

# Effects of elevated CO<sub>2</sub> on bacterioplankton community structure in subtropical eutrophicated coastal mesocosms

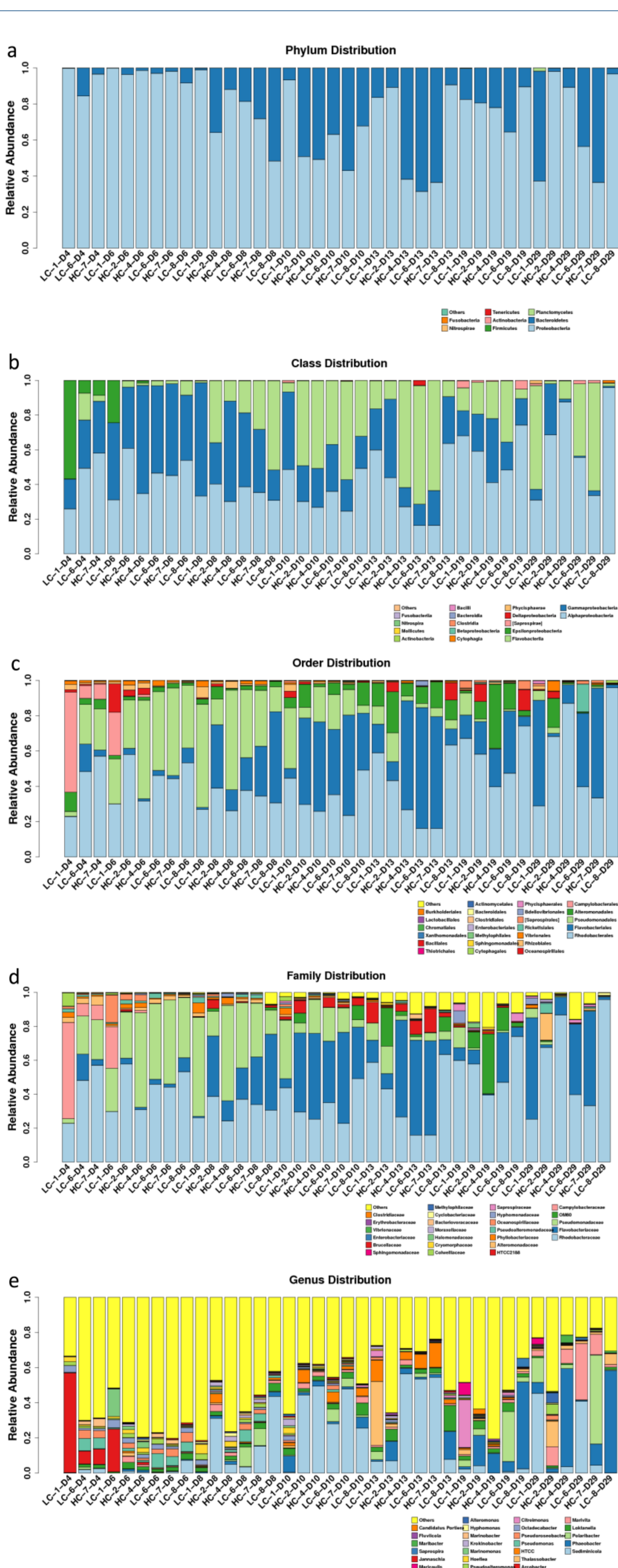
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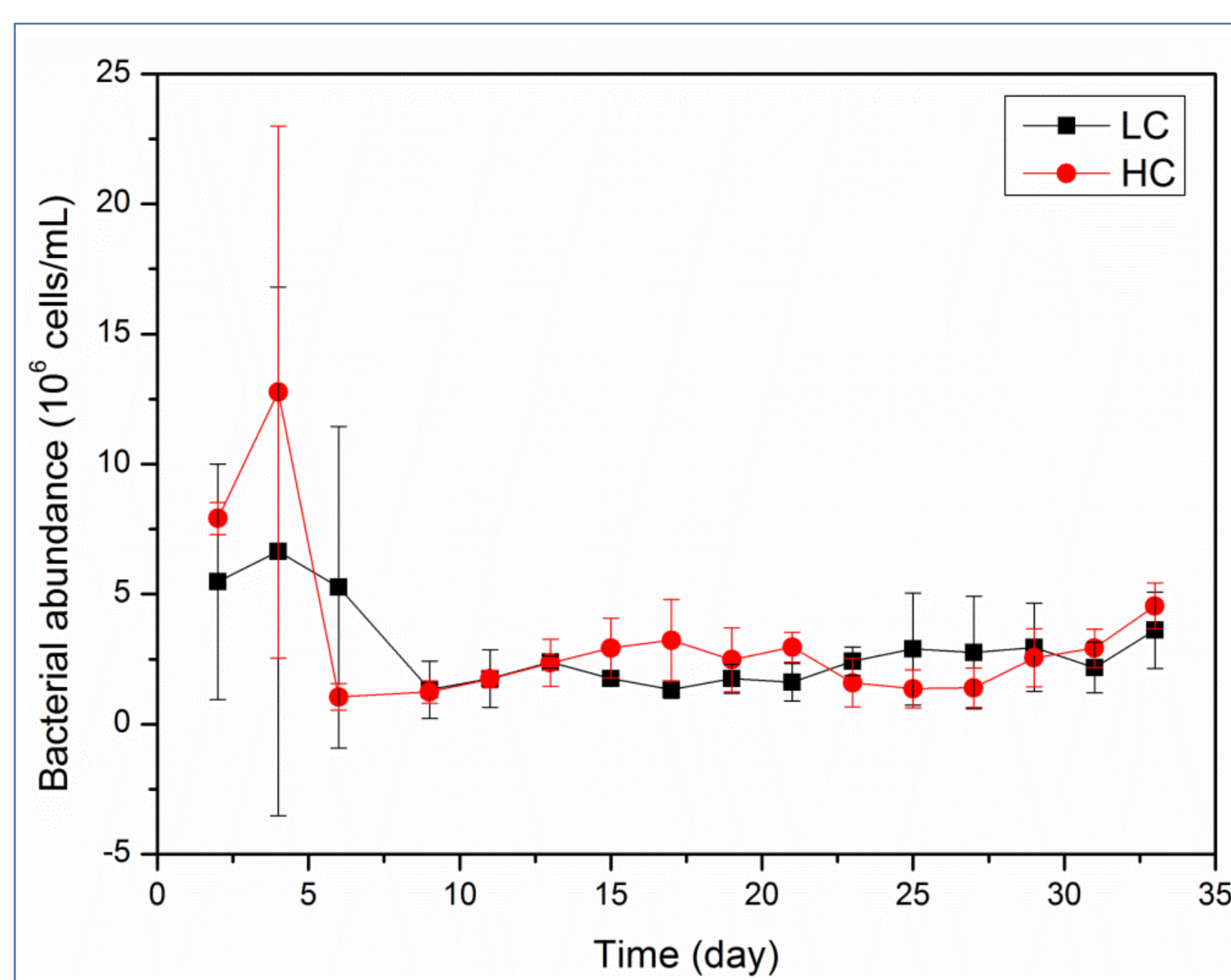
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**Introduction:** There is an increasing concern on effects of ocean acidification on marine bacteria and subsequent biogeochemical and ecological processes. Here, we show that effects of elevated CO<sub>2</sub> on changes in bacterioplankton communities during a mesocosm experiment in subtropical and eutrophicated coastal water of Southern China. These changes were evaluated by sequencing the 16S rRNA V3-V4 region. The results demonstrated that no significant differences were observed between high CO<sub>2</sub> (HC) and low CO<sub>2</sub> (LC) treatments in bacterioplankton community abundance, structure or composition. Analysis with the data from ecological networks indicated that HC did not significantly alter ecological network relationships between bacterioplankton species with high abundance, which implies the insensitiveness of the bacterioplankton community to HC. Nevertheless, Flavobacteria, which is known to be associated with phytoplankton and play an important role in the microbial carbon pump, showed higher relative abundance under HC during the early stage of phytoplankton bloom in the mesocosms.

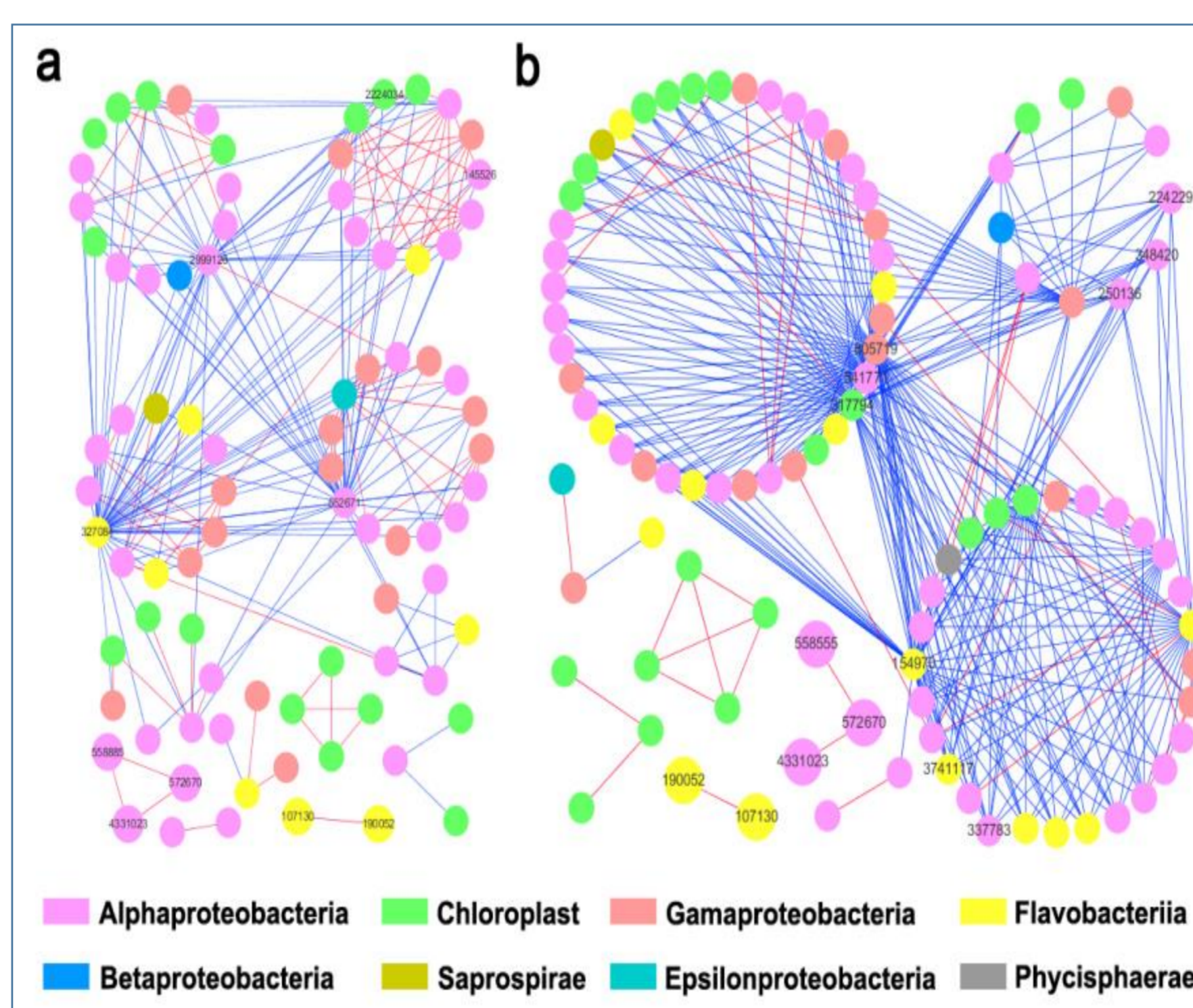
**Key-words:** ocean acidification, mesocosm, eutrophication, ecological network, Flavobacteria



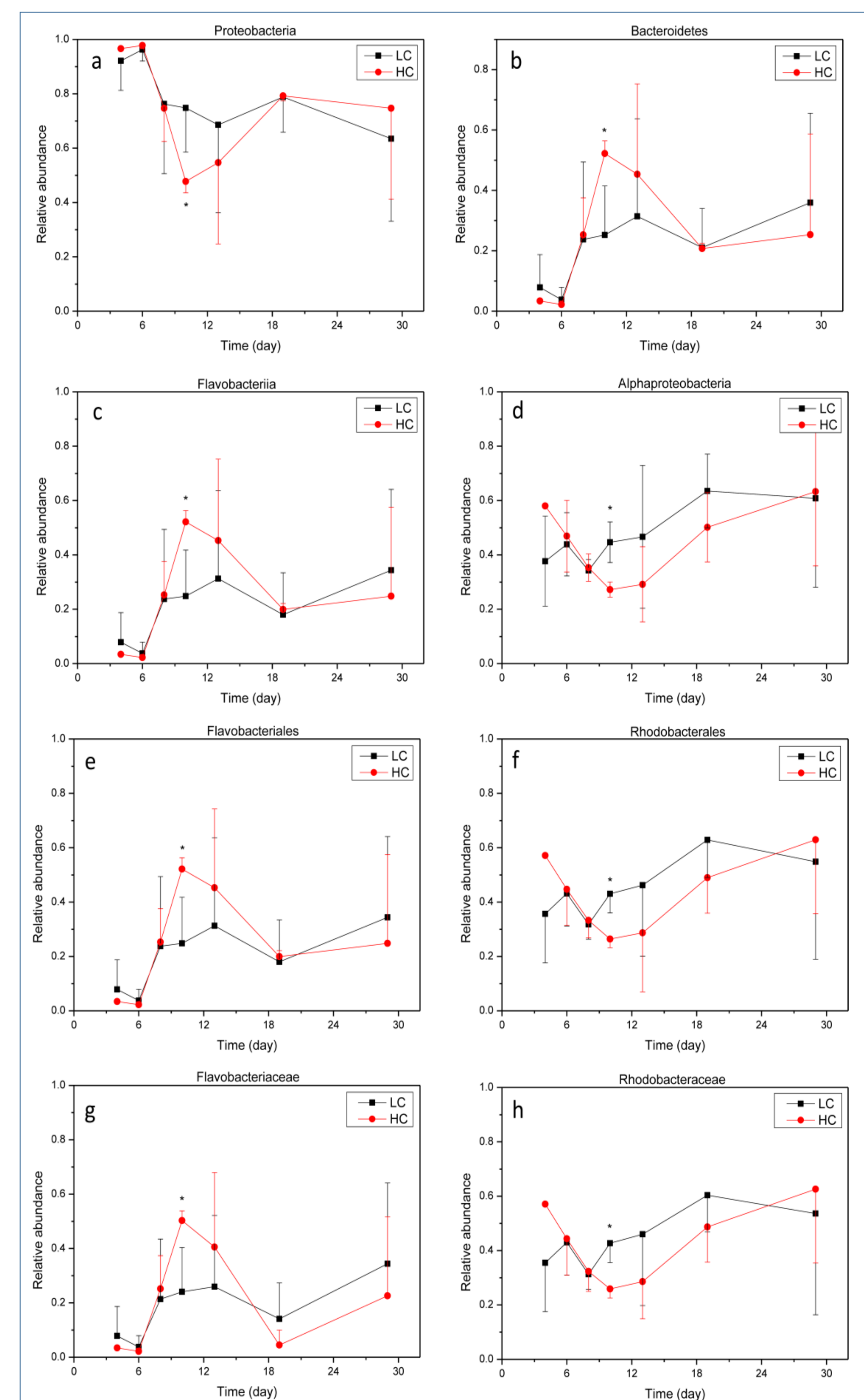
**Fig.2** Bacterioplankton community structure overview at different taxonomic levels during day 4, 6, 8, 10, 13, 19 and 29. X-axis represents sample name (for example, LC-1-D4 refers to bacterioplankton in mesocosm bag 1 with LC treatment collected on day 4) and the Y-axis represents relative abundance of different groups of bacterioplankton.



**Fig.1** Bacterial abundance at different time points throughout the duration of the experiment. The red line represents the average bacterial abundance in HC mesocosm bags 2, 4, 7. The black line represents the average bacterial abundance in LC mesocosm bags 1, 6, 8. Data are the means  $\pm$  SD



**Fig.4** Bacterioplankton network interactions under HC and LC conditions. Each node represents an OTU. Node colors demonstrate different taxon. Each line connects two OTUs. A blue line indicates a negative interaction between nodes suggesting a predation or competition while a red line indicates a positive interaction suggesting mutualism or cooperation. OTUs with importance are marked with OTU identification numbers.



**Fig.3** The relative abundance over time of primary taxa of the bacterioplankton community; HC (2, 4, 7 mesocosm bags) in red and LC (1, 6, 8 mesocosm bags) in black. Data are the means  $\pm$  SD, Proteobacteria (a) and Bacteroidetes (b) are phylum level; Flavobacteria (c) and Alphaproteobacteria (d) are class level; Flavobacteriales (e) and Rhodobacterales (f) are order level; Flavobacteriaceae (g) and Rhodobacteraceae (h) are family level. The asterisk represents a difference at  $p < 0.05$ .

**Conclusion:** This FOANIC-XMU mesocosm study described here provides novel insights into how elevated CO<sub>2</sub> combined with eutrophication effect the bacterioplankton community structure and ecological network in subtropical coastal sea. The results reported here indicate that overall community structure and diversity of bacterioplankton were not significantly altered by elevated CO<sub>2</sub> combined with eutrophication. Results reported here indicate that in the context of eutrophication, the relative abundance of phytoplankton associated Flavobacteria, which play an important role in HMW DOM degradation in the ocean, was higher under HC at an early stage of phytoplankton bloom. The results reported here further highlight the influence of ocean acidification on marine carbon cycling regulated by bacterioplankton and the underlying mechanisms. These may increase attention in this area leading to much needed further investigation.