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Isolation, characterisation and phylogenetic diversity of culturable bacteria associated with marine microalgae from saline habitats of south India

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ABSTRACT: Cultivated microalgae are an essential source of nutrition to several farmed finfish, shellfish and many other commercially significant aquaculture species. Knowledge of microalgae-associated microhabitat is important for the development of a successful, pathogen-free hatchery rearing system. Therefore, an attempt was made to isolate (1), characterise (2) and determine the phylogenetic diversity of (3) bacteria associated with cultured microalgae, which are used as live feeds in many finfish and shellfish hatcheries. From 10 selected microalgal cultures, 34 bacterial isolates were obtained with total bacterial counts of 10^1 to 10^5 CFU ml⁻¹. Most notably, we checked the presence of *Vibrio* spp., the major aquaculture pathogen in all tested microalgae and their absence suggests the suitability of these microalgae for use in aquaculture systems. Phylogenetic analysis based on 16S rDNA sequencing revealed that the bacterial phylotypes associated with these microalgae were affiliated to *Gammaproteobacteria*, *Alphaproteobacteria* and *Flavobacteriia* classes. The genus *Marinobacter* (47%) was found to be the most predominant cultivable bacterium followed by *Alteromonas*, *Labrenzia*, *Oceanicaulis*, *Ponticoccus*, *Stappia* and *Rheinheimera*. Bacteria belonging to the genera *Gaetbulibacter* and *Maritalea* were also detected and, to the best of our knowledge, this is the first report of association of these bacterial groups with microalgae. The biochemical, enzymatic and antibacterial characteristics and tolerance to various abiotic stress factors of these bacterial isolates are also described in the present paper. Altogether, the present study gives an insight into the phycosphere of cultivated microalgae, which can be further explored for improving the productivity and reliability of indoor and outdoor microalgal culture systems.

KEYWORDS: Microalgal-bacterial interaction · Microalgae · Associated bacteria · 16S rDNA · Phylogeny

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