Supplementary materials

Short-Term Effects of Different Forest Management Methods on Soil Microbial Communities of a Natural *Quercus aliena* var. *acuteserrata* Forest in Xiaolongshan, China

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Supplementary methods

Close-to-natural forest management (CNFM)

CNFM is a forest management measure that is designed according to the target tree management method to cultivate large diameter wood. The management process was as follows:

(1) All the trees were classified according a method on Kraft tree classification, and the objective trees, target trees, disturbance trees, special target tree and ordinary trees are determined, respectively. The method is as follows:

①Objective trees: *Quercus aliena* var. *acuteserrata*, *Quercus wutaishansea* Mary, and *Pinus tabuliformis* are determined to be the objective tree.

②Target trees: The healthy and strong tree with a straight trunk and vitality that was selected from grade I and II trees were determined to be target tree.

③Disturbance trees: The trees that interfere with target tree growth were determined to be disturbance trees.

④Special target trees: Precious tree species, endangered tree species, rare tree species were determined to be the special target trees.

⑤Ordinary tree: Other trees that besides the objective trees, target trees, disturbance trees, and special target trees were determined to be the ordinary tree.

(2) The number of target trees is 250 plants per hectare, and the distance between target trees is 7 m, while the target trees are uniformly distributed according to the shape of the triangle.

(3) The disturbance trees that interfere with target tree growth were removed. When a special target tree interacts with a target tree, the special target trees in the stand were preferentially retained.

The actual number of harvested plants in A1–A4 was 8, 9, 16 and 10, and the respective harvesting intensities were 6.3, 15.9, 16.6, and 20.4%, respectively.

Structure-based forest management (SBFM)

Structured forest management is a forest management measure for optimizing forest structure in order to cultivate healthy and stable forests. The management process was as follows:

(1) Precious, rare, and endangered tree species in the stand were retained, and all Pinus armandii and Pinus tabulaeformis individuals (including seedlings with DBH ≥ 5 cm), large-diameter trees, and precious and endangered species were regulated by competition.

(2) Trees with poor dryness status, pests and disease, and trunk (root neck) decay, as well as bushy trees, were preferentially felled to maintain the health of the stand. Competing trees that were unfavourable for the growth of trees that were to be retained were removed. This ensured that the trees were prevented from being covered or squeezed, and prevented the disintegration of the stand. Trees of the same species that were distributed to the side of the preserved trees were preferentially removed to reduce the risk of diseases spreading and increase degree of mixing. Trees that exhibited the target diameter of DBH ≧ 45 cm were harvested (continuous harvesting is not allowed in the double tree height range). This increased the wood production of the stand, promoted its stand, and created the conditions necessary for natural regeneration. Harvesting intensity was not permitted to exceed 20%.

The actual number of harvested plants in B1–B4 was 23, 32, 28 and 24, and the respective harvesting intensities were 16.6, 17.6, 18.1, and 12.1%, respectively.

Secondary forest comprehensive silvicuture (SFCS)

Secondary forest comprehensive silvicuture is a forest management measures that is selectively harvested based on wood utilization. The management process was as follows:

(1) The unhealthy trees in the stand were removed. (2) High density trees with DBH<12 cm were removed to reduce density, but this thinning does not cause canopy gaps in the stand.

(2) The trees that were twin trees or sprouting of canopy trees with DBH in [12 cm, 20 cm) were harvested.

(3)The trees with DBH in [20 cm, 26 cm] were retained.

(4)The trees with DBH>26 cm were harvested, but this thinning does not cause a canopy gaps in the stand.

The actual number of harvested plants in D1–D4 was 29, 15, 22 and 24, and the respective harvesting intensities were 18.4, 11.3, 18.8, and 16.0%, respectively.

Table 1. Differences among the three forest management methods.

Forest management methods	Management object	Treatment method	Management purpose	Management method characteristics
CNFM	Target trees（I, II grade trees）	Harvest or cut the disturbance trees affecting target trees	Develop forests with high stability and long-term productivity	Trees are classified into target trees and disturbance trees by determining the density of the target trees and individual harvest
SBFM	Rare tree species, climax tree species, medium and large diameter trees of main associated tree species	Stand pattern optimization (including the horizontal distribution pattern of tree, tree species isolation degree, crowding density and competitiveness)	Develop health, stable and sustainable high-quality forests	Adjust stand pattern, individual harvest with mild interference
SFCC	Stand population (including all trees in the stand)	Adjusting stand density	Sustained yield timber management	Adjust stand density (regardless of tree species) and selective cutting with large interference

Supplementary data

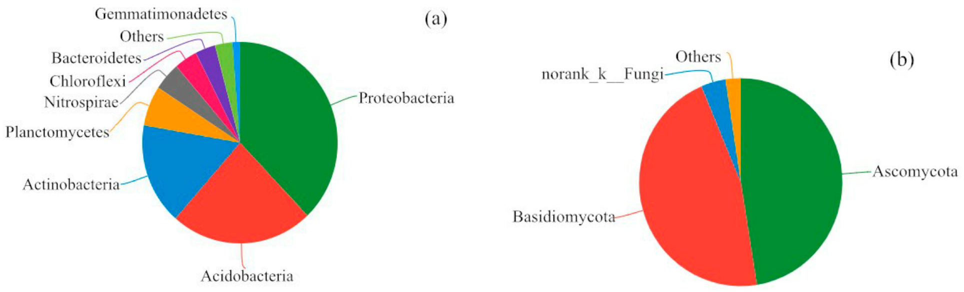

Figure. S1. Core microbial community composition of bacterial (**a**) and fungal (**b**) in four treatments.

Table S2 Composition of bacterial community at the phylum level

Dominant phyla	A	B	C	D
Proteobacteria	38.07±0.91ab	36.86±0.61b	38.66±1.33a	37.83±2.61ab
Acidobacteria	21.35±1.53a	26.24±1.17b	21.06±2.04ac	26.20±3.59ab
Actinobacteria	17.80±3.44a	13.81±1.46a	17.89±3.30a	15.26±2.78a
Planctomycetes	6.74±1.27a	5.90±0.63a	6.32±0.73a	6.76±0.54a
Nitrospirae	3.76±0.43a	5.62±1.05b	4.92±1.51ab	3.71±1.15ab
Chloroflexi	4.31±0.38a	3.69±0.55ab	3.69±0.64ab	3.55±0.34b
Bacteroidetes	3.38±0.14a	2.76±0.29b	2.64±0.52b	2.69±0.69ab
Gemmatimonadetes	1.21±0.08a	1.41±0.20a	1.19±0.13a	1.11±0.29a

The values in the table are mean value (± SD, n=4). Significant differences among different management are indicated by different letters at the 0.05 level. A indicates close-to-nature forest management(CNFM), B indicates structure-based forest management (SBFM), C indicates unmanaged (CK), D indicates secondary forest comprehensive silviculture (SFCS)

Table S3 Composition of fungi community at the phylum level

Dominant phyla	A	B	C	D
Ascomycota	68.46±9.29a	37.08±11.03b	45.95±15.6b	36.89±16.82b
Basidiomycota	23.60±9.23a	56.22±11.73b	47.79±17.01b	58.94±17.47b
norank_k__Fungi	4.34±0.75a	4.14±0.79a	4.04±1.47a	2.78±1.03a
unclassified_k__Fungi	1.08±0.53a	1.05±0.19a	1.12±0.4a	0.68±0.29a
Ciliophora	1.14±0.65a	0.62±0.30a	0.42±0.22ab	0.21±0.05bc

The values in the table are mean value (± SD, n=4). Significant differences among different management are indicated by different letters at the 0.05 level. A indicates close-to-nature forest management(CNFM), B indicates structure-based forest management (SBFM), C indicates unmanaged (CK), D indicates secondary forest comprehensive silviculture (SFCS)

Table S4 Correlation between soil nutrients and relative abundance of the dominant phyla in the bacterial community

Dominant phyla	SOM	TN	TP	TK	AN	AP	AK	pH
Proteobacteria	0.203	0.259	-0.013	0.088	0.294	-0.200	-0.134	-0.228
Acidobacteria	0.368	0.371	-0.111	0.009	0.335	-0.144	0.259	-0.262
Actinobacteria	0.285	0.306	0.493	-0.097	0.282	-0.147	-0.199	0.115
Planctomycetes	-0.262	-0.185	-0.433	0.459	-0.129	-0.015	0.078	0.022
Nitrospirae	0.224	0.222	0.395	-0.303	0.253	-0.424	-0.228	-0.231
Chloroflexi	0.118	0.044	-0.031	0.091	0.068	-0.379	-0.102	0.231
Bacteroidetes	0.15	0.15	-0.084	0.121	0.244	-0.341	0.081	0.152
Gemmatimonadetes	-0.088	-0.05	0.068	-0.112	-0.029	-0.421	-0.349	-0.082

**(*P*<0.01) and *(*P*<0.05) indicate significant differences among values of soil sample parameters based on a one-way ANOVA followed by an LSD test. SOM indicates soil organic matter; TN indicates total nitrogen; TP indicates total phosphorus; TK indicates total potassium ; AN indicates available nitrogen; AP indicates available phosphorus; AK indicates Available potassium.

Table S5 Correlation between soil nutrients and relative abundance of the dominant order in the bacterial community

Dominant order	SOM	TN	TP	TK	AN	AP	AK	pH
Rhizobiales	0.276	0.344	0.109	-0.188	0.397	-0.132	-0.237	-0.306
norank_c__Acidobacteria	**0.712****	**0.706****	0.127	-0.174	**0.659****	-0.1	0.368	-0.128
Planctomycetales	-0.318	-0.25	-0.514	0.482	-0.209	0.038	0.096	0.015
Rhodospirillales	-0.256	-0.156	-0.334	**0.532***	-0.135	0.256	0.216	-0.205
norank_c__Nitrospira	0.224	0.222	0.395	-0.303	0.253	-0.424	-0.228	-0.231
Gaiellales	0.479	0.482	**0.677****	-0.444	0.432	-0.185	-0.255	-0.315
Solirubrobacterales	0.281	0.33	0.3	-0.019	0.305	0.18	-0.04	0.083
Xanthomonadales	0.288	0.347	0.139	0.259	0.365	-0.2	0.225	0.075
Desulfurellales	0.041	0.003	0.132	-0.035	0.009	-0.405	-0.219	-0.279

**(P<0.01) and *(P<0.05) indicate significant differences among values of soil sample parameters based on a one-way ANOVA followed by an LSD test. SOM indicates soil organic matter; TN indicates total nitrogen; TP indicates total phosphorus; TK indicates total potassium ; AN indicates available nitrogen; AP indicates available phosphorus; AK indicates Available potassium.

Table S6 Correlation between soil nutrients and relative abundance of the dominant phyla in the fungal community

Dominant phyla	SOM	TN	TP	TK	AN	AP	AK	pH
Ascomycota	-0.203	-0.285	-0.058	-0.15	-0.256	-0.338	-0.434	0.324
Basidiomycota	0.247	0.329	0.12	-0.079	0.294	0.259	0.171	**-0.521***
norank_k__Fungi	0.262	0.159	0.355	**-0.518***	0.138	-0.347	-0.469	-0.099
unclassified_k__Fungi	0.509*	0.441	**0.523***	**-0.521***	0.418	-0.244	-0.288	-0.137
Ciliophora	0.209	0.159	0.363	**-0.515***	0.200	-0.529*	-0.33	0.365

**(P<0.01) and *(P<0.05) indicate significant differences among values of soil sample parameters based on a one-way ANOVA followed by an LSD test. SOM indicates soil organic matter; TN indicates total nitrogen; TP indicates total phosphorus; TK indicates total potassium ; AN indicates available nitrogen; AP indicates available phosphorus; AK indicates Available potassium.

Table S7 Correlation between soil nutrients and relative abundance of the dominant order in the fungal community

Dominant order	SOM	TN	TP	TK	AN	AP	AK	pH
unclassified_c__Agaricomycetes	0.218	0.224	0.412	-0.021	0.182	0.321	0.316	-0.462
unclassified_p__Ascomycota	0.047	-0.038	0.189	-0.344	-0.044	-0.132	-0.356	0.077
norank_c__Agaricomycetes	0.262	0.309	-0.173	-0.171	0.247	-0.132	-0.1	-0.448
Eurotiales	-0.265	-0.229	-0.219	0.241	-0.25	0.359	-0.132	0.171
Hypocreales	-0.182	-0.241	-0.015	-0.018	-0.218	-0.441	-0.293	0.409
Tremellales	-0.124	-0.191	-0.127	-0.341	-0.279	0.153	-0.412	-0.337
Sordariales	**0.55***	**0.526***	**0.518***	-0.206	**0.559***	-0.247	0.091	0.295
norank_k__Fungi	0.262	0.159	0.355	-0.518	0.138	-0.347	**-0.469***	-0.099
Agaricales	-0.294	-0.282	-0.347	-0.047	-0.365	-0.009	-0.406	-0.346

**(P<0.01) and *(P<0.05) indicate significant differences among values of soil sample parameters based on a one-way ANOVA followed by an LSD test. SOM indicates soil organic matter; TN indicates total nitrogen; TP indicates total phosphorus; TK indicates total potassium ; AN indicates available nitrogen; AP indicates available phosphorus; AK indicates Available potassium.