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Interactive comment on "Plant functional traits determined the latitudinal variations in soil microbial functions: evidence from a forest transect in China" *by* Zhiwei Xu et al.

Zhiwei Xu et al.

xuzw647@nenu.edu.cn

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(17) The paper seeks to explore relationships between plant traits and microbial communities in soil. This is a pertinent question, especially in the context of ecological resilience and resistance. The main overall finding is that labile carbon is associated with microbial community composition, a clear but relatively unsurprising or limited conclusion. There are some weaknesses in written presentation and in the presentation of data. The Abstract does not mirror the content of the main paper and lacks quantitative information. It is rather difficult to follow. In particular, the title does not reflect the real findings, as it is really a study of litter quality effects rather than

plant functional traits. Response: We have rewritten the abstract and added some quantitative information (P2, Line 35-41; Line 44-49; Line 51-53). We have add some detailed information about the latitudinal pattern of soil microbial carbon substrate use (P10, Line 280-282) and pertinent discussion (P13, Line 347-357). In order to explain the effect of plant traits on soil microbial function, we have added the scatter plots of the plant functional traits and carbon substrates use (Figure S2, supporting information). In our study, we did not directly analysis the influence of the litter quantity and quality on soil microbial function. However, we have added discussion about the influence of plant functional traits on litter (P14, Line 358-364). (18) In terms of format, the paper contains too many acronyms, which make the text hard to follow. Some of the acronyms not explained well enough. The text does flow well in many places and should be checked for readability. The "community weighted mean" is central to the analysis, but the CWM abbreviation is not defined or discussed. Response: We have defined the CWM abbreviation in our manuscript: "We also calculated the community-weighted means (CWM) values of the tree traits using the cover of each tree." (P8, Line 214-215) "To measure the leaf traits at the community level, we calculated the CWM of the tree layer, as follows: CWM=$\sum$_($i = 1$)$pi\times$ trait_i Where pi is the relative contribution of the species i to the cover of the whole community, n is the number of the most abundant species, and trait i is the trait value of species i, as described by Garnier et al. (2004). The diversity of the tree species and plant functional traits are summarized in Table S2." (P9, Line 221-226). In section 4.2 of discussion, we mainly discussed the effect of CWM of LDMC, leaf C, and leaf N on soil microbial carbon source use. We have added "Abbreviations" sections including all important full and shortened names as follow (P3, Line 54-81): Abbreviations: NSTEC North-South Transect of Eastern China AWCD Average well color development RDA Redundancy analysis Soil microbial community PLFAs Phospholipid fatty-acids G+ Gram positive bacteria G− Gram negative bacteria F/B Fungi/Bacteria Soil enzyme activities BG β-glucosidase NAG N-acetylglucosaminidase AP Acid phosphatase LAP Leucine aminopeptidase Soil properties SMC Soil moisture content SOM Soil

organic matter SOC Soil organic carbon TN Total Nitrogen DOC Dissolved organic carbon MBC Microbial biomass carbon Silt Soil silt fractions (<53 μm) Plant functional properties: CWM Community-weighted means SLA The specific leaf area LDMC Leaf dry matter content Leaf C Leaf C concentrations Leaf N Leaf N concentrations (19) The content lacks coherence and is occasionally repetitive. The text should have a more linear transition from plant to microbial function - and to isolate consideration of activity from diversity of community and community structure. The spatial dependence of microbial activity should be mentioned once at the outset, noting the issues of scales of spatial dependence. Response: we have carefully read our manuscript again and deleted that repeated part all through the text especially in section 4.3. (P16, Line 409-455) We mainly discussed the effect of plant functional traits on soil microbial function on section 4.2. (P14, Line 374-398) In addition, we added the spatial dependence of microbial activities in section 4.2 as "Of the six groups of C substrates, microbial communities in the temperate forests mainly used carbohydrates, carboxylic acids, and amino acids, which suggests that microorganisms in temperate forests probably use high-energy substrates that degrade easily (Kunito et al., 2009). The carbon substrate use was lowest in the coniferous forest. This shows that, compared with coniferous species, broadleaved tree species produce root exudates and litter high in water-soluble sugars, organic acids, and amino acids that are more favourable for microbial activity (Priha et al. 2001). There was no significant latitudinal pattern in the C metabolic intensity of soil microbes in our study, which was inconsistent with hypothesis (1). Our results show that MAP only had a moderate effect on the soil microbial function (Fig. 4). However, there was significant spatial variation in the use of different carbon sources, which was also related, to a lesser extent, to climate. Consistent with hypothesis (2), soil microbial functions were similar in closely related tree species and diverged as the variability between tree species and forest types increased (Fig. 4), which suggests that plant traits have more influence on soil microbial functions than climate." (P13, Line 347-357) (20) The paper only briefly mentions plant functional traits as a determinant of ecosystem properties, especially

for soil biogeochemical processes. The nature of the connection to microbial activity and function is poorly elucidated. Response: We have discussed connection to microbial community and soil carbon substrate use, enzyme activities, and SOM decomposition rate as in section 4.3 (P16, Line 419-436). (21) The introduction does not focus down to the study content until the end. It is difficult to understand the context of the study, since most of the introduction addresses how individual factors affects microbial activity individually. Response: in the second paragraph, we focus on the spatial pattern of soil microbial communities, enzyme activities, and metabolic activities in different scales. However, there was no studies about the variation of the microbial substrate use in large scale which support our hypotheses (1). (P4, Line 91-106) In the third paragraph we focus on the environmental properties which influence the soil microbial communities and activities. However, we still don't know about climate and plant functional traits which one is more important for the variation in soil microbial substrate use and this support our hypotheses (2) and hypotheses (3). (P4, Line 107-125) In the fourth paragraph, we focus on the relationship between soil microbial communities and function (hypotheses (4)). (P5, Line 126-148) (22) Hypotheses are offered, but not in testable, directional form. They are broad and could be better stated as overarching questions considering how microbial substrates correlate with latitude as a reflection of litter quality / substrate input. Response: We have rewritten our Hypotheses as "We tested four hypotheses in this study, as follows: (1) The profiles of soil microbial substrate use vary along a latitudinal gradient, (2) the functional characteristics of soil microbes are similar in closely related forest types, (3) biogeographical patterns of soil microbial substrate use are constrained by climate and plant functional traits, and (4) different soil microbial communities may have substrate use profiles and SOM decomposition rates." (P6, Line 160-164).

Please also note the supplement to this comment:
https://www.biogeosciences-discuss.net/bg-2018-499/bg-2018-499-AC3-supplement.pdf

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