

Back to soil: awakening the production of cryptic antibiotics in *Streptomyces*

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Introduction Most of the antibiotic biosynthetic gene clusters (BGCs) in *Streptomyces* are not expressed under laboratory conditions, however they are maintained in the genomes, therefore indicating that they must play important roles in adaptation and survival within their ecological niches. These cryptic pathways represent an untapped resource in terms of novel chemistry that could be very useful if we can awaken their expression.

Aim Understanding the global regulation patterns that affect transcription of BGCs in these strains under soil conditions versus laboratory conditions and identify the compounds via metabolomics.

Next steps: Untargeted Metabolomics

Ethyl Acetate and Methanol extraction

Can we find compounds from cryptic or silent BGC?

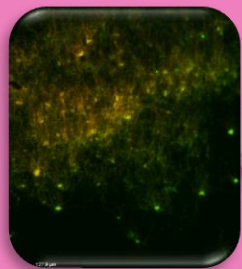


Summary

We found conditions to grow *Streptomyces* in soil and preliminary results indicate that BGC are expressed differently in soil compared to standard growth medium.

Unbiased metabolomics will be the next step to identify compounds produced in soil as well as a closer look at regulatory gene expression in the RNA-Seq data.

S. venezuelae

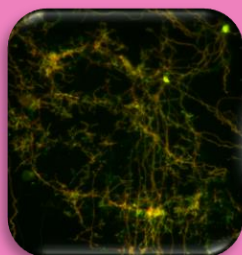


ISP-2

Sterile soil (SS)

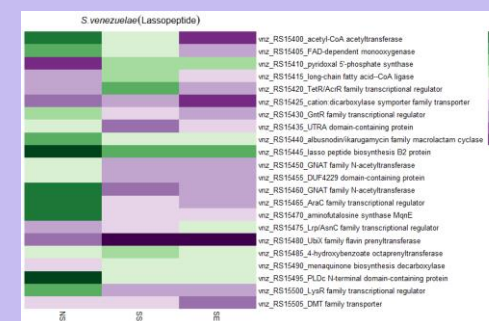
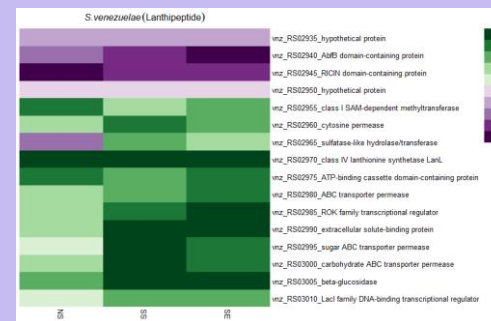
Non-sterile soil (NS)

Soil extract (SE)



S. rimosus

Transcriptomics – differential gene expression of selected BGCs comparing soil versus ISP-2 medium



For both organisms we observe changes in expression in various biosynthetic gene clusters (BGCs) on soil compared to the control condition ISP-2 medium

