



The functional diversity of bacterial microbiota associated with toxigenic *Prorocentrum* species

Oral

Microbiomes, Biological & Chemical Interactions

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Interactions between bacterial microbiota and epibenthic dinoflagellates such as *Prorocentrum* may influence the initiation, toxigenicity, and persistence of benthic harmful algal blooms (bHABs). These interactions likely involve complex chemical exchanges, including metabolites, toxins, and undefined bioactive compounds. This study characterized the bacterial diversity and core microbiota associated with 11 strains of three epibenthic *Prorocentrum* species from geographically distinct Mexican coastal waters. Using 16S rRNA gene (V3-V4) sequencing of monoclonal cultures, we identified 13 bacterial classes, with Alphaproteobacteria, Gammaproteobacteria, and Bacteroidia consistently dominant. Bacterial community structure varied significantly by dinoflagellate geographical origin but not between free-living (culture medium) and direct host-associated fractions. Twelve core bacterial taxa were identified, including *Algiphilus*, *Cohaesibacter*, *Labrenzia*, *Marinobacter*, and members of the Rhodobacteraceae. The bacterial profiles suggest mutualistic or commensal relationships with *Prorocentrum*. While these core members likely contribute to both primary and secondary metabolic functions, no direct link to dinoflagellate toxigenicity was identified. Further research on bacterial-dinoflagellate gene functions and

interactions is essential to elucidate their roles in toxigenesis and bHAB dynamics.

Palabras Clave

(1) Benthic dinoflagellates, (2) microbiome, (3) phycosphere.

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