

Metagenomic sample selection: A guided approach to Natural product discovery?

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The Bottlenecks:

We have **more samples** than we can process; and **rediscovery** of known molecules is a significant problem

A Solution?

Use culture independent techniques to assess the **microbial composition prior** to culture:

- 1. Abundance
- 2. Diversity
- 3. Novelty

Hypothesis and Methodology

Hypothesis: Diversity and abundance of the total microbiota relates to the diversity and abundance of the culturable microbiota

Metagenomics

- I. eDNA extracted, 16S amplified (515F/926R) and sequenced illumina MiSeq as per the Earth Microbiome Project standards
- II. Data analysed using Qiime2 software with denoising completed with DADA2
- III. Reads were assigned taxonomy using the Silva 16S database at 99% similarity





16S analysis of 24 sponges

Almost 40% of actinobacteria reads from 24 samples were found in ONLY two sponges

Actinobacteria Sequence Frequency



Individual Sample Assessment

Bacterial abundance, diversity and novelty from metagenomics

Bacterial Phyla Breakdown - Sponge B01140





Future Objectives

- Assess the usefulness of the 16S metagenomic data to guide culturable bacteria
- 2. Isolate and characterise novel bacteria that produce novel antimicrobials

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