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REVIEW

Exploring the oceanic microeukaryotic interactome with metaomics approaches

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ABSTRACT: Biological communities are systems composed of many interacting parts (species, populations or single cells) that in combination constitute the functional basis of the biosphere. Animal and plant ecologists have advanced substantially our understanding of ecological interactions. In contrast, our knowledge of ecological interaction in microbes is still rudimentary. This represents a major knowledge gap, as microbes are key players in almost all ecosystems, particularly in the oceans. Several studies still pool together widely different marine microbes into broad functional categories (e.g. grazers) and therefore overlook fine-grained species/population-specific interactions. Increasing our understanding of ecological interactions is particularly needed for oceanic microeukaryotes, which include a large diversity of poorly understood symbiotic relationships that range from mutualistic to parasitic. The reason for the current state of affairs is that determining ecological interactions between microbes has proven to be highly challenging. However, recent technological developments in genomics and transcriptomics (metaomics for short), coupled with microfluidics and high-performance computing are making it increasingly feasible to determine ecological interactions at the microscale. Here, we present our views on how this field will advance thanks to the progress in metaomics approaches as well as potential avenues for future research.

KEY WORDS: Microeukaryotes · Interactions · Single-cell genomics · Single-cell transcriptomics · High-throughput sequencing

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