

Bioinformatic Screening of Metagenomic Fosmid Libraries for Identification of Biosynthetic Pathways Derived from the Colombian Soils

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Abstract : Microorganisms from tropical ecosystems can be novel in terms of adaptations and conservation. Given the macrodiversity of Colombian ecosystems, it is possible that this diversity is also present in Colombian soils. Tropical soil bacteria could offer a potentially novel source of bioactive compounds. In this study we analyzed a metagenomic fosmid library constructed with tropical bacterial DNAs with the aim of understanding its underlying diversity and functional potential. 8640 clones from the fosmid library were sequenced by NANOPORE MiniOn technology, then analyzed with bioinformatic tools such as Prokka, AntiSMASH and Bagel4 in order to identify functional biosynthetic pathways in the sequences. The strains showed ample difference when it comes to biosynthetic pathways. In total we identified 4 pathways related to aryl polyene synthesis, 12 related to terpenes, 22 related to NRPs (Non ribosomal peptides), 11 related PKs (Polyketide synthases) and 7 related to RiPPs (bacteriocins). We designed primers for the metagenomic clones with the most BGCs (sample 6 and sample 2). Results show the biotechnological / pharmacological potential of tropical ecosystems. Overall, this work provides an overview of the genomic and functional potential of Colombian soil and sets the groundwork for additional exploration of tropical metagenomic sequencing.

Keywords : bioactives, biosynthetic pathways, bioinformatic, bacterial gene clusters, secondary metabolites

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