Teng Z, Cui J, Wang J, Fu X, Xu X (2018).
Effects of nitrogen and phosphorus additions on soil bacterial community composition in secondary *Castanopsis sclerophylla* forest in east China
iForest – Biogeosciences and Forestry – doi: 10.3832/ifor2673-011

Supplementary Material

Tab. S1 - Effects of N and P additions on soil physiochemical properties in the secondary subtropical *Castanopsis sclerophylla* forest. Data are indicated as means ± standard error (n=3). Different letters in the same row indicate significant difference at 5% level of probability (LSD).

Treatments	**Units**	**CK**	**N**	**N+P**	**P**
SWC	%	14.51 ± 0.63 a	16.49 ± 0.30 a	29.02 ± 0.74 a	25.30 ± 1.73 b
pH	H_2O	4.8 ± 0.05 a	4.3 ± 0.06 c	4.3 ± 0.05 c	4.5 ± 0.07 b
EC	$\mu S \cdot cm^{-1}$	31.63 ± 0.61 c	57.79 ± 4.63 b	86.89 ± 3.58 a	77.69 ± 2.86 a
NH_4^+-N	$mg \cdot kg^{-1}$	3.39 ± 0.08 b	5.06 ± 0.08a	5.44 ± 0.32 a	5.08 ± 0.21 a
NO_3^--N	$mg \cdot kg^{-1}$	1.04 ± 0.05 c	5.54 ± 0.36b	10.35 ± 0.72 a	10.76 ± 0.81 a
DOC	$mg \cdot kg^{-1}$	183.85 ± 2.35 b	207.97 ± 3.75 b	271.53 ± 2.21 a	211.43 ± 22.57 b
DON	$mg \cdot kg^{-1}$	21.23 ± 0.50 bc	26.11 ± 1.46 a	20.80 ± 0.67 c	23.66 ± 0.90 ab
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Tab. S2 - Outcome of the GLMMs model on the effect of N, P additions, interaction effect and interactive treatment: block effects on soil bacterial diversity indexes. Chao1, species richness estimator; df, degree of freedom; significant difference at 5% level of probability.

Variable	Model	df	Sum of Squares	F	*P*
Observed species	N	8	94251	0.583	0.467
	P	8	323	0.002	0.966
	N:P	8	84001	0.519	0.492
	treatment:block	4	729205	1.756	0.294
Shannon–Wiener index	N	8	0.027	0.265	0.620
	P	8	0.000	0.000	0.996
	N:P	8	0.013	0.125	0.733
	treatment:block	4	0.337	0.962	0.492
Simpson index	N	8	6.870e-09	0.006	0.940
	P	8	4.658e-07	0.411	0.539
	N:P	8	3.200e-09	0.003	0.959
	treatment:block	4	3.132e-06	0.704	0.598
Chao1 index	N	8	517264	0.786	0.401
	P	8	70826	0.108	0.751
	N:P	8	524246	0.796	0.398
	treatment:block	4	3525486	2.956	0.199

Tab. S3 - Outcome of the GLMMs model on the effect of N and P additions on the phylum-level OTUs of soil bacteria. Bold values indicate $P < 0.05$.

Variables	N		P		N:P	
	F	***P***	**F**	***P***	**F**	***P***
Proteobacteria	2.723	0.150	1.592	0.254	0.361	0.570
Acidobacteria	10.201	**0.013**	1.433	0.266	0.729	0.418
Actinobacteria	0.024	0.883	0.155	0.707	1.848	0.223
Chloroflexi	0.031	0.865	0.200	0.670	0.001	0.980
AD3	2.008	0.206	0.457	0.524	0.153	0.709
Planctomycetes	1.430	0.278	0.741	0.422	0.383	0.559
Bacteroidetes	11.242	**0.015**	2.295	0.181	2.492	0.166
WPS-2	2.229	0.186	0.033	0.862	0.314	0.596
Verrucomicrobia	2.691	0.140	1.592	0.243	3.956	0.082
Firmicutes	1.682	0.242	3.664	0.104	1.444	0.275
Gemmatimonadetes	5.099	0.065	0.184	0.683	0.148	0.714
Elusimicrobia	10.786	**0.011**	3.597	0.094	1.599	0.242
Nitrospirae	46.211	**< 0.001**	30.380	**0.001**	14.688	**0.009**
Cyanobacteria	0.473	0.518	3.464	0.112	3.290	0.120
Chloroplast	4.994	0.056	0.620	0454	0.957	0.357
TM6	9.346	**0.016**	1.657	0.234	6.265	**0.037**
candidatus Saccharibacteria	4.228	0.086	4.228	0.086	2.278	0.182
FCPU426	2.851	0.142	0.017	0.901	0.001	0.977

Tab. S4 - The most abundant OTUs at phylum and genus level with significant differences in treatments. Number of total OUTs > 10. Data are indicated as means ± standard error (n=3). Different letters in the same row indicate significant difference at 5% level of probability (LSD).

Phylum	Genus	CK	N	N+P	P
Proteobacteria	*Burkholderia*	499 ± 247 a	92 ± 19 b	67 ± 11 b	153 ± 94 b
	Rhizobium	69 ± 42 a	4 ± 3 b	4 ± 1 b	28 ± 22 ab
	Nitrospirillum	39 ± 24 a	25 ± 12 ab	10 ± 4 b	11 ± 9 ab
	Nitrobacter	31 ± 13 a	22 ± 2 ab	12 ±3 b	28 ± 4 a
	Kofleria	28 ± 4 a	8 ± 3 b	15 ± 5 b	16 ± 7 b
	Rhodopila	25 ± 13 a	16 ± 5 ab	8 ± 4b	10 ± 6 ab
	Labrys	24 ± 11 a	3 ± 2 b	6 ± 5 b	6 ± 5 b
	Bdellovibrio	23 ± 9 a	8 ± 2 b	9 ± 1 b	11 ± 8 b
	Myxococcus	17 ± 11 a	1 ± 1 b	4 ± 3 b	4 ± 6 b
	Methylibium	16 ± 2 a	2 ± 2 b	1 ± 1 b	1 ± 1 b
	Hyphomicrobium	14 ± 12 a	3 ± 2 ab		3 ± 2 ab
	Rudaea	11 ± 4 a	1 ± 1 b	1 ± 1 b	2 ± 2 b
	Variovorax	10 ± 7 a			2 ± 1 b
Acidobacteria	*Gp2*	3006 ± 1153 a	830 ± 499 b	660 ± 479 b	1996 ± 814 ab
	Gp3	1506 ± 490 a	336 ± 122 b	335 ± 25 b	717 ± 512 b
	Gp6	255 ± 44 a	51 ± 11 c	31 ± 3 c	167 ± 47 b
	Granulicella	176 ± 17 a	101 ± 91 ab	53 ± 41 b	93 ± 20 ab
	Gp5	138 ± 48 a	43 ± 12 b	55 ± 39 b	113 ± 43 ab
	Edaphobacter	97 ± 1 ab	39 ± 11 b	70 ± 41 ab	159 ± 80 a
	Candidatus Solibacter	55 ± 10 a	15 ± 6 b	15 ± 3 b	26 ± 21 b
	Gp7	37 ± 24 a	5 ± 1 b	2 ± 1 b	9 ± 2 b
	Gp10	24 ± 15 a	3 ± 4 b		9 ± 5 ab
	Gp17	14 ± 8 a			
	Gp13	11 ± 5 a	4 ± 2 b	3 ± 2 b	8 ± 2 ab
Actinobacteria	*Conexibacter*	163 ± 55 b	190 ± 76 b	361 ± 29 a	200 ± 86 b
	Kitasatospora	66 ± 23 ab	37 ± 17 b	85 ± 24 a	74 ± 24 ab
	Actinocorallia	17 ± 2 b	25 ± 17 ab	43 ± 11 a	27 ± 10 ab
	Actinospica	10 ± 1 b	16 ± 5 b	30 ± 6 a	12 ± 4 b
Bacteroidetes	*Ohtaekwangia*	31 ± 20 a		2 ± 3 b	18 ± 9 ab
	Flavitalea	11 ± 6 a		1 ± 1 b	5 ± 3 ab
candidatus Saccharibacteria	*Saccharibacteria_genera_incertae_sedis*	15 ± 4 b	41 ± 17 b	95 ± 19 a	41 ± 33 b
Firmicutes	*Cohnella*	21 ± 1 a	12 ± 4 b	11 ± 2 b	4 ± 2 c
	Paenibacillus	19 ± 6 a	7 ± 4 b	11 ± 5 ab	9 ±3 b
Nitrospirae	*Nitrospira*	17 ± 6 a			4 ± 4 b
Planctomycetes	*Gemmata*	14 ± 4 ab	15 ± 10 a	3 ± 4 b	5 ± 3 ab

Tab. S5 - Monte Carlo permutation tests of the impact of soil chemical properties on the bacterial populations based on the OTUs. Bold values indicate $P < 0.05$.

Variables	$\mathbf{r^2}$	***P***
pH	0.622	**0.015**
NH_4^+-N	0.485	0.052
NO_3^--N	0.350	0.149
DOC	0.468	0.057
DON	0.069	0.777
TP	0.503	0.058
TN	0.117	0.563
SOC	0.129	0.533
AP	0.106	0.588
K	0.037	0.876
Mg	0.313	0.210