XIX CONGRESO DE LA SOCIEDAD ARGENTINA DE MICROBIOLOGÍA GENERAL

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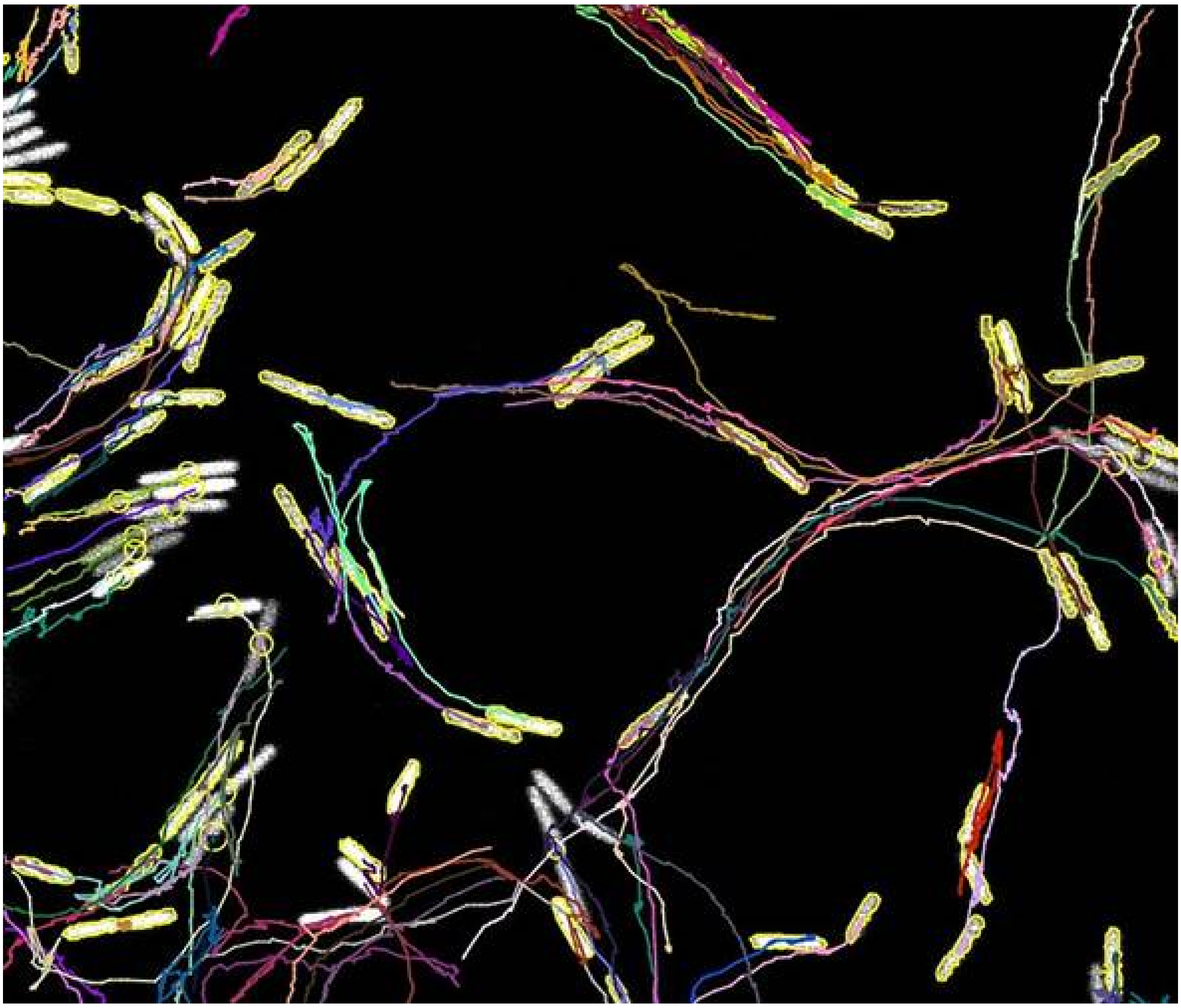

Foto: Se hace camino al andar. Celeste Dea. 1er puesto. Concurso fotográfico SAMIGE 20 años.

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BACTERIAL COMMUNITIES THAT INHABIT THE SEDIMENTS OF THE DEEP SEAFLOOR OF THE NORTHERN ARGENTINE CONTINENTAL MARGIN

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The metagenome of marine deep sediment could be a valuable resource for the energy industry. The migration of gasses and hydrocarbons from the seafloor could act as an energy or carbon source, modifying the composition of the communities. Although the presence of hydrocarbons is expected to cause changes in the microbial communities, the actual effects on their function and structure remain poorly understood. The aim of this work was to characterize bacterial communities in marine sediments from the Colorado sedimentary offshore basin of the Northern Argentine Continental Margin (NACM) collected during an ARA-Austral ship campaign (CONICET–Y-TEC). Sediment samples (15 gravity-cores, GC) were collected from depths of 20 to 600 cm at sampling sites located 500 to 3175 meters below the sea surface. DNA was extracted from 29 sections of the sediment samples using a commercial kit. The V3-V4 region of the 16S rDNA was amplified and sequenced using Illumina technology. Amplicon Sequence Variants (DADA2) were classified with Qiime2 and analyzed using phyloseq, microViz, and PICRUSt in Rstudio. Alpha diversity measures of sediment samples were within the ranges described for deep sea-floor bacterial communities. In each GC we observed a trend of higher diversity at intermediate sections (~200-400 cm). Bacterial communities in the sediments were dominated by the classes *Alphaproteobacteria*, *Gammaproteobacteria*, *Bacilli*, *Halanaerobiia*, and *Bacteroidia*. Within these classes, the families with higher abundance were *Burkholderiaceae*, *Pseudoalteromonadaceae, Bacillaceae, Rhodobacteraceae, Salisediminibacteriaceae, Flavobacteriaceae, Colwelliaceae,* and *Moraxellaceae*. Dissimilatory sulfate reduction and thiosulfate oxidation using SOX system were predicted for sequences belonging to *Halanaerobiia*, *Desulfovibrionia*, and *Alphaproteobacteria*, among the most abundant ones. On the other hand, the most abundant sequences related to dissimilatory nitrate reduction belonged to the families *Burkholderiaceae*, *Xanthobacteraceae*, *Vibrionaceae*, *Sulfurospirellaceae* and *Marinilabiliceaea*. Fermenters were found in high abundance in all samples. The functional prediction of the sequenced communities showed a potentially high abundance of genes involved in the aerobic degradation of n-alkanes, methanol oxidation, beta-oxidation and the Wood-Ljundahl and methylmalonyl-CoA pathways. These results suggest that

these communities have the genetic potential to use n-alkanes as sources of carbon and energy. On the other hand, these communities were not enriched in taxa capable of degrading methane, propane, naphthalene or benzoate. The characterization of these bacterial communities could serve as a baseline study of the sediments in this region of the NACM. The generated data could be compared in the future with communities from areas with suspected or confirmed the presence of migrated hydrocarbons to analyze their influence on the deep seafloor biosphere.

Palabras clave: Marine deep sediment – Sequencing – Hydrocarbon migration – Bacterial communities