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Monthly dynamics of microbial community structure and their controlling factors in three floodplain soils

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ABSTRACT

Seasonal dynamics of microbial community under frequently fluctuating oxidized and reduced conditions in floodplain soils are poorly understood, but are considered to be important for understanding microbial community and carbon cycling dynamics in these ecosystems. We determined the microbial community structure using phospholipid fatty acid analysis (PLFA) of three different floodplain soils (Eutric Gleysol = GLe, Eutric Fluvisol = FLe, and Mollic Fluvisol = FLm) at the Elbe River, Germany, for 17 months. Flood duration, soil moisture, soil temperature were also monitored, and hot and cold water extractable carbon (C_{HWE}, C_{CWE}) were determined. Flood duration seems to have a negative impact on total PLFA biomass which increased in the order GLe < FLe << FLm. All PLFA profiles were dominated by Gram-positive bacteria (GPB) and actinomycetes, respectively, and a low content of fungi and arbuscular mycorrhizal fungi (AMF). In the briefly flooded relatively quickly drained soils (FLe and FLm) Gram-negative bacteria (GNB) were abundant compared to the longer flooded, relatively slow drained soil (GLe). This was also obvious in the significant lowest fungi-bacteria ratio and aerobe-anaerobe ratio of GLe. Non-metric dimensional scaling (NMDS) and canonical discriminant analysis (CDA) as multivariate statistical procedures reveal that FLm could be separated from GLe and FLe probably due to aerobic conditions and available soil organic carbon. The GLe can be discriminated from FLe and FLm mainly due to different flooding durations. The GNB, fungi and AMF were more affected by changes of soil moisture and extractable carbon than the GPB, actinomycetes and anaerobes. We conclude that more stable properties of bulk soil such as the magnitude of soil organic carbon, soil texture, and associated flood duration had a stronger impact on soil microbial community than monthly fluctuations of more dynamic properties, such as soil moisture, soil temperature, and C_{HWE}, C_{CWE} in our soils.

1. Introduction

Floodplain soils are semi-terrestrial soils formed by periodical deposition of suspended sediments from river water during flood events (Rinklebe et al., 2007; Du Laing et al., 2009; Luster et al., 2014). They have large fluctuations in water table and reveal therefore various soil moisture conditions (Gutknecht et al., 2006; Du Laing et al., 2009; Shaheen et al., 2014a). These soils have both, oxidic and anoxic zones, allowing a wide range of anaerobic and aerobic processes (Gutknecht et al., 2006; Shaheen and Rinklebe, 2014). Three major types of floodplain soils have been identified in the past. They are often characterized through high carbon contents due to the high intensity of organic matter accumulation (Rinklebe, 2004; Rinklebe et al., 2007; Du Laing et al., 2009; Rinklebe and Shaheen, 2014). Dominating soils on upper riverine terraces are Eutric Fluvisols (FLe) consisting of floodplain loams while Eutric Gleysols (GLe) made up of floodplain silt–clay are characteristic soils in lower topographical positions, such as flood channels, depressions, and ditches embedded in fluvial loamy terraces (Du Laing et al., 2009; soil classification according to IUSS Working Group WRB, 2014). These GLe are showing frequently gleyic, fluvic, and stagnic properties (Rinklebe et al., 2007; Rinklebe and Shaheen, 2014). Mollic Fluvisols (FLm) are common on low-lying terraces consisting of floodplain silt and showing both, high content and high-quality soil organic matter (Rinklebe, 2004;

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Shaheen and Rinklebe, 2014). The hydrology of all floodplain soils is a crucial factor influencing the microbial community (Bossio and Scow, 1995; Rinklebe and Langer, 2010). One reason for this is that changes of flood-dry-periods cause fluctuating redox conditions (Frohne et al., 2014; Shaheen et al., 2014b) which in turn leads to varying electron donor and acceptor availability for microbial growth and functioning (Balasooriya et al., 2013). Moreover, the microbial community composition and the total phospholipid fatty acid (PLFA) biomass largely depend on flood duration and the time since the soil was last flooded (Rinklebe and Langer, 2006; Langer and Rinklebe, 2009). Fast growing Gram-negative bacteria (GNB) were found in well-aerated horizons near the surface metabolizing a variety of carbon sources, whereas Gram-positive bacteria (GPB) dominate deeper horizons where anaerobic conditions are found frequently (Bossio et al., 2006). Fungi and arbuscular mycorrhizal fungi (AMF) are also sensitive to flooding duration and are thus less abundant in less quickly draining wetland soils (Mentzer et al., 2006). Further factors affecting microbial community in wetland soils are (i) seasonality of soil water content which influences redox conditions and nutrient transport, (ii) soil texture which is important for water flow and gas exchange, (iii) seasonality of soil temperature, and (iv) surrounding plant community which is responsible for the type of plant residues and processes in the rhizosphere (Bossio et al., 1998; Waldrop and Firestone, 2006; Bapiri et al., 2010). Rinklebe and Langer (2006) found that the total PLFA biomass increased in the order GLe < FLe < FLm; however, as a static approach, microbial community composition was determined once at a given time. Nevertheless, microbial community composition varies with time due to change of climatic and environmental conditions (Bossio et al., 2006; Dong et al., 2014). Recently, it has been proposed that heavy rainfall events, strong fluctuations between floods and droughts will occur more frequently due to climate change (EEA, 2012). Such changes may influence physico-chemical conditions, particular in floodplain soils, which should have certain impacts on soil microbial community. At the same time the PRESS-report (Maes et al., 2012) highlights the potential of wetlands, rivers, and streams to regulate matter fluxes which are governed by soil microorganisms to certain extend. Especially for wetlands, soil organic carbon is recognized as important component of global carbon budgets and future climate change. This emphasizes that a better understanding of major biogeochemical processes is a prerequisite sustainable management and conservation functions delivered by those ecosystems including soil microbial functions for maintenance and re-vitalization of river-floodplain ecosystems within the context of climate change adaptation and mitigation.

Several studies about seasonal dynamics of microbial community have either been conducted at laboratory scale, (Jin et al., 2012; Kwon et al., 2013), or at field scale, (Sundh et al., 1997; Bossio et al., 2006; Bellinger et al., 2012; Dong et al., 2014). In boreal peatlands seasonal dynamics of PLFA composition were negligible during growing season (Sundh et al., 1997), in permanent flooded wetlands changes between winter and spring were larger than those due to flooding or high organic matter inputs (Bossio et al., 2006), and in paddy fields total PLFA biomass, bacterial and fungal biomass were highest in autumn and decreased sharply from autumn to winter (Dong et al., 2014). However, those studies were not directly addressed to peculiarities of floodplain ecosystems, such as periodically flooding with large changes of water level and long dry periods; moreover soil samples were collected solely 3–4 times in one year. To our best knowledge, studies of dynamics of soil microbial community in different floodplain soils in higher temporal resolution are lacking.

Therefore, our aims were (i) to determine on a monthly basis the seasonal dynamics of the total PLFA biomass and the microbial community composition using PLFA in three different floodplain soils along the Central Elbe River, Germany, during a 17 month monitoring period, (ii) to quantify the impacts of the dynamics of soil moisture, soil temperature, and available carbon (hot and cold water extractable carbon; C_{HWE} and C_{CWE}, respectively) on the soil microbial community and (iii) to use non-metric multidimensional scaling (NMDS) and canonical discriminant analysis (CDA) as multivariate statistical procedures to determine how and why the three floodplain soils can be discriminated by their individual microbial community composition.

2. Materials and methods

2.1. Study sites and soils

Two study areas which have served as model regions for common floodplains in Europe (Henle et al., 2006) were chosen. The study area "Steckby" is located at Elbe stream kilometer 284, 51°54′51″N, 11°58′33″E. The area "Wörlitz" is located at stream kilometer 242, 51°51′59″N, 12°23′11″E. This region is characterized by an average annual precipitation of 449 mm and an annual mean air temperature of 8.0 °C. Flood events depend on hydrometeorological conditions in the catchment area such as snow melting in winter and spring and heavy rainfalls in spring and summer. The plant communities are determined as *Rumici – Alopecuretum aequalis* on GLe, *Cuscuto europaeae – Convolvuletum sepium* on FLm, and *Galio molluginis – Alopecuretum pratensis* on FLe according to Schubert et al. (1995).

Based on large-scale conventional soil mapping of the study areas and plenty of years of comprehensive field pedological research in these floodplains (e.g. Rinklebe et al., 2000a,b; Rinklebe, 2004; Wälder et al., 2008) three reference soils which are common in these floodplain ecosystems were selected for the current study: an Eutric Gleysol (GLe) and a Mollic Fluvisol (FLm) (both at the area "Steckby") as well as an Eutric Fluvisol (FLe) (area "Wörlitz"). The soil profiles were classified according to the IUSS Working Group WRB (2014). One soil horizon of each soil profile was chosen to monitor the monthly dynamics of microbial community composition as well as water level, soil moisture, soil temperature, C_{HWE} and C_{CWE}. Characteristics of respective soil horizons are given in Table 1.

2.2. Soil sampling and preparation

Soil samples were collected at each site in four replicates and thereafter pooled into one sample (Rinklebe, 2004). Before analyses all visible roots, macro fauna and fresh litter material were removed. For physico-chemical analyses the samples were air dried and sieved to 2 mm. Microbial samples were collected at the beginning of every month except during flood events. At each sampling date approximately 20 cm of the entire soil profile were removed before sampling the respective fresh soil horizon. During transportation samples were cooled and thereafter sieved to 2 mm and stored at −20 °C. Before the extraction and measuring procedure the microbial samples were freeze-dried (−80 °C) for 2 days and thereafter stored until extraction at 4 °C. Hydrological monitoring stations equipped with suction cups, temperature sensors, and tensiometers were installed at each soil profile. Sensors and suction cups were arranged in the center of the studied horizons and were used to determine soil moisture and soil temperature in three replications in a high temporal resolution (every two hours). The water level was additionally monitored by piezometers at each soil profile every two hours during the monitoring period. Technical details about monitoring stations see Rinklebe (2004).