***Phyllostachys edulis* (moso bamboo) ages significantly affect soil nitrogen transformation and endophytic microbes but niche differentiations outweigh ages in shaping microbial communities of moso bamboo-soil system**

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**Fig. S3.** The relative abundances of bacterial distribution at: (a) predominant phyla; (b) predominant genera and (c) predicted function analyses of bacteria with PICRUSt. A0.5y, 0.5-year above-ground tissues; A2.5y, 2.5-year above-ground tissues; A4.5y, 4.5-year above-ground tissues; A6.5y, 6.5-year above-ground tissues; R0.5y, 0.5-year roots; R2.5y, 2.5-year roots; R4.5y, 4.5-year roots; R6.5y, 6.5 roots; S0.5y, rhizospheric soils of 0.5-year bamboos; S2.5y, rhizospheric soils of 2.5-year bamboos; S4.5y, rhizospheric soils of 4.5-year bamboos; and S6.5y, rhizospheric soils of 6.5-year bamboos.

**Fig. S4.** The relative abundances of bacterial phyla with significant differences among different groups: (a) *Acidobacteria*, (b) *Actinobacteria*, (c) *Bacteroidetes*, (d) *Chloroflexi*, (e) *Dependentiae*, (f) *Elusimicrobia*, (g) *Firmicutes*, (h) *Gemmatimonadetes*, (i) *Latescibacteria*, (j) *Nitrospirae*, (k) *Planctomycetes*, (l) *Proteobacteria* and (m) *Verrucomicrobia*. Vertical bars indicate the maximum and minimum values. Lowercase letters show significant differences among the same samples of different ages, and capital letters show significant differences among different niches of the same age.

**Fig. S5.** The relative abundances of fungal distribution at: (a) predominant phyla; (b) predominant genera and (c) predicted function analyses of fungi with Fungi Functional Guild. A0.5y, 0.5-year above-ground tissues; A2.5y, 2.5-year above-ground tissues; A4.5y, 4.5-year above-ground tissues; A6.5y, 6.5-year above-ground tissues; R0.5y, 0.5-year roots; R2.5y, 2.5-year roots; R4.5y, 4.5-year roots; R6.5y, 6.5 roots; S0.5y, rhizospheric soils of 0.5-year bamboos; S2.5y, rhizospheric soils of 2.5-year bamboos; S4.5y, rhizospheric soils of 4.5-year bamboos; and S6.5y, rhizospheric soils of 6.5-year bamboos.

**Fig. S6.** The relative abundances of fungal phyla with significant differences among different groups: (a) *Ascomycota*, (b) *Basidiomycota*, (c) *Chytridiomycota*, (d) *Glomeromycota* and (e) *Mortierellomycota*. Vertical bars indicate the maximum and minimum values. Lowercase letters show significant differences among the same samples of different ages, and capital letters show significant differences among different niches of the same age.

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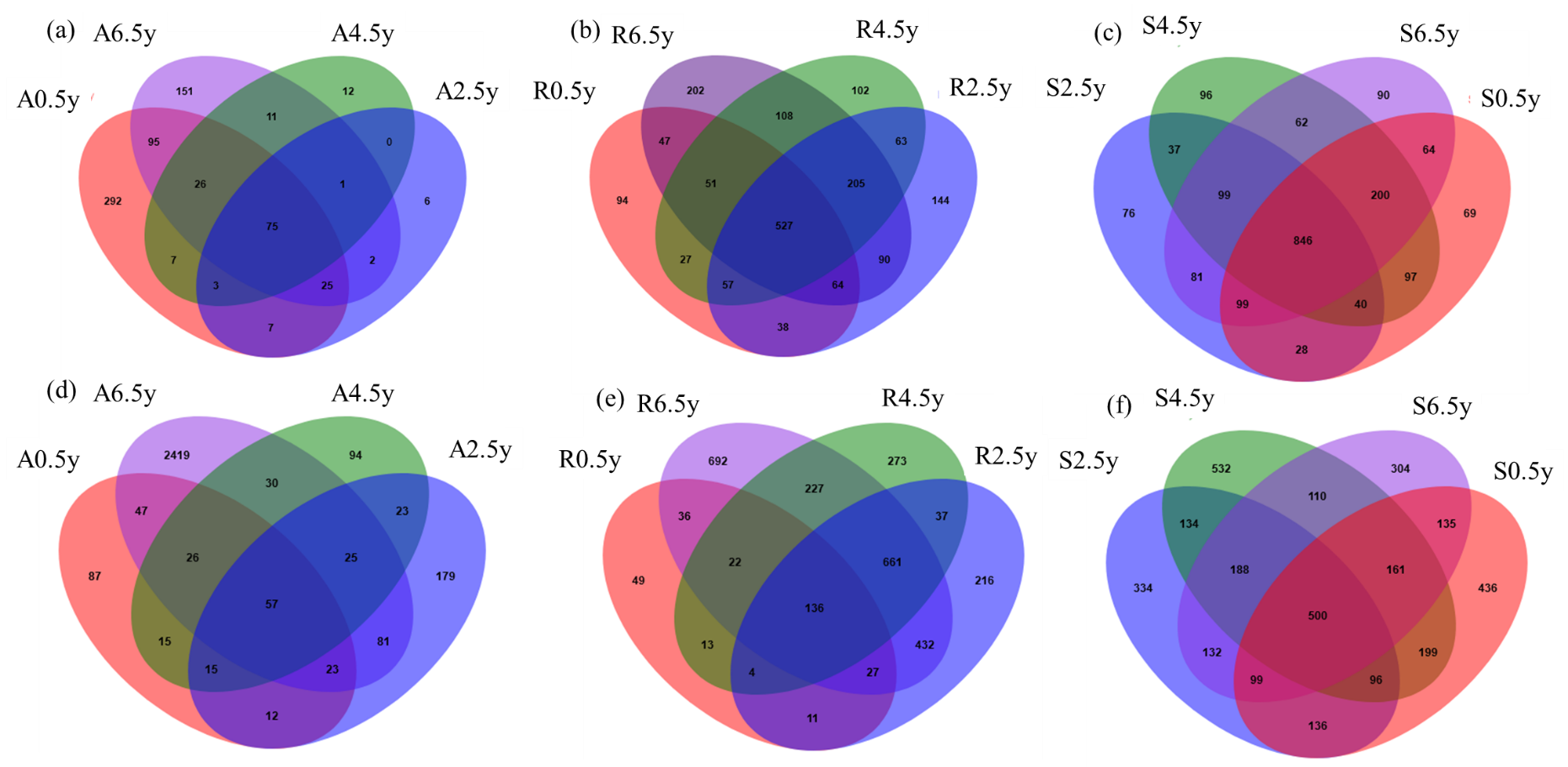
|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Functional genes** | **Primers** | **Sequence 5’-3’** | **References** | **Amplification efficiency** | **R2** |
| *npr*Agene | FP npr I  RP npr II | GTDGAYGCHCAYTAYTAYGC  ACMGCATGBGTYADYTCATG | Bach et al. [1] | 85.0% | ≥ 0.99 |
| *chi*Agene | chif2  chir | GACGGCATCGACATCGATTGG  CSGTCCAGCCGCGSCCRTA | Xiao et al. [2] | 90.5% | ≥ 0.99 |
| AOA *amo*A gene | amoAF  amoAR | STAATGGTCTGGCTTAGACG  GCGGCCATCCATCTGTATGT | Francis et al. [3] | 83.5% | ≥ 0.99 |
| AOB *amo*A gene | amoA-1F  amoA-2R | GGGGTTTCTACTGGTGGT  CCCCTCKGSAAAGCCTTCTTC | Rotthauwe et al. [4] | 84.5% | ≥ 0.99 |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Samples** | **Bacterial communities** | | | | **Fungal communities** | | | |
| **Average sequence number** | **Sequence number range** | **Average sequence length** | **Sequence length range** | **Average sequence number** | **Sequence number range** | **Average sequence length** | **Sequence length range** |
| 0.5 y above-ground tissues | 20703 | 16600 - 23299 | 376.4 | 375.2 - 377.3 | 67652 | 59258 - 72000 | 231.1 | 228.5 - 234.5 |
| 2.5 y above-ground tissues | 18126 | 11873 - 24139 | 376.9 | 376.3 - 377.2 | 69624 | 59206 - 73997 | 231.0 | 227.7 - 233.2 |
| 4.5 y above-ground tissues | 18839 | 11654 - 24924 | 377.3 | 377.1 - 377.6 | 70630 | 67490 - 74723 | 238.2 | 221.4 - 253.5 |
| 6.5 y above-ground tissues | 23990 | 22848 - 24793 | 376.4 | 375.1 - 377.7 | 62141 | 47634 - 74347 | 246.2 | 225.7 - 268.6 |
| 0.5 y roots | 19402 | 13468 - 24413 | 376.3 | 375.1 - 378 | 56793 | 50263 - 67320 | 239.3 | 229.0 - 249.6 |
| 2.5 y roots | 23359 | 21240 - 24505 | 376.4 | 374.9 - 377.2 | 53024 | 47711 - 56359 | 243.1 | 228.5 - 268.9 |
| 4.5 y roots | 22088 | 20979 - 23590 | 377.0 | 374.9 - 378 | 52928 | 47587 - 58556 | 255.6 | 229.4 – 282.0 |
| 6.5 y roots | 23107 | 19895 - 24723 | 376.9 | 376.2 - 377.5 | 55213 | 45603 - 70614 | 251.5 | 241.7 - 259.7 |
| rhizospheric soils of 0.5 y bamboos | 18052 | 10034 - 23467 | 375.4 | 373.9 - 376.6 | 66855 | 60905 - 72268 | 229.3 | 226.5 - 233.5 |
| rhizospheric soils of 2.5 y bamboos | 22219 | 17109 - 24426 | 374.7 | 374 - 375.5 | 52757 | 33045 - 67462 | 235.3 | 233.2 - 239.8 |
| rhizospheric soils of 4.5 y bamboos | 22791 | 20639 - 24941 | 376.3 | 375.9 - 376.5 | 63636 | 57715 - 69010 | 237.4 | 229.9 - 253.9 |
| rhizospheric soils of 6.5 y bamboos | 21382 | 13062 - 24593 | 373.9 | 370.5 - 375.6 | 60991 | 48871 - 70167 | 270.1 | 237.6 - 317.3 |

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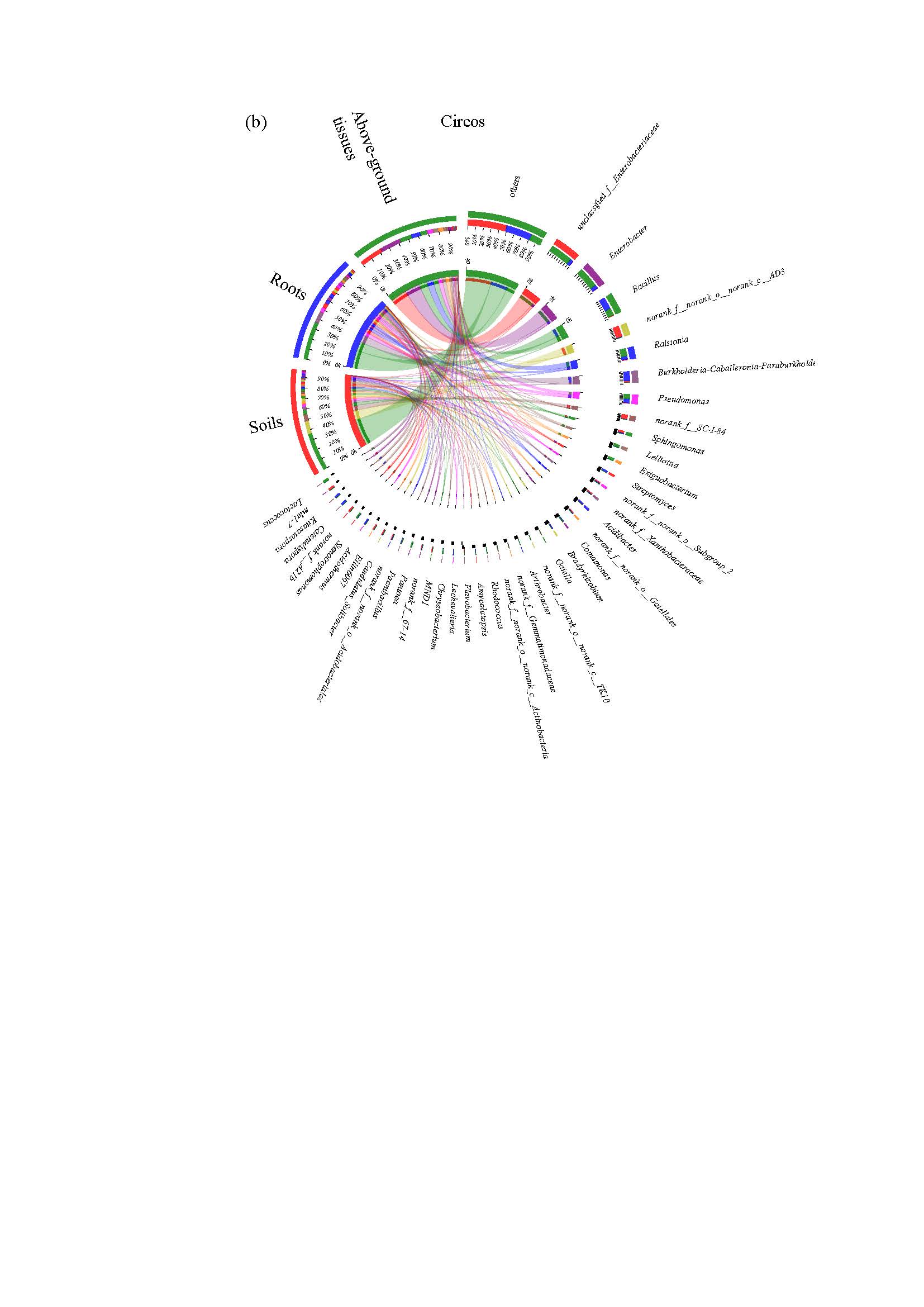


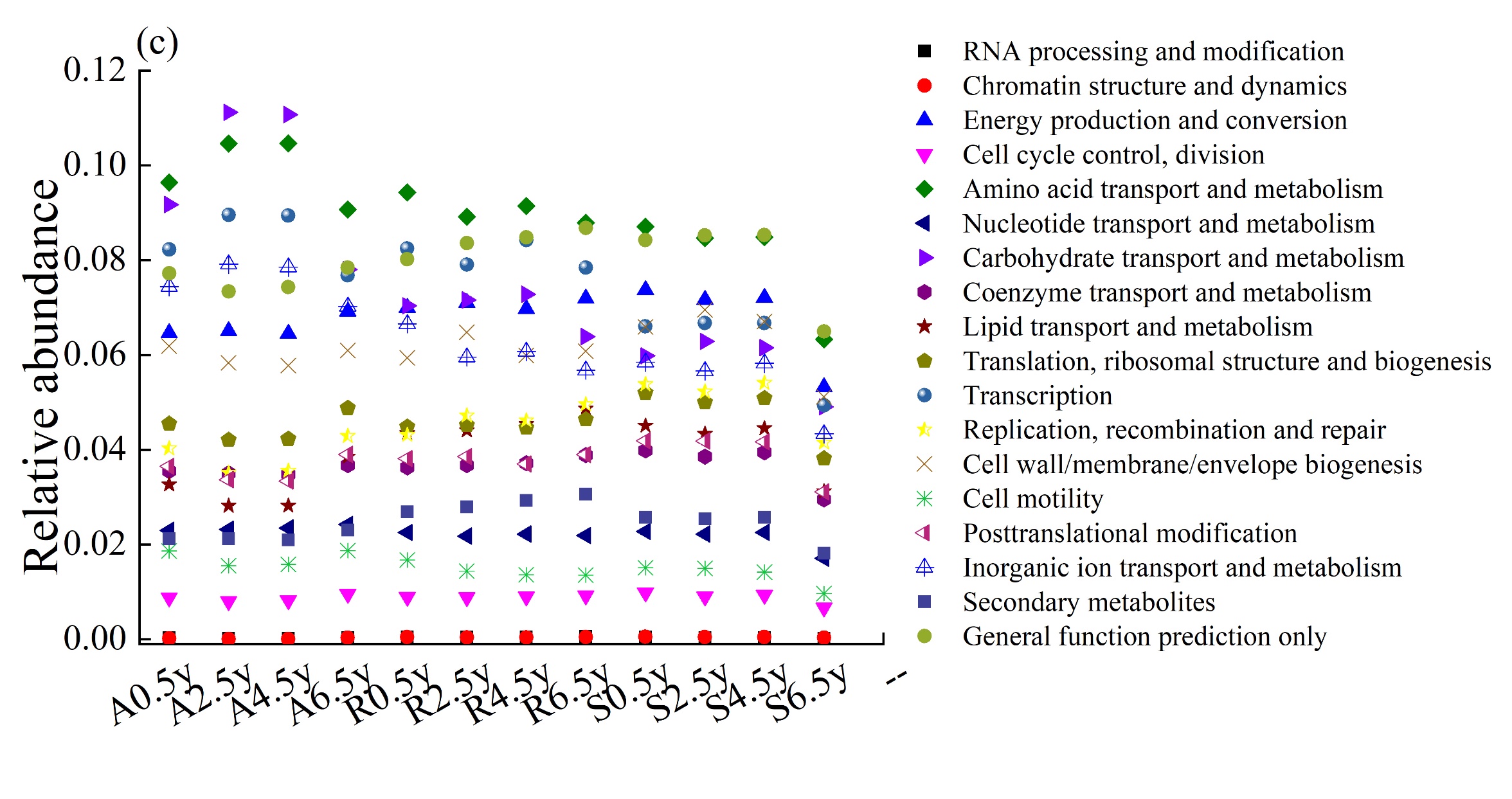
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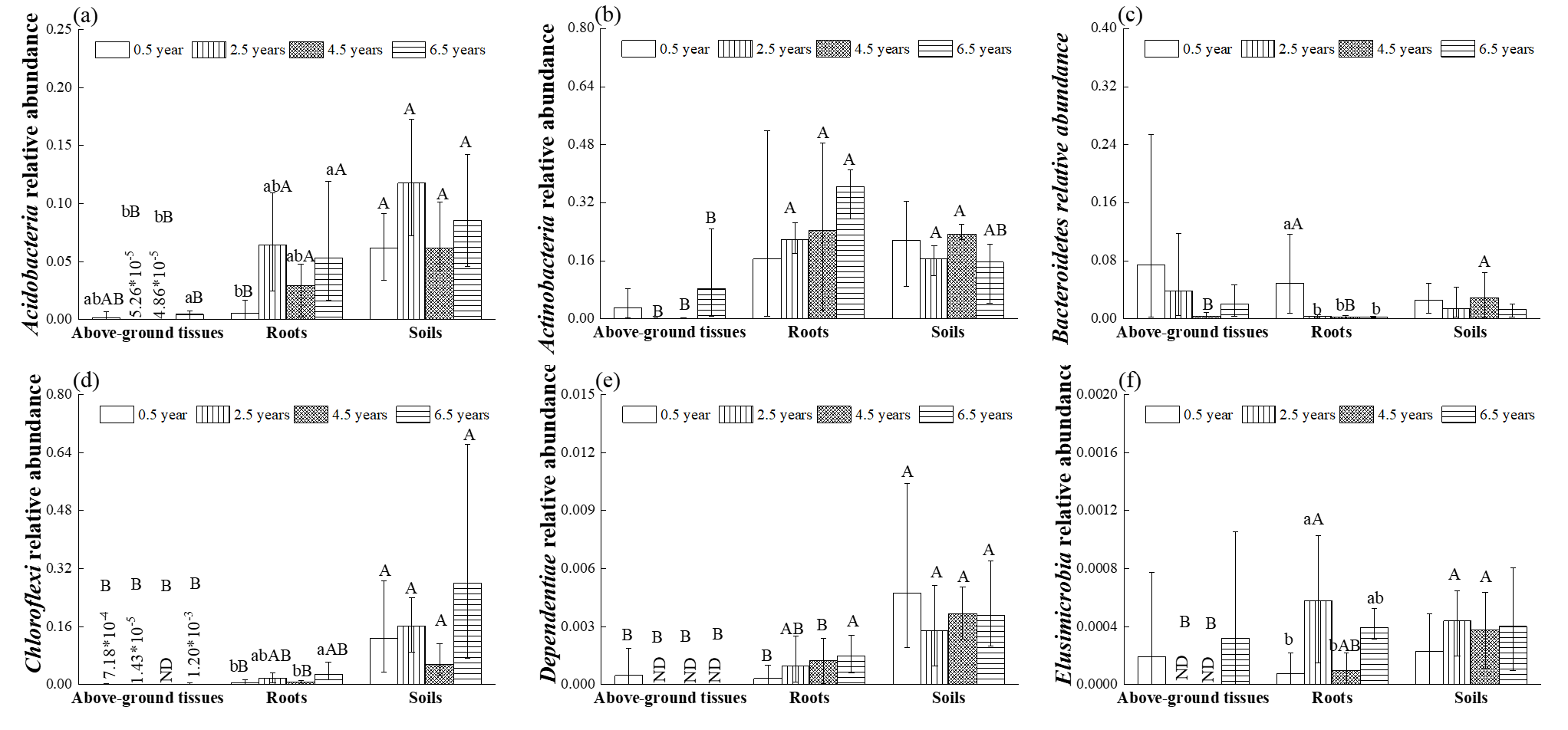
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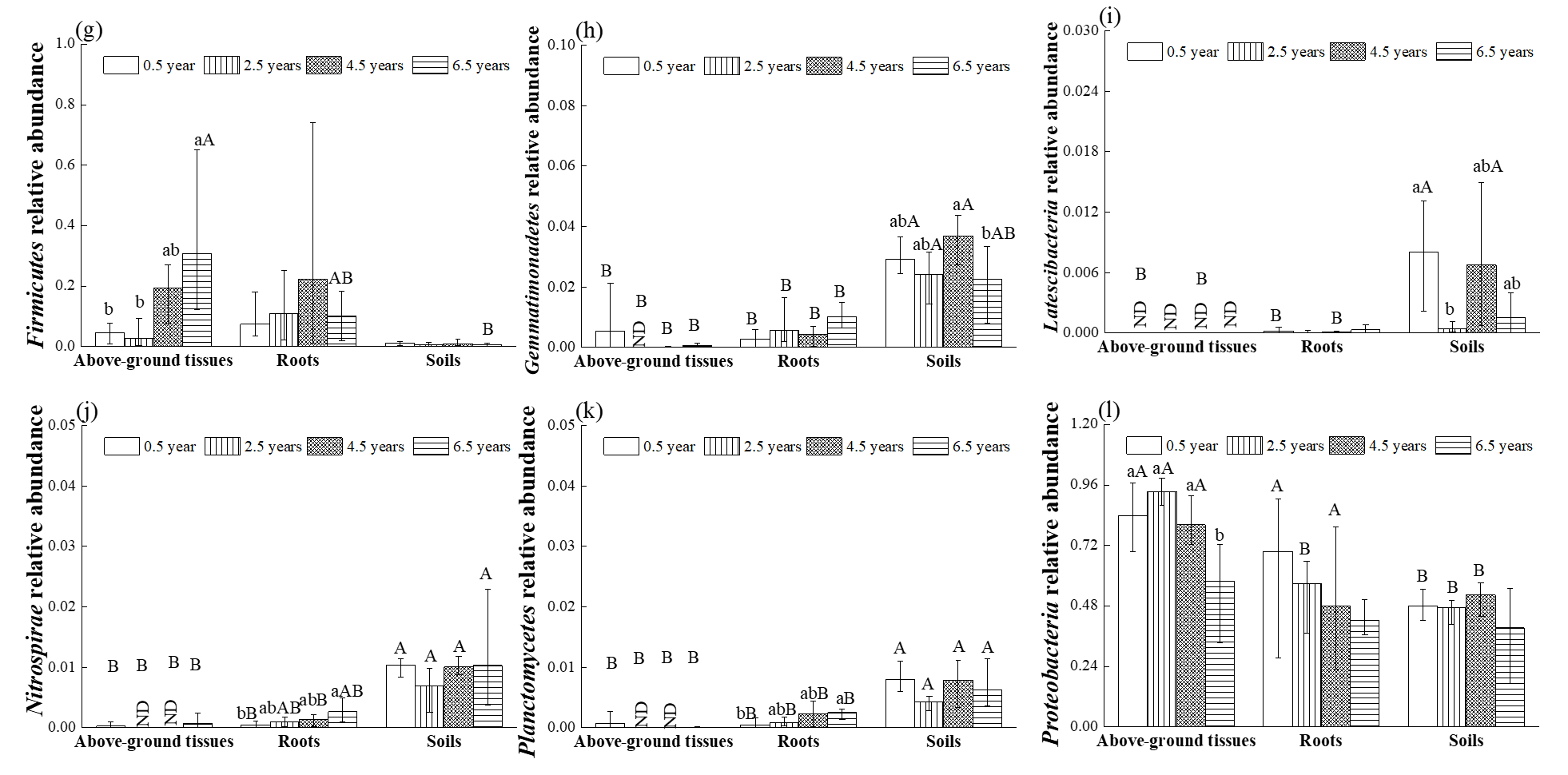


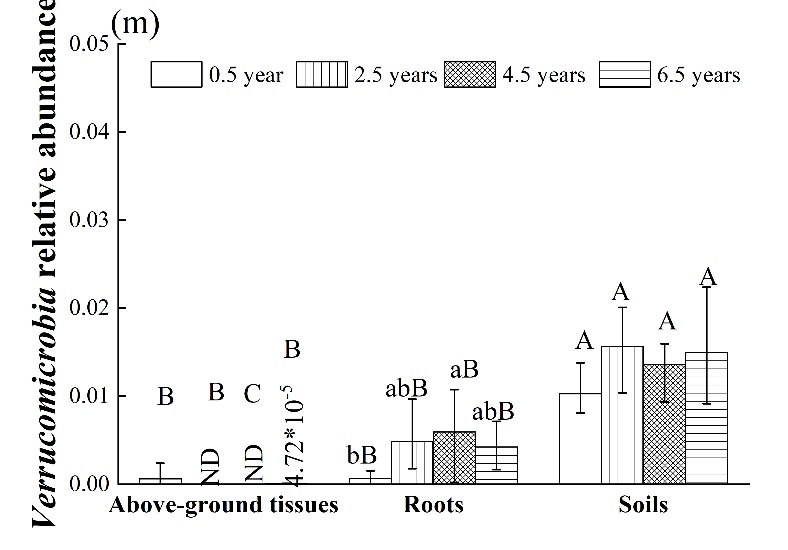




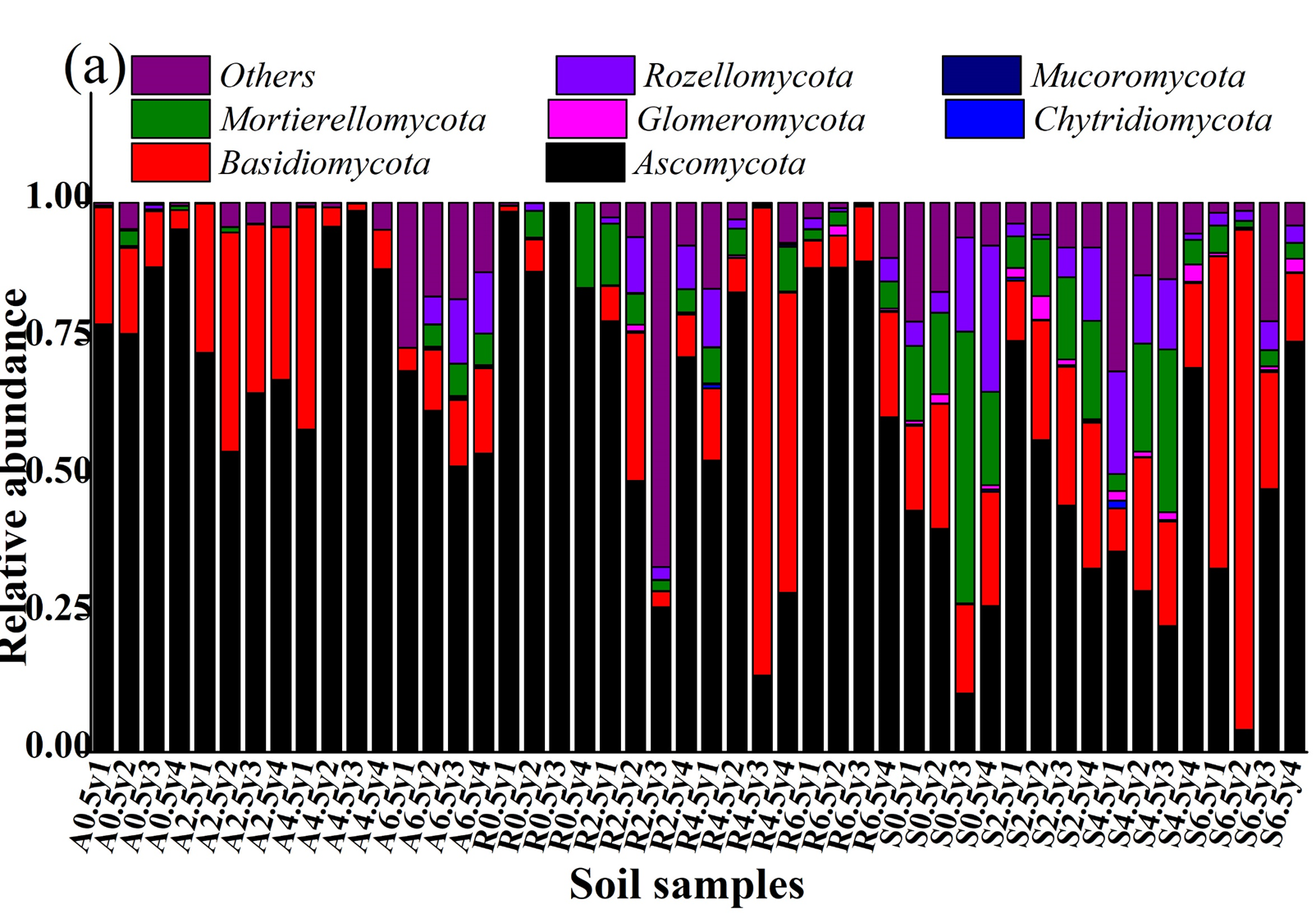
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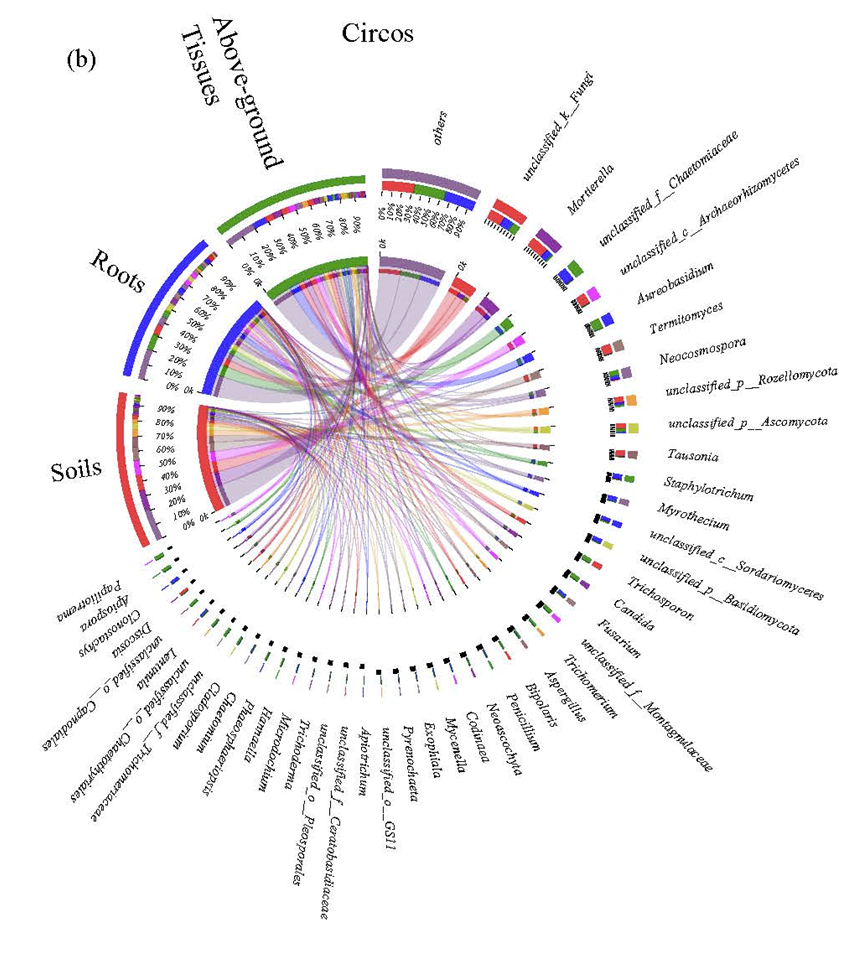


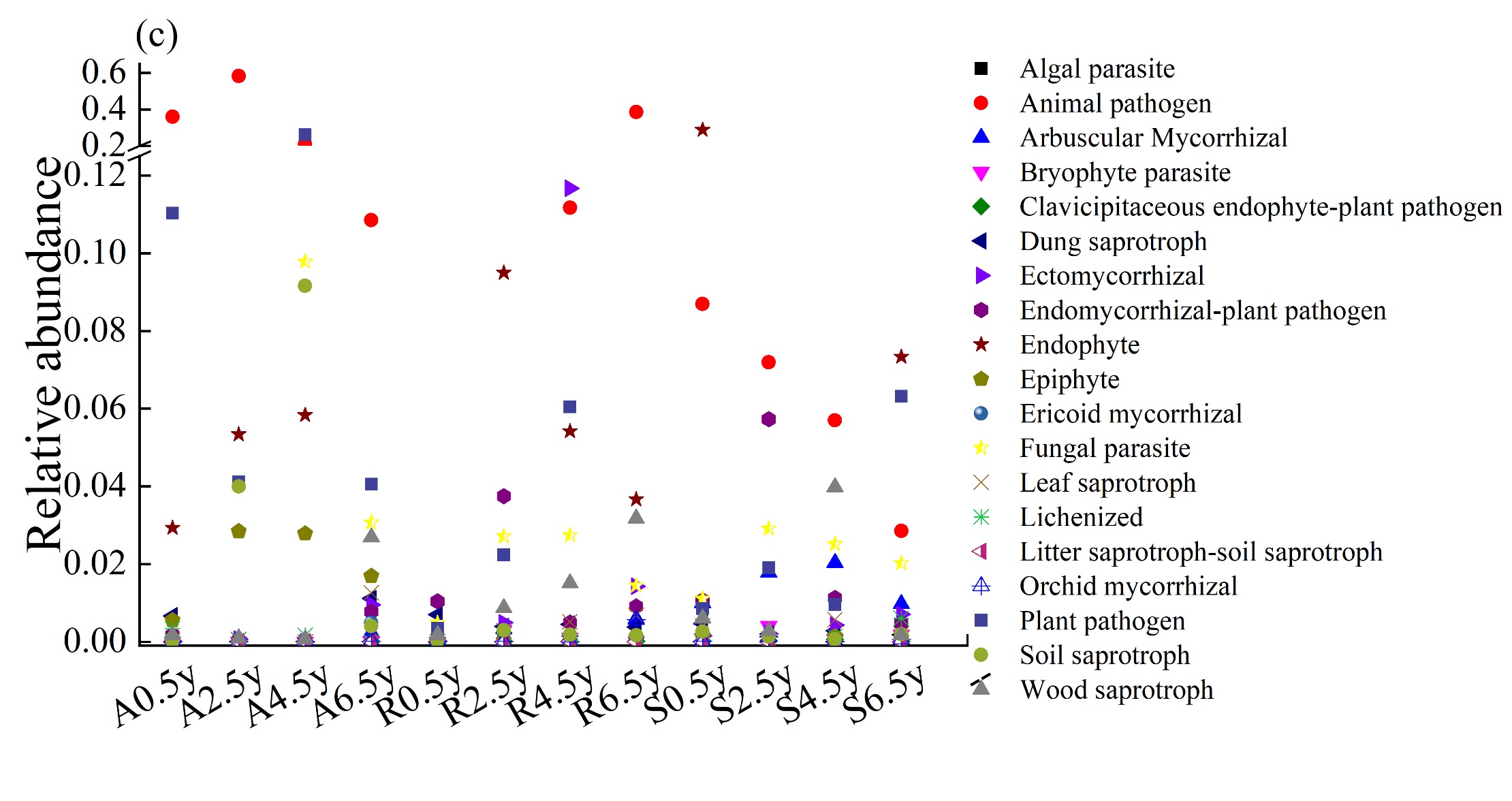


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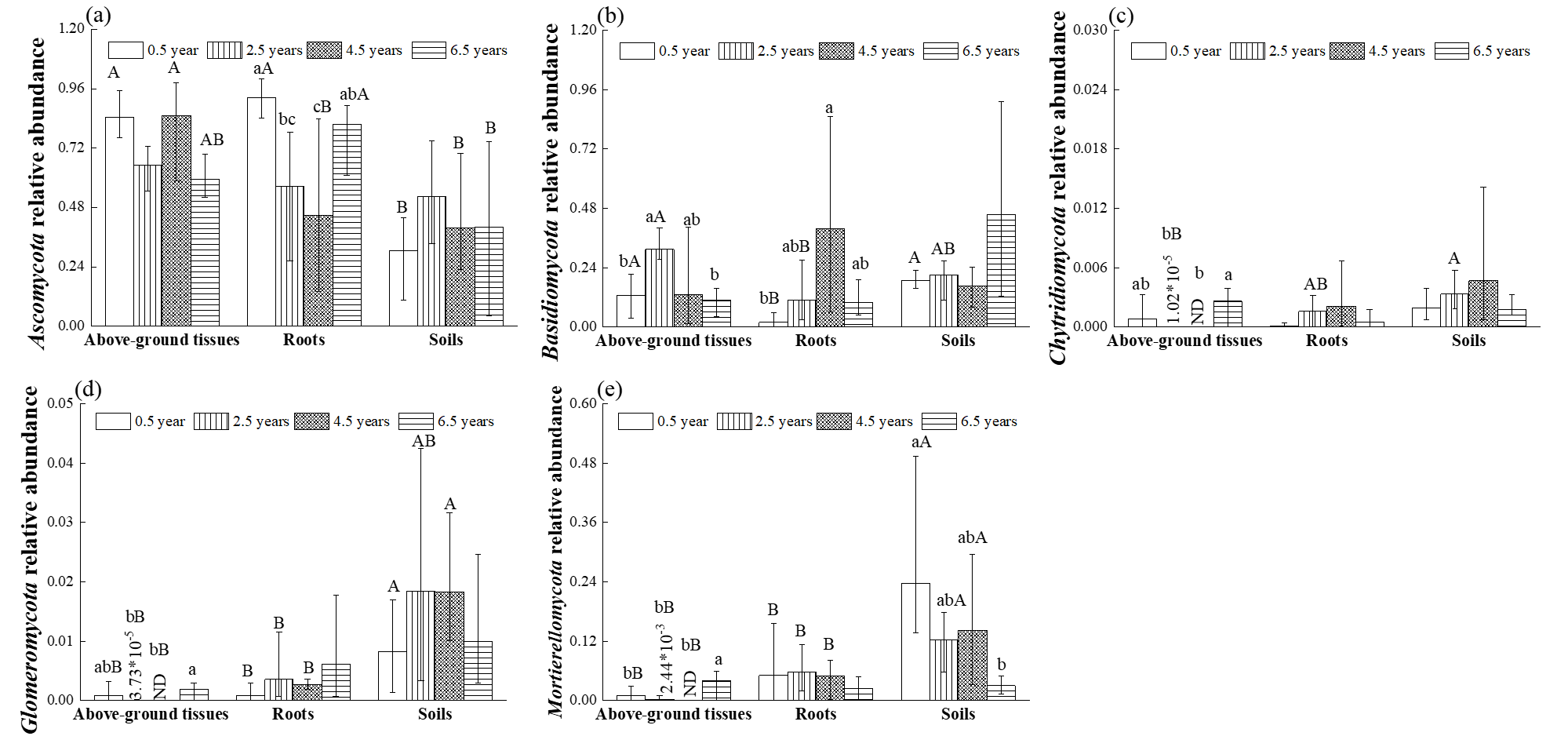
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|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Soil nutrients | | Bacterial community | | | | Fungal community | | | |
| Bacterial phyla | Above-ground tissues | Roots | Rhizospheric soil | Fungal phyla | Above-ground tissues | Roots | Rhizospheric soil |
| Soil organic matter | -0.012 | *Acidobacteria* | -0.130 | -0.075 | 0.476 | *Ascomycota* | -0.451 | 0.276 | 0.237 |
| Total N | 0.191 | *Actinobacteria* | -0.137 | -0.224 | -0.226 | *Basidiomycota* | 0.589\* | -0.444 | 0.099 |
| NH4+-N | 0.370 | *Armatimonadetes* | -0.139 | -0.157 | 0.314 | *Chytridiomycota* | 0.031 | 0.069 | 0.245 |
| NO3--N | 0.256 | *Bacteroidetes* | 0.046 | 0.165 | -0.484 | *Glomeromycota* | -0.025 | 0.176 | 0.128 |
|  |  | *Chlamydiae* | -0.113 | -0.037 | -0.598\* | *Mortierellomycota* | -0.042 | 0.255 | -0.238 |
|  |  | *Chloroflexi* | -0.022 | 0.171 | 0.083 | *Mucoromycota* | -0.057 | 0.026 | -0.072 |
|  |  | *Dependentiae* | 0.087 | -0.062 | 0.052 | *Rozellomycota* | -0.121 | 0.213 | -0.301 |
|  |  | *Elusimicrobia* | -0.077 | -0.011 | -0.214 |  |  |  |  |
|  |  | *Entotheonellaeota* | -0.030 | -0.057 | -0.329 |  |  |  |  |
|  |  | *Firmicutes* | -0.142 | 0.224 | -0.209 |  |  |  |  |
|  |  | *Gemmatimonadetes* | 0.079 | 0.165 | -0.403 |  |  |  |  |
|  |  | *Latescibacteria* | 0.000 | 0.221 | -0.365 |  |  |  |  |
|  |  | *Nitrospirae* | -0.082 | -0.017 | -0.074 |  |  |  |  |
|  |  | *Planctomycetes* | 0.093 | -0.318 | -0.437 |  |  |  |  |
|  |  | *Proteobacteria* | 0.173 | -0.034 | 0.021 |  |  |  |  |
|  |  | *Verrucomicrobia* | 0.096 | -0.212 | 0.242 |  |  |  |  |

Pearson’s correlation coefficients (r values) and *P* level (\* *P* < 0.05) were in each cell.

**References**

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1. \* Corresponding author, E-mail: zhangwenyuan@jxau.edu.cn [↑](#footnote-ref-1)