Dai Y, Wang H, Chen M, Wang D, Cao X, Chu B, Xu X (2021). **Response of soil bacterial communities to nitrogen and phosphorus additions in an age-sequence of subtropical forests**
iForest – Biogeosciences and Forestry – doi: 10.3832/ifor3655-013

Supplementary Material

Fig. S1 - The map of plot distribution.

Fig. S2 - Rarefaction curves of bacterial communities (n=9).

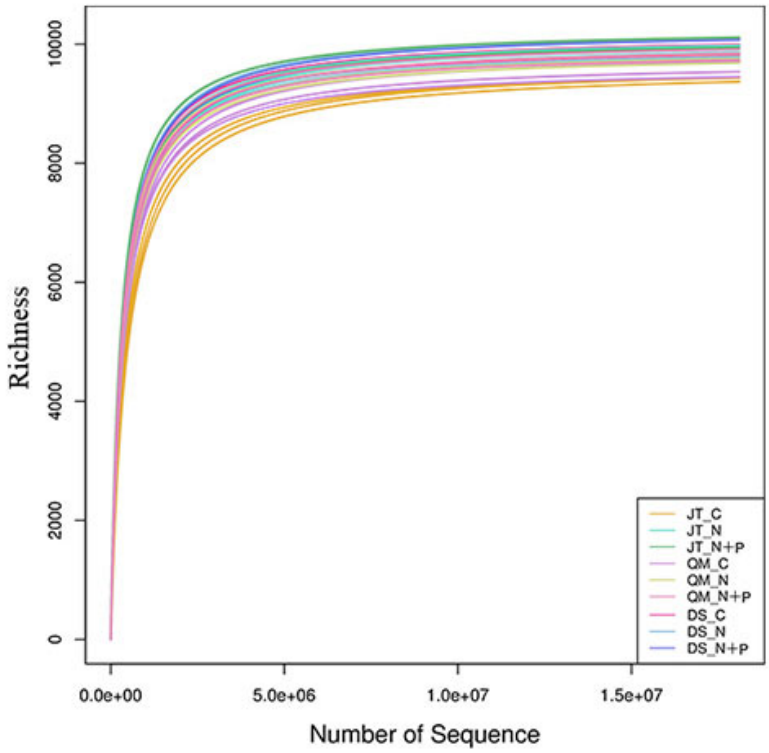


Fig. S3 - Interactive effects of treatment and stand age on the unigenes abundance of soil bacterial dominate phylum. Treatments are control (CK), nitrogen addition (N), and N and phosphorus addition (N+P). Values are bootstrapped means ± 95% confidence intervals (CIs) for individual samples and their sum (n=9). Difference between stand ages, or treatments is significant at α = 0.05 if their CIs do not overlap the other's mean.

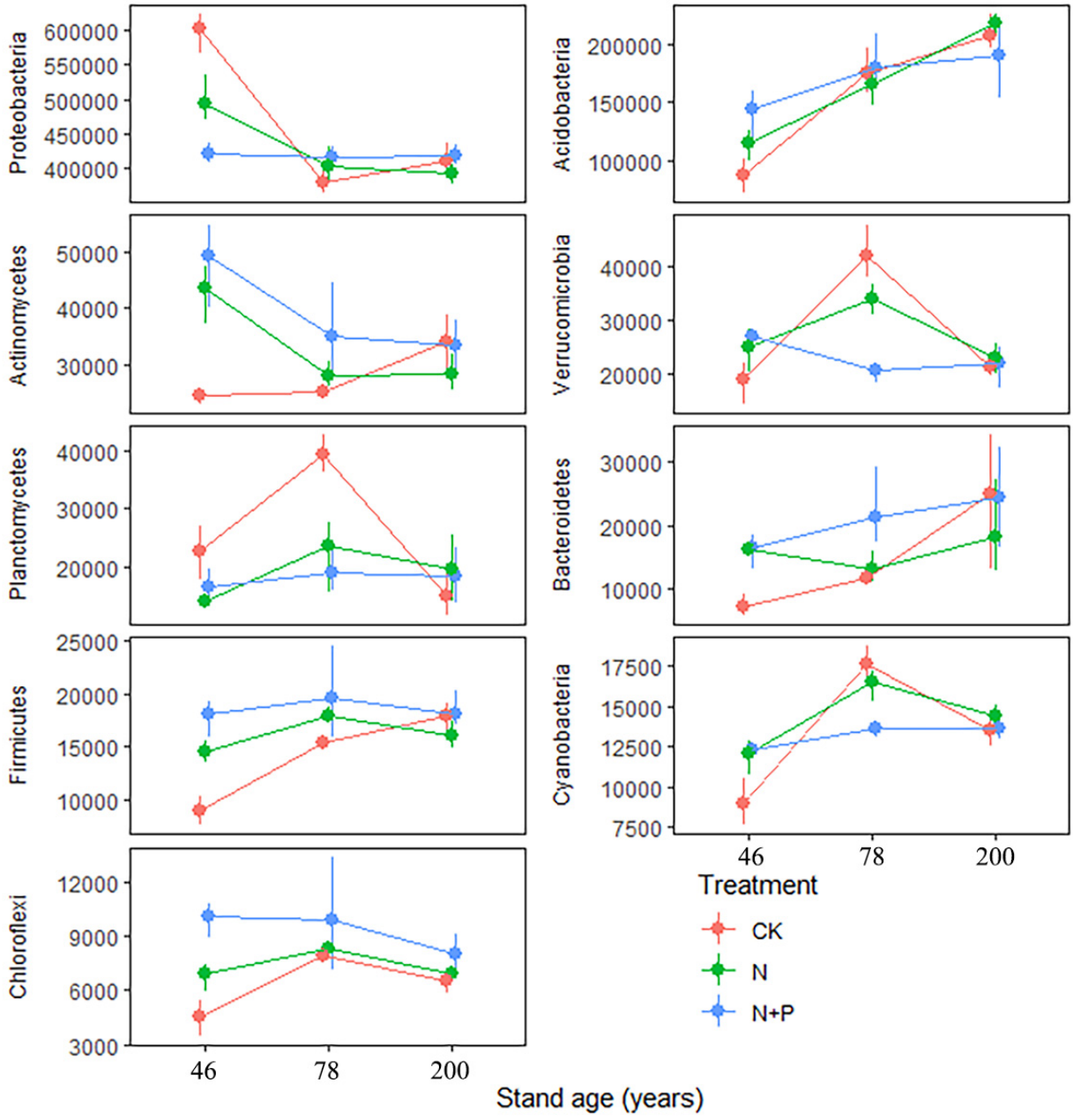


Fig. S4 - Interactive effects of treatment and stand age on the unigenes abundance of soil bacterial dominate genus. Treatments are control (CK), nitrogen addition (N), and N and phosphorus addition (N+P). Values are bootstrapped means ± 95% confidence intervals (CIs) for individual samples and their sum (n=9). Difference between stand ages, or treatments is significant at α = 0.05 if their CIs do not overlap the other's mean.

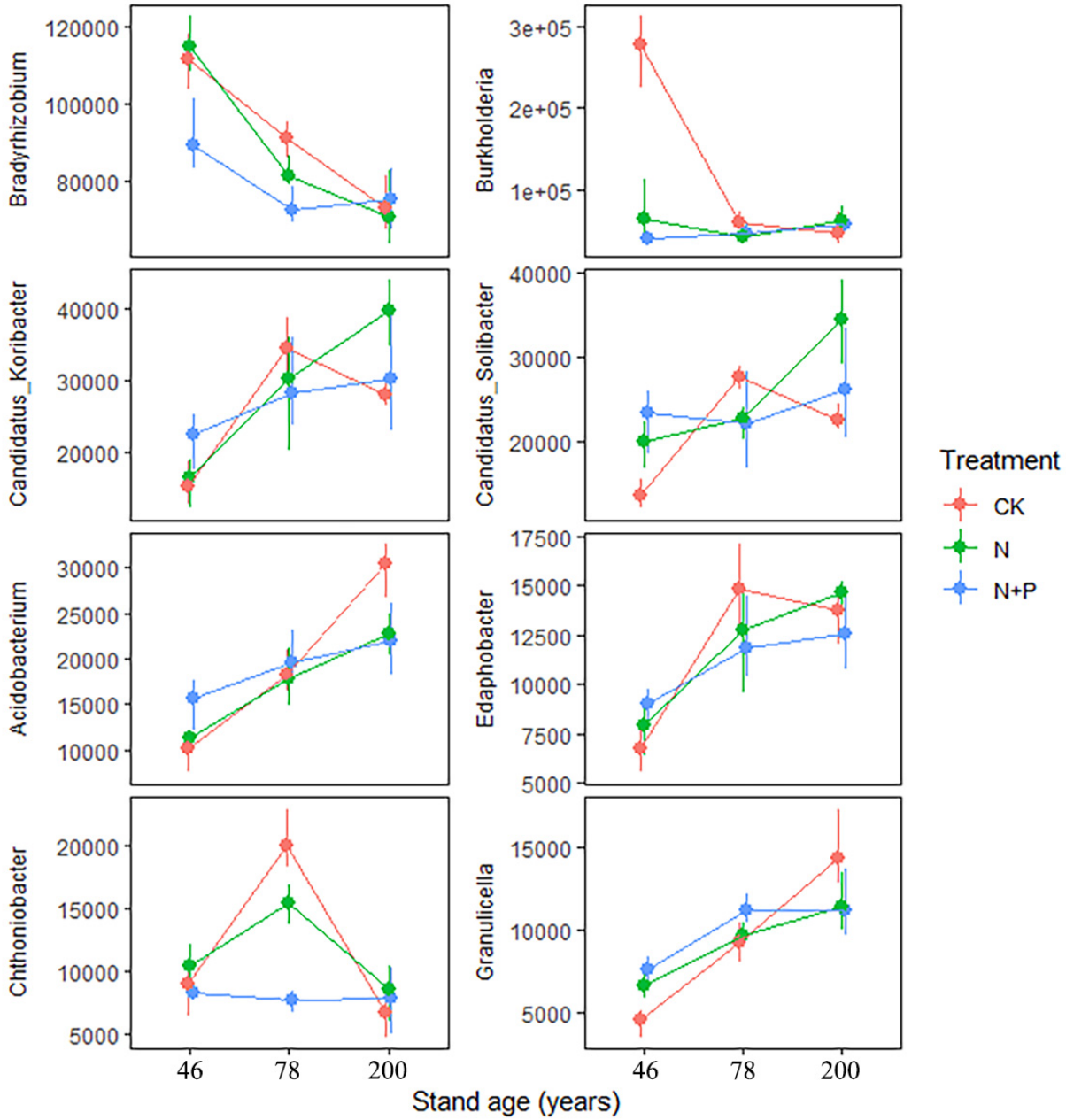


Fig. S5 - Interactive effects of treatment and stand age on the unigenes abundance of soil bacterial dominate species. Treatments are control (CK), nitrogen addition (N), and N and phosphorus addition (N+P). Values are bootstrapped means ± 95% confidence intervals (CIs) for individual samples and their sum (n=9). Difference between stand ages, or treatments is significant at α =0.05 if their CIs do not overlap the other's mean.

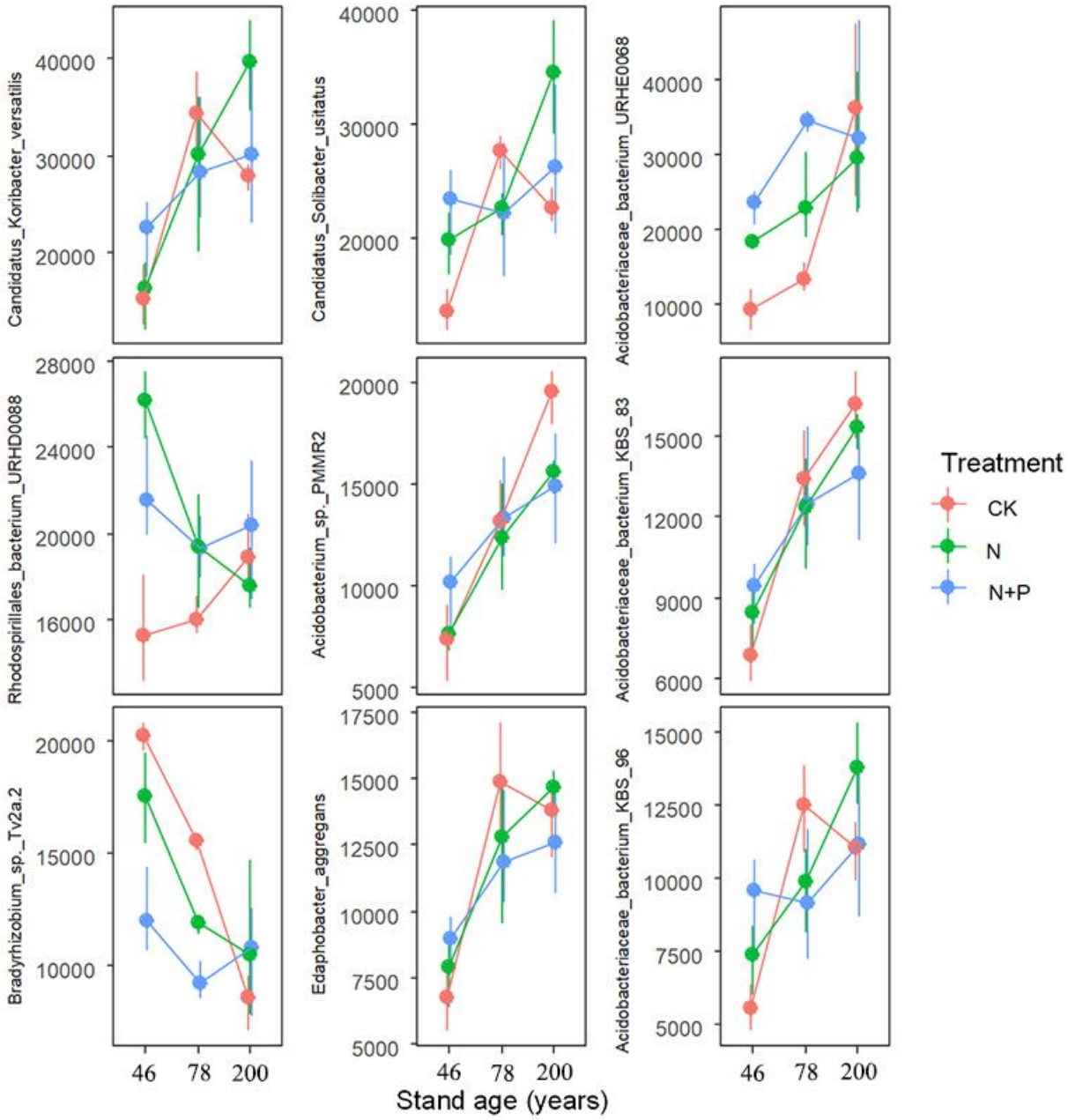
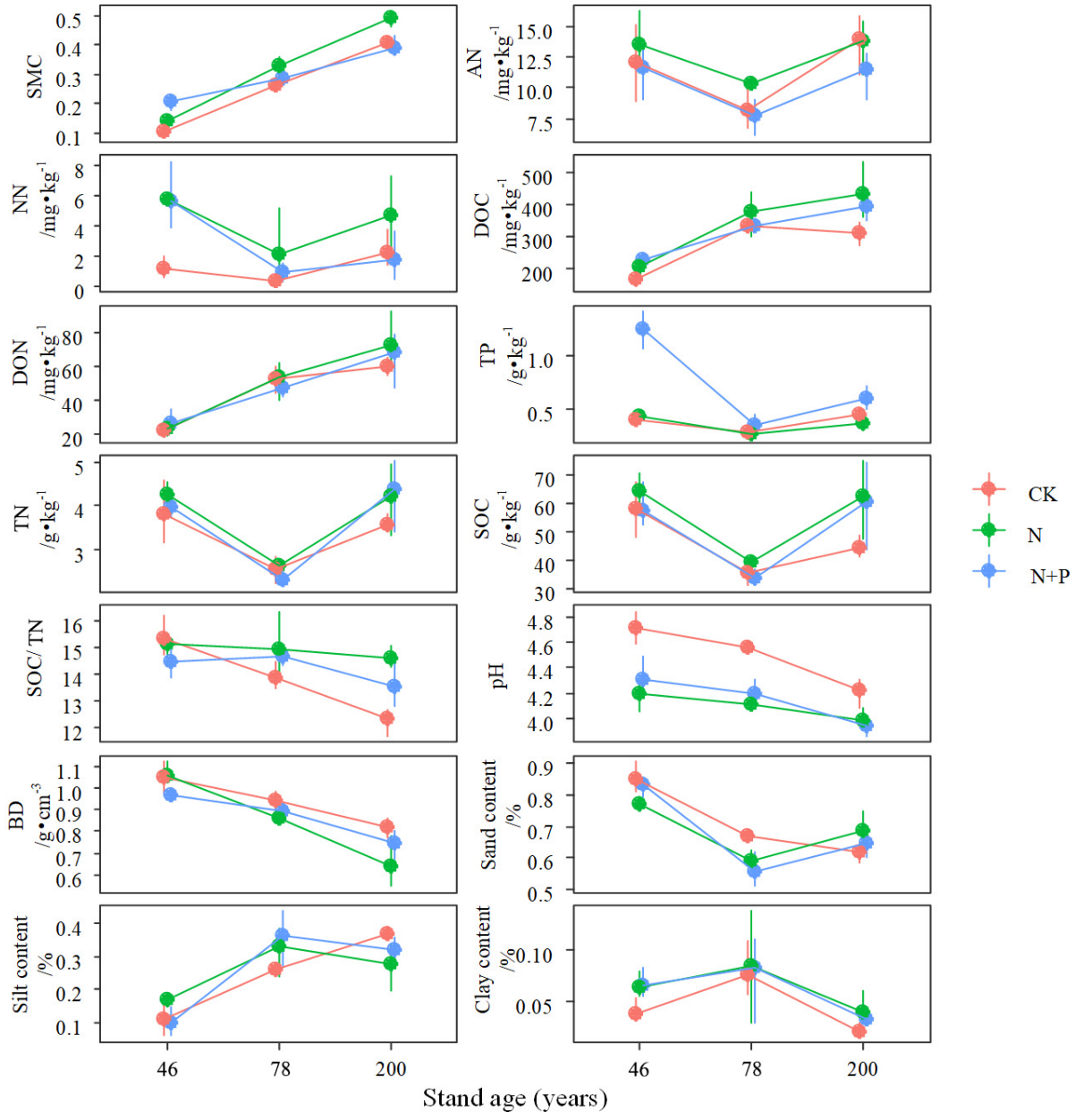


Fig. S6 - Interactive effects of treatment and stand age on soil parameters. Treatments are control (CK), nitrogen addition (N), and N and phosphorus addition (N+P). Values are bootstrapped means ± 95% confidence intervals (CIs) for individual samples and their sum (n=9). Difference between stand ages, or treatments is significant at α =0.05 if their CIs do not overlap the other's mean. SMC, soil moisture content; AN, ammonium; NN, nitrate; C/N, SOC/ TN; SOC, soil organic carbon; TN, soil total nitrogen; TP, total phosphorus; DOC, dissolved organic carbon; DON, dissolved organic nitrogen; Sand, soil sand content; Clay, soil clay content; Silt, soil silt content; BD, bulk density.



Tab. S1 - Soil texture analysed by the fractionation test described by Hunt & Gilkes (1992).

Plot	Stand age	Treatment	Sand /%	Silt /%	Clay /%	Soil texture
1	46	CK	83.15	11.53	5.32	sand loam
2	46	CK	90.80	6.29	2.91	sand
3	46	CK	81.08	15.97	2.95	sand loam
4	46	N	79.49	14.98	5.53	sand loam
5	46	N	76.39	18.06	5.56	sand loam
6	46	N	75.16	16.99	7.84	sand loam
7	46	N+P	84.56	9.56	5.88	sand loam
8	46	N+P	79.49	14.98	5.53	sand loam
9	46	N+P	85.81	5.95	8.24	sand loam
10	80	CK	65.22	23.80	10.98	silty loam
11	80	CK	67.84	26.13	6.03	silty loam
12	80	CK	66.90	27.46	5.63	silty loam
13	80	N	57.28	34.13	8.59	silty loam
14	80	N	62.21	23.96	13.82	silty loam
15	80	N	57.01	40.14	2.85	silty loam
16	80	N+P	62.07	26.90	11.03	silty loam
17	80	N+P	50.91	38.24	10.86	silty loam
18	80	N+P	53.70	43.44	2.86	silty loam
19	200	CK	63.12	35.40	1.49	silty loam
20	200	CK	58.49	38.76	2.75	silty loam
21	200	CK	63.12	35.40	1.49	silty loam
22	200	N	74.63	19.40	5.97	silty loam
23	200	N	67.67	29.32	3.01	silty loam
24	200	N	63.53	33.65	2.82	silty loam
25	200	N+P	67.87	29.41	2.715	silty loam
26	200	N+P	60.36	35.38	4.26	silty loam
27	200	N+P	65.93	31.43	2.64	silty loam

Tab. S2 - Pearson correlation coefficients between soil properties, bacterial abundance and its alpha diversity indices (n=9). (*): $P<0.05$; (**): $P<0.01$.

Age	Index	Moisture content	BD	Sand	Silt	NO_3^--N	DOC	DON	TP	SOC/ TN	pH
46 years old	Abundance	-0.90**	0.55	0.04	0.30	-0.61.	-0.86*	-0.65	-0.80*	0.37	0.78**
	Shannon	0.75*	-0.33	-0.40	0.15	0.87**	0.80*	0.18	0.54	-0.43	-0.88**
	Simpson	0.66	-0.25	-0.45	0.23	0.81*	0.71*	0.12	0.48	-0.27	-0.85**
	Chao1	0.65	-0.12	-0.65	0.43	0.87**	0.64	0.21	0.46	-0.43	-0.67
	Richness	0.74*	-0.25	-0.51	0.25	0.91**	0.76*	0.16	0.53	-0.45	-0.85**
78 years old	Abundance	0.02	-0.09	-0.59	0.58	-0.03	-0.14	-0.20	0.34	-0.03	-0.28
	Shannon	0.49	-0.27	-0.58	0.50	0.07	0.42	0.17	0.55	0.10	-0.71*
	Simpson	0.37	-0.15	-0.22	0.39	-0.12	0.59.	0.57	0.30	-0.26	-0.36
	Chao1	0.30	-0.40	-0.60	0.55	0.12	0.23	0.09	0.58	0.26	-0.65
	Richness	0.42	-0.43	-0.81*	0.79*	0.24	0.25	0.10	0.35	0.22	-0.74*
200 years old	Abundance	-0.22	0.45	-0.26	0.30	-0.06	-0.48	-0.38	-0.26	-0.54	0.48
	Shannon	-0.58	0.07	0.06	0.02	-0.58	-0.27	0.33	0.74	0.07	-0.15
	Simpson	-0.60	0.14	-0.08	0.17	-0.61	-0.45	0.09	0.54	0.02	-0.02
	Chao1	0.16	-0.47	0.56	-0.58	-0.04	0.56	0.65	0.42	0.71	-0.56
	Richness	0.01	-0.44	0.51	-0.55	0.05	0.61	0.66	0.60	0.49	-0.52

Tab. S3 - Pearson correlation analysis between soil bacterial dominate phylum (the relative abundance of Unigenes >0.01) and soil factors (n=9). R^2 are presented, asterisks indicate significant effects (linear mixed effects model; *:P<0.05; **; P<0.01).

Age	Phylum	Moisture content	BD	Sand	Silt	NO_3^--N	DOC	DON	TP	SOC/ TN	pH
46 years old	Proteobacteria	-0.89**	0.51	0.14	0.11	-0.80*	-0.86**	-0.27	-0.75*	0.60	0.76*
	Acidobacteria	0.76*	-0.43	-0.10	-0.03	0.73*	0.70*	-0.03	0.66	-0.64	-0.54
	Actinomycetes	0.75*	-0.28	-0.36	0.16	0.86**	0.75*	0.06	0.56	-0.62	-0.70*
	Verrucomicrobia	0.78*	-0.51	-0.05	-0.22	0.70*	0.91**	0.42	0.55	-0.67	-0.77*
	Planctomycetes	-0.34	-0.30	0.86**	-0.73*	-0.77*	-0.33	0.07	-0.15	0.07	0.58
	Bacteroidetes	0.64	-0.15	-0.58	0.41	0.91**	0.65	-0.04	0.44	-0.40	-0.75*
	Firmicutes	0.86**	-0.48	-0.20	-0.03	0.84**	0.80*	0.13	0.72*	-0.66	-0.72*
	Cyanobacteria	0.72*	-0.41	-0.20	-0.04	0.80*	0.84**	0.18	0.48	-0.58	-0.86**
	Chloroflexi	0.90**	-0.59.	-0.02	-0.20	0.74*	0.81*	0.21	0.82*	-0.73	-0.60
	Gemmatimonadetes	0.69*	-0.53	-0.11	0.01	0.76*	0.63	-0.17	0.57	-0.77*	-0.50
78 years old	Proteobacteria	0.48	-0.33	-0.38	0.45	0.14	0.31	0.27	0.20	0.05	-0.55
	Acidobacteria	-0.35	0.14	-0.15	0.12	-0.01	-0.41	-0.42	-0.29	-0.04	0.31
	Actinomycetes	0.09	0.07	-0.69*	0.41	-0.01	-0.14	-0.37**	0.89	0.17	-0.55
	Verrucomicrobia	-0.23	0.18	0.71*	-0.53	-0.09	0.06	0.26	-0.50	-0.23	0.63
	Planctomycetes	-0.51	0.41	0.76*	-0.60.	-0.14	-0.32	0.02	-0.41	-0.27	0.86**
	Bacteroidetes	0.00	-0.19	-0.30	0.21	-0.21	0.10	-0.03	0.43	0.10	-0.38
	Firmicutes	0.23	-0.09	-0.71*	0.40	0.09	-0.01	-0.34	0.78*	0.31	-0.67
	Cyanobacteria	-0.15	0.13	0.65	-0.57	0.05	-0.04	0.08	-0.50	-0.05	0.52
	Chloroflexi	0.01	0.14	-0.53	0.22	-0.03	-0.19	-0.40	0.91**	0.20	-0.42
	Gemmatimonadetes	-0.20	0.34	0.48	-0.28	0.17	-0.33	0.06	-0.51	-0.25	0.65
200 years old	Proteobacteria	-0.54	0.43	-0.32	0.43	-0.79*	-0.64	-0.19	0.28	-0.12	0.15
	Acidobacteria	0.52	-0.02	0.08	-0.14	0.66	0.28	-0.16	-0.64	-0.25	0.26
	Actinomycetes	-0.49	0.21	-0.09	0.11	-0.20	-0.28	0.24	0.64	-0.26	0.19
	Verrucomicrobia	-0.06	-0.05	-0.34	0.30	-0.15	-0.19	-0.48	-0.24	0.23	-0.09
	Planctomycetes	0.02	-0.25	-0.06	0.04	0.10	-0.13	-0.44	-0.43	0.31	-0.26
	Bacteroidetes	-0.32	-0.08	0.12	-0.10	-0.18	0.14	0.50	0.77*	-0.05	-0.20
	Firmicutes	-0.52	-0.07	0.13	-0.05	-0.42	-0.22	0.30	0.60	0.07	-0.14
	Cyanobacteria	0.27	-0.20	-0.02	0.03	-0.08	-0.03	-0.29	-0.51	0.40	-0.18
	Chloroflexi	-0.40	-0.33	0.22	-0.22	-0.30	0.12	0.26	0.61	0.50	-0.64
	Gemmatimonadetes	0.40	-0.26	0.04	-0.09	0.34	0.14	-0.40	-0.72	0.30	-0.16