

**Dataset of 16S ribosomal DNA sequences of bacteria isolated from marine red algae
*Kappapycus alvarezii***

ABSTRACT

The data provided in the article contains bacterial community profiles present on the surface of red algae (*Kappapycus alvarezii*) isolated directly after collection and after 30 days of cultivation in a closed circulation system. The explants of *Kappapycus alvarezii* were cultivated in a laboratory setting under controlled growth conditions for 30 days in order to determine bacteria that could adapt to controlled culture conditions. Amplification and sequencing of bacterial 16S rDNA amplicons were performed on bacterial isolates associated with the seedlings. The 16S rDNA gene sequences were analyzed, trimmed, and assembled into contigs using DNA Baser Sequence Assembler (V5) software. Taxonomic identification for the assembled sequences was achieved using the online BLAST (blastn) algorithm, and the construction of a phylogenetic tree was performed using the MEGA7 software. The data reveals a distinct set of microbial variations between day one and day 30. The phylogenetic tree depicts four major clusters, *Vibrio*, *Pseudoalteromonas*, *Alteromonas*, and *Bacterioplanes* resident on the surface of the *K. alvarezii*. Comparison between these two bacterial groups provides evidence of the persistent marine bacteria that adapt to the long-term culture in closed circulation systems. Raw data files are available at the GenBank, NCBI database under the accession number of MZ570560 to MZ570580.