

Dynamics of bacterial community composition associated with a harmful raphidophyte, *Chattonella marina*

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Abstract

Chattonella marina (*C. marina*) is one of the most common harmful red tide algae in western part of Japan. *C. marina* has been shown to interact with various kinds of marine bacteria that are either mutualistic or antagonistic to the algae. Some of the bacterial isolates from the algal blooming sites have been examined for their ability to kill *C. marina* (Imai et al. 1991, 1993, 2006). Growth of *C. marina* can also be promoted by other bacteria capable of producing chemical substances to enhance algal growth (Park et al. 2016). In non-axenic culture of *C. marina* strain A85, bacteria cells grew rapidly during early-exponential and late-exponential period of algal growth (Wada et al. 2017). As the algal culture has been maintained in laboratory conditions for more than three decades, the algal-bacterial interaction may be regarded as equilibrated. The aim of this study is to gain further insights into the relationship between *C. marina* strain A85 and associated bacteria. We took culture-dependent and culture-independent approaches to address the relationship. As a culture-dependent approach, heterotrophic bacterial colonies isolated from subsamples of *C. marina* A85 culture were purified onto 1/2 Zobell agar plates. The 16s rRNA genes of the isolates were sequenced by using the ABI PRISM 3100 genetic analyzer. Sequences were analyzed with the MEGA 6 and BLAST. In a culture independent approach, DNA samples extracted from subsamples of *C. marina* A85 culture were used for amplicon sequencing of the bacterial 16s rRNA genes with the Miseq platform. The 16s rRNA data were analyzed with R studio and Primer 6 software. We obtained a total of 14 bacterial isolates from *C. marina* A85 culture, all of which belonged to *Proteobacteria*. More than half of them were affiliated with *Alteromonadales* in *Gammaproteobacteria* regardless of the algal growth phase. On the other hand, amplicon sequencing of the 16SrRNA genes from associated bacterial community revealed that *Firmicutes* and *Bacteroidetes* were predominant during the initial phase of algal growth, while *Proteobacteria* and *Cyanobacteria* became dominant after the mid-exponential growth. The present results suggest that *C. marina* exerts substantial impacts on the composition and growth of associated bacteria.