterial communities (Nemergut et al., 2016; Thompson et al., 2017). Here we  
135 extended this line of research and used the distribution of *rrn* copy to reveal the existence of  
136 three types of bacterial communities in nature: those dominated by oligotrophs, copiotrophs  
137 or neither. Our analysis of a comprehensive collection of environmental samples indicates  
138 that most free-living and plant-associated bacterial communities are dominated by

139 oligotrophs while animal and human-associated communities are dominated by copiotrophs.  
140 This pattern is consistent with our understanding of nutrient availability in the environment. In  
141 general, soil and water are considered nutrient poor (Barber & Lynch, 1977; Kuznetsov et  
142 al., 1979; Maeda et al., 2000; Ohta & Hattori, 1983) while animal-associated sites (gut, skin,  
143 etc) are considered nutrient rich. Despite the vast compositional differences among the  
144 communities analyzed in this study, the emergence of a global pattern in the relative  
145 abundance of oligotroph and copiotroph suggests that nutrient plays a key role in shaping  
146 the ecological strategy and the structure of the bacterial communities in nature. More  
147 generally, our results suggest that in nature selection exerts strong influence on the  
148 assembly of bacterial community compared to the other processes such as drift and  
149 dispersal. Interestingly, although the vast majority of groundwater samples were dominated  
150 by oligotrophs (90.9% of samples), only 9.5% of contaminated groundwater samples were  
151 dominated by oligotrophs. Similarly, the relative abundance of oligotrophs also decreased in  
152 the contaminated open ocean and soil. In addition, we did observe outliers in some  
153 environments. For example, Antarctic soil supplemented with organic carbon (Van Horn et  
154 al., 2014) had extremely high ACN (8.9) compared to untreated soil (3.1). Together, they  
155 provide compelling evidence that nutrient dictates the ecological strategy and the structure of  
156 the bacterial communities.

157 We have demonstrated that the average and distribution of *rrn* copy number are simple yet  
158 robust predictors of the ecological strategy of bacterial communities. Unlike other imprinted  
159 genomic features (Lauro et al., 2009) that require shotgun metagenomic sequences, *rrn*  
160 copy number can be estimated from 16S rRNA gene sequences alone and therefore is  
161 applicable to both shotgun metagenomic and 16S rRNA amplicon sequence data. As such,  
162 the metrics of average and distribution of *rrn* copy number can be applied in all sequence-  
163 based microbial surveys. Additionally, as the average copy number of *rrn* is weighted by the  
164 relative cell abundance, it will capture the overall ecological strategy of a community even at  
165 relatively low sequencing depth. These features make the community *rrn* copy number an

166 extremely useful quantitative trait for studying the microbial ecosystem. By providing a link  
167 between the community structure and function, it adds values to 16S rRNA sequence data  
168 beyond simply quantifying species composition, and can help researchers generate  
169 hypotheses on how communities assemble in response to nutrient availability and other  
170 environmental factors. In addition, it can be used as proxies of the average growth rate and  
171 carbon use efficiency of bacterial communities to improve the current global carbon cycling  
172 models that have fixed values for these parameters, as has been suggested previously  
173 (Roller et al., 2016).

## 174 **Methods**

### 175 Classifying oligotrophic and copiotrophic bacteria with the *rrn* copy number

176 Using 43 genomic features, Lauro *et al* classified 126 strains of bacteria as either  
177 oligotrophic or copiotrophic (Lauro et al., 2009). We used these strains as a training set to  
178 identify an optimal *rrn* copy number cutoff for oligotroph/copiotroph classification. To reduce  
179 overrepresentation of certain clades, we selected one representative species from each of  
180 the 63 genera represented by the 126 strains and whose complete genome sequence was  
181 available (Supplementary Table 2). To evaluate the performance of using *rrn* copy number  
182 for oligotroph/copiotroph classification, we calculated the true-positive rate and the false-  
183 positive rate using each integer from 1 to 15 as the copy number cutoff, plotted the ROC  
184 curve and calculated the AUC. To find the optimal cutoff, we computed Youden's J statistic  
185 for each cutoff, and selected the copy number that had the maximum Youden's J statistic as  
186 the optimal cutoff. We then classified bacterial species whose *rrn* copy number was greater  
187 than the cutoff as copiotroph, and oligotroph otherwise.

### 188 Compilation of Data

189 We used data from the Tara Oceans Expedition (Pesant et al., 2015) to test if the *rrn* copy  
190 number captured the oligotrophic ecological strategy of marine bacteria in the open ocean.  
191 The TARA dataset includes 139 bacterial community profiles derived from WGS



192 metagenomic sequencing and focused specifically on the free-living bacterial communities in  
193 the open ocean across the globe. We downloaded the OTU abundance table and the  
194 environmental metadata from the TARA companion website (Sunagawa et al., 2015). We  
195 also downloaded the SILVA 16S rRNA reference sequences that were used in the TARA  
196 study to pick OTU at 97% similarity, and estimated their *rrn* copy numbers using the method  
197 described below. We analyzed 63 samples from the surface layer.

198 To explore the global ecological strategies of bacterial communities in nature, we compiled  
199 bacterial diversity survey data from two large microbial survey repositories, the EBI  
200 Metagenomics (Mitchell et al., 2018) and the EMP (Thompson et al., 2017). For the EBI  
201 Metagenomics dataset, we included 12,486 WGS metagenomic and 69,385 amplicon  
202 sequencing runs processed by the version 2.0 or 3.0 pipeline of the EBI Metagenomics  
203 (Mitchell et al., 2018). Sequencing runs of the same type (16S rRNA amplicon or WGS  
204 metagenomics) that were associated with the same sample were combined together. For the  
205 EMP dataset, we included 23,228 amplicon sequencing samples from its first release. We  
206 downloaded OTU abundance table and the metadata associated with each sample. The  
207 GreenGene 13.8 16S rRNA reference sequences were used for OTU picking at 97%  
208 similarity in both repositories. The *rrn* copy numbers of GreenGene reference sequences  
209 were estimated as described below. We filtered out WGS metagenomic runs whose 16S  
210 rRNA reads exceeded 5% of the total sequence reads and amplicon runs if less than 95% of  
211 the sequence reads were 16S rRNA reads, as these samples were likely 16S rRNA  
212 amplicon sequencing data mislabeled as WGS metagenomic data or *vice versa*. We then  
213 removed samples if less than 80% of their 16S rRNA reads could be mapped to the  
214 GreenGene reference sequences or if the total mapped reads were fewer than 400. We  
215 removed samples that only surveyed or were enriched for a specific bacterial clade. We also  
216 removed samples whose environmental types were too general or mislabelled, and  
217 environmental types that contained less than 5 samples. At the end, a total of 44,045  
218 samples (2,528 WGS metagenomic and 41,517 amplicon sequencing) remained after the

219 quality filtering. Together, they cover a total of 78 environmental types. We grouped these  
220 environmental types into 11 categories: air, indoor surface, sediment, freshwater, marine,  
221 non-marine saline, biofilm, soil, plant-associated, animal-associated and human-associated  
222 (Supplementary table 1).

### 223 Estimation of the average *rrn* copy number (ACN) of a community

224 The 16S rRNA gene copy number of each OTU in the SILVA and the GreenGene reference  
225 databases was estimated using the phylogenetic ancestral state reconstruction method  
226 described in Kembel *et al* (Kembel et al., 2012) with an updated reference tree of 1,197  
227 bacterial species whose genomes were sequenced and 16S rRNA gene copy numbers were  
228 known. The ACN of the bacterial community in a sample was weighted by the relative cell  
229 abundance of OTUs, as shown in Equation (1),

230

$$ACN = \sum_i n_i C_i$$

231

(1)

232 where  $n_i$  and  $C_i$  are the relative cell abundance and 16S rRNA gene copy number,  
233 respectively. The relative cell abundances  $n_i$  was in turn computed by Equation (2) proposed  
234 in Kembel *et al* (Kembel et al., 2012).

235

$$n_i = \frac{\frac{g_i}{C_i}}{\sum_i \frac{g_i}{C_i}}$$

236

(2)

237 where  $g_i$  is the relative gene abundance of an OTU estimated by the read number.

### 238 Estimation of the distribution of *rrn* copy number in communities of an environment type

239 The relative cell abundance of bacteria with a certain *rrn* copy number was calculated by  
240 summing the relative cell abundance of all species in a community with that *rrn* copy number  
241 (rounded to the nearest integer). To generate the distribution plot for an environmental type  
242 (Figure 2C), we repeated the analysis for all samples (communities) of that environmental  
243 type and calculated the average relative cell abundance of bacterial species with a certain  
244 *rrn* copy number.

245

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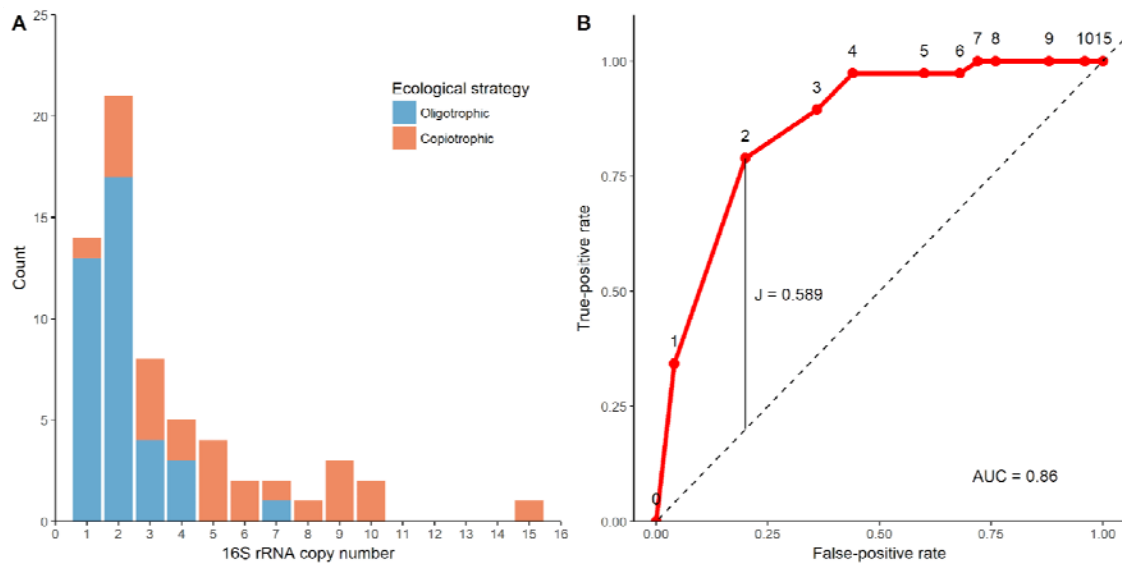
321

322 **Competing interests**

323 The authors declare no competing financial interests.

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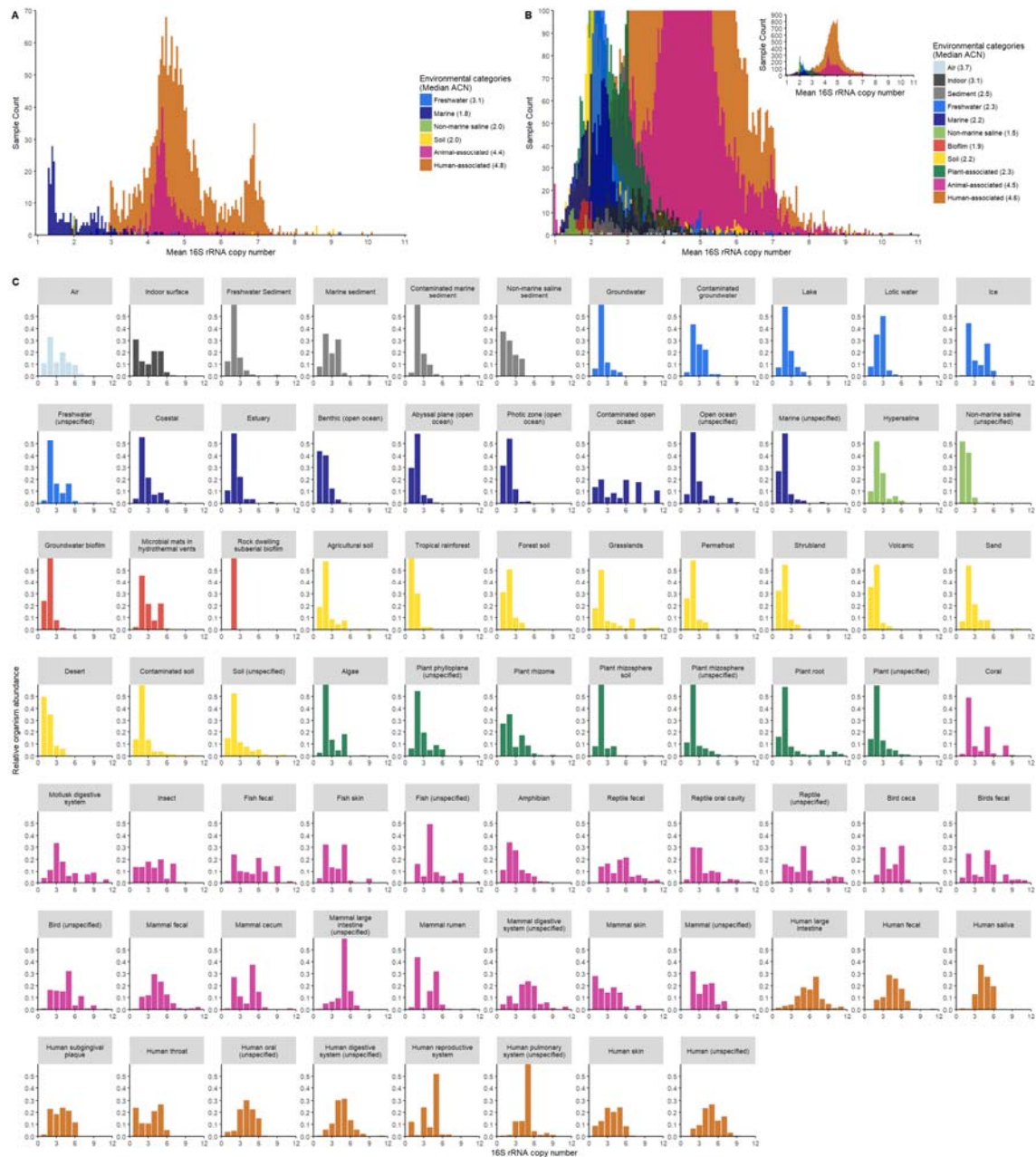


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328 Figure 1. (A) The distribution of *rrn* copy number of the 63 representative species that were  
329 identified as either oligotrophic (blue) or copiotrophic (orange). (B) The ROC curve for using  
330 the *rrn* copy number to distinguish oligotrophic and copiotrophic bacteria, with an AUC of  
331 0.86. The best copy number cutoff is 2 with a maximum Youden's J statistic of 0.589.

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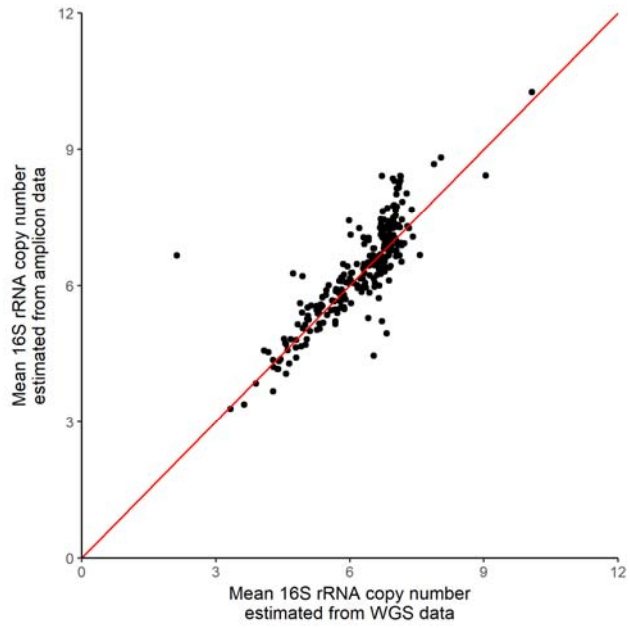


333

334 Figure 2. Distribution of the ACN of 2,528 samples surveyed by WGS metagenomics (A) and  
 335 41,517 samples surveyed by 16S rRNA amplicon sequencing (B) in the EBI Metagenomics  
 336 and the EMP databases. The relative abundance of bacterial species was plotted against  
 337 their *rrm* copy number for the amplicon sequencing samples (C). Samples were colored by  
 338 the environment categories.

339



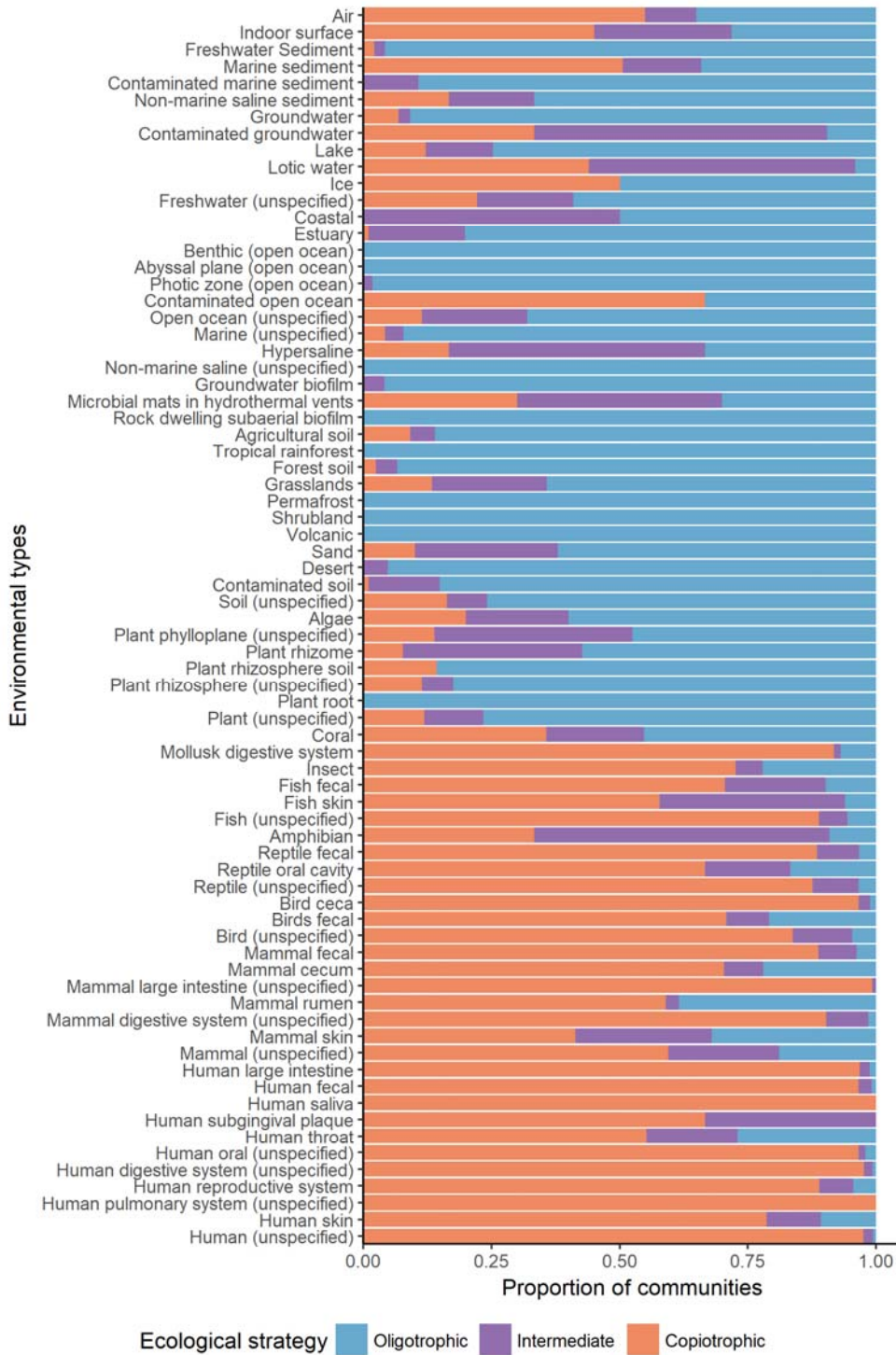


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342 Figure 3. The ACN of 275 animal and human-associated bacterial communities surveyed by  
343 both 16S rRNA amplicon and WGS metagenomic sequencing methods. Red line illustrates  
344 the one-to-one fit between the ACN estimated from the two methods. The r-squared of the fit  
345 is 0.708.

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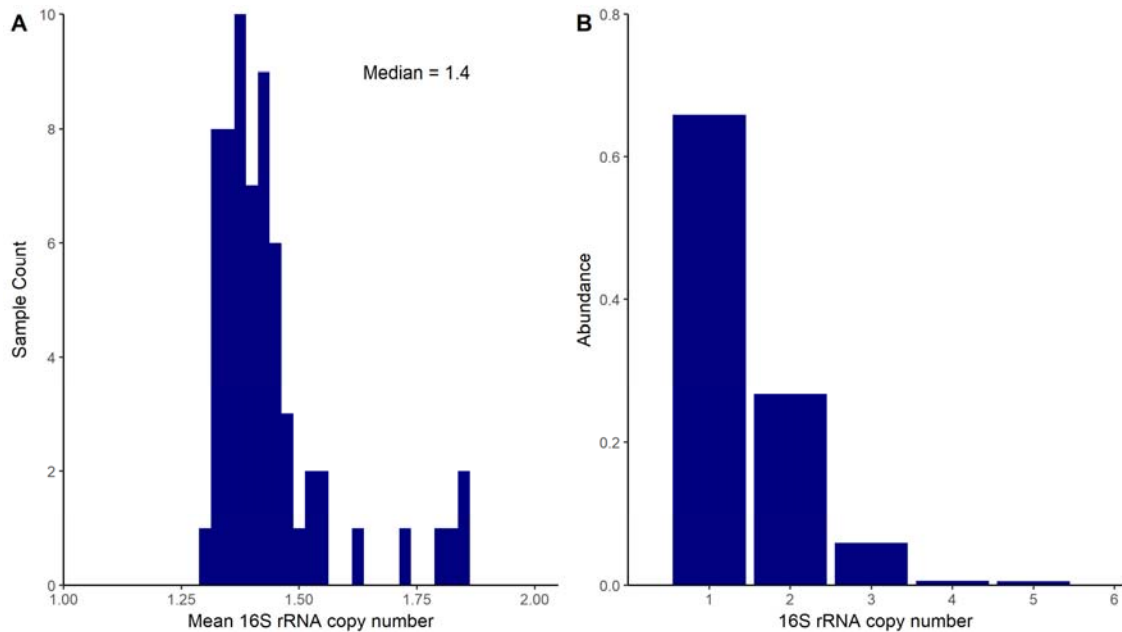
348 Figure 4. The proportion of 41,517 16S rRNA amplicon sequenced samples from 74  
 349 environmental types that are dominated (more than 60%) by oligotrophs (species with 1 or 2  
 350 copies or *rrn*, orange) or by copiotrophs (species with 3 or more copies of *rrn*, blue), or are  
 351 intermediate (neither group was dominant, purple).

352

353 **Supplementary Data**

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357 Supplementary Figure 1. (A) The average copy number of *rrn* copy of the 63 bacterial  
358 communities from the surface layer in TARA. (B) The distribution of *rrn* copy number in the  
359 63 bacterial communities. The abundances of species with more than 6 *rrn* copies are  
360 negligible and not shown.

361

362 Supplementary Table 1. Environmental types covered by samples from WGS metagenomics  
363 in the EBI Metagenomics (A) and 16S rRNA amplicon sequencing in the EBI Metagenomics  
364 and the Earth Microbiome Project (B), and their statistics.

365 Supplementary Table 2. The *rrn* copy number of 116 strains of oligotrophic or copiotrophic  
366 bacteria whose complete genome sequences were available.