Bioprospecting soil metagenomes for potential new antibiotics

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0.1 Abstract

Many soil-dwelling microbes have the natural capacity to produce toxic compounds that inhibit growth of competing bacteria; most traditional antibiotics have been derived from small molecules made by such soil-based microorganisms, of which only a small fraction can be grown in the laboratory. Since techniques that require culturing of these microbes in the lab have been the starting point for studying them in the past, our knowledge of the uncultured majority remains limited. Functional metagenomics is a method that circumvents the need for culturing, and thus has the potential to revel a yet untapped reservoir of antibacterial compounds. Here we present a potential application of functional metagenomics using genes isolated from soil microbes that employs high throughput sequencing to identify microbial genes encoding novel compounds that inhibit bacterial growth.

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0.3 Table of Contents

0.4 List of Figures

0.6 List of Tables

0.7 Abbreviations

eDNA: environmental DNA

pBAD: pBAD/*Myc*-His B, the plasmid cloning vector used

NGS: next generation sequencing

PCR: polymerase chain reaction

E. coli: *Escherichia coli*

TOPO: PCR8/GW/TOPO cloning vector (Invitrogen)

TSS: transformation and storage solution

LB: lysogeny broth

SOC: super optimal broth with catabolite repression

bp: base pairs

kbp or kb: kilo base pairs

OD600: optical density at 600nm. Indicator of bacterial growth.

ORF: open reading frame