

## Abstract

The description of soil microbial community structure by phospholipid fatty acid (PLFA) profiles is based on the relationship between the phylogeny of microorganisms and their PLFA profiles. Based on this relationship, two community based microbiological measurements, namely, potential C source utilization patterns in Biolog microtiter plates and PLFA profiles were used to examine metabolic fingerprints of soil microbial communities and changes in species composition between field and greenhouse soils. Field and greenhouse experiments were conducted using Palouse and Ritzville silt loams. Soil sampled under wheat (*Triticum aestivum* L.), barley (*Hordeum vulgare* L.), pea (*Pisum sativa* L.), jointed goatgrass (*Aegilops cylindrica* L.), downy brome (*Bromus tectorum* L.), and control soils (no plants) were used for these analyses. Principal component analysis (PCA) of PLFA profiles and C source utilization patterns were used to describe changes in microbial biomass and metabolic fingerprints from the two soil types under field and greenhouse conditions. Biomass measurements from extractable PLFA profiles per g dry weight ranged from 28.8 nmol in wheat soil in the greenhouse to 71.4 nmol in pea soil in the field. In general, biomass was higher in all the field samples than in greenhouse samples. Principal component analysis of the two soils with different plants in the field and greenhouse showed clear separation. Principal component analysis of C utilization patterns on the effects of environment on soil microbial community yielded similar results with PLFA measurements. However, higher variability observed among different plants with the Biolog data resulted in the low amount of variance for Biolog data explained by the first two dimensions of the PCA. This suggests that PLFA may be more sensitive for community analysis than the Biolog technique. © 1998 Published by Elsevier Science B.V. All rights reserved.

**Keywords:** Phospholipid fatty acid; Carbon source utilization; Biolog; Metabolic fingerprint; Microbial community structure; Microbial biomass; Principal component analysis