Metagenomic analysis of the protistan plankton communities along the coastal waters of Qatar (Arabian Gulf)

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The coastal waters of Qatar belongs to the least studied and exploited marine environments worldwide, when it comes to microbial diversity. This is unsatisfying not only because coastal habitats are economically and ecologically extremely important (ecosystem services) but also because Qatari waters may hold as yet unknown and valuable microbial resources. Therefore, we set out for the first time in the Gulf a microbial eukaryote plankton diversity survey at 14 different coastal sampling sites subjected to diverse human activities. One pristine sampling site was included as a benchmark and reference site, as well as a hypersaline sampling site from an inland sea (Khor Al-Odaid) to exploit the full deck of protistan plankton diversity. From high-throughput sequencing (Illumina), we obtained and analyzed 6,725,058 amplicons of the hypervariable V4 region of the small subunit ribosomal RNA gene (18S rRNA) from all 14 sampling sites. Rarefaction analyses showed complete coverage of eukaryotic diversity for all but two sites. In general, most abundant and diverse amplicons were taxonomically assigned to dinoflagellates, ciliates, green algae, stramenopiles, haptophytes, cryptophytes and picozoa. Shannon alpha diversity was highest in and around Doha Bay and at the sampling site off Messaeid Industrial City southeast of Qatar. The by-far lowest diversity was found at the inland sea site, where salinity was twice as high as in other Arabian Gulf areas. This confirms salt as a strong environmental selection factor for plankton communities. Interestingly, coastal sites exposed to hydrocarbon exploitation did not exhibit a significantly lower diversity compared to the pristine site at Simaisma. However, as revealed by the Jaccard beta-diversity index, the community structures (composition and abundances) of protists are profoundly different at these sites compared to the pristine and to the Doha Bay sites. The environmental factors responsible for these community shifts still remain to be identified in further analyses. Global analyses of microbial diversity in Qatari coastal waters indicate high degree of novel diversity hidden in the investigated ecosystems and pinpointing the high microbial potential yet to be exploited in these waters.

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