



Development and validation of a LC-IRMS methodology for the determination of amino sugars in soil

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Within the global warming context, C-sequestration in soils is of growing importance. Therefore a better understanding of C-biogeochemistry is indispensable.

Cell walls of fungi, bacteria and actinomycetes are partially constructed of amino sugars which can be used as biomarkers for microbial necromas. The relative and absolute amounts of amino sugars in soil, together with their individual $\delta^{13}\text{C}$ values can thus be used for the determination of microbial soil communities, their turnover times and contribution to C-sequestration.

For this purpose the development of adequate component specific methods for determination of $\delta^{13}\text{C}$ of individual amino sugars is essential. Several GC-c-IRMS methods have been proposed in literature. Although these methods were used with some success in biogeochemical studies, the variability on the measured $\delta^{13}\text{C}$ is too large for precise quantification of turnover rates. This uncertainty can partially be attributed to the need for derivatization. The latter introduces uncertainties on the $\delta^{13}\text{C}$ value of the derivatization product, on the yield and on possible ^{13}C fractionation during the derivatization reaction.

A HPLC-IRMS methodology, which doesn't include a derivatization step, for the determination of $\delta^{13}\text{C}$ and concentration of individual amino sugars present in soil was developed and validated. The chromatographic method consists of two separated isocratic systems, both using the same anion-exchange column, one for the basic amino sugars (glucosamine, galactosamine and mannosamine) and one for the acidic amino sugars (muramic acid) with standard errors for $\delta^{13}\text{C}$ lower than 0.5‰

Additionally, results of amino sugar extracted from soils with a historical alteration of the $\delta^{13}\text{C}$ signature of the carbon input (specific C3-C4 plant growth history and FACE (Free-Air Carbon Dioxide Enrichment) experiment) will be presented and calculated turnover times of the these biomarkers will be reported.