

Discovering prokaryotic dynamic in marine environment by using a combination of genetic analysis and numerical ecosystem models

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Despite the many important roles, they play, bacteria are one of the least known components of the marine biogeochemical cycles. Even if they have highly diverse functional roles in the ecosystem, their representation in the marine biogeochemical models is constrained by only one functional group. In the gene-centric model approaches that uses functional gene abundance as a state variable allows for the integration of environmental genomics data and biogeochemical models. In order to determine the temporal dynamics of the species composition, the community structure, the abundances of the bacteria that play significant roles in the cycling nitrogen and phosphorus and the rates of the reactions that the bacteria perform we have used a combination of genetic analyses, biochemical measurements and numerical models in the Mediterranean. Samples (in total 65) were collected from 6 different water column depth in the oligotrophic observation station of Erdemli Time Series with monthly intervals for one year and sequenced by NGS platform using 16S rDNA Metagenomics approach. Among which, 1993 sequence variants observed, Pelagibacteraceae, Alphaproteobacteria and Flavobacteriaceae classes and *Candidatus portiera* were the highly dominantly discovered taxa. Water column stratification can be concluded as the main driving factor influencing the communities' composition. These results were further analyzed for the integration of different functional groups to numeric ecosystem model for better understanding of marine microbial reactions and carbon and nitrogen cycle in the changing marine ecosystems.

Keywords: 16S rDNA, amplicon sequencing, numerical models

Identification of Fish Species in Eurasian Otter (*Lutra lutra*) Diet Using DNA Metabarcoding of Faecal Samples

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The aim of this study is to analyze how human activities affected Eurasian Otter's nutritional behavior and test the availability of DNA metabarcoding as a tool for diet composition analysis. For this purpose, we began by studying a specific lake in Turkey inhabited by a single endemic fish species together with several non-indigenous fish species. In this preliminary study, six fresh faeces were collected throughout the perimeter of the lake area. DNA was extracted from all faecal samples using a stool DNA purification kit. For the diet analysis, hyper variable region of 12S rRNA gene was amplified using universal fish specific primers and PCR products were pooled into libraries. Then the libraries were sequenced on Illumina MiSeq platform. Raw FASTQ reads were quality-filtered using FastQC software. Further data processing and taxonomic classification through comparison with databases were performed by OBITools. Our results show that, nine fish species were identified with DNA metabarcoding of faecal samples. Species with the highest read counts were *Tinca tinca*, *Salmo trutta* and *Gobio gobio*. Therefore the results suggest that, otter's diet comprises both endemic, indigenous and non-indigenous species. However, we also obtained some false positive results through alignments from global databases (NCBI and EMBL). This alignment related bias can be prevented by building a local database