



Composition of hydrolysable amino acids in soil organic matter and soil microbial biomass

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Abstract

We hydrolysed (6 M HCl) soil organic matter (SOM) from mineral top-soil horizons, litter, and the fraction rendered extractable by 0.5 M K₂SO₄ after chloroform fumigation from eight soils under arable, grassland and forest use, covering a wide range of site conditions. Our aims were to quantify amino acid contents in the hydrolysate derived from whole soil, litter and soil microbial biomass, respectively. We also wanted to test if the pattern of hydrolysable amino acids of the whole soil is uniform irrespective of site conditions and land use, and if there is a relation with the amino acid pattern of the respective soil microbial community. The content of hydrolysable amino acids in the whole soil was higher in the soil samples from grassland and forest use than from arable land, and highly correlated with soil total N (N_t) and total organic carbon (TOC) contents. About 28–50% of N_t was found as N in hydrolysable amino acids. This is in accordance with percentages reported for hydrolysable amino acid N in the literature. Much higher values found for amide/peptide N by ¹⁵N-NMR spectroscopy are presumably due to non-hydrolysable peptides in the SOM. Amino acids derived from the soil microbial biomass also had lowest contents in arable soils and were highly correlated with microbial N (N_{mic}) and C (C_{mic}) contents. About 1–5% of TOC and 2–7% of N_t were bound in soil micro-organisms. The percentage of ‘microbial’ amino acid–N in relation to hydrolysable amino acid–N in the whole soil ranged from 1.4 to 5.1%. The pattern of hydrolysable amino acids in the whole soil and the litter was rather uniform irrespective of site conditions and land use. The pattern of microbial amino acids was much more variable. It was different from that in the whole soil in a principal component analysis and showed no consistent relationship with it. Soil pH values are presumably one major factor inducing the variability in the microbial amino acid pattern. An assimilation of the amino acid composition of litter to that found in mineral soil seems to occur already in the early stages of decomposition. © 2002 Elsevier Science Ltd. All rights reserved.

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1. Introduction

Most of the nitrogen (N) in soils (>90%) is organic N. With chemical methods, between 20 and 51% of total N in SOM was found in amino acids, releasable by acid hydrolysis (Aldag and Kickuth, 1973a; Stevenson, 1982; Scheller, 1996a; Senwo and Tabatabai, 1998). Their origin are proteins and amino acids derived from plants, animals and micro-organisms which are transformed and stabilised in the SOM. In ¹⁵N-CPMAS spectra, however, more than 80% of the soil humic material has been found in the amide/peptide region (Knicker et al., 1993). Obviously, only part of the peptide or protein in the soil is hydrolysable. This is confirmed by the study of Knicker and Hatcher (1997),

where the presence of protein-derived material in the non-hydrolysable part (6 M HCl) of an organic-rich sediment was clearly indicated by thermochemolysis.

In soils, the ratio of N in hydrolysable protein to total soil N (N_t) remains almost constant despite increases or decreases in SOM due to different management practices, e.g. manuring and fertilisation (Sowden, 1968; Christensen and Bech-Andersen, 1989). Cultivation was shown to decrease soil N contents as well as the hydrolysable amino acid N (Keeney and Bremner, 1964). An increase in the return of organic N residues (e.g. legumes in the crop rotation), on the other hand, can raise the amount of hydrolysable amino compounds in soils (Gupta and Reuszer, 1967; Stevenson, 1982; Campbell et al., 1991).

Despite substantial quantitative differences in contents of hydrolysable amino acids under different cropping or cultivation systems, only minor differences in the soil amino acid composition were found (Stevenson, 1956; Gupta and

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