Sociedad Argentina de Microbiología General

XIX CONGRESO DE LA SOCIEDAD ARGENTINA DE MICROBIOLOGÍA GENERAL

22 al 25 de octubre del 2024
Centro cultural y Pabellón Argentina de la Universidad Nacional de Córdoba, Córdoba, ARGENTINA.

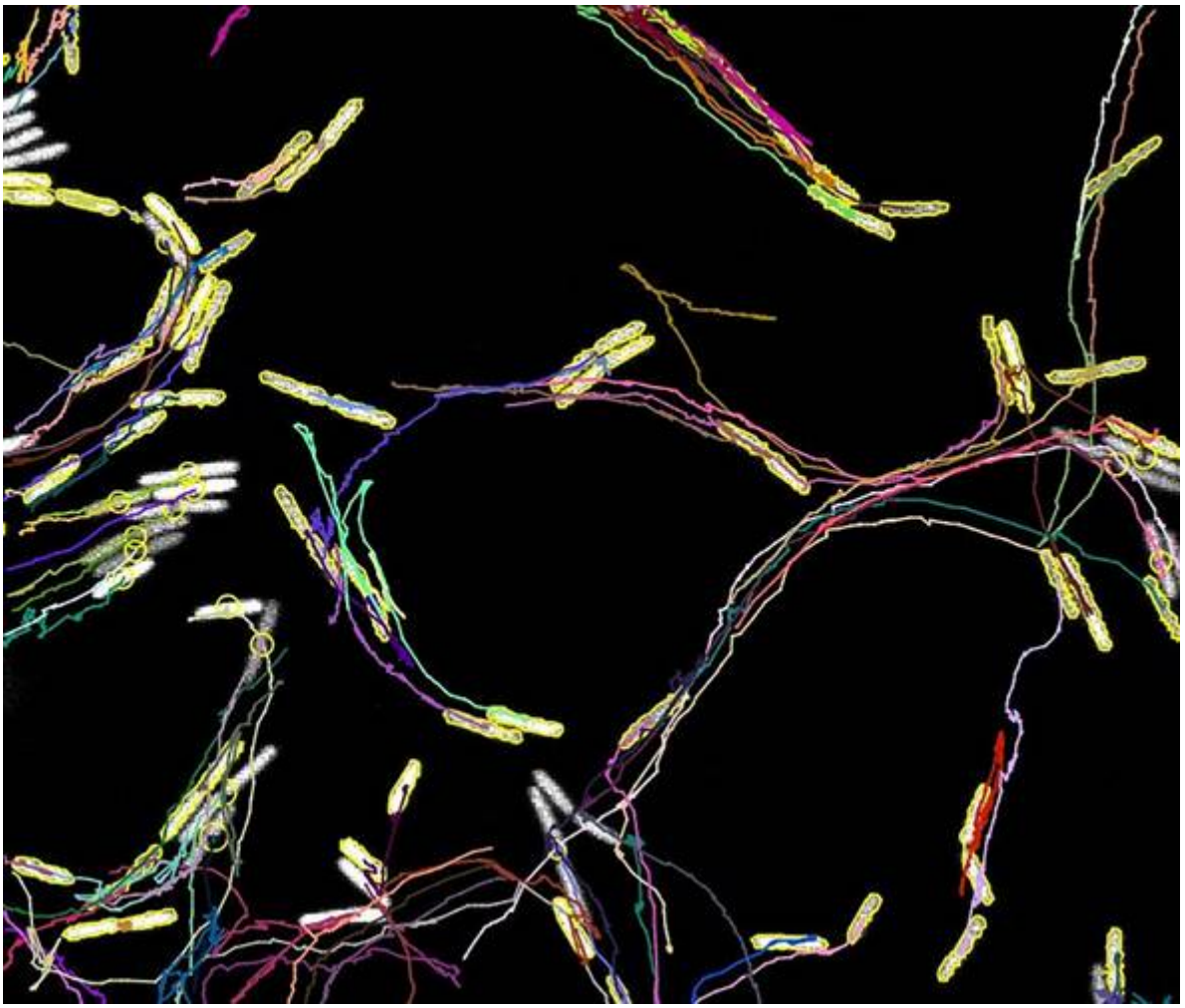

Foto: Se hace camino al andar. Celeste Dea. 1er puesto. Concurso fotográfico SAMIGE 20 años.

191 - Microbiología Ambiental, Agrícola y del Suelo

EXTREMOPHILES IN THE YUNGAS FOREST

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Hot springs usually have a remarkable diversity of associated organisms, where a gradient of temperature and chemical compounds shape the microbial communities. They represent an opportunity for the search of thermostable enzymes. The Yungas provide a setting with a thriving biodiversity, presenting a unique opportunity to find unusual organisms and metabolisms. The proposed study site for this work is Laguna La Quinta, also known as Hediondilla, in the east of the province of Jujuy. The site is well known locally, and its thermal and geological features have been characterized, but the microbiology of the site remains unexplored. Environmental DNA was extracted with DNeasy Powersoil kit (QIAGEN) from two mats, a “black mat” (HMNa) and a “green mat” (HMAb). Shotgun metagenomic sequencing was performed with Illumina 2 x 150 PE technology. Quality control and assembly were performed with Trim Galore 0.6.5dev and metaSPAdes v3.13.0 in the BV-BRC server. Reads were mapped to the assembly with bowtie2. Annotation was performed in the KBase server with Kaiju v1.9.0, prokka 1.14.5, RASTtk v1.073, dbCAN2 v10, and microTrait v1.0. Viruses were identified with VirSorter2 and characterized with a series of bioinformatics tools. Sequencing produced around 80 million reads for each sample. Taxonomic classification indicated that the same phyla were dominant on both samples. Proteobacteria (mainly Alphaproteobacteria) was the dominant phylum, with relevant abundances for Chloroflexi, Bacteroidetes and Planctomycetes. Actinobacteria and Cyanobacteria were only abundant at HMNa. Viruses were present with very low abundances but we were able to identify and characterize 18 high-quality viral genomes, 11 from a HMNa and 7 from HMAb. Assembly produced 92812 contigs with N50 5934 bp for HMNa, and 55601 contigs with N50 11648 bp for HMAb. The assemblies included 50% of the reads in HMNa and 78% in HMAb. Biogeochemical cycles were assessed with microTrait based on marker genes. In both samples, nitrogen cycle was not complete, with nitrification and anammox metabolisms absent. Carbon fixation pathways present included Calvin cycle, Wood-Ljungdahl, and Reductive citrate cycle. Photosynthesis genes were related to purple bacteria and Cyanobacteria, pointing to both oxygenic and anoxygenic photosynthesis as sources of energy. The abundance of membrane arsenite oxidases suggested alternative sources. Finally, several types of CAZymes were found. Interestingly, lytic polysaccharide

monooxygenases (LPMO or auxiliary activities, AA10) were present. These are increasingly described in recent years as they actively contribute to the degradation of plant biomass and enhance the action of hydrolases (GH). Further work will select promising thermostable AA10 + GH pairs for experimental assays in the degradation of (hemi)cellulose and possibly other complex substrates.

Palabras clave: metagenomics - extremophiles - DNA sequencing - CAZymes