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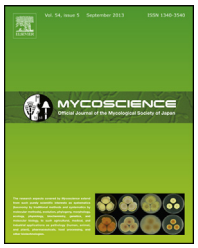

Full paper

Effect of plant species on communities of arbuscular mycorrhizal fungi in the Mongolian steppe

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ABSTRACT

Communities of arbuscular mycorrhizal (AM) fungi were investigated in *Stipa krylovii*, *Leymus chinensis* (Poaceae), *Allium bidentatum* (Liliaceae), and *Astragalus brevifolius* (Fabaceae) in the Mongolian steppe to examine the effect of plant species on the communities in this study. The AM fungal communities were examined by molecular analysis based on the partial sequences of a small subunit of the ribosomal RNA gene. The sequences obtained were divided into 23 phylotypes by the sequence similarity >98%. Many of the AM fungal phylotypes included AM fungi previously detected in high-altitude regions in the Tibet and Loes plateaus, which suggested that these AM fungi may have wide distribution with stressful conditions of aridity and coldness. Among the 23 phylotypes, 12 phylotypes were found in all four plants, and 87.4% of the all obtained sequences were affiliated into these 12 types. For the distribution of the AM fungal phylotypes, overlapping of the phylotypes among the four plant species were significantly higher than that simulated by random chance. These results suggested that AM fungal communities were less diversified among the examined plant species.

1. Introduction

The arbuscular mycorrhiza (AM) is a ubiquitous symbiosis between terrestrial plants and fungi in the phylum Glomeromycota (Smith and Read 2008). In this symbiosis, AM fungi provide the host plant with soil nutrients, particularly phosphate (Jayachandran and Shetty 2003). Furthermore, alleviations of plant disease and abiotic stresses on host plants are known effects of AM symbiosis (Rabie 1998; Ruiz-Lozano et al. 2001). AM fungi usually have broad host ranges, although some preferences or functional diversifications between plants and AM fungi have been suggested (Helgason et al. 2002; Vandenkoornhuyse et al. 2003). Differential responses of AM fungi depending on the host plant could affect plant community composition (van der Hejiden et al. 1998; van der Hejiden et al. 2006). Therefore, AM fungal community can be a determinant of plant community. Meanwhile, many studies showed that AM fungal communities are diversified among different plant species (Sanders and Fitter 1992; Bever et al. 1996; Vandenkoornhuyse et al. 2002, 2003). Thus, it is also considered that plant community also could be a determinant of the AM fungal community.

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The Mongolian steppe, including mountain forest steppe and desert steppe, is a part of the Eurasian steppe that extends from Hungary in the west to northeastern China in the east. It covers approximately 70% of Mongolia with an annual precipitation of 100–300 mm (Jigjidsuren and Johnson 2003). The steppe zone is mainly used as a rangeland for livestock. After privatization of livestock farming due to the democratization of Mongolia in 1990, overgrazing by livestock became a problem in steppe vegetation. Consequently, changes of floristic composition caused by overgrazing have been reported (Li 1989; Nakamura et al. 1998, 2000).

The most plant families in the steppe vegetation, such as Poaceae, Asteraceae, Fabaceae, and Liliaceae, form the arbuscular mycorrhiza (Wang and Qiu 2006). The effect of grazing on AM fungal colonization and communities has been examined in some steppe vegetations (Tian et al. 2009; Ba et al. 2012). These studies examined AM fungal communities based on the number of spores collected from soil samples. The spore numbers can be used as quantitative values, but they do not usually reflect the AM fungal colonization because of differences in sporulation depending on the AM fungal species.

In the Mongolian steppe, the AM fungal community in *Stipa krylovii* Roshev. (Poaceae) was examined by molecular analysis (Goomaral et al. 2013). This plant is one of the dominant plant species in steppe vegetation and is known as a preferred feed for livestock (Wallis de Vries et al. 1996). However, the AM fungal diversity in the environment may have been underestimated because of the single plant species examined. We hypothesized in this study that AM fungal communities may be diversified among the different plant species in the Mongolian steppe and that increasing the number of plant species examined may detect more AM fungal taxa in the environment. Understanding the AM fungal community in the environment could provide further insight into the restoration of degraded vegetation due to overgrazing. Accordingly, AM fungal communities in *Leymus chinensis* (Trin.) Tzvel. (Poaceae), *Allium bidentatum* Fisch. ex Prokh. (Liliaceae), *Astragalus brevifolius* Ledeb. (Fabaceae), and *S. krylovii* (Poaceae) in the Mongolian steppe were examined in this study.

2. Materials and methods

2.1. Sampling

Sampling was conducted at Hustai National Park in the steppe zone of Mongolia at the end of July 2011. The mean temperatures in January and July, and the mean annual precipitation were −20.5 °C, 19.0 °C, and 222.5 mm, respectively (averaged for the period of 1996–2010). The steppe vegetation is covered with herbaceous plants with some shrubs. We selected four dominant plant species in the area, *S. krylovii*, *L. chinensis*, *Al. bidentatum*, and *As. brevifolius*, to investigate the AM fungal communities. Eight sampling plots of 1 × 1 m^2 containing all four plant species were established in the area (N47°29′20″, E105°46′17″ – N47°42′09″, E106°02′01″; Fig. 1, Table 1). In each plot, soil core samples (5 cm in diameter and 10 cm in depth) containing plant roots were collected under the shoot of each plant species examined. One soil core sample was collected for one plant species in each sampling plot. Accordingly, 32 soil core samples were collected in total.

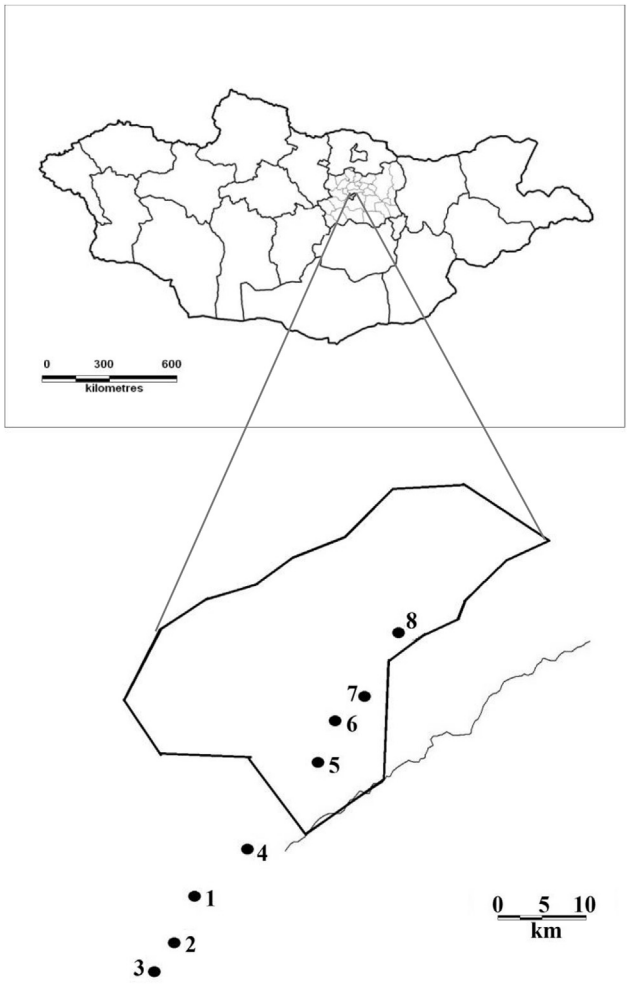

Fig. 1 – Location of the sampling plots in Hustai National Park, Mongolia.

2.2. Soil chemical analysis

The four soil cores in each sampling plot, one each for the four plant species, were combined and mixed to make one soil sample. Soil pH (soil:water, 1:2.5 v/v) and available phosphorus (Truog-P; Truog 1930) were measured for the samples.

Table 1 – Locations of sampling plots.

Plot	Latitude	Longitude	Altitude (m)
1	N 47°29′20.3″	E 105°46′17.7″	1205
2	N 47°26′59.5″	E 105°44′41.7″	1142
3	N 47°25′56.2″	E 105°43′40.9″	1137
4	N 47°32′09.4″	E 105°50′20.6″	1135
5	N 47°36′08.1″	E 105°56′00.9″	1151
6	N 47°38′06.2″	E 105°57′16.6″	1209
7	N 47°39′05.5″	E 105°58′47.9″	1205
8	N 47°42′09.0″	E 106°02′01.5″	1239