

Cultivation and genomic insights into marine bacteria of the SAR202 clade (난배양성 해양세균 SAR202 분기군의 배양 및 유전체 특성)

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The SAR202 clade is one of the most abundant bacterioplankton groups in mesopelagic and bathypelagic ocean. Previous studies based on single-amplified genomes and metagenome-assembled genomes showed several ecologically relevant genomic features of the SAR202 clade, such as subclade-specific expansion of several enzyme families. However, no isolates of the SAR202 clade have been cultured, hampering experimental characterization of the clade. Here, we report the first successful cultivation of the SAR202 clade. A total of 24 strains that are very closely related to each other and affiliated with the SAR202 clade group I were cultivated from coastal surface water by dilution-to-extinction cultivation. Four strains selected for further characterization showed very slow growth with a doubling time of approximately 80 hours. Light had a negative effect on the growth of the SAR202 strains, ranging from growth retardation at weak intensities to cell death at strong intensities. The genomes of four strains were ~3.08 Mbp long, with G+C ratio of 51.8%, and showed features of organoheterotrophs. A gene cluster for archaella (archaeal flagella) was found in the genomes: to our knowledge, this is the first report of archaella genes in bacterial isolates. In accordance with previous studies, a huge expansion of COG4948 (enolase superfamily) was observed; more than 2.8% (80 of 2,854) of predicted proteins were assigned to COG4948. Comparison to representative genomes of GTDB showed that the expansion of COG4948 is a distinguishing feature of the SAR202 group I among all prokaryotes. Several substrates such as L-fucose and L-rhamnose and their lactone and acid forms, the utilization of which is predicted to require COG4948 enzymes, promoted the growth of the SAR202 strains.