

Article

# Phylogenetic Structure of Soil Bacterial Communities along Age Sequence of Subtropical Cunninghamia Lanceolata Plantations

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**Table S1.** Description of the sampling sites of *C. lanceolata* plantations.

Sites	Slope Gradient	Slope Orientation	Understory Vegetation
Young	32°	E	I. pubescens, M. dodecandrum
Middle	35°	E	Misanthus, D. dichotoma
Mature	30°	E	I. pubescens, D. dichotoma

I. pubescens: *Ilex pubescens*; D. dichotoma: *Dicranopteris dichotoma*; M. dodecandrum: *Melastoma dodecandrum*

**Table S2.** Bacterial sequences and OTUs in each soil sample at different age of *C. lanceolata* plantations.

Stand Age	Sequence	OTU Number
Young 1	45298	2123
Young 2	46437	2211
Young 3	54278	2201
Young 4	68006	2260
Young 5	60223	2270
Middle 1	70260	2264
Middle 2	72152	2399
Middle 3	56610	2347
Middle 4	85503	2186
Middle 5	57324	2122
Mature 1	66314	2497
Mature 2	75017	2485
Mature 3	71550	2159
Mature 4	69047	2416
Mature 5	74782	2395

**Table S3.** Significant test of bacterial community taxonomic (Bray-Curtis) and phylogenetic (Unifrac) composition between different ages of *C. lanceolata* plantations based on PerMANOVA analysis.

	Taxonomic community			Phylogenetic Community		
	F	R <sup>2</sup>	p	F	R <sup>2</sup>	p
<b>Young vs Middle</b>	7.12	0.47	0.008	11.07	0.58	0.009
<b>Young vs Mature</b>	10.37	0.56	0.010	19.04	0.71	0.011
<b>Middle vs Mature</b>	3.17	0.28	0.033	0.38	0.046	0.721

**Table S4.** Results of redundancy analysis.

Matrix	Variance explained	F	p
Stand age	40.3%	8.8	0.002
Soil moisture (%)	1.7%	0.4	0.431
TC (g kg <sup>-1</sup> )	12.9%	3.3	0.010
TN (g kg <sup>-1</sup> )	4.1%	1	0.384
AP (mg kg <sup>-1</sup> )	2.3%	0.5	0.202
NO <sub>3</sub> <sup>-</sup> -N (mg kg <sup>-1</sup> )	3.2%	0.8	0.162
DOC (mg kg <sup>-1</sup> )	2.1%	0.5	0.444
pH (H <sub>2</sub> O)	0.4%	0.05	0.318
NH <sub>4</sub> <sup>+</sup> -N (mg kg <sup>-1</sup> )	1.7%	0.4	0.484

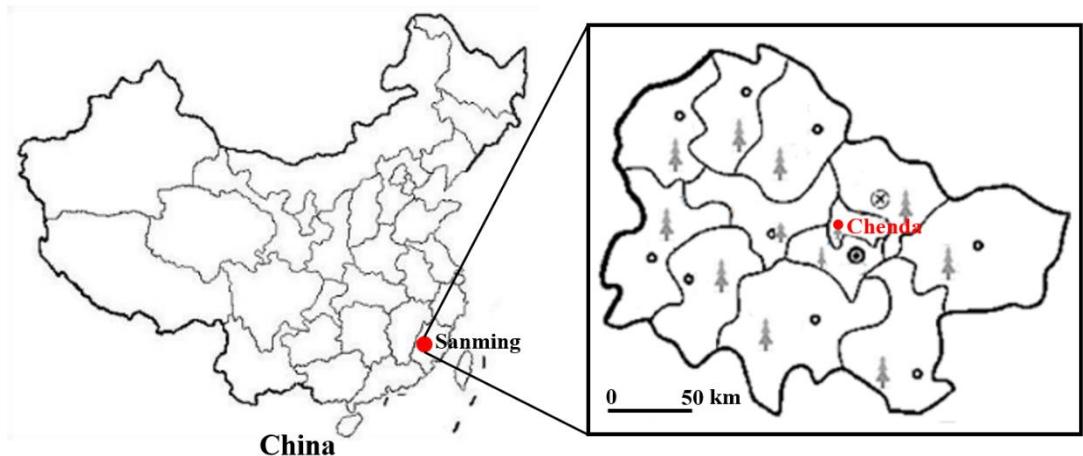
p values were calculated based on 999 permutations; p values in bold are statistically significant ( $p < 0.05$ ).

**Table S5.** Pearson correlations between soil properties and MPD, NRI and phylogenetic diversity.

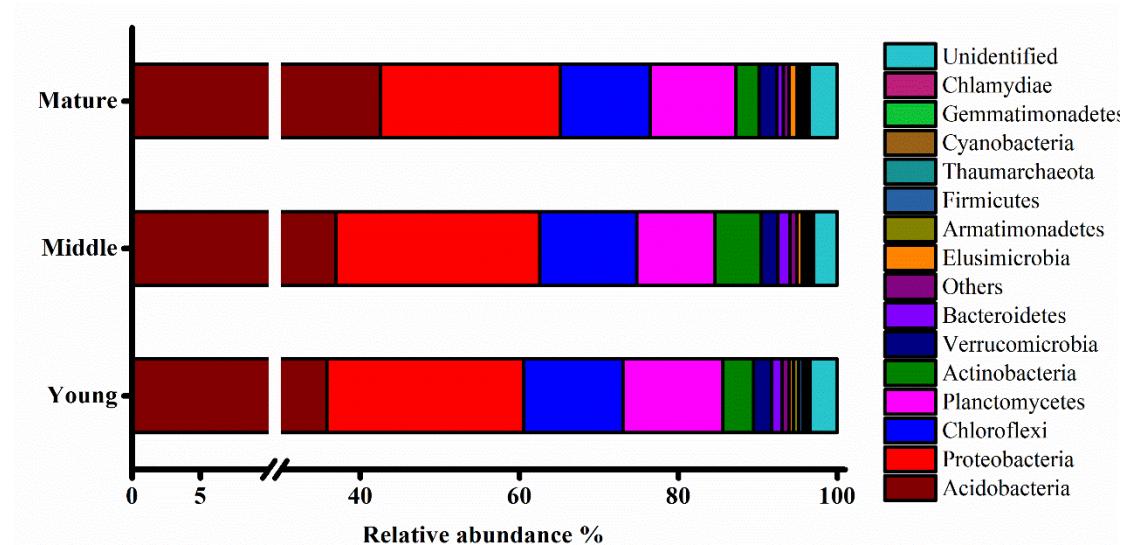
	MPD	NRI	OTU richness	Phylogenetic diversity
pH (H <sub>2</sub> O)	0.121	-0.401	-0.094	-0.487
Soil moisture (%)	-0.093	0.246	-0.334	0.249
TC (g kg <sup>-1</sup> )	0.638 *	0.542*	0.003	0.669 *
TN (g kg <sup>-1</sup> )	0.374	-0.420	0.025	-0.640
DOC (mg kg <sup>-1</sup> )	0.416	-0.315	-0.577 *	-0.142
NH <sub>4</sub> <sup>+</sup> -N (mg kg <sup>-1</sup> )	-0.030	0.329	-0.187	0.242
NO <sub>3</sub> <sup>-</sup> -N (mg kg <sup>-1</sup> )	0.287	-0.097	-0.506	0.027
AP (mg kg <sup>-1</sup> )	0.527 *	-0.303	-0.154	-0.477

TC, total carbon; TN, total nitrogen; DOC, dissolved organic carbon; AP, available phosphorus;

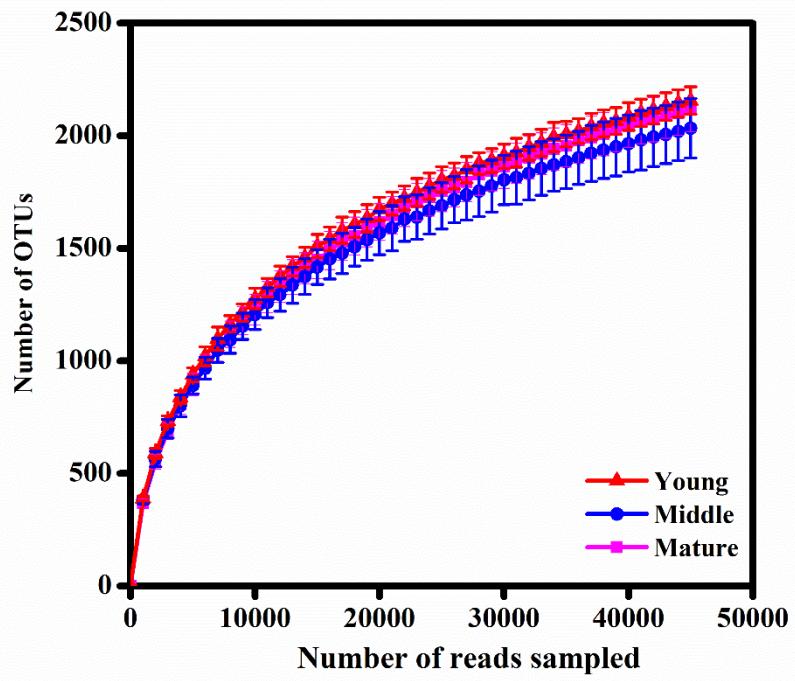
\*,  $p < 0.05$



**Figure S1.** Location of study area in Chenda Town, Fujian Province, China.



**Figure S2.** Taxonomic composition of soil bacterial communities at the phylum level under different age of *C. lanceolata* plantations.



**Figure S3** Rarefaction curves of observed bacterial OTUs among different age of *C. lanceolata* plantations.