Population analysis of the toxic dinoflagellate genus *Alexandrium* by novel molecular markers

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The geographic expansion of the toxic dinoflagellates genus *Alexandrium* has been shown to be world wide ranging. The members of the genus *Alexandrium* ocnstituted of 20-30 species did not show substantial differences in their morphology, which is mostly referred in the 'tamarensis species complex', except some species. Though rDNA sequences variations are very few and pseudogene types are so diverse that it is difficult to use them as the specific markers.

In this study, we outlined Korean and Japanese *A. tamarense* and *A. catenella* regional isolates by phylogenetic analysis inferred from no cutting alignments of LSU rDNA D1-D2 and SSU rDNA sequences to group these regional isolates. The results were compared to RFLP patterns of PCR products targeted chloroplast DNA. Lastly screening of highly repeated microsatellite DNA which is frequently used for population analysis in eukaryotes was conducted.

A. catenella regional strains identified by the sequencing of rDNA D1-D2 domain were divided into at least 3 groups of type E, CMC and Chinese type, divergence root may not be deep comparing with that of *A. tamarense* whose pseudogenes are very variable. Results of RFLP pattern and the phylogeny of the unknown gene targeting chloroplast showed that Korean and Japanese *A. catenella* regional isolates were divided into 3 types: Korean, Japanese and the third CMC types. Population-specific PCR amplification with Japanese *A. catenella* type-specific PCR primers was useful method for population analysis of *A. catenella*. Various types of satellite sequences such as 5 nucleotides repeats were obtained from *A.*

tamarense and *A. catenella*. The 5 nucleotides repeats were primed at the both 3′ and 5′ ends, and these repeats were prominent as longer repeated motifs. This repeated DNA was intercalated as internal sequences containing various types subrepeats. It is expected that these satellite DNA would be a useful molecular population marker through detail comparison among *Alexandrium* regional isolates to trace their transferring pathway and to prevent their human-associated their regional extents.