Supplementary Material S1

Diversity Patterns and Determinants of Soil Microorganisms and Nematodes along Elevation Gradients in a Temperate Forest in South Korea

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1.1 Materials and Methods

Quantification of tree diversity and identity

To examine the relationship among taxonomic diversity and SMND, we employed three indices of taxonomic diversity: species richness, Shannon-Wiener H, and Pielou's species evenness. Species richness was quantified as the total number of species in each plot. Shannon-Wiener H was calculated in each plot using the following equation:

$$\text{Shannon H} = -\sum_{i=1}^{n} p_i \ln p_i$$

where n and p_i are the number of species and the relative abundance of the ith species in each quadrat, respectively. Species evenness was also quantified in each plot using an equation:

$$\text{SE} = \frac{H}{\ln(S)}$$

where H and S indicate the Shannon-Wiener H index and species richness, respectively.

To calculate phylogenetic diversity indices, we constructed a phylogenetic tree that included all tree species occurring in the total plots (Fig. S1). We used the "GBOTB.extended" megatree as the backbone tree (Jin and Qian, 2019). The GBOTB.extended is a time-calibrated molecular phylogeny of 74,533 vascular plant species, including all families of extant seed plants, and it is the most extensive dated phylogeny for vascular plants available to date (Jin and Qian, 2019). The backbone trees used in this study were pruned using the phylo.maker function of the "V.PhyloMaker" package in R. Then, we calculated four phylogenetic diversity indices: phylogenetic species richness (PSR), phylogenetic species variability (PSV), phylogenetic species clustering (PSC), and phylogenetic species evenness (PSE). These indices are usually used to analyze the effect of evolutionary history and properties on AGB in a community (Helmus et al., 2007). Phylogenetic species richness is the number of species in a community multiplied by PSV. The PSR value is maximum at species richness and decreases toward zero as relatedness increases. Whereas, PSV is the measurement of the deviation from a star phylogeny and its values range from one, when all species are phylogenetically unrelated, to zero, when species are phylogenetically more related. Phylogenetic species clustering is a metric of the branch-tip clustering of species across a phylogenetic tree. The values of PSC range from zero, when species at the tips of the phylogenetic tree are closely related, to one, when species at the tips of the phylogenetic tree are less closely related to one another. Phylogenetic species evenness is the PSV metric that has been modified to incorporate relative species abundances with its values ranging from zero, when there is unequal abundance of phylogenetically close species, to one, when there are equal abundances of phylogenetically distant species. All phylogenetic diversity indices were calculated using the R package *picante* in R 3.6.2.

To quantify functional diversity and the community-weighted mean (CWM), four functional traits of tree species, maximum height (m), leaf size (cm), wood density (g cm^{-3}), and seed mass (mg) were used in this study to represent important aspects of plant strategy and fundamental functional trade-offs directly related to survival and the growth of tree species (Cornelissen et al., 2003; Rose and Poorter, 2003; Garnier et al., 2016). Generally, maximum height is the dominant factor influencing access to light and represents a major axis of life-history variation (Mole et al., 2009). Leaf size is related to resource acquisition and has important consequences for leaf energy and water balance (Cornelissen et al., 2003). In this study, we used the sum of leaf length and width as a proxy of leaf area because some leaf traits such as leaf area and photosynthetic activity correlated well with the sum of leaf length and width in previous studies (Kim and Um, 1998; Paik et al., 1998; Lee et al., 2014). Therefore, the previous studies suggested the use of this simple index because of a non-destructive method in the field. Wood density is associated with a trade-off between structural investment and growth and mortality rates (Swenson et al., 2012). Seed mass is related to resource conservation and affects the tree's ability to survive under environmental stresses (Kitajima and Myers, 2008). A mean trait value of a trait for a given woody species was used, and the mean trait values were used to analyze functional diversity and the CWM. Thus, this study does not reflect trait variation among and within tree species (Swenson et al., 2012).

We calculated functional dispersion (FDis; Mason et al., 2005; Laliberté and Legendre, 2010) as a proxy of functional diversity based on the multivariate-trait and each trait space and thus five FDis indices were calculated in this study. The species' relative basal area was used to weight the species' traits (Prado-Junior et al., 2016; Ali et al., 2018).

The CWM was calculated for each trait in each plot following (Díaz et al., 2007):

$$\mathrm{CWM}_x = \sum_{i=1}^{n} p_i \, t_i$$

where CWM_x is the CWM for trait x n is the number of species in a plot, and p_i and t_i represent the relative basal area and the trait value of ith species in each plot, respectively. All functional diversity indices and CWMs were quantified using the R packages *vegan* and *FD* using R 3.6.2.

References

Ali, A., Lohbeck, M., Yan, E.R., 2018. Forest strata-dependent functional evenness explains whole-community aboveground biomass through opposing mechanisms. For. Ecol. Manage. 424, 439–447.

Cornelissen, J.H.C., Lavorel, S., Garnier, E., Díaz, S., Buchmann, N., Gurvich, D.E., Reich, P.B., ter Steege, H., Morgan, H.D., van der Heijden, M.G.A., Pausas, J.G., Poorter, H., 2003. A handbook of

protocols for standardized and easy measurement of plant functional traits worldwide. Aust. J. Bot. 51, 335–380.

Díaz, S., Lavorel, S., de Bello, F., Quétier, F., Grigulis, K, Robson, T.M., 2007. Incorporating plant functional diversity effects in ecosystem service assessments. Proc. Natl. Acad. Sci. U.S.A. 104, 20684–20689.

Garnier, E., Navas, M.L., Grigulis, K., 2016. *Plant functional diversity: organism traits, community structure, and ecosystem properties*. Oxford University Press, UK.

Helmus, M.R., Bland, T.J., Williams, C.K., Ives, A.R., 2007. Phylogenetic measures of biodiversity. Am. Nat. 169, E68–E83.

Jin, Y, Qian, H., 2019. V.PhyloMaker: an R package that can generate very large phylogenies for vascular plants. Ecography 42, 1353–1359.

Kim, G.T., Um, T.W., 1997. A study on the distribution of wild edible herb species in Mt. Kariwang. J. Korean For. Soc. 86, 422–429.

Kitajima, K., Myers, J. A., 2008. Seedling ecophysiology: strategies toward achievement of positive net carbon balance. Seedling ecology and evolution, 172-188.

Laliberté, E., Legendre, P., 2010. A distance-based framework for measuring functional diversity from multiple traits. Ecology 91, 299–305.

Lee, C.M., Kwon, T.S., Park, Y.K., Kim, S.S., Sung, J.H., Lee, Y.G., 2014. Diversity of beetles in Gariwangsan mountain, South Korea: influence of forest management and sampling efficiency of collecting method. J. Asian-Pac. Biodivers. 7, 319–346.

Mason, N.W., Mouillot, D., Lee, W.G., Wilson, J.B., 2005. Functional richness, functional evenness and functional divergence: the primary components of functional diversity. Oikos 111, 112–118.

Prado-Junior, J.A., Schiavini, I., Vale, V.S., Arantes, C.S., Sande, M.T., Lohbek, M., Poorter, L., 2016. Conservative species drive biomass productivity in tropical dry forests. J. Ecol. 104, 817–827.

Rose, S. A., Poorter, L., 2003. The importance of seed mass for early regeneration in tropical forest: a review. Long-term changes in tropical tree diversity: Studies from the Guiana Shield, Africa, Borneo and Melanesia, 19-35.

Swenson, N.G., Erickson, D.L., Mi, X., Bourg, N.A., Forero-Montaña, J., Ge, X., Howe, R., Lake, J.K., Liu, X., Ma, K., Pei, N., Thompson, J., Uriarte, M., Wolf, A., Wright, S.J., Ye, W., Zhang, J., Zimmerman, J.K., Kress, W.J., 2012. Phylogenetic and functional alpha and beta diversity in temperate and tropical tree communities. Ecology 93, S112–S125.

1.2 List of supplementary tables and figures

Table S1. Summary of the indices of tree diversity, trait identity and aboveground biomass (n = 27) in temperate forests of South Korea.

Table S2. Allometric equations for the estimation of the aboveground biomass (AGB) of the woody plant species recorded in this study. Scientific names follow The Plant List (www.theplantlist.org). AGB equations were obtained from the listed literature.

[*] *Note: Tables S2 and S5 were prepared in a different file format (i.e., Excel file). They could not be included in the supplementary materials due to the large file size.*

Table S3. Summary of the generalized least squares (GLS) models indicating the tree effects on soil microbial and nematode diversity to confirm the influence of spatial autocorrelation.

Table S4. Summary of the generalized least squares (GLS) models indicating the effect of environmental factors on soil microbial and nematode diversity in the variance partitioning plots to explain the influence of spatial autocorrelation.

Table S5. Dataset used in this study.

Figure S1. A phylogenetic tree used for the quantification of phylogenetic diversity indices.

Figure S2. Pearson's correlation coefficient among tree factors and soil microbial and nematode diversity.

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Figure S4. Standardized coefficient(β) with 95% confidence intervals and importance values of a) tree and d) environmental factors calculated using model averaging approach of a multimodel inference test.

Table S1. Summary of the indices of tree diversity, trait identity and aboveground biomass (n = 27) in temperate forests of South Korea. Abbreviations: Min, minimum; Max, maximum; SE, standard error; SR, species richness, SD, Shannon H index; SE, species evenness; PSR, phylogenetic species richness; PSV, phylogenetic species variability; PSC, phylogenetic species clustering; PSE, phylogenetic species evenness; FDis, functional dispersion; MH, maximum height; LS, leaf size; WD, wood density; SM, seed mass; CV DBH, coefficient of variation of diameter of breast height; CWM, community weighted mean; AGB, aboveground biomass; OTU, operational taxonomic unit; MAP, mean annual precipitation; MAT, mean annual temperature; TOC, total organic carbon; TN, total nitrogen; NH_4^+-N, ammonium-nitrogen; NO_3^--N, nitrate-nitrogen; TP, total phosphorus; AP, available phosphate; OM, organic matter; CEC, cation exchange capacity.

Type	Variables	Unit	Community level			
			Min	Max	Mean	SE
Tree factors	**<Tree diversity>**					
	Taxonomic diversity					
	SR	unitless	7.00	17.00	10.37	2.88
	SD	unitless	0.86	2.35	1.88	0.35
	SE	unitless	0.34	0.91	0.68	0.14
	Phylogenetic diversity					
	PSR	unitless	1.93	6.05	3.82	1.12
	PSV	unitless	0.28	0.55	0.37	0.06
	PSC	unitless	0.12	0.36	0.23	0.06
	PSE	unitless	0.28	0.55	0.37	0.06
	Functional diversity					
	FDis	unitless	0.55	2.30	1.17	0.37
	FDis MH	unitless	0.31	3.62	1.33	0.70
	FDis LS	unitless	0.16	1.78	0.80	0.45
	FDis WD	unitless	0.93	3.40	1.78	0.61
	FDis SM	unitless	< 0.01	0.12	0.02	0.02
	Structural diversity					
	CV DBH	unitless	0.54	1.31	0.87	0.20
	<Tree trait identity>					
	CWM MH	m	4.18	18.14	9.23	3.80
	CWM LS	cm	11.73	18.59	15.62	1.61
	CWM WD	g cm^{-3}	0.47	0.75	0.65	0.07
	CWM SM	mg	16.84	6078.15	1273.46	1298.02
	<Tree quantity>					
	AGB	Mg ha^{-1}	12.00	60.75	31.26	13.30
Soil biodiversity	**<Soil biodiversity>**					
	Bacterial OTU richness	unitless	1838.00	2817.00	2276.11	295.88
	Fungal OTU richness	unitless	376.00	854.00	624.96	121.31
	Nematode OTU richness	unitless	381.00	756.00	580.11	93.81

Environmental factors	**<Environmental factors>**					
	Topography					
	Elevation	m	603.00	1493.00	1039.30	271.21
	Climate					
	MAP	mm	1401.00	1836.00	1610.67	100.01
	MAT	°C	5.20	9.10	7.31	1.15
	Soil chemical property					
	pH	unitless	4.80	6.60	5.41	0.51
	TOC	%	2.67	24.08	8.79	4.53
	TN	%	0.19	1.42	0.62	0.25
	NH_4^+-N	mg kg^{-1}	7.25	81.75	28.70	17.78
	NO_3^- -N	mg kg^{-1}	0.28	12.85	6.00	3.46
	TP	mg kg^{-1}	197.40	1648.46	796.41	284.58
	AP	mg kg^{-1}	20.60	158.50	37.51	29.17
	OM	%	4.70	23.81	11.42	4.14
	CEC	cmolc kg^{-1}	19.21	32.34	25.77	2.85

Table S3. Summary of the generalized least squares (GLS) models to test the influence of spatial autocorrelation of the tree effects on soil microbial and nematode diversity. All the abbreviations for variables are described in Table S1.

GLS model	Model	Coefficient	t-value	P-value	AIC	R^2_{pseudo}
Whole community level						
Bacterial OTU richness ~ FDis LS	Non-spatial	0.529	3.114	0.005	76.289	0.279
	Spatial	0.529	3.114	0.005	80.289	0.279
Bacterial OTU richness ~ SE	Non-spatial	-0.230	-1.182	0.248	83.122	0.056
	Spatial	-0.230	-1.182	0.248	87.122	0.056
Bacterial OTU richness ~ CWM LS	Non-spatial	0.115	0.579	0.568	84.148	0.013
	Spatial	0.115	0.579	0.568	88.148	0.013
Bacterial OTU richness ~ CWM WD	Non-spatial	-0.370	-1.988	0.058	80.811	0.137
	Spatial	-0.370	-1.988	0.058	84.811	0.137
Bacterial OTU richness ~ AGB	Non-spatial	0.284	1.482	0.151	82.376	0.081
	Spatial	0.284	1.482	0.151	86.376	0.081
Fungal OTU richness ~ FDis LS	Non-spatial	0.363	1.949	0.063	80.946	0.132
	Spatial	0.346	2.025	0.054	83.084	0.139
Fungal OTU richness ~ CWM LS	Non-spatial	0.115	0.580	0.567	84.147	0.013
	Spatial	0.231	1.303	0.204	85.500	0.053
Fungal OTU richness ~ AGB	Non-spatial	0.087	0.436	0.667	84.292	0.008
	Spatial	0.097	0.519	0.608	86.574	0.008
Nematode OTU richness ~ CV DBH	Non-spatial	0.340	1.808	0.083	81.409	0.116
	Spatial	0.338	1.797	0.084	85.386	0.114
Nematode OTU richness ~ CWM LS	Non-spatial	0.179	0.908	0.373	83.670	0.032
	Spatial	0.219	1.146	0.263	87.308	0.042
Nematode OTU richness ~ AGB	Non-spatial	0.510	2.962	0.007	76.961	0.260
	Spatial	0.510	2.962	0.007	80.961	0.259

Table S4. Summary of the generalized least squares (GLS) models to test the influence of spatial autocorrelation of the environmental effects on soil microbial and nematode diversity. All the abbreviations for variables are described in Table S1.

GLS model	Model	Coefficient	t-value	P-value	AIC	R^2_{pseudo}
Environmental condition						
Bacterial OTU richness ~ MAP	Non-spatial	–0.359	–1.921	0.066	81.039	0.129
	Spatial	–0.359	–1.921	0.066	85.039	0.129
Bacterial OTU richness ~ pH	Non-spatial	0.809	6.871	0.000	57.962	0.654
	Spatial	0.809	6.871	0.000	61.962	0.654
Fungal OTU richness ~ MAP	Non-spatial	–0.191	–0.972	0.340	83.554	0.036
	Spatial	–0.125	–0.480	0.635	85.950	0.010
Fungal OTU richness ~ pH	Non-spatial	0.550	3.293	0.003	75.475	0.303
	Spatial	0.550	3.293	0.003	79.475	0.289
Nematode OTU richness ~ MAP	Non-spatial	0.095	0.479	0.636	84.253	0.009
	Spatial	0.089	0.437	0.666	88.163	0.007
Nematode OTU richness ~ NH4	Non-spatial	0.543	3.231	0.003	75.758	0.295
	Spatial	0.543	3.230	0.003	79.756	0.293

Figure S1. A phylogenetic tree used for the quantification of phylogenetic diversity indices in this study.

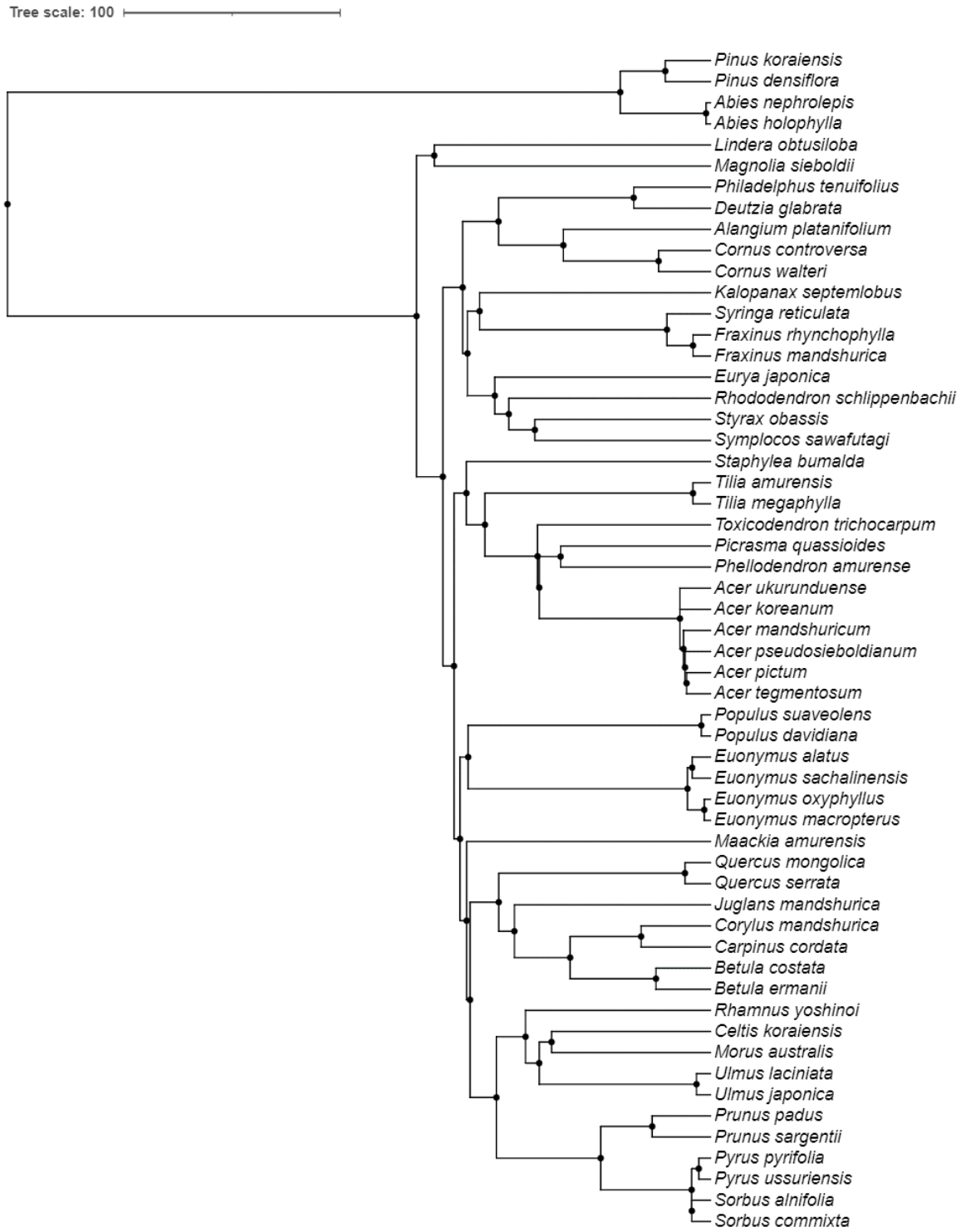


Figure S2. Pearson correlation coefficient among tree factors and soil microbial and nematode diversity. All the abbreviations for variables are described in Table S1.

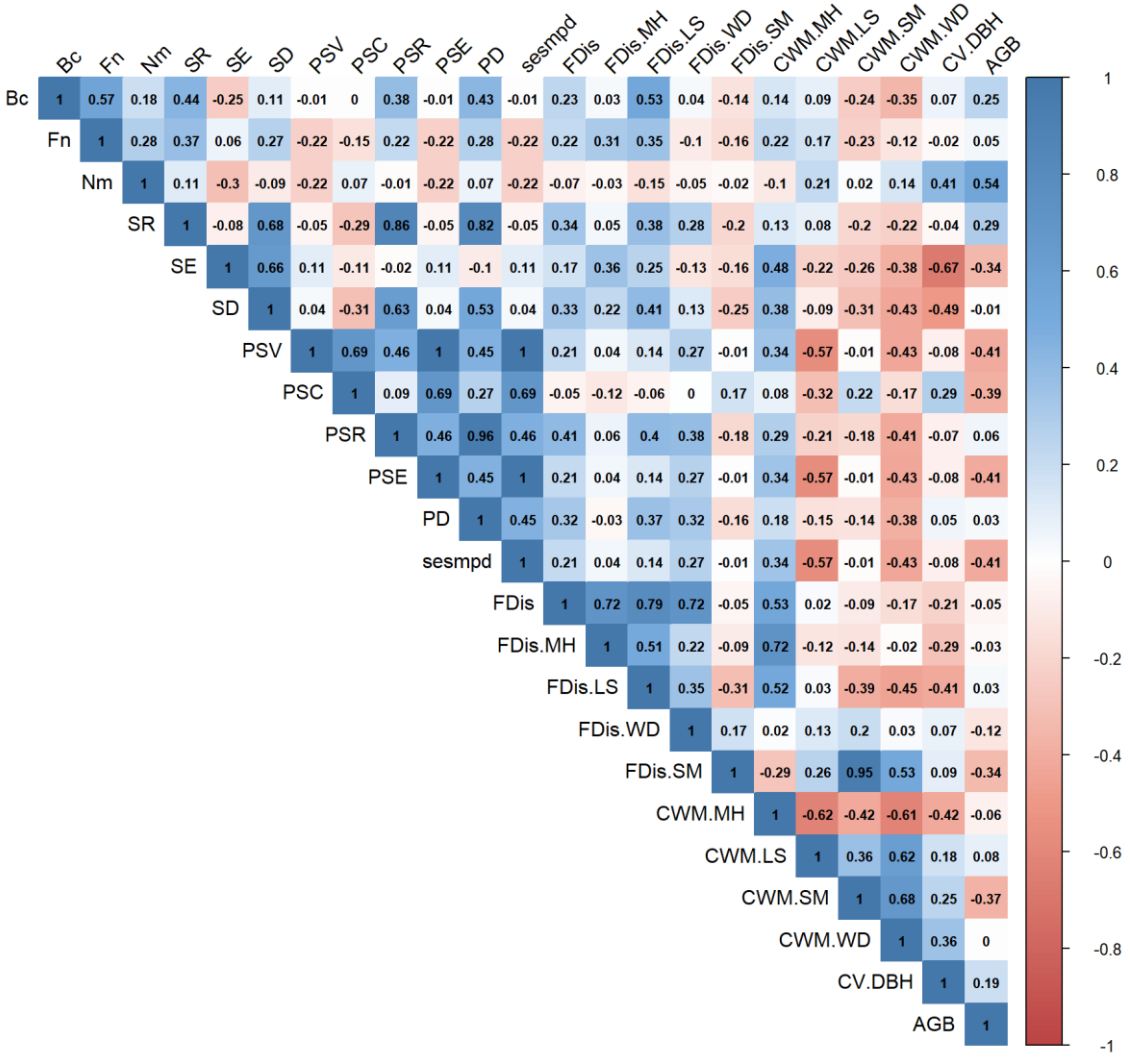


Figure S3. Pearson correlation coefficient among environmental factors and soil microbial and nematode diversity. All the abbreviations for variables are described in Table

S1.

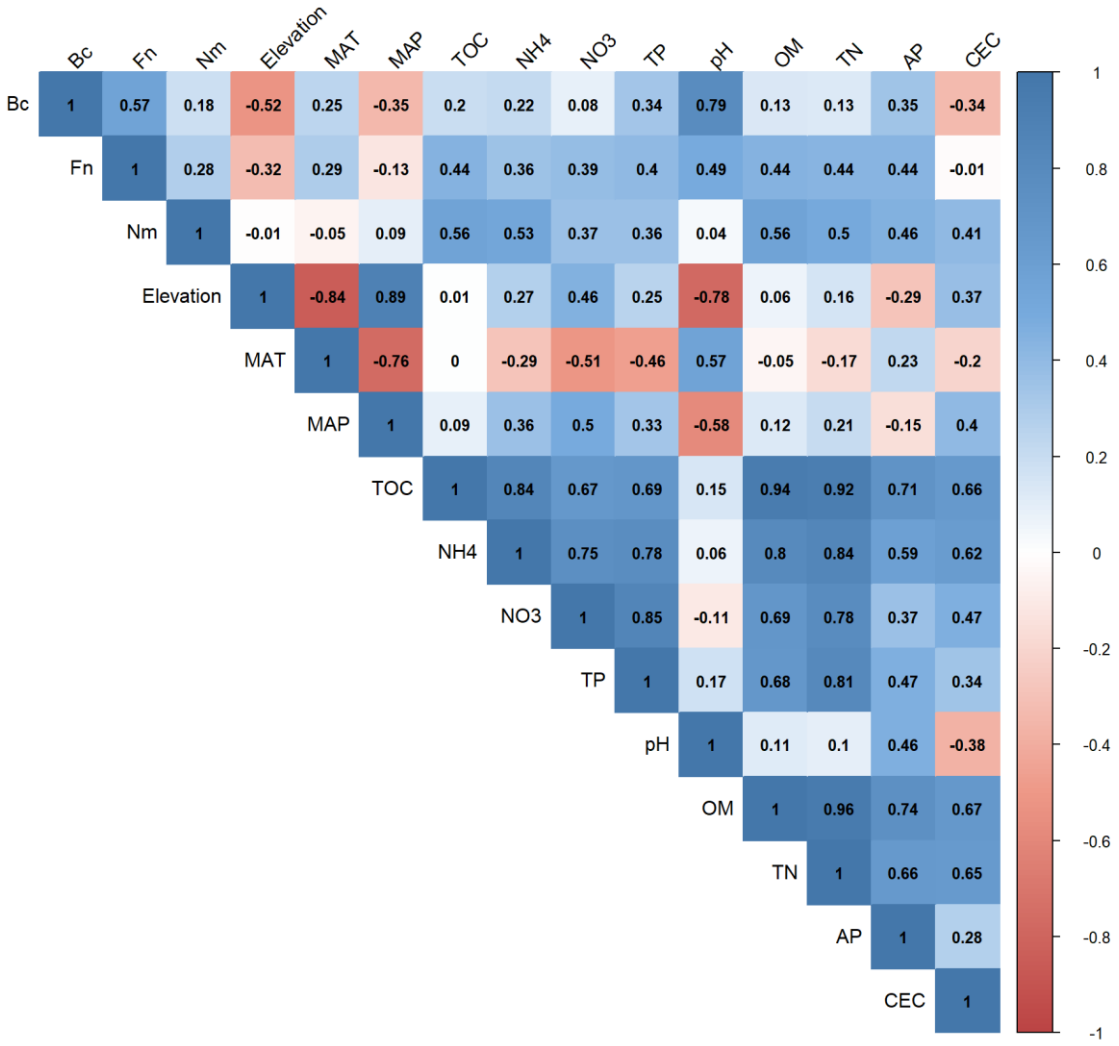
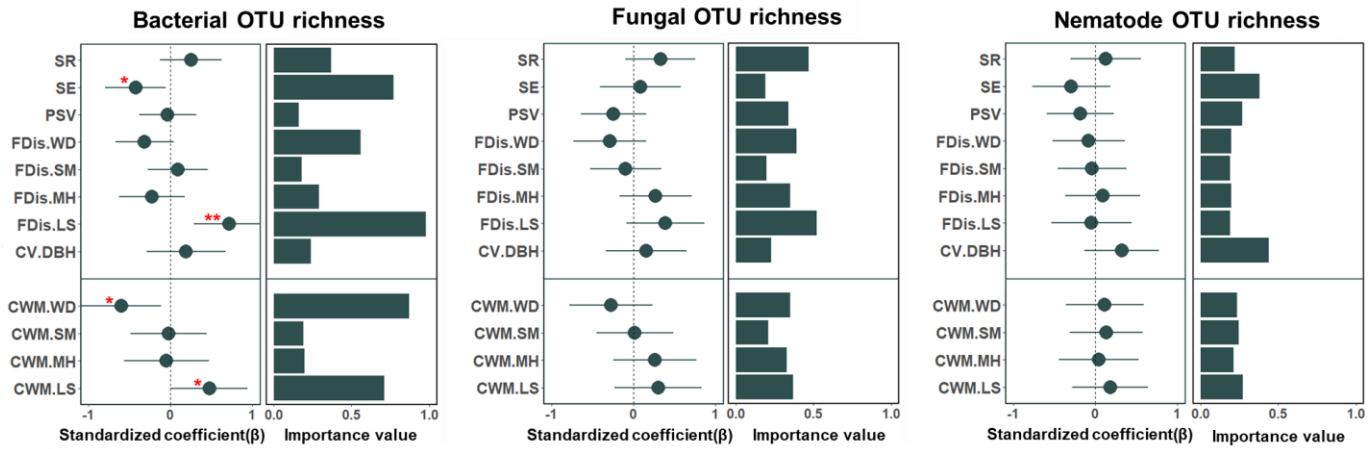

Bc Fn Nm Elevation MAT MAP TOC NH4 NO3 TP pH OM TN AP CEC
Bc 1 0.57 0.18 -0.52 0.25 -0.35 0.2 0.22 0.08 0.34 0.79 0.13 0.13 0.35 -0.34
Fn 1 0.28 -0.32 0.29 -0.13 0.44 0.36 0.39 0.4 0.49 0.44 0.44 0.44 -0.01
Nm 1 -0.01 -0.05 0.09 0.56 0.53 0.37 0.36 0.04 0.56 0.5 0.46 0.41
Elevation 1 -0.84 0.89 0.01 0.27 0.46 0.25 -0.78 0.06 0.16 -0.29 0.37
MAT 1 -0.76 0 -0.29 -0.51 -0.46 0.57 -0.05 -0.17 0.23 -0.2
MAP 1 0.09 0.36 0.5 0.33 -0.58 0.12 0.21 -0.15 0.4
TOC 1 0.84 0.67 0.69 0.15 0.94 0.92 0.71 0.66
NH4 1 0.75 0.78 0.06 0.8 0.84 0.59 0.62
NO3 1 0.85 -0.11 0.69 0.78 0.37 0.47
TP 1 0.17 0.68 0.81 0.47 0.34
pH 1 0.11 0.1 0.46 -0.38
OM 1 0.96 0.74 0.67
TN 1 0.66 0.65
AP 1 0.28
CEC 1
1
0.8
0.6
0.4
0.2
0
-0.2
-0.4
-0.6
-0.8
-1

Figure S4. Standardized coefficient (β) with 95% confidence intervals and importance values of a) tree and b) environmental factors calculated using model averaging approach of a multimodel inference test. The definitions of the variables are described in Table S1.

a) tree factors



b) environmental factors

