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Discussions

Interactive comment on "The stable carbon isotope signature of methane produced by saprotrophic fungi" *by* Moritz Schroll et al.

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Schroll and co-authors studied the stable carbon isotope values of methane emitted during the aerobic decomposition of organic matter by two fungal species. Methane production by fungi during plant litter decomposition is novel patheway of methane formation, that was recently documented by by the authors and others. This manuscript, however, is the first study of the stable carbon isotope (d13C) values associated with this novel pathway and their relationship substrate d13C values.

This study addresses closes a knowledge gap in the isotope systematics of atmospheric methane that is relevant to the Biogeosciences readership. The authors used state of the art methods, and their conclusions are well supported by their results. The

manuscript is well structured and easy to follow.

The study's strength is that this is the first study of its kind and provides unique stable isotope fractionation factors between biomass and methane produced by fungi. The study also used very rebust measurement methods (GC/IRMS with preconcetration) that exceeds the precision, accuracy, and specificity of laser-based analysers. The main limitation of the study are that the authors did not test for contaminations by other microbial species during this study (this was, however, tested by the authors in similar incubations in a previous study). Another limitation is that the authors were not able to identify controls over relatively large variations in methane isotope values beside differences between C3 and C4 plants. This, however, is understandable given that the biochemistryof aerobic methane production in fungi remains poorly understood, and the authors contribution will surely help elucidate these pathways in the future.

Main comments: - The authors used two distinct fungal species, and state that these species include both white rot and brown rot fungi. However, I was unable to find where in the manuscript the authors identify which fungal species belongs to which group.

Minor comments. L53: remove 'applications of' for easier sentence structure L54: clarify what 'they' refers to in 'they might be used..', also, avoid 'fingerprints' ('characteristic d13C values?) L57: 'global isotopic patters': Do you mean the d13C values of atmospheric CH4?' L63: 'isotope patters': stable isotope values? L74f: clarify which fungi is the white rot and which one is the brown rot one. L142: is 0.06mg correct? This seems a very low sample inweight for EA/IRMS, although not impossible. Also, did you analyse analytical replicates? A single 0.06mg inweight is likely associated with a significant subsampling error. L164: You could add a note that the low R2 resulted from the lack of a change in d13C values (emission d13C was similar to background d13C). In this case, a low R2 does not indicate a poor relation between concentration and d13C value. L167: 'The SDs are given with a confidence interval of 1 σ': sentence not needed and meaningless. L173-179: not needed, can be removed. L185: 'where': use 'in which' instead L229 and Table1: stating CH4:CO2 ratios in umol/mol instead of

nmol/mmol would improve clarity. L302: ‘distinct differences in the patterns’: redundant structure, could be simplified. L305-311: This section could use some language editing for better flow. e.g. L306: ‘the used growth substrates’: The growth substrates used for this study... or similar. L306: ‘consist of various amounts’: contain distinct amount of cellulose, [..], and other compounds. L307: structure in parenthesis: grammar L309: .. source signatures might _depend_ on the metabolic pathyways _used by_ the fungal species _as well as_ the chemical composition of the substrate (or similar) L310: Therefore, we suggest: remove this phrase. “The selected ...” L313: Figure 5 _compares_ _the_ d13C-CH4 values.. L320: ’depending on the photosynthetic pathway (C3, C4, or CAM)’

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