

New diatom predatory amoebozoans from Sagami Bay, Japan

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Diatoms are major primary producers in marine environments. The population dynamics of diatoms are affected not only by abiotic factors such as temperature and nutrient availability but also by biotic factors, including viral lysis, grazing by zooplankton, and predation by protists. Compared to zooplanktons such as copepods and other small metazoans, the diversity and ecology of protists feeding on diatoms are underexplored. These diatom predatory protists are distributed among diverse eukaryotic lineages such as aphelids and chytrids (Fungi), bigyromonads, labyrinthulids, and oomycetes (Stramenopiles), cercozoans and endomyxans (Rhizaria).

Here, we focus on diatom predatory amoebae belonging to Amoebozoa. Amoebozoa is a eukaryotic supergroup including morphologically and ecologically diverse amoebae. Diversity of algivorous amoebozoans is poorly explored in contrast to endomyxan amoebae (e.g., vampyrellids). In 2025, we found two unknown amoebozoans feeding on the diatom *Chaetoceros* sp. during a regular survey at Sagami Bay, Japan. We successfully established two-membered cultures of amoebae and *Chaetoceros* sp. (strain KS183 and KS184). In this study, we aimed to identify and characterize these amoebae by light microscopy and molecular phylogenetic analyses of 18S rDNA sequences.

Amoebae of strain KS183 were generally monopodial, elongated, with an anterior hyaline area and posterior uroidal filaments. During predation on diatom cells, an amoeboid cell attached to the diatom frustule, became rounded, engulfed the diatom cell through the pore or gap of the frustule. This feeding behavior of KS183 resembled that of a described diatom predatory amoeba, *Rhizamoeba schneppii* from North Sea. Molecular phylogenetic analysis revealed that KS183 belonged to the class Tubulinea. KS183 was not related to the order Leptomyxida, including the genus *Rhizamoeba* but sister to the order Euamoebida, indicating it represents a new family of Euamoebida or a new order. Currently, sequence comparison between *R. schneppii* and KS183 is not possible because the sequence data of *R. schneppii* is unavailable.

Amoebae of strain KS184 exhibited dactylopodial morphotype. When it fed on diatoms, an amoeba cleaved the frustule, invaded inside, and engulfed diatom cell. Molecular phylogenetic analysis showed that KS184 belonged to *Paramoeba*/*Neoparamoeba* clade of the family Paramoebidae (Dactylopodida, Discosea) and was sister to *N. longipodiida* from deep-sea sediment of the Western Atlantic Ocean. *Paramoeba* and *Neoparamoeba* are well known as pathogens causing diseases of fish and some invertebrates, or they are presumed to be bacterivorous. This is the first record of diatom predatory species in Paramoebidae.

These findings revealed overlooked lineages of diatom predatory amoebozoans, even at new family or order levels, and unexpected ecological diversity of well-known pathogenic lineages. Further investigations of diatom predatory amoebozoans are necessary to understand interaction between diatoms and diverse eukaryotic predators in marine environments.

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