Identification of lignocellulose degrading microbes in a boreal forest soil
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Introduction

Purpose of study: to identify what microbes and their associated enzymes are degrading lignocellulose in boreal forest soils.

Methods

Samples
- Fractinations from Times 0, 2, 4, 6, 8 (weeks)
- Fractions 9-14 found to contain labeled DNA
- Pooled fractions 9-14, separate samples from fractions

PCR amplification
- 16S ribosomal region for bacteria
- Primers 27F and 1525R
- ITS region for fungi
- Primers ITS1F and ITS4

ARISA results (see Table 1).
- 16S bacterial qPCR = no evidence of labeled DNA
- ITS qPCR = clearly absorbed 13C substrate in biomass

Discussion

Results

- ARISA fragments with high peaks assumed to be dominant degraders
- Higher peak indicates more DNA/PCR product present
- Some fragments correlate with others
- Abundance of 601 bp fragment at time 2; abundance of 654 bp fragment at time 6; abundance of 683 bp fragment at time 8
- Suggests microbes (assuming each fragment is single microbe) worked cooperatively over time to degrade the lignocellulose

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Literature Cited