

# Phylogenetic relations of the dinoflagellate *Gymnodinium baicalense* from Lake Baikal

## Communication

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**Abstract:** Freshwater dinoflagellates still remain poorly studied by modern biological methods. This lack of knowledge prevents us from understanding the evolution and colonization patterns of these ecologically important protists. *Gymnodinium baicalense* is the most abundant, and possibly endemic, planktonic dinoflagellate from the ancient Lake Baikal. This dinoflagellate species blooms in the spring under the ice. This study analyzed the origin of this Baikalian dinoflagellate using three markers (two ribosomal and one mitochondrial DNA). It was found that this species is a true member of the order *Gymnodiniales* and has close relatives in the glacial melt waters of the Arctic Ocean. It seems that *G. baicalense* has diversified relatively recently from the arctic marine gymnodinioids. These results shed light on dinoflagellate biogeography and their colonizations in Lake Baikal biodiversity hotspot.

**Keywords:** Protists • Baikal • Biogeography • Evolution • 18S rRNA gene • ITS-2 • COI

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## 1. Introduction

Dinoflagellates are widespread aquatic protists. They occupy various ecological niches as photosynthetic, heterotrophic, or mixotrophic organisms. Some dinoflagellates are symbionts or parasites of other organisms. Many planktonic dinoflagellate species form seasonal blooms, and some marine species are toxic for humans [1]. Freshwater dinoflagellates are less studied than marine dinoflagellates; there are more than 1700 described species of free-living marine dinoflagellates and only about 220 described freshwater species [2]. Moreover, many of the known freshwater dinoflagellates have been described before electron microscopy and molecular genetic methods became available. Thus, identifying and comparing freshwater dinoflagellates from different groups and geographic locations is challenging. This lack of knowledge precludes an understanding of the evolution and colonization patterns of these protists.

Today there are two opposing opinions about the distribution of free-living microorganisms, including dinoflagellates. Some scientists claim that protists live in all environments that they can exploit [3], while others suggest the existence of endemic microorganisms is due to natural selection and geographical barriers (the moderate endemism hypothesis) [4]. In order to reject either of these two hypotheses, there is a need for a more comprehensive description of the taxonomy and distribution of these protists. Thus, data about poorly described or unknown species are needed. Also, prior cases of dinoflagellate endemism should be revisited using modern methods. For example, Gómez [5] argued that many endemic dinoflagellates species from the Mediterranean Sea were poorly described and that they were actually cosmopolitan species. On the contrary, endemic species may not be detected due to the lack of resolution of the morphospecies concept (based on light microscopy data) and the use of taxonomic literature based on European species. Molecular genetic

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