Exploring the relationships between the biodiversity of groups of interacting organisms yields insight into ecosystem stability and function (Hooper et al. 2000; Wardle 2006). We demonstrated positive relationships between host plant richness and ectomycorrhizal (EM) fungal diversity both in a field study in subtropical China (Gutianshan) and in a meta-analysis of temperate and tropical studies (Gao et al. 2013). However, based on re-evaluation of our data sets, Tedersoo et al. (2014) argue that the observed positive correlation between EM fungal richness and EM plant richness at Gutianshan and also in our meta-studies was based mainly from (i) a sampling design with inconsistent species pool and (ii) poor data compilation for the meta-analysis. Accordingly, we checked our data sets and repeated the analysis performed by Tedersoo et al. (2014). In contrast to Tedersoo et al. (2014), our re-analysis still confirms a positive effect of plant richness on EM fungal diversity in Gutianshan, temperate and tropical ecosystems, respectively.

Keywords: community ecology, ectomycorrhizal fungal diversity, environmental DNA, host plant richness

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Relative importance of a host species richness and identity

Tedersoo et al. (2014) re-analysed our Gutianshan data using one-way ANOVA and linear regression analysis. Their one-way ANOVAs showed that the presence of two particular species, Pinus massoniana and Quercus serrata, significantly influenced ectomycorrhizal (EM) fungal richness, while the linear regression analysis indicated that particular host species or host genera may drive the ‘host richness’ effect. However, this conclusion is problematic because of the fact that EM fungal richness was also significantly correlated with EM plant richness (Gao et al. 2013), and therefore, the influences of EM plant richness and of individual plant species on EM fungal richness must be evaluated in one single model.

In addition, in order to consider the possible influence of chimeras in our initial results, which was pointed out by Tedersoo et al. (2014), we re-evaluated the ITS sequence quality and deleted chimeras and non-EM fungal sequences (Table S1, Supporting Information). Subsequent statistical analysis showed similar results as in our original study (Gao et al. 2013). Briefly, we performed univariate and stepwise multiple regression analyses as in Gao et al. (2013). The univariate regression analysis showed that EM fungal richness was significantly related to EM plant species richness ($R^2 = 0.494$, $P = 0.012$), EM plant genus richness ($R^2 = 0.717$, $P < 0.001$), EM plant family richness ($R^2 = 0.618$, $P = 0.003$) and EM plant abundance ($R^2 = 0.384$, $P = 0.032$). For the multiple regression model that EM fungal richness was predicted by EM plant species richness, EM plant genus richness, EM plant family richness and EM plant abundance, the final model only retained EM plant genus richness ($F_{1,10} = 25.3$, $P < 0.001$). These results point out that removing chimaera sequences did not affect the conclusion of Gao et al. (2013).

Consistent with the results of Tedersoo et al. (2014), we found that the EM fungal richness was significantly related to the basal area of Pinus massoniana ($R^2 = 0.659$, $P = 0.001$) and the basal area of Quercus serrata ($R^2 = 0.626$, $P = 0.002$). Subsequently, EM plant species richness, genus richness, family richness, abundance, the basal area of Pinus massoniana and the basal area of Quercus serrata were used as predictors of EM fungal species richness in a generalized least-squares (GLS) model. The models were simplified according to the corrected Akaike Information Criterion (AICc). Model selection showed that EM plant genus richness was retained in the best model ($n = 12$, $R^2_{adj} = 0.688$; EM plant genus richness: $t = 5.030$, $P < 0.001$). Thus, these results support the ‘host richness’ effect on EM fungal richness.

Besides, in order to account for the influence brought in by the experiment design that three plots in each plant richness level were not independent, the number of data
points was reduced from 12 to 4 by calculating the average value of EM fungal diversity and other variables. The univariate regression analysis showed that the EM fungal species richness was significantly related to EM plant genus richness ($R^2 = 0.984, P = 0.009$) and EM plant abundance ($R^2 = 0.944, P = 0.029$), but not significantly related to EM plant species richness ($R^2 = 0.678, P = 0.177$), family richness ($R^2 = 0.849, P = 0.079$), the basal area of *P. massoniana* ($R^2 = 0.800, P = 0.106$) and the basal area of *Q. serrata* ($R^2 = 0.890, P = 0.057$). Subsequently, EM plant genus richness and abundance were used as predictors of EM fungal species richness in a GLS model, and the models were simplified according to the AIC (because the AICc values were infinite). The final multiple regression model retained EM plant genus richness ($n = 4, R^2_{adj} = 0.688$; EM plant genus richness: $t = 10.987, P = 0.009$). Thus, these results support the ‘host richness’ effect on EM fungal richness.

**Meta-analysis – data compilation**

For the metastudy, we considered some of the suggestions of Tedersoo *et al.* (2014) and removed some data sets and references: (i) study 12 examined fruit bodies and study 58 investigated Ericaceae plants; (ii) studies 22, 24, 43, 44, 45, 57, 61, 62, 63 and 83 mainly sampled plant seedlings; (iii) studies 8, 14, 37, 38, 81 and 91 sampled twice; and (iv) studies 2, 55, 60, 71 included many sites >10 km apart, which cannot be separated into different <10 km groups for analysis. In addition, we corrected (i) EM fungal richness of studies 9, 36, 62, 64, 68, 70, 87 and 87 and (ii) EM plant richness of studies 1, 4, 6, 7, 9, 34, 36, 47, 70, 78, 89, 90 and 99 as commented by Tedersoo *et al.* (2014).

However, we disagree on the exclusion of some references, which are still included in our revised analyses. This includes (i) studies 3, 29, 42, 49 that can be separated into several <10 km sites according to the criterion stated in our paper (Gao *et al.* 2013); (ii) studies 53 and 65 that comprised <15 samples, as sampling number was used as predictor variable in statistic analysis; (iii) studies 3 and 29 that focused on *Alnus* plants, as the data compilation should include various plant groups; (iv) studies 17 and 25 that investigated exotic pine plantations, because plant native status is not a concern in our data compilation and Tedersoo *et al.* (2014) also included study 13 on exotic eucalypt plantation and study 85 on exotic pine plantation in their analyses; (v) studies 39, 40, 41, 48 and 50 that pooled stands of different hosts and richness, as this is a common method used in investigating EM fungal diversity.

**Fig. 1** Ectomycorrhizal (EM) plant genus richness significantly positively related to the partial residuals in EM fungal species richness that the effects of sample number and sample number$^{0.5}$ are controlled for the newly revised (A) tropical, (B) temperate and (C) combined both data sets.

**Fig. 2** Ectomycorrhizal (EM) plant genus richness significantly positively related to (A) EM fungal species richness for the further revised tropical data set, significantly positively related to (B) the partial residuals in EM fungal species richness that the effects of sample number and sample number$^{0.5}$ that are significant in final generalized least-squares (GLS) models are controlled for the further revised temperate data set and not significantly related to (C) the partial residuals in EM fungal species richness that the effects of sample number and sample number$^{0.5}$ that are significant in final GLS models are controlled for the combined further revised tropical and temperate data set.
community of multiple host species within a study site (Table S2, Supporting Information).

The newly revised data set was also analysed following the procedure used by Tedersoo et al. (2014). Briefly, EM plant species richness, genus richness, family richness, sampling number, square-root-transformed sampling number, sampling volume and square-root-transformed sampling volume were used as predictors of EM fungal species richness in GLS. The models were simplified according to the AICc. In addition, the selected model with smallest AICc value was further simplified until $P < 0.05$ for all retained predictors. Furthermore, if sampling variables were retained in the final model, the residuals in EM fungal species richness will be calculated by partialling out the effects of significant sampling variables (Kraft & Jetz 2007). The pure plant richness effect will be demonstrated by plotting the partial residual in EM fungal species richness against EM plant genus richness.

Model selection showed that EM plant genus richness, sampling number and sample number$^{0.5}$ were retained in the best models in temperate ($n = 78$; $R^2_{adj} = 0.434$; EM plant genus richness: $t = 4.011$, $P < 0.001$; sampling number: $t = -5.072$, $P < 0.001$; sampling number$^{0.5}$: $t = 5.840$, $P < 0.001$), tropical ($n = 16$; $R^2_{adj} = 0.723$; EM plant genus richness: $t = 2.809$, $P = 0.016$; sampling number: $t = -3.102$, $P = 0.009$; sampling number$^{0.5}$: $t = 3.022$, $P = 0.011$) and both temperate and tropical regions combined ($n = 94$; $R^2_{adj} = 0.367$; EM plant genus richness: $t = 2.630$, $P = 0.010$; sampling number: $t = -5.518$, $P < 0.001$; sampling number$^{0.5}$: $t = 6.106$, $P < 0.001$). Furthermore, after the influences of sample number and sampling number$^{0.5}$ on EM fungal species richness were partialled out, the partial residuals in EM fungal species richness were 20.6% ($P = 0.044$, Fig. 1A), 16.5% ($P < 0.001$, Fig. 1B) and 5.8% ($P = 0.012$, Fig. 1C) explained by EM plant genus richness in tropical, temperate and combined both ecosystems, respectively (Fig. 1).

Besides, although we do not agree with Tedersoo et al. (2014) for the exclusion of studies 17 and 25 that investigated exotic pine plantation species, and studies 39, 40, 41, 48 and 50 that pooled stands of different hosts and richness, to evaluate whether the inclusion of them affects the results, we further excluded these nine sites and re-ran the analysis using data from 85 sites. For the further revised tropical data set, only EM plant genus richness was retained in the best model in tropic ecosystem ($n = 14$, $R^2_{adj} = 0.541$; EM plant genus richness: $t = 4.041$, $P = 0.002$, Fig. 2A). For the further revised temperate data set, EM plant genus richness, sampling number and sample number$^{0.5}$ were retained in the best model ($n = 71$; $R^2_{adj} = 0.436$; EM plant genus richness: $t = 2.920$, $P = 0.005$; sampling number: $t = -4.340$, $P < 0.001$; sampling number$^{0.5}$: $t = 5.412$, $P < 0.001$), and EM plant genus richness accounted for 9.86% ($P = 0.005$) of the partial residuals in EM fungal species richness after the influences of sample number and sampling number$^{0.5}$ were partialled out (Fig. 2B). For the combined further revised tropical and temperate data set, the final model retained sample number and sampling number$^{0.5}$ ($n = 85$; $R^2_{adj} = 0.391$; sampling number: $t = -5.393$, $P < 0.001$; sampling number$^{0.5}$: $t = 6.506$, $P < 0.001$), and EM plant genus richness accounted for <1% ($P = 1$) of the partial residuals in EM fungal species richness after the influences of sample number and sampling number$^{0.5}$ were partialled out (Fig. 2C).

Finally, our revised results demonstrate ‘plant richness effect’ on EM fungal diversity in our Gutianshan field site and for metastudy analysis on the tropical and temperate ecosystems, respectively. However, there was no consistent ‘plant richness effect’ in the combined temperate and tropical metadata analyses, when different data filtering criteria were employed. Our conclusions partially differ from the results by Tedersoo et al. (2014), who conclude that EM fungal diversity in metastudy analysis on temperate, tropical and both combined was all only influenced by sampling effects, but not by host richness. Other field studies (Molina et al. 1992; Richard et al. 2005; Ishida et al. 2007; Tedersoo et al. 2008, 2010) and meta-analyses (Schmit et al. 2005; Dickie 2007) have found evidence that host preference can drive a positive relationship between host plant richness and EM fungal diversity, while some studies demonstrated that large EM fungal diversity was recovered from small host diversity (Richard et al. 2005, 2011; Parrent & Vilgalys 2007). The differences between our results and those of Tedersoo et al. (2014) suggest that no definitive conclusion can be drawn on the most prominent driver of EM fungal diversity, especially when different criteria were adopted in metastudy analysis. In addition, because the numbers of studies were unevenly distributed among tropical, subtropical and temperate ecosystems, the conclusion of the global-scale metastudy is therefore dubious (Tedersoo et al., 2012, 2014). Furthermore, not only the effect of host richness, but also the effects of soil biotic and abiotic factors on EM fungal diversity are still open questions that need to be addressed (Pölme et al. 2013; Roy et al. 2013). Future studies should take both sampling effects (Wardle 1999) and the contribution of biotic and abiotic variables into consideration (Dickie 2007; Lilleskov & Parrent 2007). While we respectfully disagree with the result of Tedersoo et al.’s re-analysis of our data set, we agree that large-scale multidisciplinary projects coupled with next-generation sequencing techniques (Lindahl et al. 2013) to investigate spatial and temporal variation of fungal communities and statistical analysis combining extensively collected environmental variables will help to address these key questions.

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C.G. and L.G. analysed data, C.G., N.S., Y.L., Y.Z., Q.D., X.M., K.M., T.W., F.B. and L.G. wrote the manuscript.

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Data accessibility

All data are available in Table S1 and S2.

Supporting information

Additional supporting information may be found in the online version of this article.

**Table S1** The number of positive clones for every ectomycorrhizal (EM) fungal OTU in every quadrat in Gutianshan study.

**Table S2** Metadata for study. Those highlighted are changed from Tedersoo et al. (2013).