Metabarcoding using eDNA reveals depth-stratified microbial community dynamics in the coastal zones of the Southwest Indian Ocean.

Girish Rameshan[1,2] and Thulani Makhalanyane[1,2]

[1.] Department of Microbiology, Stellenbosch University, Stellenbosch, 7600, South Africa.

[2.] School for Data Science and Computational Thinking, Stellenbosch University, Stellenbosch, 7600, South Africa

In the Southwest Indian Ocean, coastal cities including those on the African continent are under threat due to urbanization, plastic contaminants, and other emerging contaminants from untreated wastewater-treatment plants. Microbes are the key contributors in coastal marine ecosystem playing extensive roles in carbon sequestration and nutrient recycling, but we lack fundamental baseline datasets regarding their biogeography, and interactions with other marine biota. These baseline studies act as a primer for the development of effective coastal and marine strategies, especially in the ecologically distinct and threatened coastal ecosystems. Several factors control the diversity and composition of microbial communities in these ecosystems. Among this, vertical stratification significantly influences the dynamics of ocean microbial community by creating environmental gradients along the water column. The depth-based ecological adaptations might significantly influence marine food-webs, indirectly contributing to ecosystem sustainability. We used environmental DNA (eDNA) metabarcoding to investigate marine bacteria and archaea, fungi, and other eukaryotes using 16S, ITS and 18S rRNA genes, respectively, at five stations in coastal waters near Durban, South Africa. The data showed that *Exophiala*, *Ascomycota*, and *Basidomycota* were dominant among fungi. The *SAR11 clade*s of *Alphaproteobacteria* were prominent and core constituents of bacterial communities. The results showed that *Opisthokonta*, *Stramenopiles*, *Alveolata*, and *Rhizaria* were dominant eukaryotes. Statistical analysis suggests that microbial communities varied significantly based on sampling depths. Species richness was higher in the top photosynthetic zone, and these communities were influenced substantially by nutrient input, ocean currents, temperature, salinity, and light availability. Predictive functional profiling suggests depth-related variations in the abundances of metabolic pathways and functional orthologs related to bacteria, archaea, and fungi. The analysis also showed distinct differences in metabolic capacity, based on sampling depth. Taken together,

the results suggest strong variability in microbial community structural patterns along the water column. This highlights the role of depth-related factors and environmental factors as drivers of microbiota in coastal marine ecosystems.