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Harmful Algae

journal homepage: www.elsevier.com/locate/hal



Phylogenetic analysis of the toxigenic genus *Amphidinium* (Amphidiniales, Dinophyceae) revealed an unexpectedly high diversity in the Asia-Pacific region

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ARTICLE INFO

Keywords: Amphidinols Benthic dinoflagellates DNA metabarcoding Molecular phylogeny Morphology

ABSTRACT

The dinoflagellate genus Amphidinium encompasses several toxic species known to cause harmful algal blooms. Despite their ecological significance, the diversity within this genus may be underestimated due to the morphological similarities among species. In this study, we established 82 strains of Amphidinium by isolating single cells from the Asia-Pacific region. We examined their morphology using light and transmission electron microscopy. Additionally, we obtained partial sequences of the large subunit ribosomal (LSU) DNA and/or internal transcribed spacer regions for all strains, Furthermore, DNA metabarcoding targeting the LSU D1-D2 region was employed to detect species in the Bohai Sea, Yellow Sea, Mediterranean Sea, and Red Sea, where strain data is limited. The 82 strains were classified into 13 Amphidinium species. Among these were four undescribed species, provisionally named Amphidinium sp. 1 to Amphidinium sp. 4, as well as A. cupulatisquama, A. fijiensis, A. gibbosum, A. massartii, A. operculatum, A. pseudomassartii, A. thermaeum, A. tomasii, and A. trulla, based on both morphological and molecular analyses. DNA metabarcoding detected nine Amphidinium species. While Amphidinium gibbosum and A. tomasii are confined to tropical and warm subtropical waters, the other species exhibit a broader distribution. Molecular phylogenetic analysis revealed two distinct clades within the genus Amphidinium. Species in clade A, including A. uduigamense, A. stirisquamtum, A. operculatum, Amphidinium sp. 1, and Amphidinium sp. 2, share a characteristic sulcus that originates in the posterior one-third of the hypocone. In contrast, species in clade B are characterized by a sulcus that originates in the anterior or middle part of the cell. Additionally, amphidinol analysis was conducted on ten strains of five Amphidinium species using liquid chromatography-tandem mass spectrometry (LC-MS/MS), but amphidinols were below the detection limit. However, one strain of A. massartii produces a new amphidinol variant with a molecular mass of 1402.7 Da (34.47 fg cell-1) and hemolysis assays suggest the potential presence of novel amphidinols or related compounds in A. operculatum. Our findings underscore the significant diversity and potential risk posed by Amphidinium species in the Asia-Pacific region and beyond.

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https://doi.org/10.1016/j.hal.2025.102934

Received 10 April 2025; Received in revised form 18 July 2025; Accepted 22 July 2025 Available online 23 July 2025

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