The role of biological interactions during bloom outbreak of *Karenia mikimotoi* in northern Fujian, China

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ABSTRACT

The blooms of *Karenia mikimotoi* have frequently occurred globally, posing a serious threat to marine ecosystems and the marine economy. Several blooms of *K. mikimotoi* occurred in the waters of Fuzhou and Ningde. We adopted a combined approach using microscopy observation, high-throughput sequencing technologies targeting 28S and 16S rRNA genes, and metagenomics to investigate the potential contributions of heterotrophic dinoflagellates, parasitic dinoflagellates, and microorganisms to the decline of these blooms. During the demise phase of two *K. mikimotoi* blooms in the Fuzhou waters, a significant presence of heterotrophic *Gyrodinium* spp. was observed, indicating their role in promoting the decline of the *K. mikimotoi* blooms through predation. Although a large number of parasitic dinoflagellates were detected in the water, none were found inside the cells of *K. mikimotoi*, suggesting their limited impact. Throughout the process of *K. mikimotoi* bloom, changes in microbial functional metabolism were observed, reflecting the effects of different stages of the bloom on microbial basal metabolic pathways, the synthesis of secondary metabolites, and amino acid biosynthesis. These changes may be linked to the adaptive strategies of microorganisms in the bloom environment.

MATERIAL AND METHODS

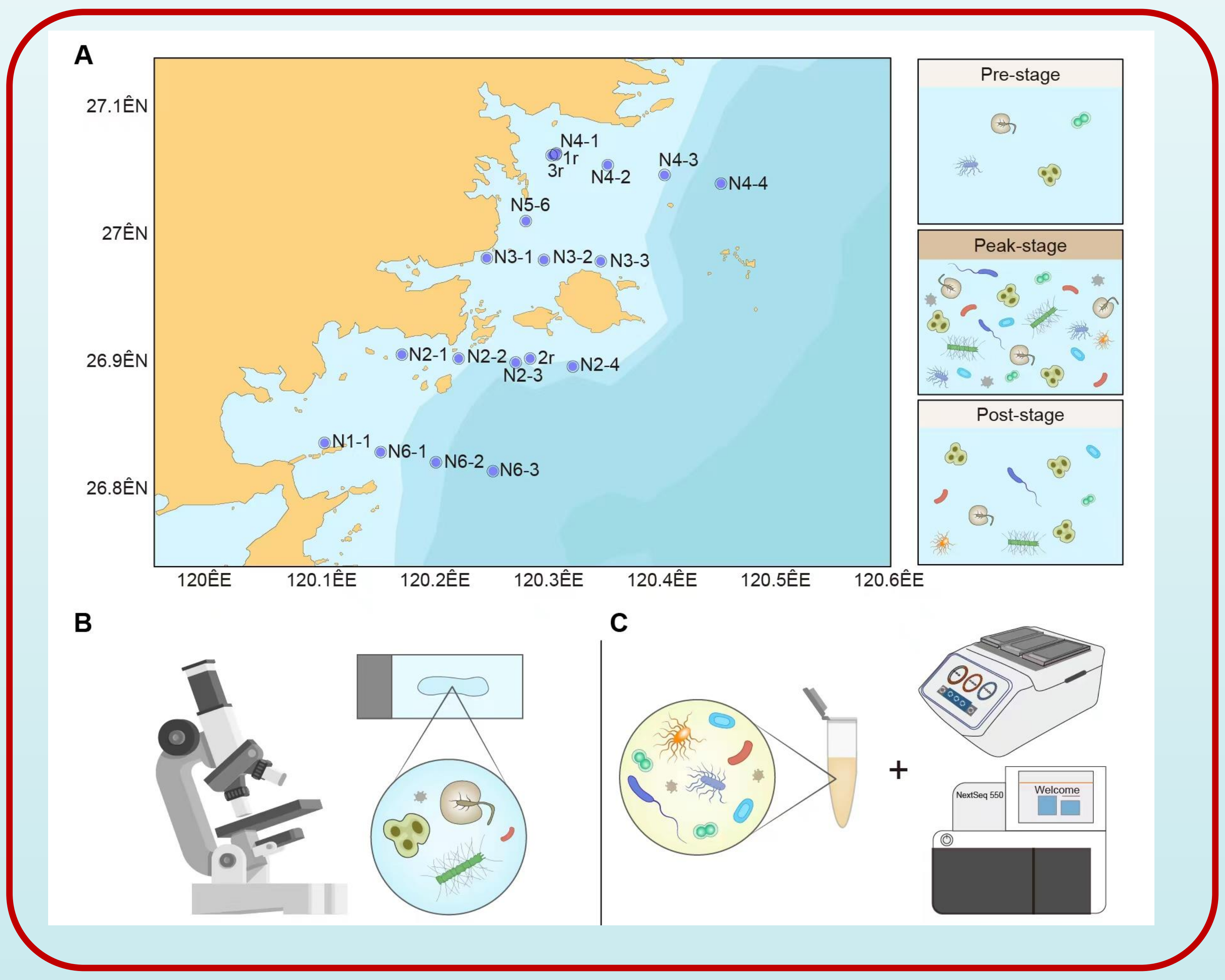

Fig. 1 A: sampling stations; B: light microscipy; C: DNA extraction and highthroughput sequencing

RESULTS

In late May 2021, a large-scale bloom of *Karenia mikimotoi* occurred in the waters of Fuzhou. Water samples collected on June 1 were examined by light microscopy. The density of *K. mikimotoi* reached 1.0 × 10^6 ind./L, along with two *Gyrodinium* species that were *G. moestrupii* and *G. fusiforme* (Fig. 2), with the larger species having a density of 1.0 × 10^5 ind./L. The bloom disappeared the next day, suggeting that the predation from *Gyrodinium* contributed the bloom decline.

A bloom of *Karenia mikimotoi* broke out in Sansha Bay, Ningde in June 2021. 16S rRNA gene high-throughput sequencing and metagenomics were employed. In the early stages, there was a positive correlation between the microbial community and parameters such as pH, temperature, and salinity. However, this relationship shifted to a negative correlation as the bloom developed and subsequently declined (Fig. 3). Notably, cyanobacteria were enriched before the *K. mikimotoi* bloom, with their relative abundance decreasing during the bloom, while the relative abundance of Thermoplasmatota increased and remained high after the *K. mikimotoi* decline.

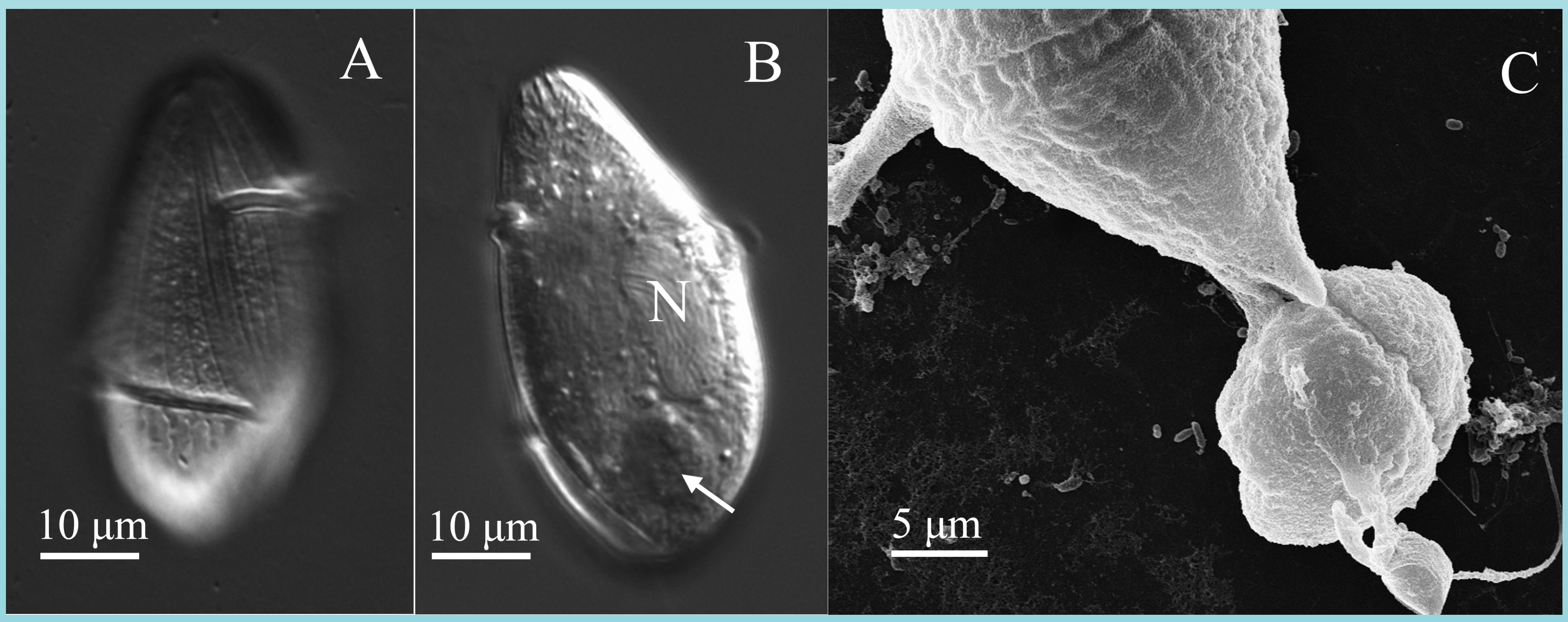

Fig. 2. A: *Gyrodinium moestrupii* (LM); B: The same cell showing a nucleus (N) and a prey inside (arrow). C: *Gyrodinium fusiforme* feeding on *Karenia mikimotoi*.

Throughout the *K. mikimotoi* bloom, changes in microbial functional metabolism were observed, reflecting the effects of different stages of the bloom on microbial basal metabolic pathways, the synthesis of secondary metabolites, and amino acid biosynthesis.

Bloom samples of *Karenia mikimotoi* were collected in Fuzhou in June 2024 and examined by light microscopy for parasitic dinoflagellate. However, no infection by the *Amoebophrya ceratii* complex was detected in the cells although the bloom is at a later stage, suggesting that parasitism is not vital for bloom termination.

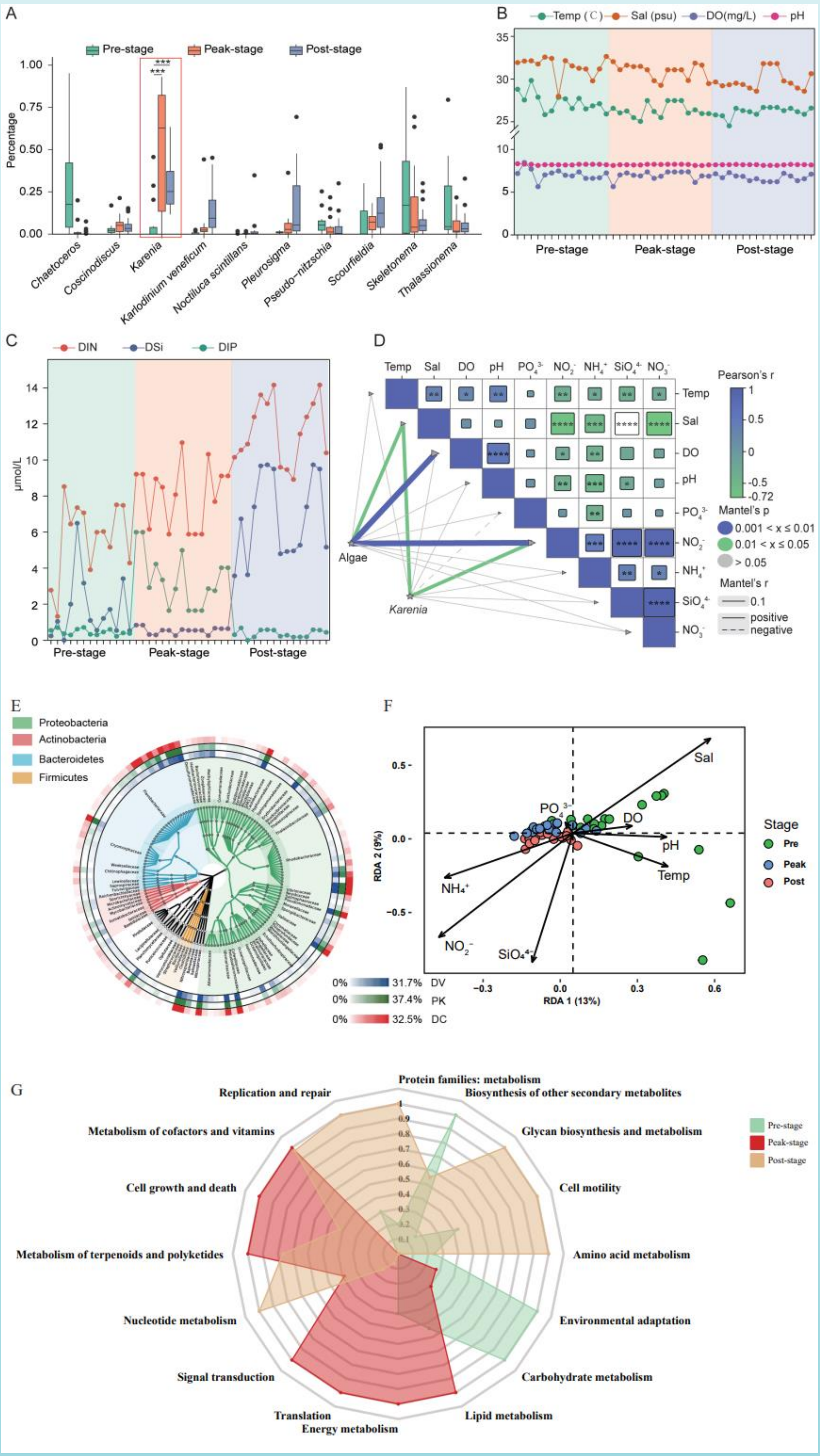

Fig. 3. A: Three stages of *Karenia mikimotoi* bloom; B: Environmental changes during the bloom; C: Nutrients changes during the bloom; D: Correlation between *Karenia mikimotoi* and environmental factors; E: Composition of microbial communities; F: Correlation analysis between microbial communities and environmental factors; G: Differences in microbial functions