

Detection of biosynthetic genes of microbially-synthesized secondary metabolites in a contaminated tropical agricultural soil

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Abstract

The hunt for microbially-synthesized secondary metabolites have long generate exceptional interest due to their unique functionalities. In this study, shotgun metagenomic was used to decipher the array of secondary metabolites present in a contaminated agricultural soil (AB1) via detection of their biosynthetic genes. Functional annotation of AB1 metagenome's putative open reading frames (ORFs) for polyketide synthases (PKSs) and non-ribosomal peptide synthetases (NRPSs) revealed that majority of the detected biosynthetic genes belong to type I polyketides and non-ribosomal peptides. Biosynthetic genes for type I polyketides such as macrolides, polyene macrolides, rapamycin-related compounds (FK506, FKF20), myxobacterial compounds (epothilone A, soraphen A), lovastatin, enediynes, among others were detected. Similarly, biosynthetic genes for non-ribosomal peptides such as surfactin, fengycin, iturin, lichenysin, arthrofactin, vibriobactin, mycobactin, bacitracin, gramicidin S, viomycin, bleomycin, vancomycin, pristinamycin, tyrocidine, fumiquinazoline and several others were also detected. Taxonomic characterization of the detected biosynthetic genes revealed microorganisms that are not known to be natural producers of the secondary metabolites, thus pointing to the possibility of horizontal gene transfer. The huge repository of these genes in the soil environment is a clear reminder of the pivotal role the soil as a natural resource can play as a source of exciting natural products that can be deployed as viable alternatives to solve myriad of challenges facing the medical, industrial, and environmental settings.

Keywords: Secondary metabolite ; Agricultural soil ; shotgun metagenomics ; polyketide synthase ; non-ribosomal peptide synthetase

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