

Large distinct carbon and hydrogen isotope variation of biomarkers in the Nakafusa hot-spring bacterial mat.

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http://www.desc.okayama-u.ac.jp/Geo/HP_New/staff_e/Naraoka/Naraoka_e.html

Various bacterial communities have sometimes been developed around hydrothermal vents. The bacterial activities depend on reduced inorganic chemical species such as H₂S and H₂ as energy sources for carbon fixation. In terrestrial hot springs, faunal activities are restricted around the vents due to high temperature to produce a bacterial mat or stream structure. With respect to bacterial ecology and metabolism, lipid biomarkers including their isotopic compositions will provide valuable information on source identification and biochemical mechanisms. In this study, we determined both carbon and hydrogen isotopic compositions of fatty acids and hydrocarbons from bacterial mat at the Nakafusa hot spring in Nagano Prefecture to clarify the bacterial community.

Bacterial mats are developed well around a hydrothermal vent (~70°C), where three kinds of bacterial mat (white, green and brown) were observed. Water temperature and pH of bacterial mat during sampling ranged from 59.4-65.5°C and 8.6-9.0, respectively. After freeze-dried, each mat was extracted with organic solvents by sonication, subsequently the lipid extract was saponified. The lipid biomarkers were analyzed by gas chromatography (GC) for quantification, GC/mass spectrometry (MS) for identification, and GC/combustion and pyrolysis/isotope ratio MS for compound-specific carbon and hydrogen isotope measurements.

Compound-specific δ¹³C and δD of biomarkers ranged very widely from ~-33 to ~0 per mil (vs. PDB) and ~-470 to ~-160 per mil (vs. SMOW), respectively. White bacterial mat distributed closely to the vent was the most abundant and accompanied with molecular sulfur, suggesting that the white bacterial mat is composed mainly of sulfur-oxidizing bacteria. The carbon isotopic composition of C₁₆ saturated fatty acid (-22.6 per mil) from the white bacterial mat is also consistent with the activity of sulfur-oxidizing bacteria. Green bacterial mat outside the white bacterial mat contained C₁₇ n-alkane (δ¹³C=-33 per mil) and diploptene (δ¹³C=-33 per mil), suggesting that the green mat is cyanobacteria. C₂₀:1 unsaturated fatty acid from brown bacterial mat is extremely ¹³C-enriched (+0.2 per mil). This unusual isotope signature clearly indicates that the brown bacteria utilize reverse TCA cycle for carbon fixation. Furthermore, C₂₀:1 unsaturated fatty acid is extremely D-depleted (-468 per mil), which is probably produced by hydrogen-oxidizing bacteria. Iso- and anteiso-C₁₅ and C₁₇ fatty acids observed from the green and brown mat have δ¹³C of -13 to -11 per mil and δD of -210 to -170 per mil. The δ¹³C of iso- and anteiso-fatty acids is close to bulk organic δ¹³C of bacterial mats, and the δD is the most enriched in D relative to other fatty acids. These branched-chain fatty acids could be produced by heterotrophs such as sulfur-reducing bacteria.