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Influence of irrigated agriculture on soil microbial diversity

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ABSTRACT

Organic carbon (C), bacterial biomass and structural community diversity were measured in Southern Idaho soils with long term cropping histories. The soils tested were native sagebrush vegetation (NSB), irrigated moldboard plowed crops (IMP), irrigated conservation – chisel – tilled crops (ICT) and irrigated pasture systems (IP). Organic C concentration in soils decreased in the order NSB 0–5 cm > IP 0–30 cm = ICT 0–15 cm > IMP 0–30 cm > NSB 5–15 cm = NSB 15–30 cm. Active bacterial, fungal and microbial biomass correlated with soil C as measured by the Walkely Black method in positive curvilinear relationships (r^2 = 0.93, 0.80 and 0.76, respectively). Amplicon length heterogeneity (LH-PCR) DNA profiling was used to access the eubacterial diversity in all soils and at all depths. The Shannon–Weaver diversity index was used to measure the differences using the combined data from three hypervariable domains of the eubacterial 16S rRNA genes. Diversity was greatest in NSB 15–30 cm soil and lowest in the IMP soil. With the exception of IMP with the lowest diversity index, the samples highest in C (NSB 0–5 cm, IP 0–30 cm, ICT 0–15 cm) reflected lower diversity indices. However, these indices were not significantly different from each other. ICT and IP increase soil C and to some extent increase diversity relative to IMP. Since soil bacteria respond quickly to environmental changes, monitoring microbial communities may be one way to assess the impact of agricultural practices such as irrigation and tillage regimes.

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1. Introduction

Land use changes can impact the amount of organic carbon (C) stored in the soil by altering C inputs and losses. In forest, grassland and wetland ecosystems, conversion of native vegetation to agricultural cropping has resulted in substantial C transfer to the atmosphere as a result of loss of climax vegetation to the lower equilibrium C concentration in soil (Baker et al., 2007; VandenBygaart et al., 2003; Wang et al., 1999). Farm management practices, including conservation tillage and erosion control, have reduced the amount of CO_2 emitted to the atmosphere in both Canada and the United States (VandenBygaart et al., 2003; West and Marland, 2002; Paustian et al., 1997). Irrigation also increases C input to soils via increased litter and root production. In arid and semi-arid environments, plant survival and growth is limited by available water and irrigation is required to increase plant production to the point where crops become economically viable. Intensively managed crop or pastureland has potential for C gain through the use of improved grazing regimes, fertilization practices and irrigation management (Entry et al., 2002; Follett, 2001; Bruce et al., 1999).

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Soil microbial diversity is important because it is often regarded as an important index of soil ecosystem health. As the biodiversity of an ecosystem increases, the resilience and stability of the ecosystem should increase (Garbeva et al., 2004; Torsvik and Ovreas, 2002). Conversely, as ecosystems degrade, ecosystem biodiversity decreases (Garbeva et al., 2004; Sun et al., 2004). Loss of biodiversity leads to loss of ecosystem resistance and resilience to anthropogenic as well as natural stresses (Garbeva et al., 2004; van Elsas et al., 2002). Ecosystem resistance is the ability of the system to absorb the reduction of numbers of a species or set of species as a result of natural catastrophes such as hurricanes, periodic droughts, and insect or disease epidemics. Ecosystem resilience is the ability of ecosystem processes such as nutrient cycling, to survive and recover from these natural catastrophes.

Microorganisms exhibit an impressive diversity in their metabolic activities and in their interactions with other microbes, plants, and animals. Microbes have much shorter turnover rates than higher plants and therefore, respond more quickly to changes in land management than plants and may be the most sensitive indicator to anthropogenic activities. In the past it has been nearly impossible to discern underlying patterns within ecosystems because of the intrinsic structural and functional diversity of microbial communities. To date, only 1–5% of the world's microorganisms have been identified (Mills et al., 2007; Nannipieri et al., 2003; Hugenholtz et al., 1998) As a result, microbial processes, the microbes are often placed in a 'black box', inputs and outputs measured, but most of the processes that go on inside 'the box' are based on inference (Mills et al., 2007; Swift et al., 2004; Brussaard et al., 1997). Recently, there has been an explosion in the identification of microorganisms in the natural world using culture-independent techniques. The structure and function of these microbial communities using new molecular technologies can be determined (Mills et al., 2007; Thies, 2007; Nakatsu, 2007; Rogers et al., 2007; Suzuki et al., 1998).

Ribosomal molecules have highly conserved sequence domains interspersed with hypervariable regions (Kirk et al., 2004; Head et al., 1998), and it is these variable domains that can be used distinguish one microbe from another and therefore, can be used as molecular markers to discriminate among taxa. The use of ribosomal DNA profiles as phylogenetic markers has provided a rapid and economical method to assess microbial diversity, although at lower resolution than nucleic acid sequencing (Thies, 2007; Nakatsu, 2007; Mills et al., 2007, 2006). The application of the amplicon length heterogeneity-PCR (LH-PCR) technique as a profiling tool to assess microbial communities has been shown to extend the current knowledge of the dynamics of microbial communities in their natural environment (Mills et al., 2006; Bernhard et al., 2005; Ritchie et al., 2000). For example, LH-PCR has been compared with fatty acid methyl ester (FAME) profiles in an effort to see which method could better assess the diversity present in the soil communities (Ritchie et al., 2000). LH-PCR has proven to be highly reproducible, robust and capable of monitoring microbial communities in a variety of soil, water and sediment ecosystems (Mills et al., 2003, 2006, 2007; Ritchie et al., 2000; Suzuki et al., 1998). Since increasing plant growth on arid and semi-arid lands by conversion to irrigated agriculture increases C storage in soils (Entry et al., 2002), we hypothesize that irrigated agriculture will also increase active bacterial biomass, and eubacterial structural diversity. Given that soil type and spatial distribution of resources have been found to be key drivers in the organization of soil communities (Johnson et al., 2003; Girvan et al., 2003; Zhou et al., 2002), organic carbon, microbial biomass and eubacterial structural diversity measures were used to assess the impact of ''disturbance'' or land management practices on Idaho soil under irrigation and different tillage regimes.

2. Materials and methods

2.1. Site descriptions

The study area is located on the Snake River Plain, between 42°30′00″ and 43°30′00″N and 114°20′00″ and 116°30′00″W. The sites occur across an elevation gradient ranging from 860 to 1300 m. The area is classified as a temperate semi-desert ecosystem (Bailey, 1998). The climate is typified by cool, moist winters and hot, dry summers with annual precipitation ranging from 175 to 305 mm, two-thirds of which occurs during October through March (Collett, 1982). Air temperatures range from 0 to 30 °C with annual average of 9–10 °C. Soils are typically well-drained loams and silt loams derived from loess deposits overlying basalt. Soil was classified as a fine, montmorillonitic, mesic Xerollic Haplargid on the Brown's Creek site, a coarse-loamy, mixed non-acid, mesic Xeric Torriorthents on the Simco site and a loamy, mixed, mesic lithic Xerollic Camborthids on the Kuna Butte site (Collett, 1982).

Vegetation throughout the general area was historically dominated by basin big sagebrush (*Artemisia tridentata* var. *tridentata* Nutt.), Wyoming big sagebrush (*Artemisia tridentata* var. *wyomingensis* Nutt.), and perennial bunch grasses, including Sandberg bluegrass (*Poa secunda* J. Presl), bottlebrush squirreltail (*Elymus elymoides* Raf. Swezy.), bluebunch wheatgrass (*Pseudoroegneria spicata* Pursh. A. Love), and Thurber's needlegrass (*Achnatherum thurberianum* (Piper) Barkworth).

2.2. Native vegetation sagebrush sites

Native sagebrush sites (NSB) were vegetated with native steppe vegetation and a low composition of exotic annual grasses. Sites were chosen for this study based on a history of no livestock grazing (BLM, Boise, Idaho, unpublished data). All study sites had 5–10% slope and were on areas that supported basin big sagebrush or Wyoming big sagebrush or mixed communities. Three geographically separated NSB locations, at least a minimum of 5 km apart, were sampled for this study.

2.3. Irrigated pasture (IP) sites

Three irrigated pastures were selected that were formerly crop land and converted to and maintained as irrigated pasture for the past 30 years. The Buhl site was vegetated with Kentucky bluegrass (*Poa pratensis* L.)—orchardgrass (*Dactylis glomerata* L.) on a Rakane-Blacknest soil complex, fine-loamy, mixed, mesic Xerollic Durargids soil. The Gooding site was vegetated with