

## Response to Reviewer #2

### General comments

Relationship between plant functional traits and soil microbial functions is totally important research to estimate forest soil carbon and nutrient budget at present conditions and at the global climate change conditions. And meta-analysis using multi-site data or samples is one of the major methods to know it. However in this case, we need discreet data handling, appropriate hypothesis because each forest has specific and different conditions (e.g. plant, soil, environment, history) and interaction between functions and conditions is always complex. In this MS, authors used 9 forests' soil samples and examined plant, carbon and microbe data. And authors defined this study as the relation between “plant function and the latitudinal variations in soil microbial functions (title). And authors also mentioned that this study related with a counter-hypothesis about functional redundancy of microbe (L90-L111). However this MS has some unclear points in (1) hypothesis testing, (2) relation between plant and microbe and (3) latitudinal distribution. In my opinion, this research has much, reasonable and complex information however needs major revision.

### Specific comments

(11) Hypothesis testing. At different forests and in different environmental conditions, specific (different) microbe distribution (species and activities) can happen and this must be common. Therefore in case mentioning on functional redundancy of microbe functions, careful definition of hypothesis is necessary

because dissimilarity or similarity at multi sites does not directly mean functional redundancy of ecosystem. In the papers authors referred (L90-L111), Balsler, Banerjee, Waldrop and Philippot used 1 site (or near 2 site transplanting) data and samples, and had a very clear hypothesis and testing. Strickland used several sites but experimental design was clear. In the study of Fierer, they used 71 site's samples but they focusing on bacteria (I recommend authors check this MS well.). Most of all studies conducted a specific manipulation and experiment for hypothesis testing because verification of functional redundancy in the steady state condition is difficult. On the other hand, I could not find one or several clear hypothesis in this paper. Please set more appropriate and clear hypothesis

Response: we have rewritten the hypothesis part 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)

(12) Relation between plant functional traits and soil microbial functions

In this MS, plant functional traits were defined in table S2 and used in Fig 4. Plant functional traits authors used were unclear in representativeness as plant functions. Because many researches focus on various plant functional traits

which could regulate microbial activities and species distributions (e.g. priming effect, home field advantage, and fine root production). At least, I think authors need to mention why they choose these variables as plant functional traits. And several variables were discussed in section.

Response: we have added the reason for the variables selection in the discussion as “A growing number of studies reported that vegetation type, land use, soil nutrients, and soil organic matter quality and quantity can determine large scale patterns of microbial communities (de Vries et al., 2012; Tu et al., 2016). Plant functional traits that are related to growth may determine a tree species' ability to contribute to the soil carbon pool via leaf litter inputs. For example, it was previously reported that plant traits such as the leaf N content, SLA, and LDMC could explain variations in soil nutrients and litter decomposition rates (Eichenberg et al., 2014; Laughlin, 2011). Therefore, we examined how these plant traits influenced the soil microbial function by latitude.” (P14, Line 358-364)

(13) 4.2. Each relation was reasonable but not seemed to lead to functional redundancy of microbe functions along forest sites

Response: We have rewritten this part as “The functional dissimilarity of microbes and fungi may help explain these results. However, we did not measure some key variables, such as the microbial competition and interactions, and relationship between the microbial diversity and the decomposition rates. Therefore, in the future, we will use different experimental

techniques that will help us gain an improved understanding of the mechanisms that drive the relationships between the structure and function of microbial communities.” (P17, Line 450-455)

#### (14) Latitudinal distribution

This MS was defined as “the latitudinal variations in soil microbial functions”. However I could not know about latitudinal distribution in soil microbial functions but comparison between forest and forest types. If authors wanted to assert this, I think they need focus more not on simple negative-positive relation but distribution (e.g. focusing on MAT vs plant type).

Response: we have added the description on the variation of soil microbial functions along the latitude and between forest types in 3.1 section as follow:

“The substrate microbial use ability was highest in the coniferous broad-leaved mixed forest and tropical forest soils, and lowest in the coniferous forest soil (Fig. 3).” (P11, Line 280-282).”

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 favorable 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)

We have also realized that the topic of 4.2 section was not conform with its text, so we have written it as “Mechanisms driving latitudinal variations in microbial substrate use” (P13, Line 343)

Technical comments

(15) Scatter plots CSU vs leaf N (L298), CSU vs leaf C (L308) and LDMC(L321) may support readability.

Response: we have added the scatter plots about CSU and leaf N, leaf C and LDMC (Figure S2).

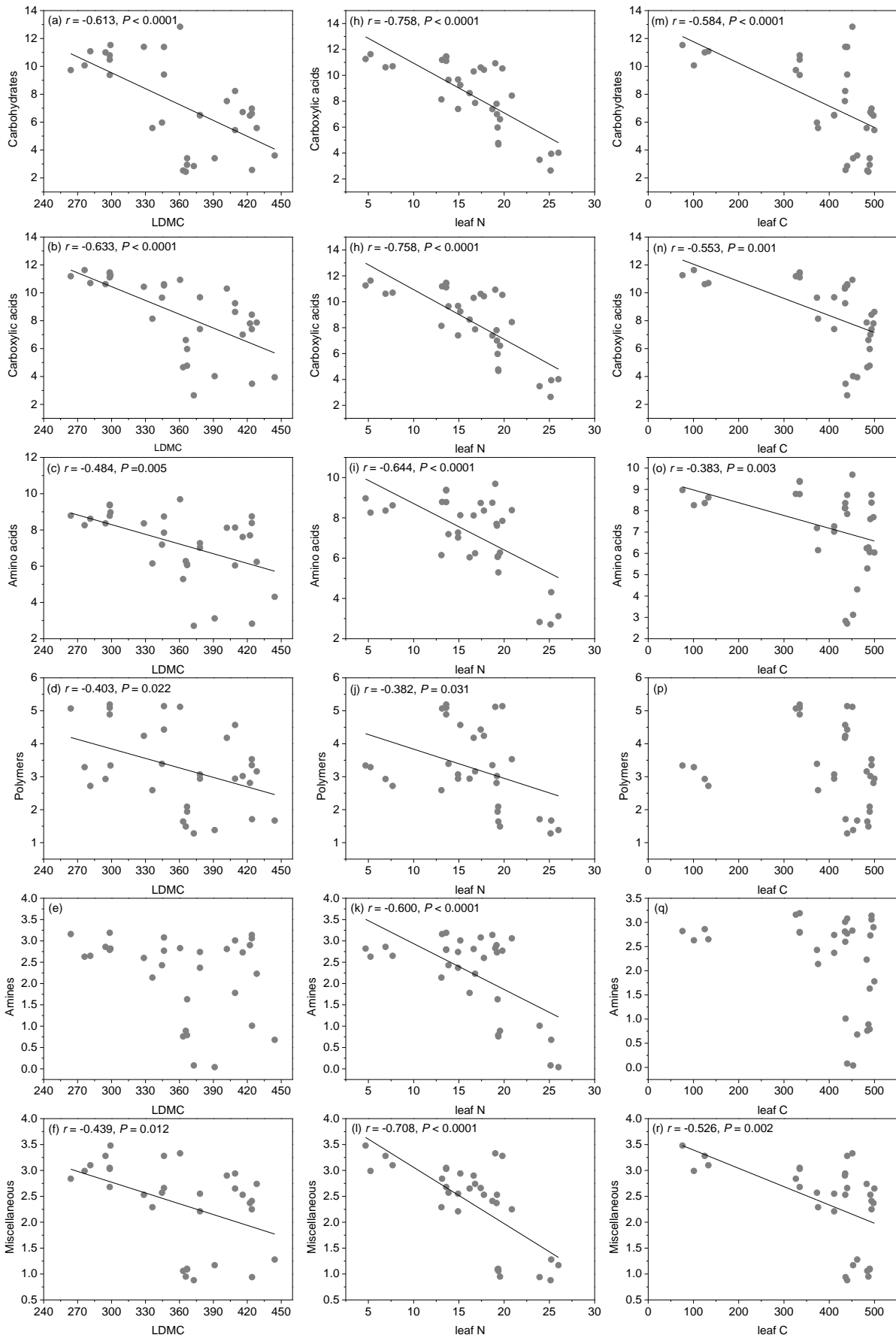


Fig.S2 The Pearson's correlation coefficients between the use of individual substrates and plant functional traits.

(16) Definition of CWM and H' was not clear.

Response: We have added the definition of the CWM and H' as follows:

We established four sampling plots (30×40 m) in each forest ecosystem. In each plot, we recorded all the tree individuals, and measured the height and diameter-at-breast-height (DBH) of each woody individual with a DBH≥2 cm. The diversity of the tree species in the sampling plots was represented by H', and the diversity (H', Shannon-Wiener) of the tree species in the community was calculated as follows:

$$H' = \sum_{i=1}^n (P_i \ln P_i)$$

Where  $P_i$  was the importance value of the species  $i$  as a proportion of all species, and  $n$  was the number of the species. (P8, Line 206-213)

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:

$$\text{CWM} = \sum_{i=1}^n p_i \times \text{trait}_i$$

Where  $p_i$  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  $\text{trait}_i$  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. (P8, Line 221-226)

