Functional and genetic diversity of soil microbial communities along a gradient of succession in a chalk grassland in north-western France

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Abstract

Plant and microbial communities were compared through their composition, their diversity and their function in a chalk grassland in north-western France. A spatialised sampling design and multivariate statistic analysis permitted to describe the plant succession and to identify four stages of succession from short grasslands to early stages of woodland. In each stage, several measures were collected on vegetation (floristic data and biomass), soil parameters (total carbon, soluble C, total nitrogen, soil polysaccharides) and soil microbial communities (microbial biomass, genetic diversity assessed by ARDRA 16S and 18S, functional diversity assessed using BIOLOG). Our first results do not show clear trends between vegetation and microbial diversity. However, soil parameters and functional microbial diversity discriminated the shrub vegetation.

Keywords : *chalk grassland, plant diversity, plant succession, soil microbial communities, genetic diversity, microbial function*

Introduction

The relationship between plant biodiversity and ecosystem functioning has emerged as a major scientific issue today (Loreau 2000). Although plant and soil microbial communities are closely associated, the relationships between plant diversity and microbial process has been little explored (Broughton et Gross 2000).

Chalk grasslands in north-western France feature very species-rich plant communities. Consequently to the abandonment of traditional sheep grazing, chalk grasslands are threatened by forest progression. In these grasslands, plant succession are one of the most prominent factors controlling plant diversity (Alard *et al.* 1998). Several rare species characteristic to grassland habitat disappear at the final stage of the succession (corresponding to forest). However, few studies have examined the impact on microbial communities and their loss of diversity and function.

This study aims to link vegetation and microbial process according the following approach: (1) Identify changes in vegetation composition, diversity and production along a successional gradient, (2) Examine variations in soil parameter and microbial genetic and functional diversity among the different stages of plant succession, (3) Point out the main factors affecting microbial communities.

Study site

The study was carried out in a chalk grassland in the Hénouville Nature Reserve $(49^{\circ}29'N; 0^{\circ}56'E)$, region of Haute-Normandie, in north-western France. The reserve is situated on a southwest-facing slope (20-30° inclination), along the convex bank of the Seine river. The underlying rocks are calcareous deposits from the Cretaceous overlain by shallow rendzina soils. The chalk grassland belongs to the *Mesobrometum erecti*.

Vegetation, soil parameters and microbial communities sampling

Vegetation was sampled according a spatialised sampling design using a grid-transect of 140 points in order to cover all stages of plant succession. For each plot, vascular plant species abundance was estimated in a $1m^2$ -quadrat. A first vegetation analysis identified four stages of succession. In each of these stages, above ground biomass (weight, cellulose and lignin content) was measured.

Soils were taken from three distinct points in each successional stage. Total carbon, soluble C, total nitrogen, soil polysaccharides and microbial biomass (fumigation/extraction method) were determined. Bacterial and fungal genetic diversity was assessed by ARDRA 16S and 18S while functional diversity was characterised using BIOLOG plates.

Data analysis

Vegetation composition was analysed using Factorial Correspondence Analysis (FCA). This analysis was completed by a Hierarchical Clustering (HC) to identify the main types of plant species assemblages in the transect area. A second HC realised on microbial data and compared to vegetation. The same diversity index (richness, Shannon) were also used to calculate vegetation and microbial diversity. These analysis were performed using the computer program ADE-4 (Thioulouse *et al.* 1997).

Results & discussion

Hierarchical Clustering of vegetation data points out 4 species assemblages corresponding to 4 successional stages: (A) open grasslands with *Sesleria albicans*; (B) tall grasslands dominated by *Brachypodium pinnatum*; (C) grassland-shrub interfaces; (D) shrub. Our first results do not show clear links between vegetation and functional microbial groups. Microbial communities do not co-vary with the whole floristic gradient of the succession. However, soil microbial communities appeared different under the shrub vegetation corresponding to the successional stage D. At this final stage of succession, vegetation is dominated by scrub its species richness is low and its biomass is high.

Soil carbon supply depends of the nature and productivity of vegetation. This nutrient supply changes significantly at the last successional stage, so it is likely that the soil microbial community is affected. Functional diversity of soil microbial community is more affected by vegetation production than its floristic diversity.

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