# Dynamic Changes of Rhizosphere Soil Microbiome and Functional Genes Involved in Carbon and Nitrogen Cycling in Chinese Fir Monoculture

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**Table. S1.** Shannon diversity index of rhizosphere soil microbial communities in different stand ages of Chinese fir plantations in subtropical China.

| Stand age | Bacterial community | Fungal community | Archaeal community |
|---|---|---|---|
| 6 | 6.98±0.06a | 4.96±0.09a | 5.72±0.01ab |
| 17 | 7.00±0.03a | 5.16±0.03a | 5.76±0.01a |
| 26 | 7.07±0.03a | 4.87±0.09a | 5.71±0.01ab |
| 45 | 7.04±0.03a | 4.95±0.04a | 5.74±0.02ab |
| 102 | 6.99±0.03a | 4.52±0.38a | 5.49±0.04b |

All data are presented as means ± standard error ($n$ = 3). Means with different lowercase letters in a column indicate significant differences in Shannon diversity index of a specific soil microbial community ($P < 0.05$).

**Table S2.** Relative abundance of the pathway ko04626 (plant-pathogen interaction).

| Stand age / year | ko04626 |
|---|---|
| 6 | 192.20 ± 14.34a |
| 17 | 180.76 ± 14.46a |
| 26 | 246.32 ± 13.74a |
| 45 | 202.07 ± 31.79a |
| 102 | 203.76 ± 24.28a |

All data are presented as means ± standard error ($n$ = 3).

**Table S3.** Relative abundance of the genus *Streptomyces*.

| Stand age / year | *Streptomyces* |
|---|---|
| 6 | 0.022 ± 0.003b |
| 17 | 0.026 ± 0.001ab |
| 26 | 0.031 ± 0.002a |
| 45 | 0.021 ± 0.003b |
| 102 | 0.025 ± 0.002ab |

All data are presented as means ± standard error ($n$ = 3). Means with different lowercase letters in a column indicate significant differences in the relative abundance of *Streptomyces* ($P < 0.05$).

**Table S4.** Relative abundance of the genus of *Methanosarcina* and *Methanobacterium.*

| Stand age / year | *Methanosarcina* | *Methanobacterium* |
|---|---|---|
| 6 | 0.073 ± 0.006b | 0.020 ± 0.0012b |
| 17 | 0.095 ± 0.002a | 0.022 ± 0.0004ab |
| 26 | 0.105 ± 0.003a | 0.023 ± 0.0003a |
| 45 | 0.095 ± 0.008a | 0.024 ± 0.0015a |
| 102 | 0.075 ± 0.003b | 0.018 ± 0.0003b |

All data are presented as means ± standard error ($n$ = 3). Means with different lowercase letters in a column indicate significant differences in the relative abundance of *Methanosarcina* and *Methanobacterium* ($P < 0.05$).

**Figure S1.** Heatmap of correlation (Pearson's rank) between the relative abundance of the potential functional pathways and soil properties. *: 0.01 < P < 0.05; **: 0.001 < P < 0.01; ***: P < 0.001.

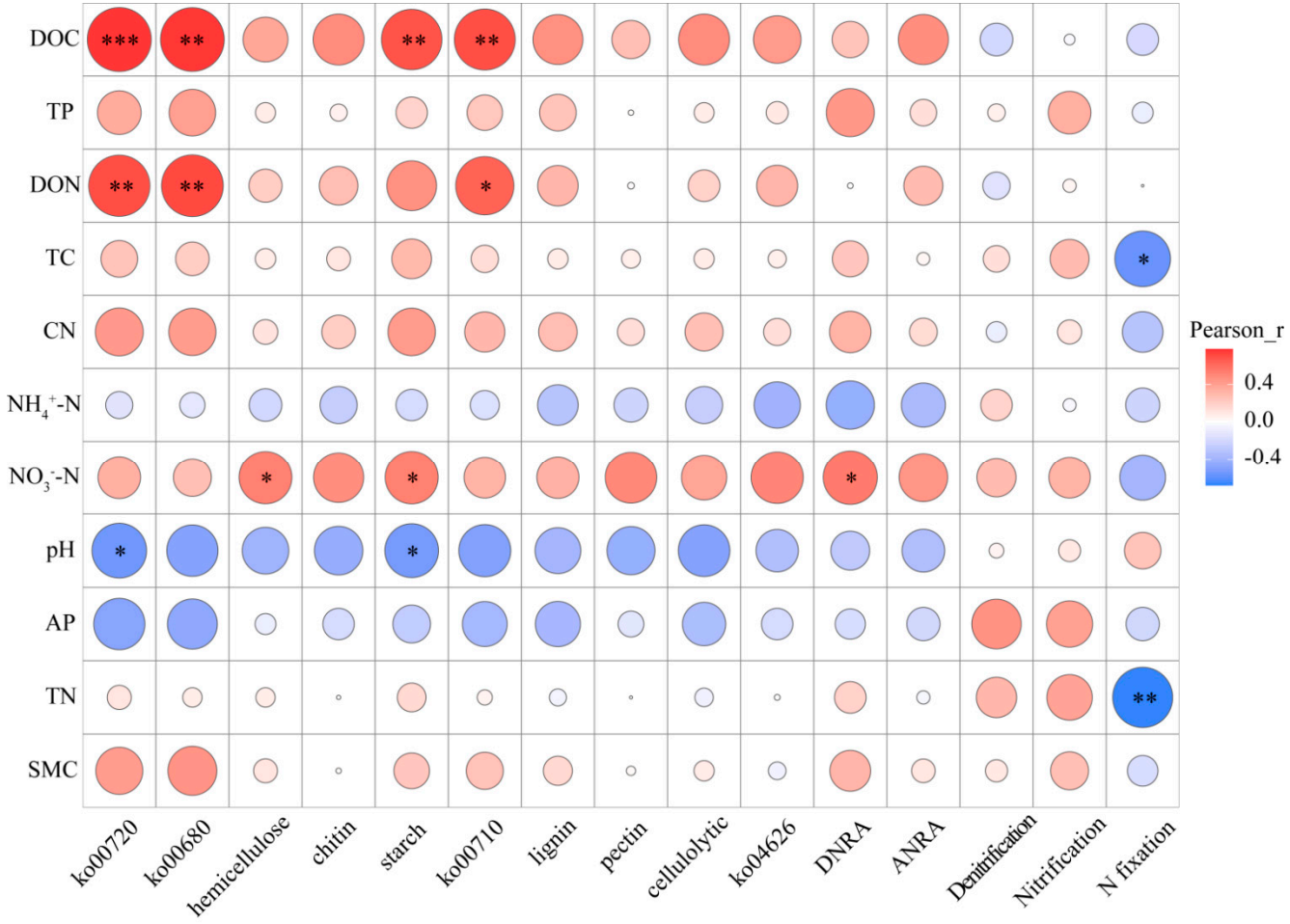


**Figure S2.** Random forest (RF) analysis was performed to explore the soil indicators of *Acidobacteria* (a) and *Actinobacteria* (b).

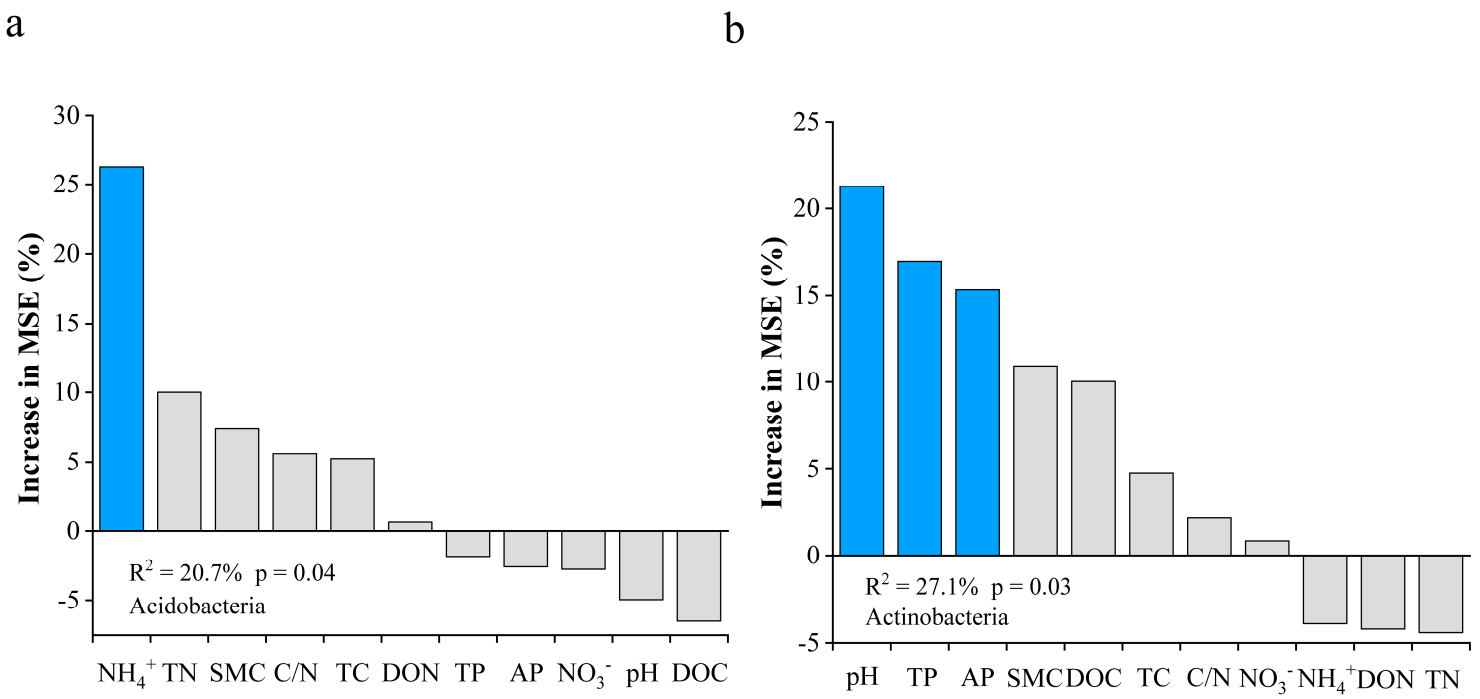


**Figure S3.** Linear regression analysis between soil nutrient concentrations and the relative abundance of selected microbial phyla.

Shading indicates 95% confidence intervals. *: 0.01 < P < 0.05; **: 0.001 < P < 0.01.

