

## AUTHOR'S CORRECTION

### Diversity of Bacteria in the Marine Sponge *Aplysina fulva* in Brazilian Coastal Waters

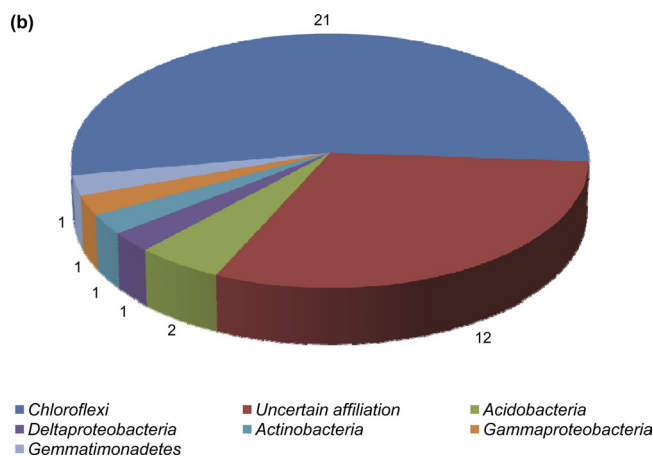
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Volume 75, no. 10, p. 3331–3343, 2009. The tentative affiliation of 20 16S rRNA gene sequences into bacterial phyla was not registered correctly as shown in Fig. 4b. This was because affiliations assigned by the RDP Classifier tool with low confidence thresholds (i.e., below 50%) were inadvertently regarded as stringent. Previously recorded as *Aquificae* (2), *Bacteroidetes* (1), *Deferribacteres* (3), *Dictyoglomi* (2), *Firmicutes* (7), and *Proteobacteria* (5), 12 of these sequences actually belong to one bacterial lineage of uncertain affiliation as described by Kamke et al. (ISME J. 4:498–508, 2010). The remaining 8 sequences are firmly affiliated with the *Chloroflexi* (4), *Acidobacteria* (2), and *Proteobacteria* (2) phyla. In addition, one clone sequence has been removed from the analyzed data set because of vector contamination. As a consequence, the following modifications to the article are needed.

Page 3337: In Fig. 4a, “40” should read “39” to indicate the number of sequences initially not classified at a 70% confidence threshold.

Page 3337: Fig. 4b should appear as shown below.



Page 3337: In the legend to Fig. 4, “reclassified at  $\leq 69\%$  CI” should read “reclassified by phylogenetic inference.”

Page 3337, column 1: Lines 22–27 should read as follows. “. . .The 39 sequences that were initially not classifiable at the phylum level could be assigned, by phylogenetic inference, to the *Acidobacteria*, *Actinobacteria*, *Chloroflexi*, *Gemmatimonadetes*, *Deltaproteobacteria*, *Gammaproteobacteria*, and to a lineage of uncertain affiliation related with the *Planctomycetes-Verrucomicrobia-Chlamydiae* superphylum.”

Page 3338: In Fig. 5, clone i126 belongs to a bacterial lineage of uncertain affiliation.

Page 3341, column 1, lines 46–48: The sentence beginning with “Sequences resembling. . .” should be deleted.