

Taxonomic composition of microbial communities associated to *Caulerpa prolifera* along acidified Vulcano shallow hydrothermal vent

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Siphonous green seaweeds are complex algae capable of hosting rich and diversified endo- and epibiont bacterial communities, whose specificity is still largely unknown (1). Understanding the mechanisms underlying the complex seaweed-bacteria association in nature may provide information on the fitness of these species, especially in peculiar environments like marine hydrothermal vents. The green algae *Caulerpa prolifera*, collected from the shallow hydrothermal vent of Baia di Levante in Vulcano Island (Aeolian Islands, Italy) is considered, along the seagrass *Cymodocea nodosa*, the most abundant vegetal species of this site (2). Here, we propose to investigate the microbial community associated with specimens of *C. prolifera* inhabiting this hydrothermal vent area. Our results demonstrated that the taxonomic structure of the associated microbial communities is related to the physical-chemical parameters detected at the sampling site. Metabarcoding analysis carried out through sequencing of V3-V4 region of 16S rDNA showed that Proteobacteria, Bacteroidota, Planctomycetota, Cyanobacteria and Actinobacteriota were the most abundant Phyla, showing a similar community to that previously reported for water samples at the same time and in the same area (3) and to the same genera *Caulerpa* collected in different areas (4). A high microbial diversity was detected at genus level, with 73 different genera representing 5 main families: *Rhodobacteraceae* (41 genera), *Flavobacteraceae* (19 genera), *Pirellulaceae* (9 genera), *Thiotricaceae* (3 genera), and *Thalassospiraceae* (1 genus). This study provided new insights into the complex association

between bacteria and these algal species, suggesting a defined composition of microbial communities.

References:

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