



Antimicrobial Resistance in Soils

The Phylogenetic Diversity of Ceftriaxone-resistant Isolates in Soil, Diversity of their ESBL Genes, and their Capacity for Multi-drug resistance

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Introduction

The third-generation cephalosporins have been useful in treating infections by Gram negative bacteria as they exhibit wide antimicrobial activity. However, in recent years, increasing levels of resistance have been observed in clinical isolates. Since the soil microbiome is considered to be a natural reservoir of antibiotic resistance genes, soil microbes could potentially pose a risk to public health. However, few studies have reported the presence of extended-spectrum β -lactamase (ESBL) genes in undisturbed soils.

Objectives

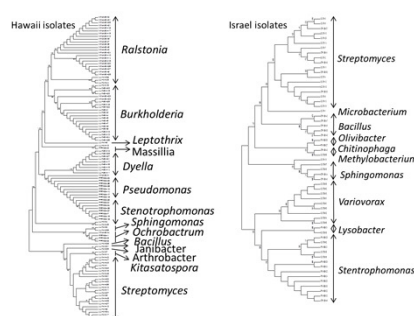
1. Determine the phylogenetic diversity of ceftriaxone-resistant soil isolates.
2. Determine the extent of multi-drug resistance in ceftriaxone-resistant soil isolates.
3. Determine the diversity of ESBL genes in ceftriaxone-resistant soil isolates.

Methods

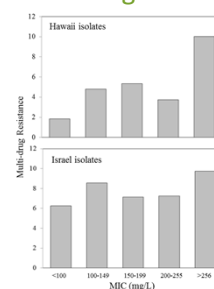
- Six undisturbed (non-agricultural or human-impacted) and physiochemically diverse soils were collected from Hawaii (USA) and Israel.
- Ceftriaxone-resistant soil isolates were obtained either by irrigation of soil microbiomes with clinically relevant concentrations of ceftriaxone, or by creating soil slurries amended with ceftriaxone.
- The identities of the isolates were determined by sequencing their 16S rRNA genes.
- To determine their multidrug-resistance, the microdilution method was used to find their minimum inhibitory concentrations (MIC) against 13 other antibiotics as well as ceftriaxone.
- The isolates were screened for three common ESBL genes by multiplex PCR.

Results

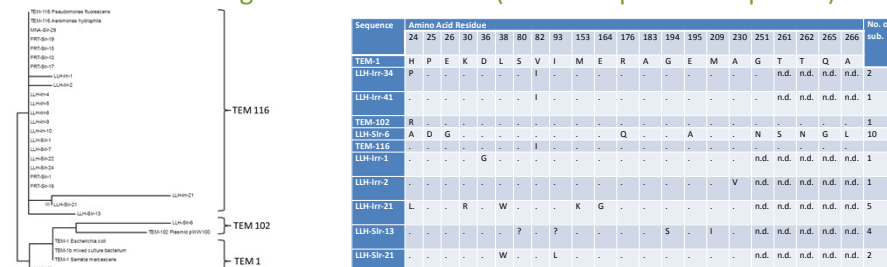
There was a large diversity of ceftriaxone resistant isolates



Soils exposed to higher concentrations of ceftriaxone gave more multi-drug resistant isolates



Three distinct ESBL genes were detected (based on protein sequence)



Conclusions

Ceftriaxone-resistance was conferred by a diverse group of microorganisms (within the *Proteobacteria*, *Actinobacteria*, *Firmicutes* and *Bacteroides*). Higher levels of ceftriaxone-resistance correlated with higher levels of multi-drug resistance. Three distinct ESBL genes were detected in nine genera, suggesting its ubiquitous presence and/or horizontal gene transfer in soil microbiomes.

Future Work

We are currently mapping the extent of antimicrobial resistance in Scottish soils and surface waters by detecting 300+ antibiotic resistance genes. The National Soils Archive contains soils on a 20km grid. The National Waters Archive contains 200 waters representing end of catchment locations.

Acknowledgements

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