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EDITORIAL

Functional traits along a transect

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Functional traits, which usually develop over evolutionary timescales to maximize plant survivorship and functional performances in changing environment, are important indices to explore how ecosystems respond and adapt to a changing environment. Many ecologists have argued that identifying regional to global-scale patterns in functional traits, at organismal to ecosystem scales, in combination with responses to environmental changes, is necessary to increase our ability to predict how ecosystems will function in the future (Katja & Jeanfrançois, 2009; Reich, Walters, & Ellsworth, 1997; Wright et al., 2017). Global models that have been used to simulate changes in ecosystem function primarily incorporate biogeochemical and ecophysiological processes (Bonan, 2008; Taylor, Stouffer, & Meehl, 2012). These models, however, could not well predict community compositional change (Fisher et al., 2017). Traditionally, plant functional types have been used to represent community composition changes in dynamic global vegetation models (DGVM). That scheme remains poor at predicting ecosystem functions and their responses to climatic change (Sitch et al., 2008). Recently, trait-based modelling has emerged as one of the most promising approach to simulation of community dynamics under global changes (Markus, Michael, Mahecha, Jens, & Baldocchi, 2014; van Bodegom, Douma, & Verheijen, 2014; Van Bodegom et al., 2012; Violle, Reich, Pacala, Enquist, & Kattge, 2014). To support this trait-based modelling, it is urgent to compile empirical evidence, develop comprehensive datasets, and reveal the large-scale patterns and controlling factors of functional traits and their variations along environmental gradients.

The global scientific community has actively studied functional traits in the past decades, with noticeable advances in our understanding on plant functional traits (Katja & Jeanfrançois, 2009; Onoda et al., 2011; Reich et al., 1997; Wright et al., 2004, 2017), microbial functional traits as well as their correlations with ecosystem functions (Martiny, Treseder, & Pusch, 2013; Xu et al., 2017). In spite of these advances, challenges still exist, such as how to scale traits measured at the individual species level to community level, and then link them to ecosystem functions (Markus et al., 2014). Given the diversity of plant species and their different contributions to the natural community, community-aggregated traits can bridge the gap between plant traits at the organismal scale and key biogeochemical processes measured at the ecosystem scale, such as above-ground net primary productivity, litter decomposition and digestibility (Garnier & Navas, 2012; Karel, Julian, & Stephen, 2008). These studies across scales require the systematic investigation of plant functional traits for each of the observed plant species as well as for the overall community. To date, the well-designed, comprehensive sampling of leaf, root and microbial traits with ecosystem functions is uncommon-especially with the goal of integrating these data across a range of forest types. This lack of data integration limits our capacity to evaluate and calibrate trait-based models. Thus, it is imperative to investigate how multiple plant and microbial functional traits are related to ecosystem functions to regulate plant–soil–microbe interactions.

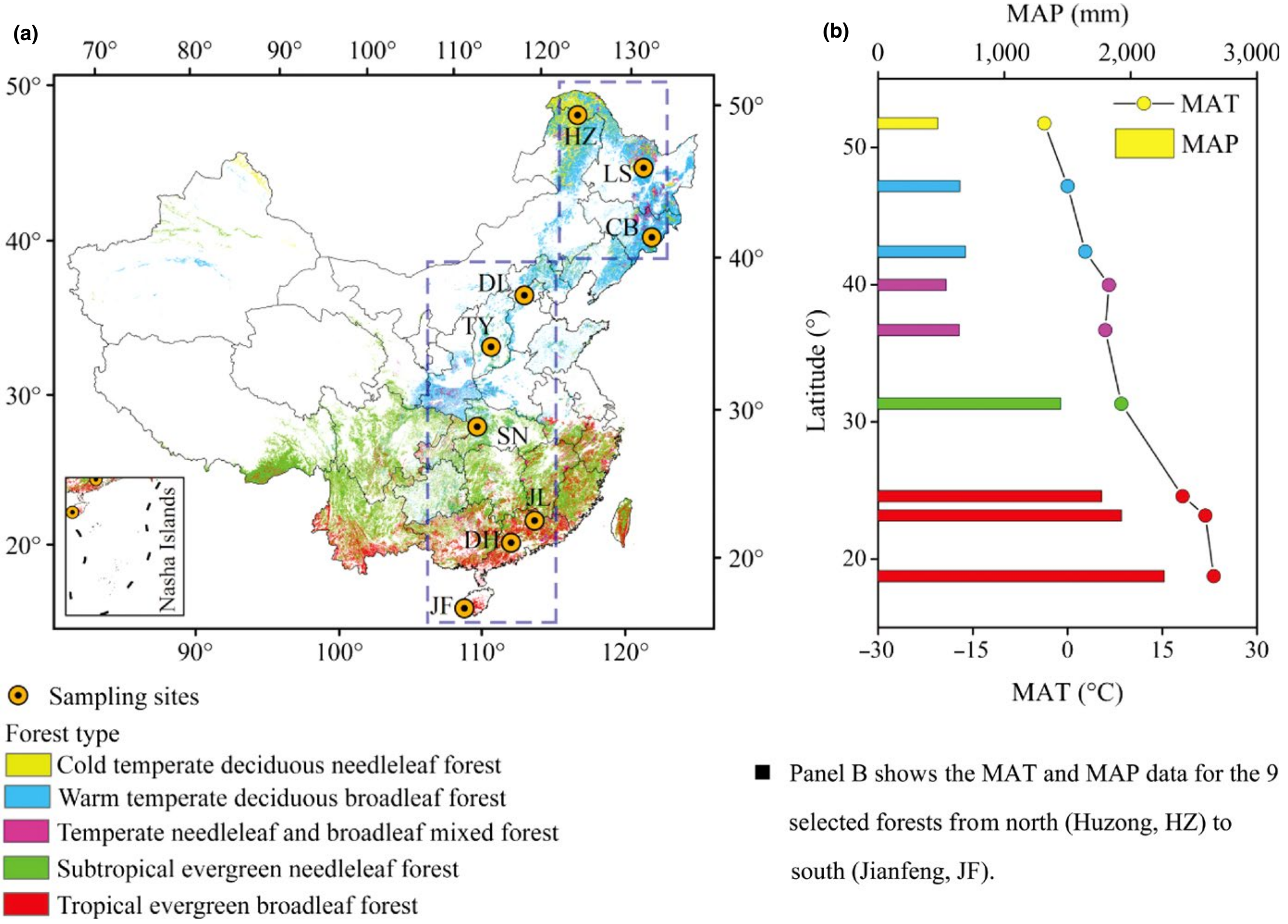
Transect studies are considered as an efficient approach to investigate the spatial patterns of functional traits and their underlying mechanisms from the sites to the regional scale. Environmental gradients along a transect provide excellent opportunities for researchers to explore the drivers of community structure and ecosystem functions in response to environmental heterogeneity and global changes (Mayor et al., 2017). Given these characteristics, the Asian continent offers a diverse array of environmental gradients, highly heterogeneous topography, and a distinct geographic and evolutionary history. Thus, it is ideal for exploring the relationships among climate, traits and functions. Within Asia, China is one of the most biologically diverse countries in the world (Fang et al., 2012; Sanders, 2012) and it is possible to establish a research transect spanning the tropics to boreal zones—a gradient that represents all of the forest types in the Northern Hemisphere (Figure 1). The transect of North–South Transect of Eastern China (NSTEC) is the official 15th standard transect of the International Geosphere and Biosphere Program (IGBP). This diverse gradient of forest ecosystems and climates across China enables researchers to explore how biodiversity, climate, organismal traits and ecosystem functions influence and interact with one another across a range of forest biomes. Such studies have the potential to provide the trait-based understanding so as to improve DGVM models and their predictions.

This special feature uses the NSTEC to explore spatial patterns of multiple biological functional traits (e.g. plant leaf, branch, trunk, root, soil and soil microbes) and associated ecosystem functions. The NSTCE extends across eastern China and encompasses a gradient of tropical to cold-temperate forests (Zhang & Yang, 1995). In fact, it encompasses nine vegetation types (36 plots), 1,100 plant species, 3,700 km from north to south with latitude ranging from 51.8°N to 18.7°N and longitude ranging from 108.9°E to 123.0°E (Figure 1). The mean annual temperature (MAT) of the transect ranges from −4.4 to 20.9°C. The mean annual precipitation (MAP) is about 481.6–2,449 mm. The large environmental heterogeneity encompassed by the NSTEC makes it an ideal "natural laboratory" to examine the ecological responses of plant traits, soil microbial traits and ecosystem functions to environmental changes across scales, climates and biomes.

Studies published in this special issue all used standard protocols (Figure 2) to collect comprehensive datasets on plant, soil, and microbial traits as well as ecosystem functions (Table 1). The authors then used these unique datasets to address following questions:

1. How do functional traits of plant, microbe, and ecosystem vary from tropical to cold-temperate forests and what environment factors, if any, account for this variation?
2. How plant and microbial functional traits are related to ecosystem functions across forest types?
3. How do soil microbial communities and their diversity vary across forest biomes (tropical to cold-temperate) and what controls their diversity patterns?
4. Do plant–soil interactions influence ecosystem function across forest biomes?

To answer the above questions, the papers in this issue explored the spatial patterns and controlling factors of leaf stomatal and anatomical traits, root traits from species to community level (He et al., 2018; Liu et al., 2018; Wang, Wang, Zhao, et al., 2018; Zhao et al., 2018). Across the papers, the spatial patterns of plant functional traits were distinctly different at various levels. For example, the concentrations of 15 elements in the fine roots of 281 species showed that root element composition could be used to distinguish different forest types as well as



■ Panel B shows the MAT and MAP data for the 9 selected forests from north (Huzong, HZ) to south (Jianfeng, JF).

FIGURE 1 Overview of (a) the North–South Transect of Eastern China (NSTEC, blue frame) and the nine selected forest ecosystems, and (b) their mean annual temperature (MAT) and precipitation (MAP)

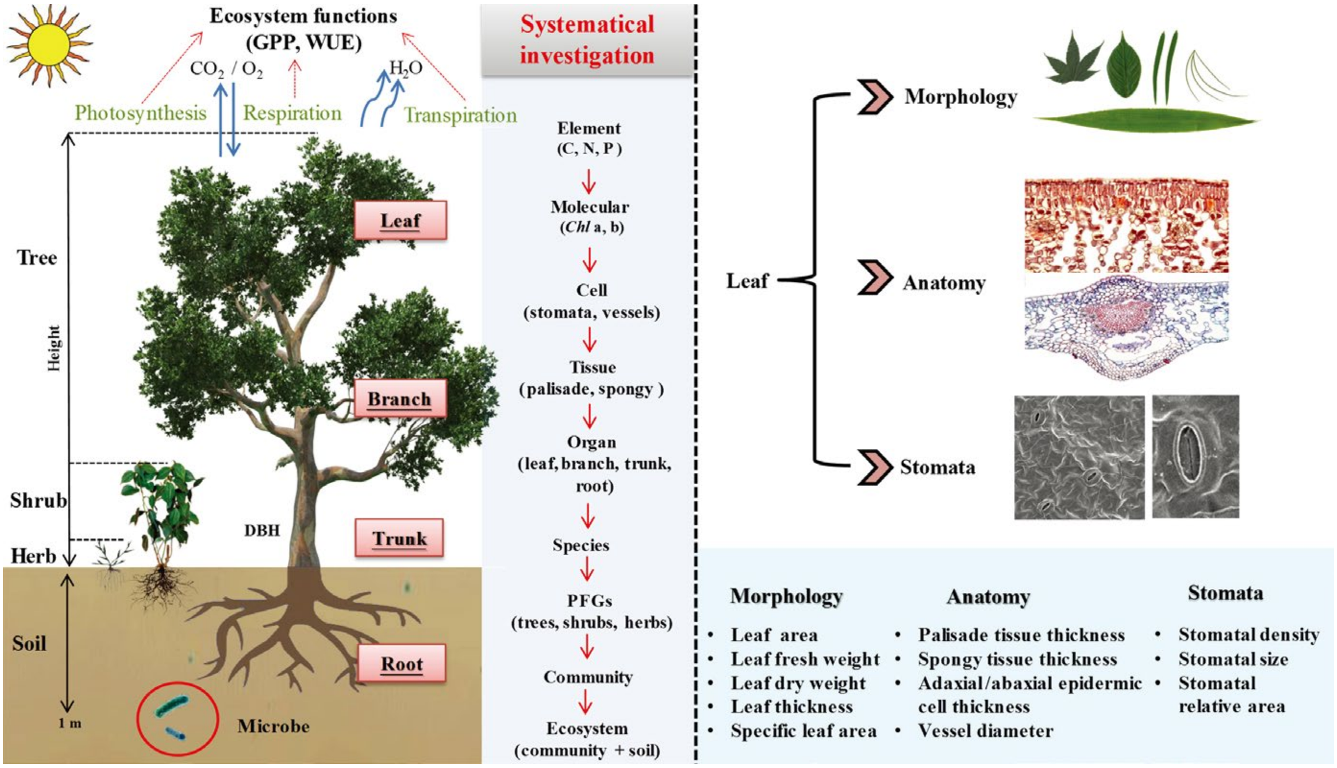


FIGURE 2 Overview of the traits that were investigated in this special issue along the North–South Transect of Eastern China (NSTEC)

individual species (Zhao et al. 2018). Species had specialized root element compositions, yet each species retained some degree of plasticity to environmental changes. Moreover, the variations of six first-order root traits (root diameter, specific root length, root tissue density, root carbon concentration, root nitrogen concentration and root C:N ratio) measured along the transect were mainly determined by species phylogenetic history, while community-level traits were mainly driven by temperature through shifts in species composition (Wang, Wang, Zhao, et al., 2018). Furthermore, two papers in this special issue comprehensively illustrated the spatial patterns and their underlying mechanisms of leaf stomatal traits (density, size and relative area) (Liu et al., 2018) and leaf anatomical traits (adaxial epidermis thickness, abaxial epidermis thickness, leaf thickness, palisade-spongy tissue ratio, palisade tissue-leaf thickness ratio and spongy tissue-leaf thickness ratio) (He et al., 2018) at the species, plant functional group and community level from tropical to cold-temperate forests. Those findings filled the gaps about large-scale patterns of plant traits and their controlling environmental factors, which is fundamentally important for benchmarking trait-based models.

Furthermore, the researchers found that when plant traits scaled up to plant community level, they connected well with ecosystem functioning. For example, Zhang, Zhao, et al. (2018) scaled up the measured carbon, nitrogen and phosphorus content in leaf, stem, root and soil using the data of community composition to estimate the spatial patterns of carbon:nitrogen:phosphorus stoichiometry at plant, community and ecosystem levels. They found that ecosystem carbon:nitrogen:phosphorus stoichiometry might be underestimated without considering plant community structure. Similarly Liu et al. (2018) demonstrated that ecosystem WUE correlated well with stomata traits only at the community level. Those studies provided new insights to better understand the relationship between plant traits and ecosystem functioning. Given the diversity of plant species and the species-specific contributions to the natural community, the individual plant traits, without the integration of plant community composition, could not really reflect the natural ecosystem functions.

Beside plant traits, soil microbial traits and diversity along the NSTEC transect also showed latitudinal patterns. Using high-throughput 16S rRNA gene sequencing, Tian et al. (2018) investigated the geographical distribution of bacterial diversity and found that soil bacterial richness and phylogenetic diversity increased linearly with latitude. Soil pH and substrate availability were the most important edaphic drivers for bacterial community structure along the transect. Zhang, Yang, et al. (2018) compared phosphatase activity in different forests and revealed the diverse responses to experimental soil nutrient addition. These studies established a link between soil microbes or enzymes with soil functions, providing insights into responses of soil microbial diversity to both climate and soil factors.

This special issue also explored the large-scale patterns and the controlling factors of vegetation and soil carbon turnover times, soil gross ammonification and nitrification rates along the transects. For carbon cycle, Wang, Sun, et al. (2018) quantified the large spatial scale of vegetation and soil turnover times and their controlling factors

TABLE 1 Overview of the functional traits that were studied along the North–South Transect of Eastern China

	Component	Measured parameters	Methods or instruments
Plant	Leaf	Morphology (leaf size, leaf thickness, leaf dry weight, leaf fresh weight, leaf specific area)	Vernier caliper, Balance, Scanner, Photoshop
		Stomata (stomatal size, stomatal density, stomatal relative area)	Scanning electron microscope, MIPS software
		Anatomy (Adaxial and abaxial epidermis thickness, leaf thickness, palisade tissue thickness and spongy tissue thickness)	Electron microscope, MIPS software
		Multi-elements (C, N, P, K, Ca, Mg, S and others)	Elemental analyser, Inductively coupled plasma optical emission spectrometer
		Leaf chlorophyll content (*Chl* a and *Chl* b)	Spectrophotometry, 95% ethanol
		Leaf non-structural carbohydrate (Sugars, starch)	Anthronecolorimetry
		Leaf caloric value	Oxygen bomb calorimeter
	Branch	Multi-element (C, N, P, K, Ca, Mg, S,and others)	As mentioned above
	Trunk	Multi-element (C, N, P, K, Ca, Mg, S and others)	As mentioned above
	Root	Morphology (root diameter, root length, root dry weight, root volume)	Root order method WINRHIZO software
		Multi-elements (C, N, P, K, Ca, Mg, S and others)	As mentioned above
Soil	Physical property	Soil particle size (Sand, silt and clay)	Malvern laser particle size analyser
		Soil moisture content	Oven drying method
	Chemical property	Multi-elements (C, N, P, K, Ca, Mg, S and others)	As mentioned above
		Soil pH	Potentiometric method
	SOC composition	Soil organic C	As mentioned above
		Easy-oxidized organic C	Potassium permanganate method
		Humic acid C	Extraction method (Sodium pyrophosphate Sodium hydroxide)
		Humin C	
Soil microbe	Microbes	Microbial community structure	Phospholipid fatty acid
		Microbial biomass C	Chloroform fumigation
	Enzymes	Soil enzyme activity	Enzymatic analyser
		Metabolic activity	Biolog microplate technique
Soil C/N turnover	C turnover	Soil C mineralization rate	Incubation experiment
		Temperature sensitivity	Incubation with temperature gradient
		Soil C turnover time	Data synthesis
	N turnover	Soil N mineralization rate	Incubation experiment
		Soil gross N transformation rate	Labelled by $^{15}NO_3^-$ and $^{15}NH_4^+$in situ
		Soil gross N transformation potential	Labelled by $^{15}NO_3^-$ and $^{15}NH_4^+$ in Lab

C, carbon; N, nitrogen; P, phosphorus; K, potassium; Ca, calcium; Mg, magnesium; S, sulfur; SOC, soil organic carbon.

along the transect. Their findings are essential to constrain the model parameters related to carbon turnover times and benchmark model performance so as to reduce uncertainty in prediction of the carbon-climate feedback. For nitrogen cycle functions, Wang, Wang, Zhu, et al. (2018) conducted both in situ incubation and experimental incubation using ^{15}N-labelled technology and found that the rates of soil gross ammonification and nitrification rates were significantly lower in warm temperate deciduous forests compared to tropical and cold-temperate forests. Soil nitrogen content, microbial biomass nitrogen and bacterial quantity jointly affected soil gross nitrogen transformations along the forest transect. These findings potentially advance our understanding of the factors (substrate vs. microbe vs. climate) that drive soil nutrient supply at a large scale.

Overall, this special feature provides a continental-scale view of the spatial patterns of functional traits in forest ecosystems, the link between functional traits and ecosystem functioning, and the responses to future climate changes. The species-specific plant traits suggest the importance of major differences among species and within plant functional groups. The relationships between functional traits and environment factors demonstrate adaptation and feedback between vegetation and its environment. Those mechanisms are largely neglected by traditional DGVMs. We hope the findings on the critical impotence of traits variation and their link to ecosystem functions will stimulate the continued incorporation of traits into the global models. In addition, the large gradient datasets, which are presented in this special issue and will be publically available, could be used to test numerous ecological theories, explore the mechanisms underlying ecosystem responses to changing environment, and provide new perspectives on contemporary debates in macroecology and benchmark ecological models.

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