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Vegetation Diversity in Native Mixed-Korean Pine Forests

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Abstract

The relationship between biodiversity and ecosystem function is a significant scientific concern today. The purpose of this study was to examine the link between plant diversity and microbial communities in native mixed-Korean pine forests and to construct a comprehensive evaluation model that utilizes both vegetation diversity and microbial functional diversity to assess the stability of the forest ecosystem. Experiments were conducted in a series of original Korean pine forests compared to adjacent artificial forests. The experimental design included five plots (HD, HZ, HY, LY, and BH), each measuring 800 m². Plant studies indicated that vegetation significantly ($P > 0.05$) affects the crown volume index of the herb, shrub, and tree layers. Species richness, diversity, and evenness of the herb, shrub, and tree layers in original Korean pine forest types were significantly ($P > 0.05$) higher than those in artificial forest types.

Keywords

Native mixed-Korean pine forests, Vegetation diversity, Microbial diversity, Biolog, Eco-environmental stability

1. Introduction

Unprecedented rates of species extinction resulting from anthropogenic disturbances, such as land-use change and climate change, have prompted extensive research on the impact of biodiversity losses on ecosystem functioning [1-3]. The potential for anthropogenic disturbance to impose selective pressure on microbial communities is well documented. Biodiversity may have an important role in the stability of ecosystem functioning. Loss of sensitive species as a result of disturbance has the potential to cause long-lasting ecological effects if the stability or functioning of the microbial community as a whole is compromised [4-6]. Many researchers have investigated community structure dynamics [7, 8], nutrient cycling characteristics [9], soil quality [10], and the impact of biodiversity on soil properties [11-13]. The diversity of soil micro-organisms is not only studied but it is believed that only about 1% of the organisms that occur in soil have been cultured, identified, and characterized [14, 15]. As a result, we selected a series of original Korean pine forests converted from subalpine natural coniferous forests compared to adjacent artificial forests. We believe that this species turnover may also drive variations in the microbial communities between different locations, Thus, in this study, we were concerned with determining just how correlated above-ground plant species diversity is with soil microorganism functional diversity, and try to construct a comprehensive evaluation model, using the vegetation diversity and microbial function diversity to evaluate the stability of the forest ecological system similar to sample plot.

2. Materials and methods

2.1 Study area

Liangshui Nature Reserve (47°10′50″N, 128°53′20″E), a preserve which is located in Yichun City, Heilongjiang province of China. It had the efficacy of protecting the Korean pine broad-leaved mixed forest ecological system. The area is 6394

hm^2, and its temperate type belongs to the continental climate. In this area, the latitude is higher, the average annual temperature is only -0.3 ℃ while the annual average minimum and maximum temperatures are -6.6 ℃ and 7.5 ℃ respectively. It belongs to the northern temperate Needle Mongolia forest area. The zonal vegetation is a mixed forest with needle and broad leaves, which is mainly Korean pine (Abbreviation broad-leaved Korean pine forest).

Eight sampling locations surrounding each original Korean pine mixed forest type (type: HY: Korean spruce & Korean pine forest; HZ: oak & Korean pine forest; HD: linden-Korean pine forest) in Liangshui Nature Reserve, which was chosen based on previous studies conducted in this site. Two adjacent artificial forest types (type: BH: birch pure forest; LY: larch pure forest) were chosen to represent the background.

2.2 Vegetation sampling

The above-ground plant species inventory was carried out between July and August of 2010. In order to avoid a possible edge effect, eight square sampling plots (25 × 25 m^2) were delimited according to the method of the species/area curve (Kent & Coker, 1992), demarcated approximately in the center of each stand. The vegetation is divided into three height classes, 0-0.5 m (herbaceous or small shrubs), 0.5-2 m (shrubs), and > 2 m (tall shrubs or trees). In each sampling plot, trees (10 × 10 m^2), shrubs (5 × 5 m^2), and herbaceous (2 × 2 m^2) were destructively measured in plots placed in each facies whose datum within the 10 × 10 m^2 plot was used for comparing with below-ground communities. Detailed measurements were made of stand and site characteristics on these plots [25]. Each plant recorded was characterized by its species name, canopy dimensions, number, and trunk circumference; habitat factors: longitude and latitude, altitude, topography, slope, soil type, etc.

2.3 Vegetation diversity calculations

Percentage cover for each plant species, calculated through visual estimation was determined. Then, the following diversity indexes were calculated (Magurran, 2004; Simpson, 1949) [16]: species richness (S), Shannon's index (H) [17], Simpson's index (D) [18], and Pielou's index (U) [19]. These four indexes were calculated for both (i) all the plant species present in the sampling plots considered as a whole [20] and (ii) each of the three different growth forms here considered (i.e., herbs, shrubs, trees) [21].

3. Results

3.1 Vegetation diversity

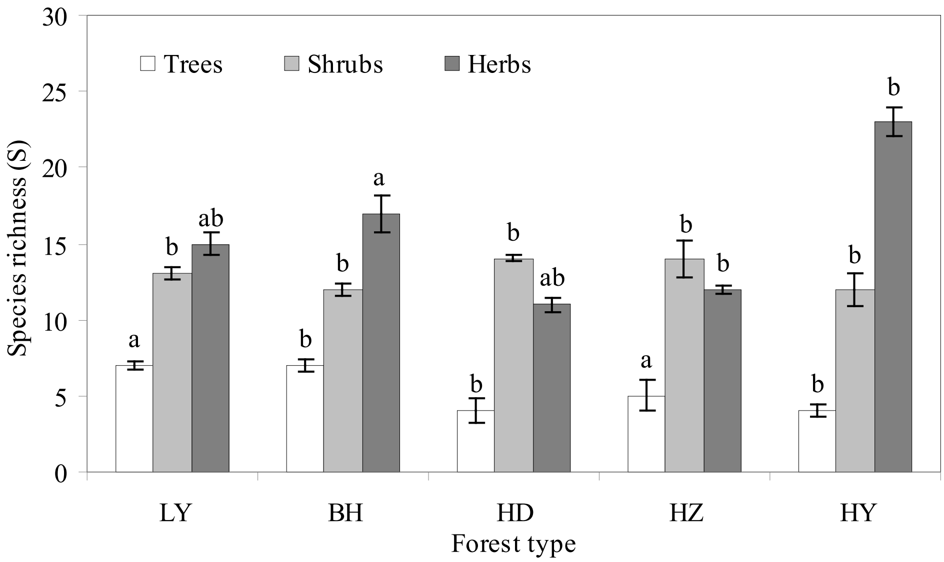


Figure 1. Mean species richness for herb, shrub, and tree layers among the different forest types. (±S.E.) Means with different letters are significantly different (by Fisher PLSD test, at *P* < 0.05) (LY, BH, HD, HZ, and HY represent forest type, LY: larch pure forest; BH-birch pure forest; HD: linden-Korean pine forest; HZ: oak & Korean pine forest; HY: Korean spruce & Korean pine forest).

The treatment groups showed (Fig. 1) similar trends during the three layers (tree, shrub, and herb layers). The species richness of the tree layer for the treatments was minimal. Both the shrub and herb layers treatments appeared to show an increase in the volume of species richness. Both the species richness of the tree and herb layers were significantly higher ($P < 0.05$) in the artificial pure forest types (LY, BH) than the original Korean pine mixed forest types (HD, HZ, and HY) at each sampling date. The species richness of the shrub layer was higher ($P < 0.05$) in the artificial pure forest types (LY, BH) than the original Korean pine mixed forest types (HD, HZ, and HY) at each sampling date, although differences were not significant (Fig. 1).

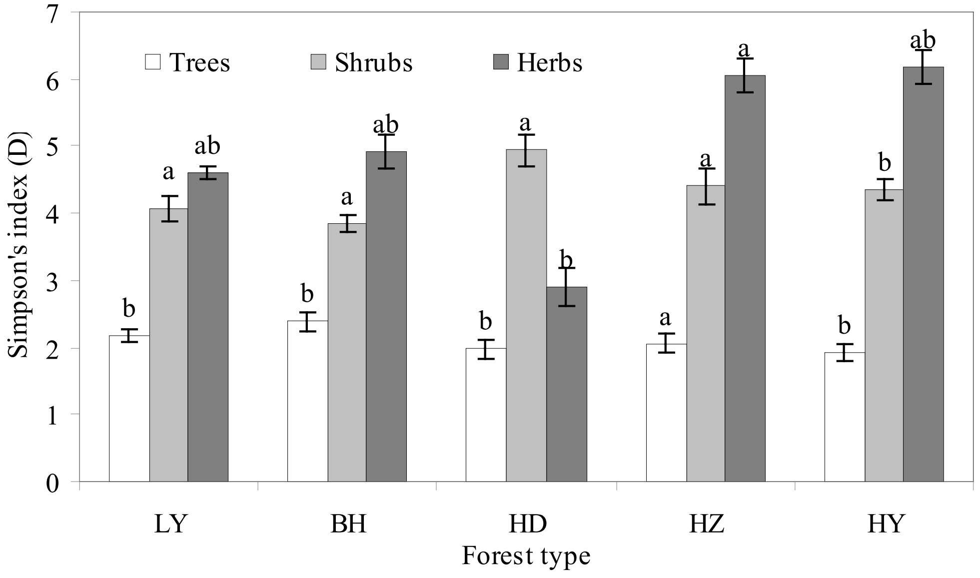


Figure 2. Mean Simpson's diversity index for herb, shrub, and tree layers among the different forest types. (±S.E.) Means with different letters are significantly different (by Fisher PLSD test, at *P* < 0.05). Refer to Fig. 1 for definitions of forest types.

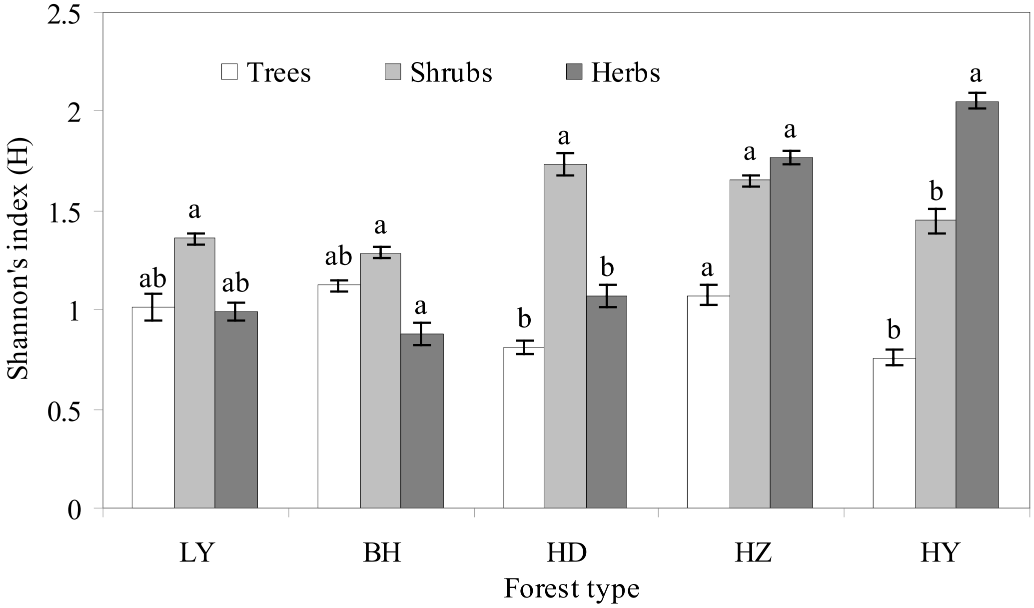


Figure 3. Mean Shannon's diversity index for herb, shrub, and tree layers among the different forest types. (±S.E.) Means with different letters are significantly different (by Fisher PLSD test, at *P* < 0.05). Refer to Fig. 1 for definitions of forest types.

Mean species diversity of the three layers was similar (Shannon's index or Pielou's index) among the treatments (Fig. 2; Fig. 3). The Shannon's index and Pielou's index for the LY, BH, and HD treatments peaked in the shrubs layer, although both the indexes for the HZ and HD treatments peaked in the herb layer.

Mean species diversity of the tree layer was similar (Shannon's index or Pielou's index) among the treatments (Fig. 2; Fig. 3). Both the artificial pure forest types (LY and BH) demonstrated the significantly higher (P < 0.05) level of tree species diversity compared with the original Korean pine mixed forest types treatments, (HD, HZ, and HY).

Mean species diversity in both of the shrub and herb layers was similar (Shannon's index or Pielou's index) among the treatments (Fig. 2; Fig. 3). To compare with both the artificial pure forest types (LY and BH), the original Korean pine mixed forest types treatments (HD, HZ, and HY) demonstrated the significantly higher (P < 0.05) level of species diversity.

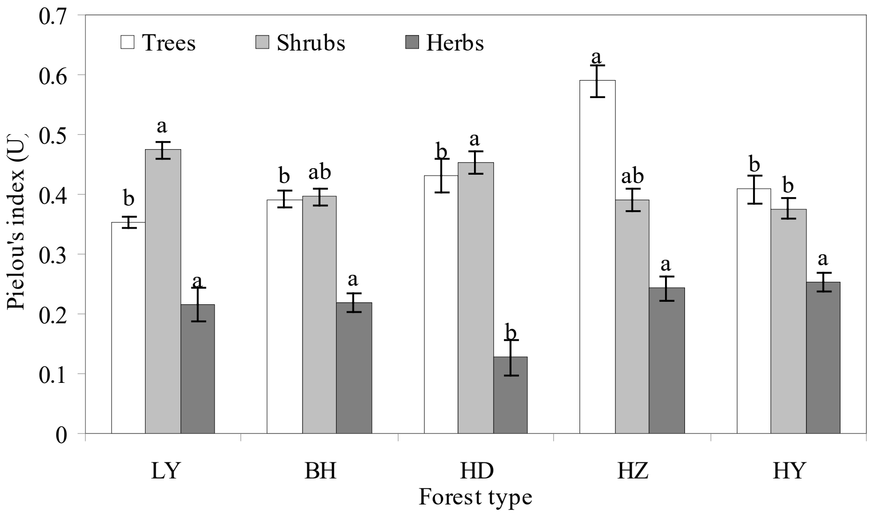


Figure 4. Mean Pielou's evenness index for herb, shrub, and tree layers among the different forest types. (±S.E.) Means with different letters are significantly different (by Fisher PLSD test, at P < 0.05). Refer to Fig. 1 for definitions of forest types.

Mean Pielou's index of the treatment groups showed similar trends during the three layers (tree, shrub, herb layers) [22]. The Pielou's index of the tree and shrub layer for the treatments was approximate and the Pielou's index of the herb layer was minimum.

Mean Pielou's index of both the tree and herb layers was similar among the treatments (Fig. 4). To compare with both the artificial pure forest types (LY and BH), the original Korean pine mixed forest types treatments (HD, HZ, and HY) demonstrated the significantly higher (P < 0.05) level of species evenness.

Mean Pielou's index of the shrub layer both of the artificial pure forest types (LY and BH), demonstrated the significantly higher (P < 0.05) level of species evenness compared with the original Korean pine mixed forest types treatments (HZ and HY). However, the mean Pielou's index of the shrub layer of treatment HD was higher than treatment BH, although lower than treatment LY.

3.2 Microbial community catabolic profile

The AWCD of surface soil, 0-10cm soil, and 10-20cm soil showed similar time trends among the treatments showed a gradual growth [23, 24]. Metabolic speed assessment was using kinetics of AWCD values (Fig. 5) which were significantly higher for the original Korean pine mixed forest types treatments (HD, HZ and HY) than the artificial pure forest types (LY and BH) from the soil of surface to 10-20 cm layers. Furthermore, trend curves of treatments showed statistically lower metabolic speed for the soil of surface than in-depth 0-10 cm and 10-20 cm in all sampling times. These data of logarithmic growth from 72 h were used to calculate the functional diversity [25].

Biolog data from the five sites were subjected to PCA (Fig. 6a). PC1, PC2 and PC3 accounted for 66.28%, 14.46% and11.20% of total variation respectively, while their eigenvalues were 20.55, 4.48 and 3.47 respectively. PC1 differed LY from the other four forest types (P < 0.05). PC2 differentiated BH from the other four forest types (P < 0.05). PC3 differed HY and HZ from the other three forest types (P < 0.05). Cluster analysis of Biolog data (Fig. 6b) showed that the microbial community structure beneath LY was different from those beneath the other forest types [26].

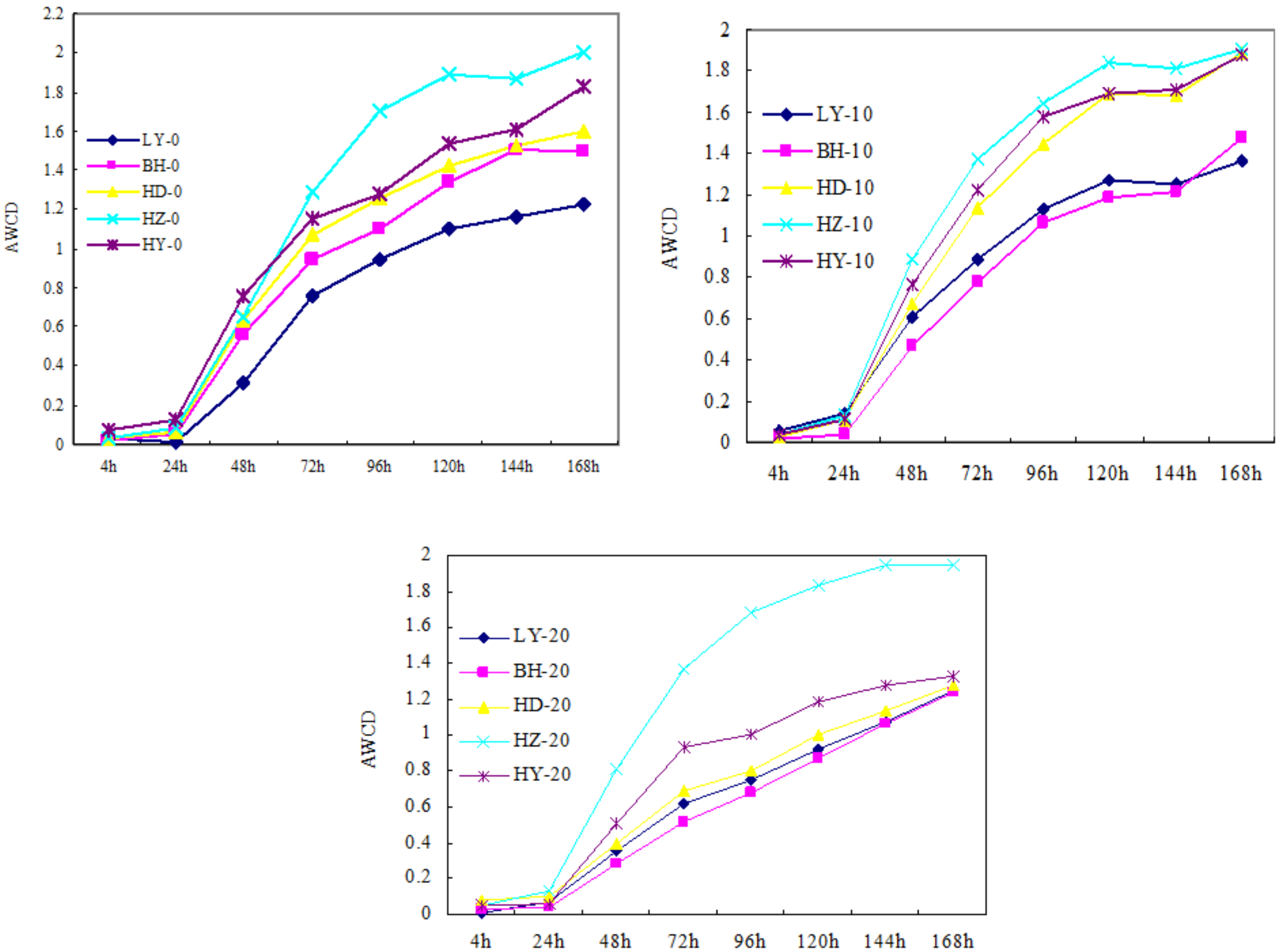
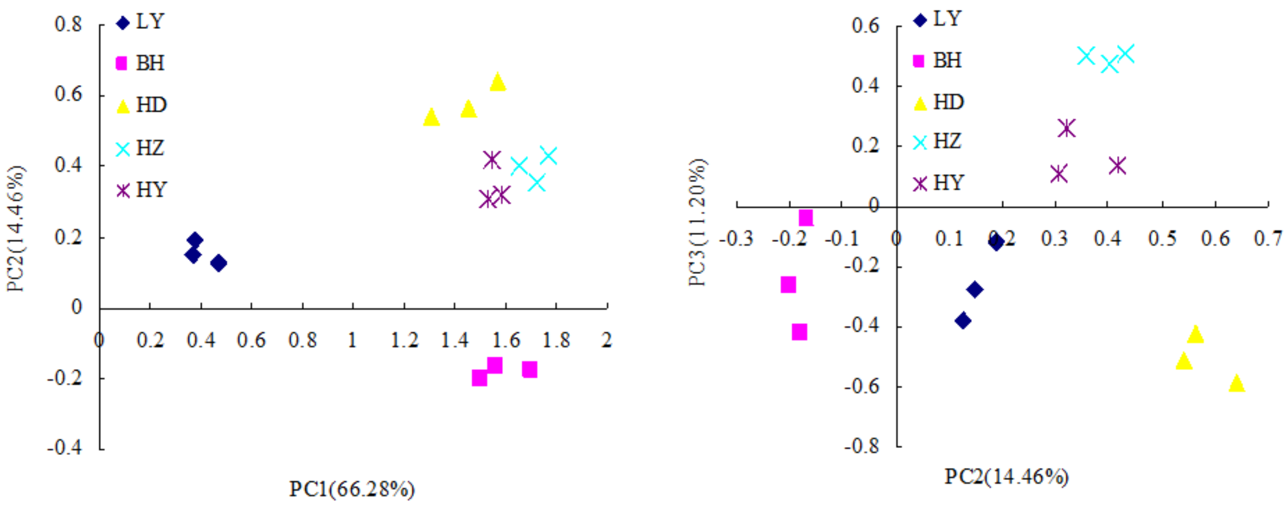
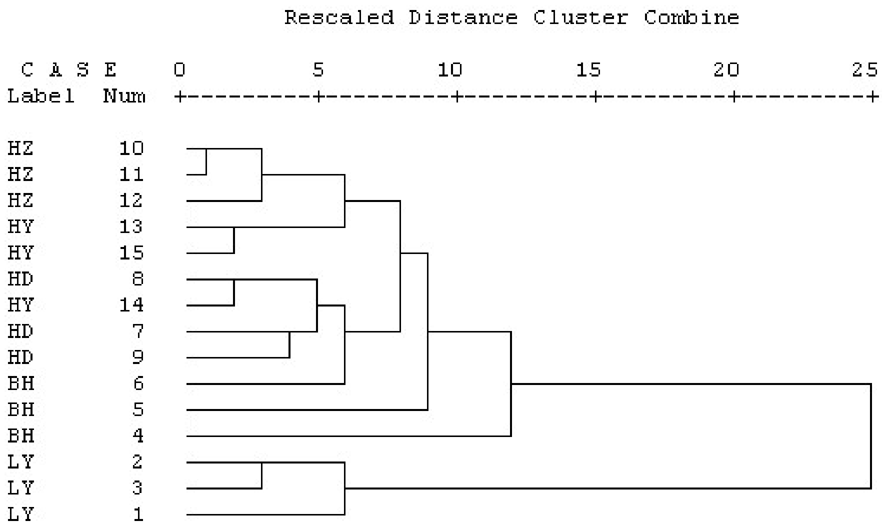


Figure 5. Kinetics of AWCD (mean average values, n = 3) of each sampling time. Refer to Fig. 1 for definitions of forest types. 0: surface soil, 10: 0-10 cm soil, and 10: 10-20 cm soil.



a. Biolog PCA.



b. Cluster tree.

Figure 6. Classification of treatments by principal component analysis (PCA). Refer to Fig. 1 for definitions of forest types.

4. Discussion

Using the important value can estimate both Shannon and Simpson diversity while Pieloub equability are useful tool to indicate areas having large and small diversity, though it may seem a controversial one (Figs. 2-4) [27, 28]. In our experiment, species richness and floristic diversity were significantly higher in natural than artificial plots at each sampling date [29].

Different research methods usually lead to varied results which were also found in this study when characteristics of soil microbial community were assessed with different analytical techniques [30, 31]. As a result of the soil microorganism, multiple selections for the C compounds on BIOLOG ECO plates soil microorganism from five different forest types and soil layers did have a different selection for a few C compounds on BIOLOG ECO plates (Fig. 5; Fig. 6). These findings coupled with the change in microbial C-to-N ratio with soil type and treatment suggested that the composition of the microbial communities had changed. However, with current BIOLOG ECO plate techniques, it is very difficult to detect any changes in the total numbers of C compounds utilized and even more difficult to predict the effect that these changes may have on long-term soil sustainability. Strong seasonal dynamics of microbial biomass and inconsistency of microbial selections for C compounds will limit the use of microbial assessments as criteria for long-term soil sustainability assessments [32].

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