Geophysical Research Abstracts
Vol. 19, EGU2017-3974-9, 2017
EGU General Assembly 2017

Sulfur isotopic fractionation of carbonyl sulfide during degradation by soil bacteria and enzyme

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Carbonyl sulfide (COS) is an atmospheric trace gas that possess great potential for tracer of carbon cycle (Campbell et al., 2008). COS is taken up by vegetation during photosynthesis like absorption of carbon dioxide but COS can not emit by respiration of vegetation, suggesting possible tracer for gross primary production. However, some studies show the COS-derived GPP is larger than the estimates by using carbon dioxide flux because COS flux by photolysis and soil flux are not distinguished (e.g. Asaf et al., 2013).

Isotope analysis is a useful tool to trace sources and transformations of trace gases. Recently our group developed a promising new analytical method for measuring the stable sulfur isotopic compositions of COS using nanomole level samples: the direct isotopic analytical technique of on-line gas chromatography-isotope ratio mass spectrometry (GC-IRMS) using fragmentation ions S+ enabling us to easily analyze sulfur isotopes in COS (Hattori et al., 2015).

Soil is thought to be important as both a source and a sink of COS in the troposphere. In particular, soil has been reported as a large environmental sink for atmospheric COS. Bacteria isolated from various soils actively degrade COS, with various enzymes such as carbonic anhydrase and COSase (Ogawa et al., 2013) involved in COS degradation. However, the mechanism and the magnitude of bacterial contribution in terms of a sink for atmospheric COS is still uncertain. Therefore, it is important to quantitatively evaluate this contribution using COS sulfur isotope analysis.

We present isotopic fractionation constants for COS by laboratory incubation experiments during degradation by soil bacteria and COSase. Incubation experiments were conducted using strains belonging to the genera *Mycobacterium, Williamsia, Cupriavidus,* and *Thiobacillus*, isolated from natural soil or activated sludge and enzyme purified from a bacteria. As a result, the isotopic compositions of OCS were increased during degradation of OCS, indicating that reaction for $OC^{32}S$ was faster than that for $OC^{33}S$ and $OC^{34}S$ (Kamezaki et al., 2016). Although OCS degradation rates divided by cell numbers were different among strains of the same genus, the isotopic fractionation constants for same genus showed no significant differences. At the presentation, we discuss the mechanism of isotopic fractionation for OCS during degradation by comparing soil bacteria with enzyme.

References

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