Effect of metagenome on stable-isotope-enabled metaproteomic analyses of soil microbial communities

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Introduction

• Metaproteomics analysis of soil using isotope-labelled glucose as a marker for metabolic activity.
• Three metagenomic databases were searched using MSGF+1 and results compared.
• Database selection can influence quality and quantity of peptide/protein identifications.

Methods

Overview

• Metaproteomic analysis of soil using isotope-labelled glucose at PNNL please visit at site.
• Metaproteomic analysis of soil using isotope-labelled glucose at PNNL please visit.

Background

• Database selection can influence the quantity and quality of peptide/protein identifications.
• Protein families that were identified from the glucose-amended samples using this metagenome included central metabolism, sugar transport, and sugar storage.

Results

• Comprehensive metagenome represents the entire microbial community as a single entity providing functional information with no taxonomic identifications.

Protein-SIP: Taxonomic profiling of label incorporation

• Provides a view of active microbes by observing incorporation of label into newly synthesized proteins.
• MetaProSIP2 software was used for data analysis.

Conclusions

• The three metagenome databases provide complementary information and demonstrate how database selection can influence peptide identification.
• Protein families that were identified from the glucose-amended samples using this metagenome included central metabolism, sugar transport, and sugar storage proteins - indicate a microbial community with an abundance of nutrients.
• Stable isotope incorporation in proteins can be an indicator of microbial activity in soil microbial communities.
• Ongoing work: Developing software for confident detection and visualization of stable isotope labelled peptides using improved fitting and optimization criteria.

References


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