## 琉球大学学術リポジトリ

巨視的群体を形成する糸状シアノバクテリアを主体 とした、沖縄沿岸産シアノバクテリアの多様性と分 類

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## Abstract

Title

Diversity and taxonomy of cyanobacteria from coasts of Okinawa, Japan, mainly macroscopic colony forming filamentous cyanobacteria

巨視的群体を形成する糸状シアノバクテリアを主体とした、沖縄沿岸産シアノバクテリアの多 様性と分類

Okinawa has extensive coastline possessing extraordinary diversity of marine cyanobacteria. This group becomes very important component for marine ecosystem due to their contribution in global primary production in the ocean. Beside their ecological importance, many species of marine cyanobacteria are well known as prolific producers of various kind of bioactive compounds with biomedical relevance. According to their ecological importance and capability to produce natural products, marine cyanobacteria have become interesting subject for various studies. Nowadays, the studies of marine cyanobacteria have increased since the introduction of modern molecular method. The molecular method based on genetic analysis have routinely been applied in various cyanobacterial studies, such as diversity, taxonomy, as well as community structures. In this study, a metabarcoding technique were applied to investigate seasonal composition of small unicellular cyanobacteria in two coral reef ecosystems around Sesoko Island. Moreover, we also characterized marine macroscopic colony-forming filamentous (MMCFF) cyanobacteria based on polyphasic taxonomy in order to reveal their diversity in Okinawan coastlines. Furthermore, more detail identification with additional analyses of ITS phylogeny and secondary structures were applied to describe novel species from genus Neolyngbya and Okeania. The result of this study showed that two unicellular marine cyanobacteria (Synechococcus and Prochlorococcus) together with two species of pico-eukaryotic algae dominated pico-phytoplankton community in two coral reefs around Sesoko Island. In general, the abundance of these two cyanobacterial species increased in summer season. Furthermore, the pico-phytoplankton compositions between two sampling sites almost had no significant differences. From investigation of MMCFF cyanobacteria, we found that MMCFF cyanobacteria were very diverse both from morphology and molecular genetics. The 16S rRNA phylogenetic inference revealed that Okinawan MMCFF cyanobacteria were genetically diverse, and clustered in some distinct clades. At least six genera were successfully identified from all samples of MMCFF cyanobacteria from Okinawan coasts. A total three cyanobacterial genera: Moorena, Okeania and Caldora showed strong cytotoxic activity against HeLa cells with IC50 below than 1 µg/ml. Furthermore, more detail characterization was also done for specimens morphologically corresponding to genus Neolyngbya and Okeania. The phylogeny 16S rRNA gene and ITS region indicated presence of new species from these two genera. The ITS secondary structures of specimens collected from Okinawa presented unique structures both in structure form and configuration. The ITS secondary structures provided additional evidence for speciation. Hence the new taxonomic names were proposed for these undescribed species from Neolyngbya and Okeania. Overall, this study may contribute to improve knowledge of marine cyanobacteria, especially in diversity, taxonomy and community structures.

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