

Postprint: Advances in the Biogeography of Arbuscular Mycorrhizal Fungi

Authors: Chen Baodong, Li Xuejing, Xu Tianle, Xie Wei

Date: 2018-03-08T00:00:00+00:00

Abstract

Arbuscular mycorrhizal fungi (AMF) are ubiquitous in terrestrial ecosystems and can form mycorrhizal symbioses with the vast majority of higher plants. AMF can promote plant absorption of mineral nutrients, enhance plant stress resistance, and play important roles in maintaining ecosystem stability and productivity. AMF biogeography primarily investigates the biogeographic distribution patterns and community assembly mechanisms of AMF, which is crucial for understanding the importance of AMF in different ecosystems. This paper summarizes the latest research progress and methodologies in AMF biogeography and proposes a theoretical framework for AMF biogeography research. It is concluded that AMF are not simply randomly distributed in nature; host plants, geographic factors, climatic factors, and soil factors jointly determine AMF community structure, and AMF community assembly at different scales conforms to the niche-neutral continuum hypothesis, but the relative importance of these driving factors differs across scales. At global and regional scales, the geographic distribution patterns of AMF are mainly influenced by geographic distance and climatic factors, with neutral theory playing a greater role than niche theory. As spatial scale decreases, the influence of host plants and environmental factors on AMF communities surpasses the effects of geographic distance and dispersal limitation, and niche theory replaces neutral theory as the dominant force in AMF community assembly. Furthermore, many studies have found that the community assembly mechanisms of AMF in the same habitat are not static and can change with environmental variations. In future research, meta-analysis and data mining should be strengthened based on field surveys and public databases to further enrich and improve AMF biogeography theory.

Full Text

Preamble

ACTA ECOLOGICA SINICA

ChinaXiv Partner Journal

Vol. 38, No. 4, Feb. 2018

DOI: 10.5846/stxb201701030009

Advances in the Biogeography of Arbuscular Mycorrhizal Fungi

Chen B D, Li X J, Xu T L, Xie W. Advances in the biogeography of arbuscular mycorrhizal fungi. *Acta Ecologica Sinica*, 2018, 38(4): 1167-1175.

Affiliations:

State Key Laboratory of Urban and Regional Ecology, Research Center for Eco-Environmental Sciences, Chinese Academy of Sciences, Beijing 100085, China
University of Chinese Academy of Sciences, Beijing 100049, China

Abstract

Arbuscular mycorrhizal fungi (AMF) are ubiquitous soil fungi in terrestrial ecosystems that form symbiotic associations with the majority of higher plants. Through mycorrhizal symbiosis, AMF facilitate plant uptake of mineral nutrients, enhance plant resistance to various environmental stresses, and play crucial roles in maintaining ecosystem stability and productivity. AMF biogeography focuses on the geographical distribution patterns and community assembly mechanisms of AMF, which is critical for understanding their ecological significance across different ecosystems. Here, we summarize recent advances in AMF biogeography, introduce the methodological approaches applied in this field, and outline a theoretical framework for future research.

Generally, AMF communities do not exhibit purely random distribution; instead, their community structure is jointly determined by host plants, geographical distance, climate factors, and soil physicochemical properties. Community assembly can be predicted by both niche theory and neutral theory at different spatial scales, supporting the niche-neutral continuum hypothesis. At global and regional scales, neutral theory plays a more important role than niche theory, with AMF distribution patterns primarily shaped by geographical distance and climate factors. However, at local and small scales, niche theory dominates. As spatial scale decreases, the influence of host plants and environmental factors on AMF communities surpasses that of geographical distance and dispersal limitation. The ecological processes driving AMF assembly change with environmental conditions, indicating that assembly mechanisms are not static but shift in response to environmental variation. Future research should strengthen integrated analysis and data mining based on systematic field surveys and public databases to further enrich and refine biogeographical theory.

Keywords: arbuscular mycorrhizal fungi; community assembly mechanism; scale; niche theory; neutral theory

1. AMF Geographic Distribution and Community Assembly Mechanisms

Community structure refers to the composition and quantitative characteristics of a community within a specific time period, typically described using parameters such as richness, dominance, and importance values. Community assembly refers to the mechanisms underlying the formation and maintenance of species diversity within a community and represents a core focus of biogeographical research. The primary hypotheses explaining community assembly mechanisms include niche theory, neutral theory, and the niche-neutral continuum hypothesis.

1.1 Neutral Theory

Hubbell proposed the unified neutral theory of biodiversity and biogeography, which posits that all species in an ecosystem are functionally equivalent and that species distributions are widespread and random, primarily influenced by geographical distance and dispersal limitation. Many studies have shown that AMF are widely distributed across global habitats, suggesting that neutral stochastic processes play crucial roles in community assembly. When studied habitats encompass large spatial scales and environmental gradients, neutral theory becomes particularly important in shaping community composition and geographical distribution patterns. Van der Gast et al. found that dispersal limitation largely determines the relative abundance of species in AMF communities, and that α -diversity decreases with increasing geographical distance, following the classic distance-decay pattern in biogeography. These findings confirm that at global scales, neutral theory dominates in explaining AMF distribution and community assembly.

1.2 Niche Theory

Grinnell originally defined the niche as the unit of limiting environmental factors occupied by a species, representing both a spatial unit of the environment and a species' position within it. Niche theory is based on deterministic processes, where environmental filtering and competitive exclusion dominate community composition. Numerous studies have demonstrated that environmental factors and host plants significantly influence AMF diversity and community structure. For example, Kohout et al. found that temperate grassland AMF communities were affected by spatial distance between sampling sites, but soil environmental factors and host plant growth stage played more important roles. Fitzsimons et al. showed that soil physicochemical factors and nitrate-nitrogen content could

effectively predict AMF community structure. These studies collectively indicate that niche theory occupies an important position in AMF community assembly.

1.3 Niche-Neutral Continuum Hypothesis

Although niche theory and neutral theory are distinct, both have successfully explained AMF community assembly and diversity patterns. Gravel et al. integrated these theories into the niche-neutral continuum hypothesis, proposing that community assembly involves both neutral processes and niche influences, with their relative importance forming a continuous spectrum from neutral to niche poles. Increasing evidence shows that the relative importance of these processes varies across ecosystems and spatial scales. Some studies suggest that AMF community structure results from the combined effects of dispersal limitation, environmental filtering, and species interactions. Others argue that the relative importance of niche and neutral theories in determining AMF community structure may shift with environmental changes. For instance, Hazard et al. found that in alpine meadow ecosystems, as toxic plant spread intensified, AMF community composition shifted from phylogenetically random to phylogenetically clustered, indicating that environmental filtering became the dominant factor in the presence of toxic plants. These results demonstrate that AMF community assembly cannot be explained by a single theory but likely involves both stochastic genetic drift and niche differentiation.

2. Scale-Dependent Patterns in AMF Geographic Distribution and Community Assembly

Scale is a fundamental concept in natural and social sciences, representing the spatial or temporal dimension of a research object. As a key paradigm in ecology, scale serves as a bridge linking pattern and process. The relative contributions of geographical distance and environmental factors to microbial distribution patterns are scale-dependent.

2.1 Global Scale

Global-scale biogeographical studies compare community distribution patterns across different continents, climate zones, and ecosystems. Research indicates that at the global scale, AMF distribution shows low heterogeneity, likely due to effective dispersal through abiotic and biotic pathways. However, community structures in different habitats are closely related to environmental factors and spatial distance. AMF taxa are phylogenetically clustered, and α -diversity decreases with geographical distance, following the distance-decay pattern. These findings confirm that neutral theory dominates in explaining AMF distribution and community assembly at global scales.

2.2 Regional Scale

Regional-scale studies typically cover large geographic areas with substantial variation in vegetation and other factors, often encompassing countries or extensive regions. At this scale, AMF distribution patterns are influenced by geographical distance and dispersal limitation, but also correlate strongly with soil physicochemical properties. Studies in northern China and Switzerland have shown that geographical factors such as latitude and soil conditions are more important than land management practices in determining AMF communities. Environmental heterogeneity emerges as a primary driver of regional-scale distribution patterns. These results indicate that neutral theory remains important, but environmental factors play increasingly significant roles in community structure.

2.3 Local Scale

Local-scale research focuses on smaller areas with relatively uniform climate but variable soil and vegetation factors. At this scale, soil factors and host plants become the dominant determinants of AMF community structure. Studies have shown that soil available phosphorus strongly influences AMF communities, and that vegetation type and soil factors are the most important environmental variables. Host plant changes can also alter soil AMF composition, with plant invasions increasing AMF richness and abundance. Overall, at local scales, community structure is closely related to soil physicochemical properties and host plants, with niche theory playing the dominant role in community assembly.

2.4 Small Scale

Small-scale studies are conducted in fixed plots with consistent climate and minimal dispersal limitation. In these settings, AMF communities often show spatial autocorrelation and respond sensitively to environmental changes. Research has demonstrated that waterlogging increases AMF species richness, fertilization significantly alters community composition, and adding nitrogen-fixing legumes enhances AMF communities. These findings indicate that ecological niche theory plays a crucial role in shaping AMF communities at small scales, and that community assembly mechanisms can shift in response to environmental changes.

2.5 Altitude and Temporal Scales

Research on AMF community patterns along altitude and temporal gradients remains limited. Studies show that AMF community structure varies with altitude, often peaking at mid-elevations, though some report decreasing diversity with increasing altitude. These differences likely result from variation in soil properties and host plant communities across elevations. Temporally, AMF communities exhibit seasonal and interannual variations, with seasonal changes related to climatic factors and interannual variations associated with ecosystem succession. These results suggest that AMF communities show clear niche

differentiation along both altitudinal and temporal gradients.

3. Summary

AMF are not randomly distributed in nature but show non-random patterns influenced by environmental factors and host plants. The primary drivers of geographic distribution and community assembly mechanisms vary across scales. Our synthesis of recent research suggests a theoretical framework where AMF community structure is shaped by both niche and neutral theories across all scales, consistent with the niche-neutral continuum hypothesis. However, the relative importance of these theories changes with scale: at global and regional scales, neutral theory dominates as geographical distance and climate factors primarily shape distribution patterns; as spatial scale decreases, host plants and environmental factors become more important than dispersal limitation, and niche theory replaces neutral theory as the dominant assembly mechanism. Importantly, these assembly mechanisms are not static but shift with environmental changes.

[Figure 1: see original paper] Theoretical framework for studies on biogeography of arbuscular mycorrhizal fungi

4. Outlook

The emergence of molecular biology, particularly high-throughput sequencing, has greatly facilitated AMF biogeography research. Future studies should combine large-scale field surveys, multi-factor experiments, and data mining of public databases to systematically investigate key factors and regulatory pathways affecting AMF community structure across different habitats. Integrating data across scales and ecosystems will provide convenient means to explore AMF biogeographical patterns and underlying mechanisms. Drawing on traditional biogeographical models such as island biogeography theory will help develop comprehensive models for AMF distribution and assembly mechanisms.

Current research has focused primarily on spatial scales, with limited reports on temporal and altitudinal gradients. Future work should examine AMF community changes during vegetation succession at small scales and preserve soil samples from the same sites across different periods for temporal dynamic studies. Combining spatial and temporal scales will provide a more comprehensive understanding of AMF community dynamics, enabling better predictions of how future environmental changes will affect ecosystem structure and function and informing environmental change mitigation strategies.

References

- [1] Crisp M D, Trewick S A, Cook L G. Hypothesis testing in biogeography. *Trends in Ecology & Evolution*, 2011, 26(2): 66-72.
- [2] Martiny J B H, Bohannan B J M, Brown J H, Colwell R K, Fuhrman J A, Green J L, Horner-Devine M C, Kane M, Krumins J A, Kuske C R, Morin P J, Naeem S, Øvreås L, Reysenbach A L, Smith V H, Staley J T. Microbial biogeography: putting microorganisms on the map. *Nature Reviews Microbiology*, 2006, 4(2): 102-112.
- [3] Fitter A H, Heinemeyer A, Husband R, Olsen E, Ridgway K P, Staddon P L. Global environmental change and the biology of arbuscular mycorrhizas: gaps and challenges. *Canadian Journal of Botany*, 2004, 82(8): 1133-1139.
- [4] [Omitted - incomplete reference]
- [5] O Malley M A. The nineteenth century roots of ‘everything is everywhere’ . *Nature Reviews Microbiology*, 2007, 5(8): 647-651.
- [6] De Wit R, Bouvier T. ‘Everything is everywhere, but, the environment selects’ ; what did Baas Becking and Beijerinck really say? *Environmental Microbiology*, 2006, 8(4): 755-758.
- [7] Lugo M A, Ferrero M, Menoyo E, Estévez M C, Sinériz F, Anton A. Arbuscular mycorrhizal fungi and rhizospheric bacteria diversity along an altitudinal gradient in South American Puna grassland. *Microbial Ecology*, 2008, 55(4): 705-713.
- [8] Harley J L, Smith S E. *Mycorrhizal Symbiosis*. London: Academic Press Inc., 1983.
- [9] Hill J O, Simpson R J, Ryan M H, Chapman D F. Root hair morphology and mycorrhizal colonisation of pasture species in response to phosphorus and nitrogen nutrition. *Crop and Pasture Science*, 2010, 61(2): 122-131.
- [10] Augé R M. Water relations, drought and vesicular-arbuscular mycorrhizal symbiosis. *Mycorrhiza*, 2001, 11(1): 3-42.
- [11] Johnson N C, Wilson G W T, Bowker M A, Wilson J A, Miller R M. Resource limitation is a driver of local adaptation in mycorrhizal symbioses. *Proceedings of the National Academy of Sciences of the United States of America*, 2010, 107(5): 2093-2098.
- [12] Sikes B A, Cottenie K, Klironomos J N. Plant and fungal identity determines pathogen protection of plant roots by arbuscular mycorrhizas. *Journal of Ecology*, 2009, 97(6): 1274-1280.
- [13] Li T, Hu Y J, Hao Z P, Li H, Wang Y S, Chen B D. First cloning and characterization of two functional aquaporin genes from an arbuscular mycorrhizal fungus *Glomus intraradices*. *New Phytologist*, 2013, 197(2): 617-630.
- [14] van der Heijden M G A, Klironomos J N, Ursic M, Moutoglis P, Streitwolf-Engel R, Boller T, Wiemken A, Sanders I R. Mycorrhizal fungal diversity determines plant biodiversity, ecosystem variability and productivity. *Nature*, 1998, 396(6706): 69-72.
- [15] Jansa J, Erb A, Oberholzer H R, Šmilauer P, Egli S. Soil and geography are more important determinants of indigenous arbuscular mycorrhizal communities than management practices in Swiss agricultural soils. *Molecular Ecology*,

2014, 23(8): 2118–2135.

[16] Sené-Guerrero C, Schüßler A. DNA-based characterization and identification of arbuscular mycorrhizal fungal species. In: Martin F, Uroz S, eds. *Microbial Environmental Genomics (MEG)*. New York: Springer, 2016, 1399: 101–123.

[17] Krüger M, Krüger C, Walker C, Stockinger H, Schüßler A. Phylogenetic reference data for systematics and phylotaxonomy of arbuscular mycorrhizal fungi from phylum to species level. *New Phytologist*, 2012, 193(4): 970–984.

[18] Öpik M, Vanatoa A, Vanatoa E, Moora M, Davison J, Kalwij J M, Reier Ü, Zobel M. The online database MaarjAM reveals global and ecosystemic distribution patterns in arbuscular mycorrhizal fungi (Glomeromycota). *New Phytologist*, 2010, 188(1): 223–241.

[19] Davison J, Moora M, Öpik M, Adholeya A, Ainsaar L, Bâ A, Burla S, Diedhiou A G, Hiesalu I, Jairus T, Johnson N C, Kane A, Koorem K, Kochhar M, Ndiaye C, Partel M, Reier Ü, Saks Ü, Singh R, Vasar M, Zobel M. Global assessment of arbuscular mycorrhizal fungus diversity reveals very low endemism. *Science*, 2015, 349(6251): 970–973.

[20] Kivlin S N, Hawkes C V, Treseder K K. Global diversity and distribution of arbuscular mycorrhizal fungi. *Soil Biology and Biochemistry*, 2011, 43(11): 2294–2303.

[21] [Omitted - incomplete reference]

[22] [Omitted - incomplete reference]

[23] Hubbell S P. *The Unified Neutral Theory of Biodiversity and Biogeography*. Princeton and Oxford: Princeton University Press, 2001.

[24] Dumbrell A J, Nelson M, Helgason T, Dytham C, Fitter A H. Relative roles of niche and neutral processes in structuring a soil microbial community. *The ISME Journal*, 2010, 4(3): 337–345.

[25] Gravel D, Canham C D, Beaudet M, Messier C. Reconciling niche and neutrality: the continuum hypothesis. *Ecology Letters*, 2006, 9(4): 399–409.

[26] Bell G. The distribution of abundance in neutral communities. *The American Naturalist*, 2000, 155(5): 606–617.

[27] [Omitted - incomplete reference]

[28] van der Gast C J, Gosling P, Tiwari B, Bending G D. Spatial scaling of arbuscular mycorrhizal fungal diversity is affected by farming practice. *Environmental Microbiology*, 2011, 13(1): 241–249.

[29] Öpik M, Zobel M, Cantero J J, Davison J, Facelli J M, Hiesalu I, Jairus T, Kalwij J M, Koorem K, Leal M E, Liira J, Metsis M, Neshataeva V, Paal J, Phosri C, Pölme S, Reier Ü, Saks Ü, Schimann H, Thiéry O, Vasar M, Moora M. Global sampling of plant roots expands the described molecular diversity of arbuscular mycorrhizal fungi. *Mycorrhiza*, 2013, 23(5): 411–430.

[30] Grinnell J. The niche-relationships of the California Thrasher. *The Auk*, 1917, 34(4): 427–433.

[31] McGill B J. A test of the unified neutral theory of biodiversity. *Nature*, 2003, 422(6934): 881–885.

[32] Leibold M A, McPeck M A. Coexistence of the niche and neutral perspectives in community ecology. *Ecology*, 2006, 87(6): 1399–1410.

- [33] Kohout P, Doubková P, Bahram M, Suda J, Tedersoo L, Vorišková J, Sudová R. Niche partitioning in arbuscular mycorrhizal communities in temperate grasslands: a lesson from adjacent serpentine and non-serpentine habitats. *Molecular Ecology*, 2015, 24(8): 1831–1843.
- [34] Fitzsimons M S, Miller R M, Jastrow J D. Scale-dependent niche axes of arbuscular mycorrhizal fungi. *Oecologia*, 2008, 158(1): 117–127.
- [35] Powell J R, Karunaratne S, Campbell C D, Yao H Y, Robinson L, Singh B K. Deterministic processes vary during community assembly for ecologically dissimilar taxa. *Nature Communications*, 2015, 6: 8444.
- [36] Ai D, Chu C J, Ellwood M D F, Hou R, Wang G. Migration and niche partitioning simultaneously increase species richness and rarity. *Ecological Modelling*, 2013, 258: 33–39.
- [37] Hazard C, Gosling P, Van der Gast C J, Mitchell D T, Doohan F M, Bending G D. The role of local environment and geographical distance in determining community composition of arbuscular mycorrhizal fungi at the landscape scale. *The ISME Journal*, 2013, 7(3): 498–508.
- [38] Shi G X, Liu Y J, Mao L, Jiang S J, Zhang Q, Cheng G, An L Z, Du G Z, Feng H Y. Relative importance of deterministic and stochastic processes in driving arbuscular mycorrhizal fungal assemblage during the spreading of a toxic plant. *PLoS One*, 2014, 9(4): e95672.
- [39] [Omitted - incomplete reference]
- [40] Peterson D L, Parker V T. *Ecological Scale: Theory and Applications*. New York: Columbia University Press, 1998.
- [41] [Omitted - incomplete reference]
- [42] Soudzilovskaia N A, Douma J C, Akhmetzhanova A A, van Bodegom P M, Cornwell W K, Moens E J, Treseder K K, Tibbett M, Wang Y P, Cornelissen J H C. Global patterns of plant root colonisation intensity by mycorrhizal fungi explained by climate and soil chemistry. *Global Ecology and Biogeography*, 2015, 24(3): 371–382.
- [43] Xiang D, Verbruggen E, Hu Y J, Veresoglou S D, Rillig M C, Zhou W P, Xu T L, Li H, Hao Z P, Chen Y L, Chen B D. Land use influences arbuscular mycorrhizal fungal communities in the farming-pastoral ecotone of northern China. *New Phytologist*, 2014, 204(4): 968–978.
- [44] Bouffaud M L, Bernaud E, Colombet A, van Tuinen D, Wipf D, Redecker D. Regional-scale analysis of arbuscular mycorrhizal fungi: the case of Burgundy vineyards. *OENO One*, 2016, 50(1): 1–8.
- [45] Xu T L, Veresoglou S D, Chen Y L, Rillig M C, Xiang D, Ondřej D, Hao Z P, Liu L, Deng Y, Hu Y J, Chen W P, Wang J T, He J Z, Chen B D. Plant community, geographic distance and abiotic factors play different roles in predicting AMF biogeography at the regional scale in northern China. *Environmental Microbiology Reports*, 2016, 8(6): 1048–1057.
- [46] Xiang D, Veresoglou S D, Rillig M C, Xu T L, Li H, Hao Z P, Chen B D. Relative importance of individual climatic drivers shaping arbuscular mycorrhizal fungal communities. *Microbial Ecology*, 2016, 72(2): 418–427.
- [47] Hu Y J, Rillig M C, Xiang D, Hao Z P, Chen B D. Changes of AM fungal abundance along environmental gradients in the arid and semi-arid grasslands

- of northern China. *PLoS One*, 2013, 8(2): e57593.
- [48] Alguacil M M, Torrecillas E, Lozano Z, Roldán A. Arbuscular mycorrhizal fungi communities in a coral cay system (Morrocoy, Venezuela) and their relationships with environmental variables. *Science of the Total Environment*, 2015, 505: 805-813.
- [49] de Beenhouwer M, Muleta D, Peeters B, Van Geel M, Lievens B, Honnay O. DNA pyrosequencing evidence for large diversity differences between natural and managed coffee mycorrhizal fungal communities. *Agronomy for Sustainable Development*, 2015, 35(1): 241-249.
- [50] Rodríguez-Echeverría S, Teixeira H, Correia M, Timóteo S, Heleno R, Öpik M, Moora M. Arbuscular mycorrhizal fungal communities from tropical Africa reveal strong ecological structure. *New Phytologist*, 2017, 213(1): 380-390.
- [51] [Omitted - incomplete reference]
- [52] Lekberg Y, Gibbons S M, Rosendahl S, Ramsey P W. Severe plant invasions can increase mycorrhizal fungal abundance and diversity. *The ISME Journal*, 2013, 7(7): 1424-1433.
- [53] Hiesalu I, Pärtel M, Davison J, Gerhold P, Metsis M, Moora M, Öpik M, Vasar M, Zobel M, Wilson S D. Species richness of arbuscular mycorrhizal fungi: associations with grassland plant richness and biomass. *New Phytologist*, 2014, 203(1): 233-244.
- [54] Liu Y J, Mao L, Li J Y, Shi G X, Jiang S J, Ma X J, An L Z, Du G Z, Feng H Y. Resource availability differentially drives community assemblages of plants and their root-associated arbuscular mycorrhizal fungi. *Plant and Soil*, 2015, 386(1/2): 341-355.
- [55] Horn S, Caruso T, Verbruggen E, Rillig M C, Hempel S. Arbuscular mycorrhizal fungal communities are phylogenetically clustered at small scales. *The ISME Journal*, 2014, 8(11): 2231-2242.
- [56] Toljander J F, Eberhardt U, Toljander Y K, Paul L R, Taylor A F S. Species composition of an ectomycorrhizal fungal community along a local nutrient gradient in a boreal forest. *New Phytologist*, 2006, 170(4): 873-884.
- [57] Yang H S, Koide R T, Zhang Q. Short-term waterlogging increases arbuscular mycorrhizal fungal species richness and shifts community composition. *Plant and Soil*, 2016, 404(1/2): 373-384.
- [58] Chen Y L, Chen B D, Hu Y J, Li T, Zhang X, Hao Z P, Wang Y S. Direct and indirect influence of arbuscular mycorrhizal fungi on abundance and community structure of ammonia oxidizing bacteria and archaea in soil microcosms. *Pedobiologia*, 2013, 56(4/6): 205-212.
- [59] Klabi R, Bell T H, Hamel C, Iwaasa A, Schellenberg M, Raies A, St-Arnaud M. Plant assemblage composition and soil P concentration differentially affect communities of AM and total fungi in a semi-arid grassland. *FEMS Microbiology Ecology*, 2015, 91(1): 1-13.
- [60] Coutinho E S, Fernandes G W, Barbara R L L, Valério H M, Goto B T. Variation of arbuscular mycorrhizal fungal communities along an altitudinal gradient in rupestrian grasslands in Brazil. *Mycorrhiza*, 2015, 25(8): 627-638.
- [61] Yang R, Li S M, Cai X B, Li X L, Christie P, Zhang J L, Gai J P. Responses of arbuscular mycorrhizal symbionts to contrasting environments: field

- evidence along a Tibetan elevation gradient. *Mycorrhiza*, 2016, 26(7): 623–632.
- [62] Wahl A L, Spiegelberger T. Arbuscular mycorrhizal fungi in changing mountain grassland ecosystems: a challenge for research. *Botany*, 2016, 94(6): 435–458.
- [63] Gai J P, Tian H, Yang F Y, Christie P, Li X L, Klironomos J N. Arbuscular mycorrhizal fungal diversity along a Tibetan elevation gradient. *Pedobiologia*, 2012, 55(3): 145–151.
- [64] Li X L, Gai J P, Cai X B, Li X L, Christie P, Zhang F S, Zhang J L. Molecular diversity of arbuscular mycorrhizal fungi associated with two co-occurring perennial plant species on a Tibetan altitudinal gradient. *Mycorrhiza*, 2014, 24(2): 95–107.
- [65] Sommerfeld H M, Díaz L M, Alvarez M, Villanueva C A, Matus F, Boon N, Boeckx P, Huygens D. High winter diversity of arbuscular mycorrhizal fungal communities in shallow and deep grassland soils. *Soil Biology and Biochemistry*, 2013, 65: 236–244.
- [66] Helgason T, Feng H Y, Sherlock D J, Young J P W, Fitter A H. Arbuscular mycorrhizal fungal communities associated with maples (spp.) in a common garden are influenced by season and host plant. *Botany*, 2014, 92(4): 321–326.
- [67] [Omitted - incomplete reference]
- [68] Escudero V, Mendoza R. Seasonal variation of arbuscular mycorrhizal fungi in temperate grasslands along a wide hydrologic gradient. *Mycorrhiza*, 2005, 15(4): 291–299.
- [69] Bainard L D, Bainard J D, Hamel C, Gan Y T. Spatial and temporal structuring of arbuscular mycorrhizal communities is differentially influenced by abiotic factors and host crop in a semi-arid prairie agroecosystem. *FEMS Microbiology Ecology*, 2014, 88(2): 333–344.
- [70] Cui X C, Hu J L, Wang J H, Yang J S, Lin X G. Reclamation negatively influences arbuscular mycorrhizal fungal community structure and diversity in coastal saline-alkaline land in Eastern China as revealed by Illumina sequencing. *Applied Soil Ecology*, 2016, 98: 140–149.

Note: Figure translations are in progress. See original paper for figures.

Source: ChinaXiv – Machine translation. Verify with original.