

TITLE: Metagenomics Sheds Light on the Ecology of Marine Microbes and Their Viruses

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ABSTRACT:

Multiple associations of marine microbes with each other, and with their environment, have recently been discovered, shedding light on their ecological niches and the community assembly process. Culture-independent approaches have drastically expanded our knowledge of the diversity of marine bacteria, archaea, microeukaryotes and viruses, redefining our understanding of the evolution of life on Earth. Omics-based approaches provided deeper insights into the contributions of both novel and previously known taxa to biogeochemical cycles and other ecosystem-sustaining processes. Most ecogenomics studies are focused on Picocyanobacteria and SAR11 from the euphotic zone, while other taxa and ecosystems have been neglected. Metagenomics revealed the massive diversity of marine viruses and showed that their influence over host communities is much broader than previously conceived. Advances brought about by omics-based approaches have revolutionized our understanding of the diversity and ecological processes involving marine archaea, bacteria, and their viruses. This broad review discusses recent examples of how genomics, metagenomics, and ecogenomics have been applied to reveal the ecology of these biological entities. Three major topics are covered in this revision: (i) the novel roles of microorganisms in ecosystem processes; (ii) virus?host associations; and (iii) ecological associations of microeukaryotes and other microbes. We also briefly comment on the discovery of novel taxa from marine ecosystems; development of a robust taxonomic framework for prokaryotes; breakthroughs on the diversity and ecology of cyanobacteria; and advances on ecological modelling. We conclude by discussing limitations of the field and suggesting directions for future research. Advances brought about by omics-based approaches have revolutionized our understanding of the diversity and ecological processes involving marine archaea, bacteria, and their viruses. This broad review discusses recent examples of how genomics, metagenomics, and ecogenomics have been applied to reveal the ecology of these biological entities. Three major topics are covered in this revision: (i) the novel roles of microorganisms in ecosystem processes; (ii) virus?host associations; and (iii) ecological associations of microeukaryotes and other microbes. We also briefly comment on the discovery of novel taxa from marine ecosystems; development of a robust taxonomic framework for prokaryotes; breakthroughs on the diversity and ecology of cyanobacteria; and advances on ecological modelling. We conclude by discussing limitations of the field and suggesting directions for future research. the combination of stochastic and deterministic processes that together shape the taxonomic composition of biological communities. approaches based on isolating microorganisms or viruses from their original environment and cultivating them in the laboratory, usually in axenic cultures. If properly executed, allows the separation of a single population from the community. a field that aims to understand the ecology of microorganisms based on their genomes/metagenomes and the evolutionary and ecological patterns that can be derived from them. the multidimensional space volume of abiotic (environmental parameters) and biotic (other organisms and viruses) conditions in which an organism can survive, grow, and reproduce. classification of novel organisms or identification of known taxa (e.g., genera, species, or strains) through comparative analysis of their genomic content. viral infection process in which the viral genome is replicated alongside the host genome without the production of the new viral particles or cell burst, thus avoiding host death. viral infection process that culminates in death of the host cell due to bursting and release of the newly produced viral particles. complete or partial genome sequences obtained by assembling reads from one or multiple metagenomes followed by binning together the assembled contigs. analysis of genomic sequences of a whole community, directly from a sample without any prior cultivation steps. an assemblage of potentially interacting microorganisms within defined spatial and temporal limits. single-celled, microscopic eukaryotic microbes, that is, the protists. reconstruction of phylogenies based on multiple genes (often the entire core genome of a group) yielding more robust results than strategies based on a single or a small number of phylogenetic markers. complete or partial genome sequence obtained by sequencing the amplified DNA of a previously isolated single cell or viral particle.

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