Increasing the power of interpretation for soil metaproteomic data

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Video Byte

Abstract

Soil and sediment microorganisms are remarkably diverse and are critical for ecosystem health. However, they are underrepresented in public databases, and assembling new metaproteomic datasets is challenging, which makes it difficult to characterize the microorganisms in specific soil samples. To increase the outputs of soil metaproteomic studies, a recent study compared various database construction strategies. Search strategies using either sample-specific metagenomic databases or public databases produced comparable peptide-spectrum matches for a floodplain soil core. However, a two-step cascaded search combining both types of databases led to greater peptide-spectrum matching. The combination strategy also improved functional annotation of the peptides, and the resulting metaproteome (MetaP) annotations correlated well with the metagenome (MetaG) annotations. Although further research on additional soil types and microbial communities is warranted, the current study provides a practical approach for obtaining more information from soil and sediment samples, which will facilitate research on the dynamics of critical microbial communities.