

Sequence analysis of partial LSU rDNA of three *Alexandrium* species (Dinophyceae) hitherto unreported

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We, for the first time, reported molecular sequences of large subunit ribosomal DNA D1-D3 region of *A. hiranoi*, *A. leei* and *A. satoanum* hitherto unreported. In addition, this study presented the full-length sequences of *A. affine*, *A. fraterculus*, *A. catenella* and *A. tamarense* occurring in Korean coastal waters. In total, 17 *Alexandrium* morphospecies were subjected to the phylogenetic analysis using the Maximum-likelihood (ML) method. The alignment result of sequences of *A. hiranoi* and *A. pseudogonyaulax* showed that there were only two substitutions without length heterogeneity implying their genetic affiliation. In ML tree, *A. leei* formed a deeply diverging branch probably because of the accelerated evolutionary rate, and its phylogenetic position was so ambiguous to resolve the phylogenetic relationship to the residual taxa. An *A. satoanum* culture showing morphological variation in the sulcal plate formed an independent divergent branch with consistent sister relationship to *A. hiranoi/A. pseudogonyaulax* clade supported by the high posterior probability (PP) value. Blast search in GenBank showed the sequence data of *A. affine*, *A. fraterculus*, *A. catenella* and *A. tamarense* corresponded to their morphological species designation. In ML tree, *Alexandrium* species were commonly split into four main clades. The inter-clade relationships were not clear and usually supported by the weak PP values. In general, the sulcal plate of *Alexandrium* species seemed to reflect the true phylogeny at the main clade level, and the connection between the 1 and the apical pore complex seemed to reflect the phylogeny at the subclade level.

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