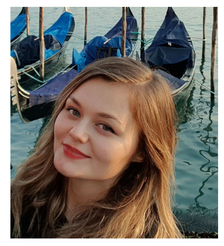
Elucidating fungal-bacterial interactions within compost systems

Mădălina Vîță, Femke van Dam, Michiel Kienhuis, Klaas Nierop, Lubos Polerecky, Francien Peterse, Jack Middelburg

Department of Earth Sciences, Faculty of Geosciences, Utrecht Univeristy, Vening Meinesz Gebouw A, Princetonlaan 8, 3584 CB Utrecht, the Netherlands, m.m.vita@uu.nl



Introduction

Agaricus bisporus, the button mushroom, is cultivated commercially on a composted mixture of straw, manure and gypsum. Different temperatures and conditions are used in substrate production with the aim to make the compost microbiologically and nutritionally specific for the mushroom. Previous studies have shown that *A. bisporus* depends on the rest of the microbial community during its life cycle, for nutrient uptake and fruiting body production. This dependence is poorly understood as is the food-web of the compost.

Aim

The aim of this project is to elucidate the food web and nutrient flows within the compost system in order to increase the yield and reduce waste in the commercial production of *Agaricus bisporus*.

Methods

Stable isotope labelling: addition of ^{13}C-glucose and ^{15}N-ammonium chloride as substrate.
Biomarker analysis: phospholipid derived fatty acids (PLFAs) as biomarkers of fungi, actinomycetes and other bacteria (Table 1). GC-c-IRMS for quantification and isotopic composition measurement.
Nanoscale secondary ion mass spectrometry (nanoSIMS): isotopic composition and imaging of fungal samples from compost or in vitro.

Results

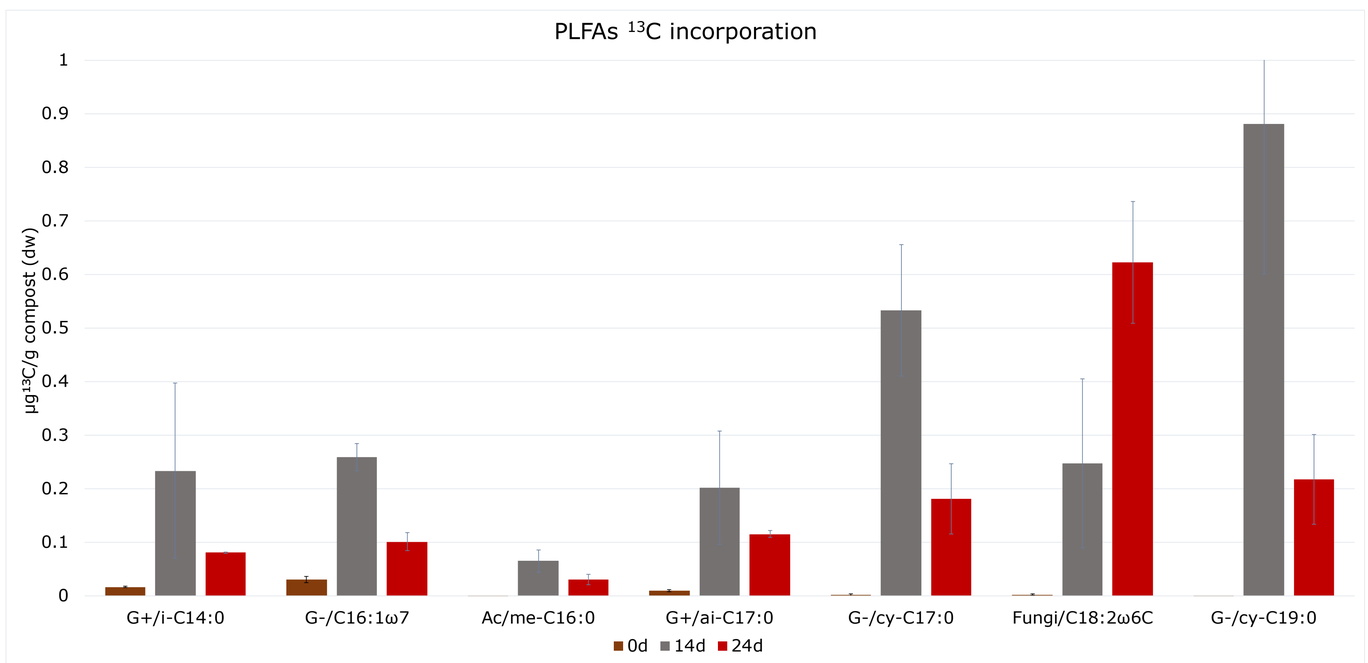


Figure 1 PLFAs ^{13}C Absolute Content represents a measurement of ^{13}C incorporation within the biomass

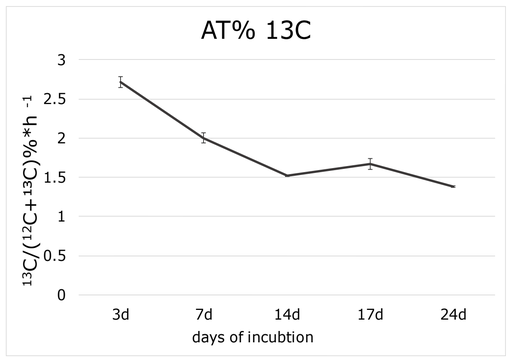


Figure 2 Fraction of ^{13}C on the total carbon trapped in sodium hydroxide

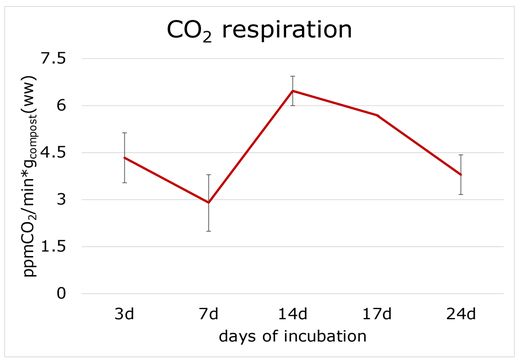


Figure 3 Total community respiration as measured with infrared carbon dioxide sensor

PLFAs	Microbial group
18:2ω6	Fungi [1][2][3]
i/ai-15,17:0	Gram positive bacteria [1][2][3]
Cy-19:0; 16:1ω7	Gram negative bacteria [1][2][3]
Me-16,18:0	Actinomycetes [1]

Table 1 Examples of PLFAs identified from compost's fatty acids

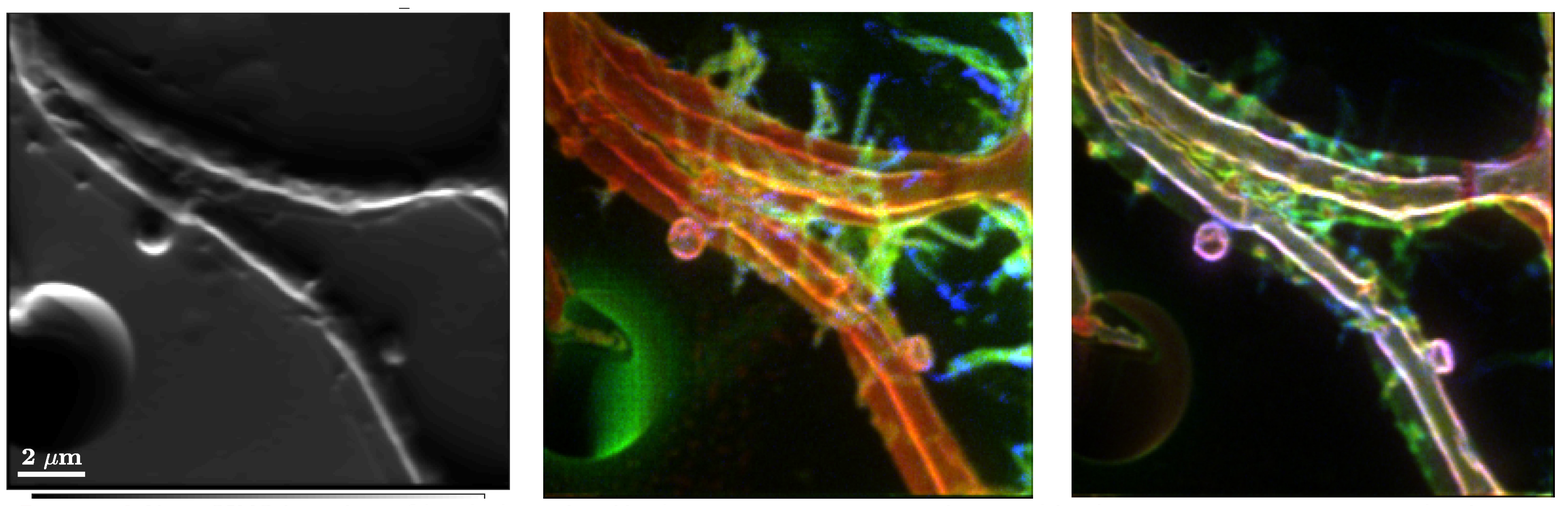


Image 1 NanoSIMS imaging of hyphal section.Hyphae grown on support inserted in the compost were prepared using a dehydration fixation protocol. Left: SEM picture; Middle: surface; Right: subsurface.

Conclusions

Stable isotope labelling and biomarker analysis are suitable methods for elucidating fungal-bacterial interactions.

Microbial communities can be prepared for nanoSIMS imaging.

Preliminary results confirm the bacterial population as a carbon source for *A.bisporus* during late vegetative state.

The start of predatory phase coincides with maximum of fungal biomass.

Acknowledgments

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References

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