

Bacterial community dynamics and predictive function of surf zone seawater in a recreational beach in Oostende, Belgium

Li Yunmeng¹, Van Acker Emmanuel², Janssen Colin², Asselman Jana³ and De Rijcke Maarten¹

¹ Flanders Marine Institute (VLIZ), InnovOcean Campus, Jacobsenstraat 1, 8400 Oostende, Belgium
E-mail: yunmeng.li@vliz.be

² Department of Animal Sciences and Aquatic Ecology, Ghent University, Coupure Links 653, 9000 Ghent, Belgium

³ Blue Growth Research Lab, Ghent University, Wetenschapspark 1, 8400 Oostende, Belgium

Coastal seawater is home to a diverse array of bacteria that play a critical role in the functioning of marine ecosystems. These bacteria perform various functions, such as decomposing organic matter, nitrogen cycling, and serving as food for other organisms. In addition to their ecological importance, bacteria present in seawater can also affect human health if they are inhaled, ingested or in contact with the skin. Understanding the bacterial community in coastal seawater is therefore essential for both ecological and public health reasons. Recreational beaches at the coast, which are visited by millions of people every year, increase the potential for exposure to potentially harmful bacteria and their toxins. The dynamic surf zone, where sea spray aerosols are formed, is of particular interest due to the potential for increased bacterial concentrations via the mixing of seawater and sediment. This study aimed to investigate the bacterial community and potential function in the surf zone seawater and to identify possible drivers affecting these variations. We collected 72 surface seawater samples from the surf zone of a recreational beach in Oostende, Belgium from March 2018 to November 2019. Bacterial communities were analyzed using full-length 16S rDNA sequencing by Nanopore sequencer MinION. Potential bacterial functions were determined using pathway prediction by phylogenetic placement (PAPRICA). Environmental data such as abiotic parameters (e.g., sea water temperature (SST) and wave height (WH)) and biotic parameters (e.g., Chlorophyll *a* (Chl *a*) and net primary production (NPP) estimates) were obtained from *Meetnet Vlaamse Banken* and *Ocean Productivity* database. The relationships among bacterial community, function, and environmental factors were determined using co-occurrence network analysis. The results of this study provide valuable insights into the bacterial community dynamics of surf zone seawater and their modulating factors, and may have implications for beach management and public health.

Keywords

Bacterial Communities; Predictive Function; Surf Zone Seawater; Long-Term Variation; Full-Length 16S rDNA Sequencing; Nanopore Sequencer Minion