

Primer Design for the Detection of Secondary Metabolite Biosynthetic Pathways in Metagenomic Data

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Abstract : Most of the known antimicrobials so far discovered are secondary metabolites. The potential for new natural products of this category increases as new microbial genomes and metagenomes are being sequenced. Despite the advances, there is no systematic way to interrogate metagenomic clones for their potential to contain clusters of genes related to these pathways. Here we analyzed 52 biosynthetic pathways from the AntiSMASH database at the protein domain level in order to identify domains of high specificity and sensitivity with respect to specific biosynthetic pathways. These domains turned out to have various degrees of divergence at the DNA level. We propose PCR assays targeting such domains in-silico and corroborated one by Sanger sequencing.

Keywords : bioinformatic, anti smash, antibiotics, secondary metabolites, natural products, protein domains

Conference Title : ICMBG 2021 : International Conference on Molecular Biology and Genomics

Conference Location : Bangkok, Thailand

Conference Dates : December 16-17, 2021