

Phylogenetic relationships in the harmful dinoflagellate *Cochlodinium polykrikoides* (Gymnodiniales, Dinophyceae) inferred from LSU rDNA sequences

Abstract

Phylogenetic relationships among chain-forming *Cochlodinium* species, including the harmful red tide forming dinoflagellate *Cochlodinium polykrikoides*, were investigated using specimens collected from coastal waters of Canada, Hong Kong, Japan, Korea, Malaysia, México, Philippines, Puerto Rico, and USA. The phylogenetic tree inferred from partial (D1-D6 regions) large subunit ribosomal RNA gene (LSU rDNA) sequences clearly differentiated between *C. polykrikoides* and a recently described species, *Cochlodinium fulvescens*. Two samples collected from the Pacific coasts of North America (British Columbia, Canada and California, USA) having typical morphological characters of *C. fulvescens* such as the sulcus located in the intermediate region of the cingulum, were closely related to *C. fulvescens* from western Japan in the phylogenetic tree. *Cochlodinium polykrikoides* formed a monophyletic group positioned as a sister group of the *C. fulvescens* clade with three well-supported sub-clades. These three clades were composed of (1) East Asian, including specimens collected from Hong Kong, western Japan, and southern Korea, (2) Philippines, from Manila Bay, Philippines and Omura Bay, Japan, and (3) American/Malaysian, from the Atlantic coasts of USA, the Pacific coast of México, Puerto Rico, and Borneo Island, Malaysia. Each of these clades is considered to be a so-called "ribotype" representing the population inhabiting each region, which is distinguished based on ribosomal RNA gene sequences in the species despite similarities in their morphological characters. © 2007 Elsevier B.V. All rights reserved.