B207 Vertical Distribution of Benthic Microalgae in Intertidal Muddy Flats

Lee, Hak Young
Department of Biology, Chonnam National University

Benthic microalgae in intertidal muddy flats in Kamami beach of Youngkwang, Chonnam was studied to determine the vertical distribution and migration of benthic microalgae. Core samples of muddy flats were collected every 3 hours intervals after 6 hours of hide tides, and cell number and chlorophyll *a* concentration were analyzed from each 1 mm depth of muddy flats. Total cell numbers and chlorophyll *a* concentrations of benthic microalgae decreased in surface layer (0-1 mm depth) after desiccation at ebb tides. Maximum increase in cell number and chlorophyll *a* concentration were observed at 1-2 mm depth of muddy flats. The major flora of benthic microalgae was pennate diatoms. Migration activity was highest just after desiccation and migration was limited to upper 3 mm depth.

B208 Diversity of Repetitive Sequences in Toxigenic Cyanobacteria Detected by Repetitive Elements-Primed PCR

Chang Won Choi[1], Jung Mo Koo[1], Soon-Ae Yoo[1], Sang Ho Park[2].
[1]Department of Biology, Division of Life Science, PaiChai University, Taejon 302-735.
[2]Research Center for Biomedicinal Resources, PaiChai University, Taejon 302-735, Korea

Under culturing condition, the filamentous cyanobacteria, *Anabaena* sp. was lacking of characteristic specialized cells such as heterocysts and alkinetes. More significantly, one of *Oscillatoria* sp. was unusual chain-shape. Instead of morphological parameters, repetitive primed PCR (rep-PCR) was used to generate unique and identifying DNA profiles for members of the cyanobacterial genera *Anabaena* and *Oscillatoria*, which are responsible for much of the production of poisonous blooms in various freshwater systems. Rep-PCR performed on 10 isolates of the cyanobacteria with STRR1A and LTRR sequences derived from cyanobacterial genome, gram-negative bacterial ERIC and REP sequences, and eukaryotic repetitive sequences, led to the identification of 10 distinct genotypes. Grouping analysis of cyanobacterial isolates based on rep-PCR using the various sources of repetitive primers showed a close correspondence but having a slight difference. A methods based on the single or the combination of repetitive oligonucleotides in a single PCR were applied to provide specific and repeatable DNA fingerprints for cyanobacterial isolates. Analysis of DNA typing results obtained clearly distinguishes between the genus *Anabaena* and *Oscillatoria*.