



Land-use and land-cover effects on soil microbial community abundance and composition in headwater riparian wetlands



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ABSTRACT

Headwater riparian wetlands are relatively small in size but functionally significant as expected hot spots of microbial activity in the landscape. Despite their roles as biogeochemical drivers, little is known about how microbial communities in headwater riparian wetlands are affected by surrounding land-uses and land-covers (LULCs). The primary objective of this study was to determine if and how wetland soil microbial abundance and community composition varied as a function of landscape metrics as mediated through on-site edaphic properties. Forty-two soil samples, collected from eight headwater riparian wetlands in the Ridge and Valley Region of central Pennsylvania, were used for phospholipid fatty acid (PLFA) profiling of soil microbial communities. These samples were used to create microbial habitat models describing plot-level relationships between edaphic properties and microbial measures (i.e., microbial biomarker abundances, ratios and composition). Soil organic matter (SOM) content was a strong predictor of microbial biomarker abundances and fungi/bacteria ratios, while soil pH was a strong predictor of microbial composition (i.e., relative abundance of individual fatty acids) and potential microbial stress indices (i.e., cy19:0a/18:1ω7c and cy17:0/16:1ω7c ratios). Soil texture, soil moisture, and litter total nitrogen had smaller, but significant effects in these empirical microbial habitat models. Microbial habitat models were subsequently used to estimate microbial measures for a larger regional headwater riparian wetland dataset (n = 87), where edaphic property information was compiled. Site-average microbial measures were correlated with wetland elevation, and with landscape composition metrics in a landscape assessment area (i.e., 125,664 m²). Wetland elevation explained high among-site variability in microbial abundance measures, as mediated through SOM content, in headwater riparian wetlands in forested landscapes. However, wetland elevation was confounded by landscape composition, for headwater riparian wetland in mixed forested-agricultural landscapes. Hydrology, geomorphology, and changes in vegetation could be used to explain SOM variation across wetland elevation and variability in surrounding landscape composition. Microbial composition measures, including the cy19:0/18:1ω7c ratio and principal component (PC) axes derived from 23 individual PLFA biomarkers were negatively related to the Landscape Development Intensity (LDI) index, and the percent area of row crops, pastures and grasslands, and positively related to the percent area of forest. The cy17:0/16:1ω7c ratio was positively related to the LDI index, and the percent area of pasture and grasslands, and negatively related to the percent area of forest and wetland elevation. Differences along PC axes were most clearly related to the relative abundances of fungal communities; headwater riparian wetland in forested landscapes had significantly higher relative abundances of saprophytic fungi biomarkers, while headwater riparian wetland in mixed landscapes had significantly higher relative abundances of the arbuscular mycorrhizal fungi biomarker. This study highlights the utility of simple landscape metrics, which describe wetland position and landscape composition, for predicting differences in edaphic

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variability and associated microbial community composition and biomass among headwater riparian wetlands at a regional scale.

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1. Introduction

The importance of characterizing wetland functioning for the delivery of services such as carbon sequestration and nitrogen removal is at the forefront of research and management efforts, exemplified by the first ever National Wetland Condition Assessment performed in the United States (U.S.) by the Environmental Protection Agency (EPA) in 2011. With advancements in molecular tools, the use of microbial indicators in wetland condition assessments has been advocated by Sims et al. (2013). Some wetland soil processes (e.g., nitrification, methanogenesis, and sulfur reduction) are directly affected by microbial composition due to the specificity of the microbial groups required to perform these functions (Schimel and Gullledge, 1998). However, more general processes, such as decomposition, can also be affected by microbial composition, particularly in the rhizosphere, in above ground litter, and in mineral soils over temporal scales where microbial resource allocation drives system dynamics (Schimel and Schaeffer, 2012). For example, fungi are expected to metabolize complex substrates more directly than bacteria (Holland and Coleman, 1987). Fungal biomass is also more resistant to decomposition than bacterial residues (Guggenberger et al., 1999), with an increase in fungal biomass expected to favor the accrual of soil carbon through the formation of stable soil structure (Jastrow and Miller, 1998; Allison et al., 2005). Further comparisons have revealed that decomposition and carbon accretion rates in soil can vary among fungal groups (Hodge et al., 2001; Averill et al., 2014).

While several studies have assessed differences in wetland microbial communities or specific functional microbial groups in created wetlands and wetland restoration efforts (Smith et al., 2007; Hartman et al., 2008; Card and Quideau, 2010; Peralta et al., 2010; Sims et al., 2012), we lack knowledge about differences in wetland microbial communities across variability in wetland landscape contexts. In this study we begin to fill this gap by assessing variability in microbial communities across various dimensions of landscape context. Landscape context can be described by factors such as landscape position (e.g., elevation) and changes in the composition and/or arrangement of land-use and land-cover (LULC) types in the areas surrounding wetlands. While being spatially separated, the surrounding landscape can be energetically linked to wetlands, through lateral flow (i.e., surface and subsurface) of water, sediments, and chemical constituents. We hypothesize that these linkages can play a major role in microbial community composition and activity by affecting edaphic properties and hence the functions which wetlands provide. We suggest this is particularly true for headwater riparian wetlands, which are commonly situated downslope of upland areas in the watershed and receive surface, subsurface, and overbank flow. These systems are considered hot spots in the landscape for biogeochemical activities (McClain et al., 2003; Vidon et al., 2010), and lie adjacent to headwater streams, which constitute 60–75 % of total stream and river miles in the U.S. (Leopold et al., 1964). Their small size relative to the surrounding watersheds, and their high perimeter to area ratios also make them potential hot spots of surrounding landscape influence.

Although linkages between wetland microbial communities and landscape context, particularly landscape composition, are not well

understood, shifts in other on-site properties have been well documented in headwater riparian wetlands and related to changes in landscape composition. For example, in the Ridge and Valley region of central Pennsylvania headwater riparian wetlands with surrounding landscapes dominated by agricultural and urban LULC categories have greater percentages of herbaceous cover and a predominance of invasive and generalist species, compared to wetlands in landscapes dominated by forest (Miller and Wardrop, 2006; Moon and Wardrop, 2013). Hydrologic disconnections between streams and adjacent wetlands have also occurred (Adamus et al., 2001; Ryan, 2005), leading to changes in the frequency and intensity of inundation (Moon and Wardrop, 2013; Wardrop et al., 2016) and the delivery of sediment. Reference standard wetlands (i.e., those deemed to be in the most pristine condition) tend to have lower sedimentation rates (Wardrop and Brooks, 1998), higher levels of soil organic matter (SOM) (Spencer et al., 1998; Freeland et al., 1999; Dinesh et al., 2004; Cohen et al., 2005; Reiss, 2006; Rokosch et al., 2009; Cleveland et al., 2011; Moon and Wardrop, 2013) lower soil bulk densities (Spencer et al., 1998; Innis et al., 2000; Pennings et al., 2002; Reiss, 2006), and lower soil pH (Reiss, 2006; Cleveland et al., 2011; Moon and Wardrop, 2013) compared to those which are considered impacted or degraded.

Changes in these wetland on-site properties further support hypothesized changes in the microbial communities because many of these on-site factors act as proximal controls of microbial communities, and thus mediate impacts arising from landscape context (distal controls). Some studies have successfully linked microbial composition and biomass directly to ecosystem type, land-use change, management regimes, and stressors within ecosystems (Allison et al., 2005; Xue et al., 2008; Burton et al., 2010; Drenovsky et al., 2010). Differences in soil microbial biomass and composition have been associated with changes across hydrologic gradients, flooding duration, water table depth and variability, and rates of sedimentation (Lockaby et al., 2005; Mentzer et al., 2006; Balasooriya et al., 2008; Unger et al., 2009; Yu and Ehrenfeld, 2010). Others have shown that soil microbial communities are strongly influenced by vegetation (Wardle et al., 2004), with a number of studies linking microbial community composition, diversity, and enzyme activity to specific plant species (Borga et al., 1994; Sundh et al., 1997; Ingham and Wilson, 1999; Ehrenfeld et al., 2001; Kourtev et al., 2002, 2003) and higher levels of ecological complexity, such as aboveground plant diversity (Carney and Matson, 2006). Further, links have been made more directly between microbial measures and differences in edaphic characteristics (Frostegård et al., 1997; Calderón et al., 2001; Fierer and Jackson, 2006; Gutknecht et al., 2006; Balasooriya et al., 2008; Lauber et al., 2008; Wakelin et al., 2008; Yu and Ehrenfeld, 2010). Litter total carbon:total nitrogen (L_{TC}:TN) ratios (Myrold, 1999; Carney and Matson, 2006), soil temperature (Klamer et al., 2000; Pietikäinen et al., 2005; Gray et al., 2011), soil moisture (Bossio and Scow, 1998; Langer and Rinklebe, 2009), carbon and nutrient availability (Fierer et al., 2007; Högberg et al., 2007), soil pH (Fierer and Jackson, 2006; Högberg et al., 2007), and soil texture (Gregorich et al., 1991; Ludvigsen et al., 1999) have all been shown to influence microbial abundance, composition, and in some cases microbial diversity (Fierer et al., 2007).

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