



## SCREENING OF A METAGENOMIC LIBRARY FOR SECONDARY METABOLITES WITH POSSIBLE ANTIBIOTIC ACTIVITY

Miguel Marfil-Santana<sup>1</sup>, César De los Santos Briones<sup>1</sup>, Rafael A. Rojas-Herrera<sup>3</sup>, Blondy Canto-Canché<sup>1</sup>, Aileen O'Connor Sánchez<sup>1</sup>, Alejandra Prieto-Davó<sup>2</sup>

1 Centro de Investigación Científica de Yucatán, A.C. Calle 43 No. 130, Colonia Chuburná de Hidalgo, fax: (52) 999 981 39 00, [miguel.marfil81@hotmail.com](mailto:miguel.marfil81@hotmail.com)

2 Facultad de Química, Unidad Sisal. Universidad Nacional Autónoma de México. Puerto de Abrigo s/n municipio de Hunucmá, C.P. 97356, Sisal, Yucatán México

3 Universidad Autónoma de Yucatán. Facultad de Ingeniería Química. Campus de Ingenierías y Ciencias Exactas. Periférico Norte Kilómetro 33.5, Tablaje Catastral 13615, Col. Chuburná de Hidalgo Inn. C.P. 97203. Mérida, Yucatán, México

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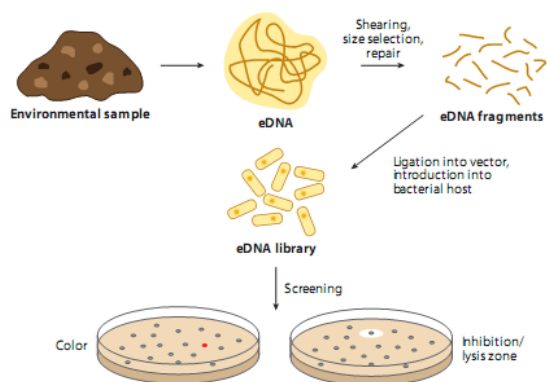
**Introduction.** For a long time, studies on bacterial metabolism were limited to cultivated strains in laboratories. Since only a very small fraction (1-20%) of microbes in any environment can be brought to culture<sup>1</sup>, studies on their biosynthetic potential have been quite limited<sup>(1)</sup>.

Metagenomic allow's us to look at a whole microbial community's genetic potential by extracting and analyzing environmental DNA without the limitation of strain cultivation. This DNA offers an excellent representation of the bacterial genomes present in the studied communities (2).

Recent studies on metagenomes from diverse environments have aided in posing fundamental questions about microbial processes present in them, e.g. aquatic ecosystems, mines and agricultural and forest soils (3, 4, 5, 6, 7).

This technique that has brought new insights onto natural products research, as it gives access to previously unreached biosynthetic pathways through the genetic and bioinformatic manipulation of DNA (8).

**Methods.** Our group has started the functional and bioinformatic screening of a metagenomic library from the underground aquifer in the Yucatán in order to find novel metabolites with antibiotic activity (Figure 1).



**Fig 1:** Esquema de la construcción de una biblioteca metagenómica (Piel Jorn 2011)

By visually screening for meta-clones producing inhibition halos against a series of pathogenic bacteria (e.g. *Staphylococcus aureus* and *Pseudomonas aeruginosa*) whilst bioinformatically screening the metagenome for PKS and NRPS genes, we intend to take advantage of the genetic potential of microbial

communities present in this underexplored and unexploited resource.

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