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Metabarcoding analysis of harmful algal bloom species in the Changjiang Estuary, China

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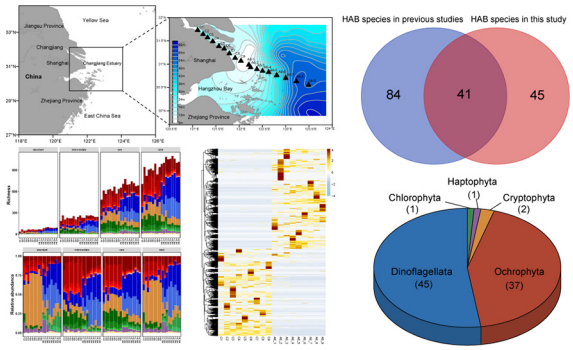
HIGHLIGHTS

- 86 HAB species identified in the Changjiang Estuary, with 45 undetected previously.
- Phytoplankton (including HAB species) distribution showed strong salinity-dependency.
- Rich *Skeletonema* species diversity revealed, with *S. marinoi* being the most abundant.

GRAPHICAL ABSTRACT



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ABSTRACT

Harmful algal blooms (HABs) frequently occur in estuaries because of their unique environmental conditions, including strong salinity gradients, rich nutrients, and complex currents. Numerous HAB species have been identified and characterized in estuaries worldwide, however, their composition and distribution patterns are still poorly understood. In this study, the first metabarcoding analysis of HAB species was conducted in the Changjiang Estuary. This study identified 86 HAB species, including 45 Dinoflagellata, 37 Ochrophyta, 2 Cryptophyta, 1 Haptophyta, and 1 Chlorophyta species. Most HAB species showed similar distribution patterns in the Changjiang Estuary, with higher relative abundances in the sampling sites outside the estuary. The results indicate that, in addition to HAB species being distributed along salinity and temperature gradients, several other key environmental factors influenced their distribution. To our knowledge, many of the HAB species identified in this study, including those that are unique to brackish water regions, such as *Katablepharis japonica* and *Skeletonema marinoi*, have not been reported in previous studies on the Changjiang Estuary. Furthermore, rich *Skeletonema* diversity was observed, with *Skeletonema marinoi* being the most abundant species. The richness of the HAB species identified in the Changjiang Estuary supports the existence of diverse HAB species, which could potentially form HABs under favorable environmental conditions. Overall, this study provides novel insights into the dynamics of HAB formation in estuaries.

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