Supplementary information

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

Sites	Age (year)	Slope gradient	Slope orientation	Average height (m)	Average basal diameter (cm)	Understory plants
Young	5	32°	E	7.5	10.6	*I. pubescens*
Middle	17	35°	E	14.5	15.6	*D. dichotoma*
Mature	40	30°	E	27.2	23.1	*M. dodecandrum*

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

Table S2 Soil chemical properties in different *C. lanceolata* plantations

Matrix	Young	Middle	Mature
pH	4.47±0.14a	4.38±0.14a	4.37±0.03a
Soil moisture (%)	10.37±1.68c	16.86±0.93a	12.81±1.57b
SOC (g kg^{-1})	10.07±0.56b	8.48±0.93c	12.11±0.89a
TN (g kg^{-1})	1.46±0.12a	1.19±0.09b	1.14±0.09b
AN (g kg^{-1})	11.74±1.13a	12.23±0.40a	10.98±0.48a
AP (g kg^{-1})	2.83±0.37a	2.63±0.22ab	2.22±0.27b
AK (g kg^{-1})	147.2±18.7b	231.2±23.4a	145.4±14.9b
DOC (g kg^{-1})	160.2±12.8b	204.6±22.6a	142.5±19.9b

Values are mean±SD. Different letters in the same column indicate significant difference (P<0.05).

Table S3 Soil AM fungal sequences and OTUs in each soil sample at different age of C. *lanceolata* plantations.

Stand age	Sequence	OTU number
Young 1	35322	31
Young 2	30692	29
Young 3	39034	29
Young 4	25727	24
Young 5	29885	27
Middle 1	34015	42
Middle 2	36759	37
Middle 3	16807	40
Middle 4	3506	22
Middle 5	21312	45
Mature 1	49280	38
Mature 2	24070	37

Mature 3	10218	41
Mature 4	22208	47
Mature 5	27628	44

Table S4 Correlations between the AM fungal community composition and AM fungal groups and GRSP contents

Matrix	NMDS axis1 (bray-Curtis)	NMDS axis1 (unifrac)	Glomeraceae	Gigasporaceae	Acaulosporaceae
EE-GRSP	**0.732****	**0.779****	-0.090	-0.05	0.402
T-GRSP	**0.679****	**0.566****	0.011	-0.226	**0.630***

Significant values were shown in bold. *, $p < 0.05$; **, $p < 0.01$

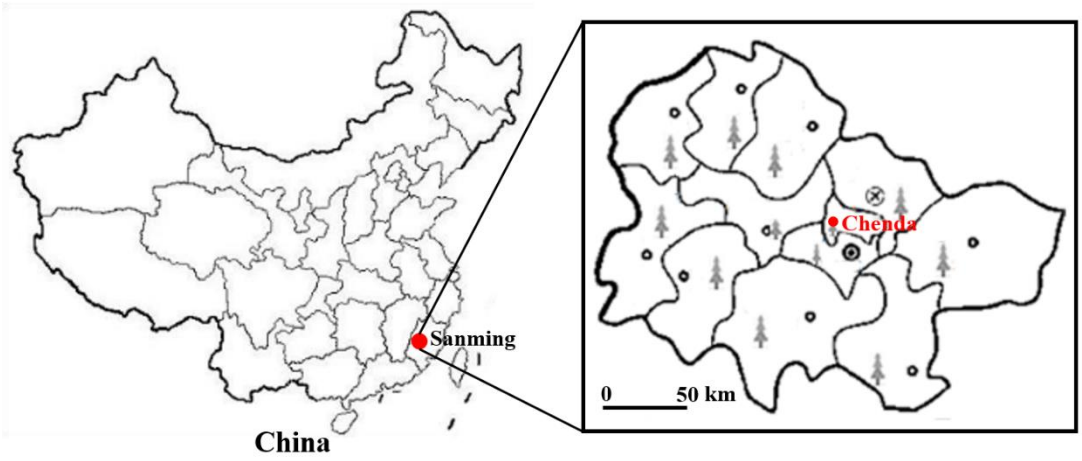

Figure S1 Location of study area in Sanming city, Fujian Province, China

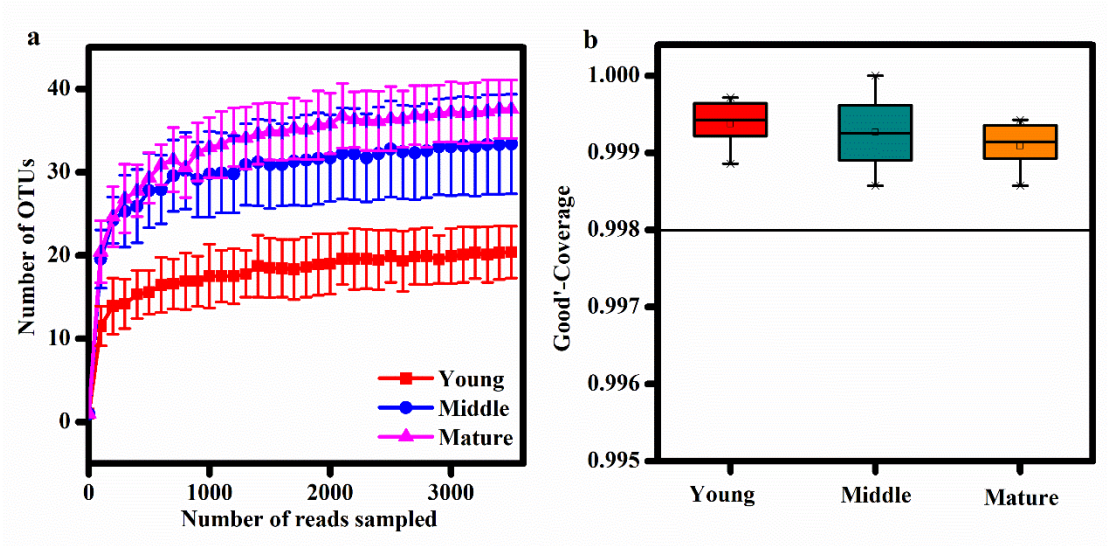

Figure S2 Rarefaction curves of observed bacterial OTUs (a) and good'coverage (b) among different age of *C. lanceolata* plantations.

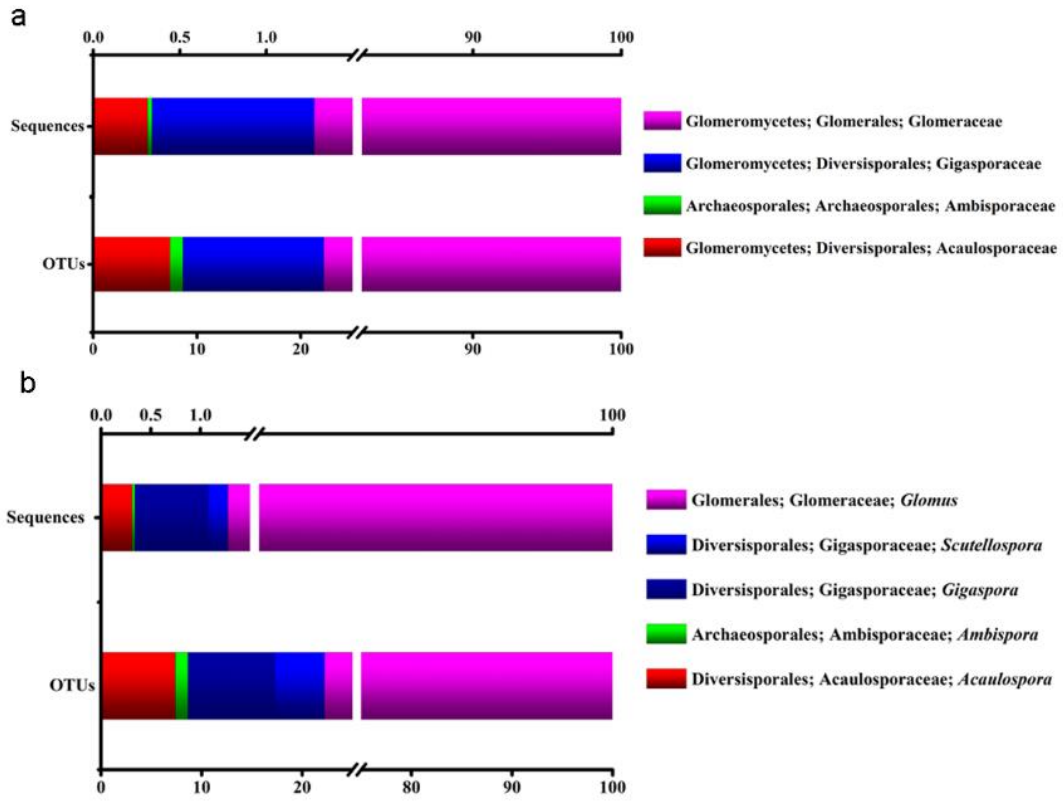

Figure S3 Taxonomic composition of soil bacterial communities at the family (a) and genus (b) levels under different age of *C. lanceolata* plantations.

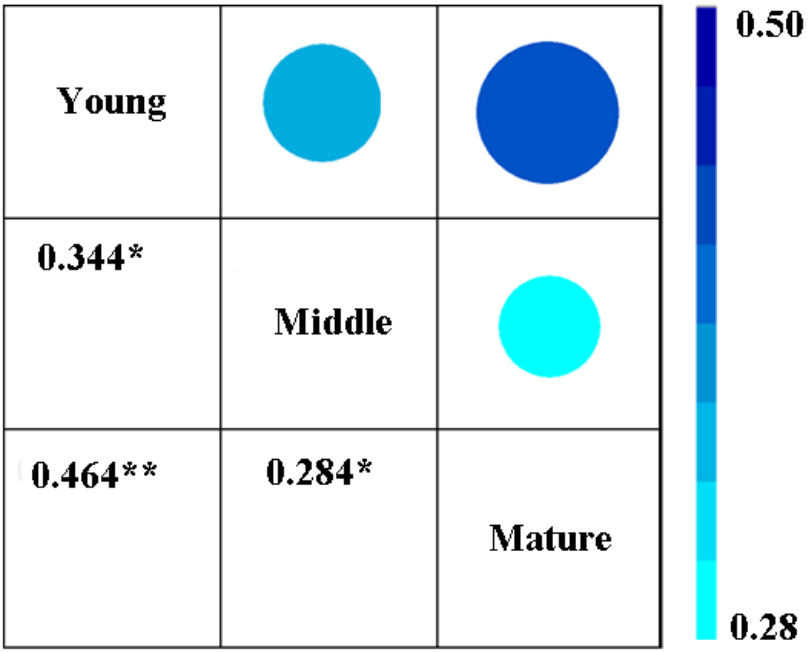

Figure S4 Significant test of bacterial community composition between different ages of *C. lanceolata* plantations based on PerMANOVA analysis.

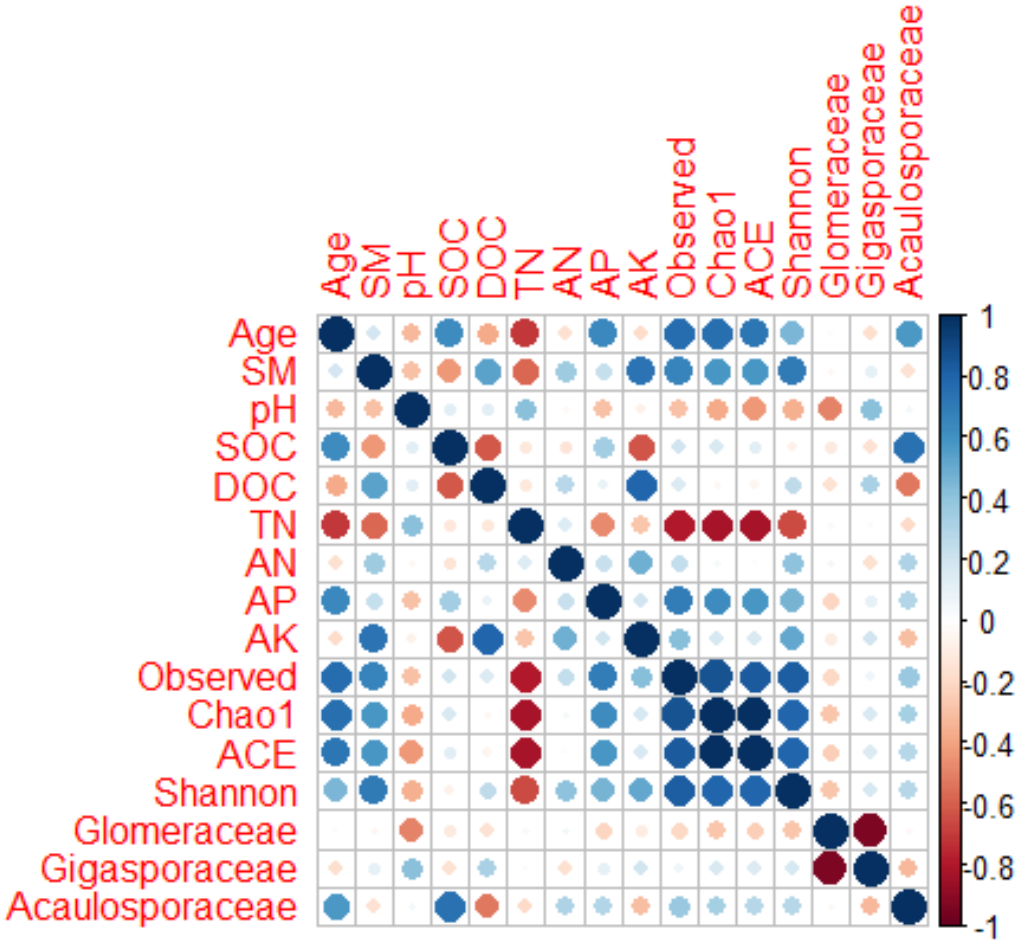

Figure S5 Correlation analysis between environmental factors and AM fungal diversity and relative abundances of AM fungal families in different ages of *C. lanceolata* plantations.