

Figure S1. Rarefaction curves based on 16S rRNA and ITS sequences among the different samples.

Table S1 The DNA concentration of each sample measuring by Qubit.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Sample ID | Concentration (ng/μL) | Sample ID | Concentration (ng/μL) | Sample ID | Concentration (ng/μL) |
| BA1 | 37.5 | BA2 | 56.1 | BA3 | 14.4 |
| BB1 | 21.8 | BB2 | 18.5 | BB3 | 26.0 |
| BC1 | 33.2 | BC2 | 30.9 | BC3 | 37.0 |
| BD1 | 47.0 | BD2 | 68.4 | BD3 | 78.6 |
| BE1 | 69.4 | BE2 | 105.9 | BE3 | 16.7 |
| BF1 | 48.5 | BF2 | 117.7 | BF3 | 88.8 |

Table S2 The curve estimation of alpha-diversity.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Alpha-diversity | Linear |  | Quadratic |  | Cubic |  |
|  | r2 | *P* | r2 | *P* | r2 | *P* |
| b- OTUs | 0.033 | 0.470 | 0.433 | 0.014 | 0.547 | **0.009** |
| b- Chao 1 | 0.000 | 0.969 | 0.220 | 0.155 | 0.220 | 0.308 |
| b- Shannon | 0.027 | 0.511 | 0.087 | 0.507 | 0.233 | 0.280 |
| b- Simpson | 0.035 | 0.457 | 0.057 | 0.644 | 0.381 | **0.074** |
| f- OTUs | 0.021 | 0.569 | 0.339 | 0.045 | 0.596 | **0.004** |
| f- Chao 1 | 0.007 | 0.737 | 0.160 | 0.271 | 0.397 | **0.062** |
| f- Shannon | 0.001 | 0.901 | 0.245 | 0.122 | 0.374 | **0.079** |
| f- Simpson | 0.003 | 0.818 | 0.199 | 0.190 | 0.280 | 0.191 |

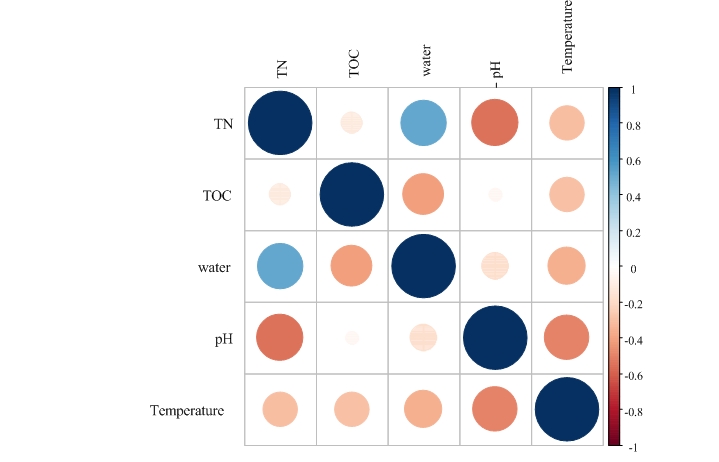


Figure S2. Pearson correlation between different environmental variables.

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Sample ID | Time (d) | Proteobacteria | Firmicutes | Bacteroidetes | Chloroflexi | Actinobacteria | Parcubacteria | Synergistetes | Deinococcus-Thermus | Gemmatimonadetes | Acidobacteria | other |
| BA | 0 | 37.5±17.1 | 12.6±5.9 | 8.2±4.3 | 9.1±4.2 | 30.3±19.0 | 0.0±0.0 | 0.0±0.0 | 0.1±0.0 | 1.6±0.5 | 0.2±0.0 | 0.2±0.0 |
| BB | 1 | 48.3±11.6 | 18.4±3.0 | 20.9±7.0 | 6.6±1.7 | 3.5±0.7 | 0.0±0.0 | 0.5±0.0 | 0.4±0.0 | 0.7±0.2 | 0.0±0.0 | 0.3±0.0 |
| BC | 2 | 47.5±1.8 | 4.9±0.4 | 41.3±2.1 | 0.6±0.1 | 5.3±1.3 | 0.0±0.0 | 0.0±0.0 | 0.0±0.0 | 0.0±0.0 | 0.0±0.0 | 0.0±0.0 |
| BD | 5 | 37.6±2.1 | 3.5±0.9 | 46.7±5.4 | 3.8±2.4 | 7.3±1.9 | 0.0±0.0 | 0.0±0.0 | 0.2±0.1 | 0.2±0.1 | 0.2±0.0 | 0.2±0.0 |
| BE | 11 | 33.5±6.9 | 4.8±3.2 | 37.3±1.7 | 8.0±6.0 | 9.7±2.0 | 1.6±1.6 | 0.0±0.0 | 2.1±2.0 | 1.1±0.8 | 0.0±0.0 | 1.5±0.6 |
| BF | 20 | 37.1±3.5 | 4.4±2.5 | 54.1±2.7 | 1.1±0.7 | 2.8±1.2 | 0.0±0.0 | 0.0±0.0 | 0.2±0.0 | 0.0±0.0 | 0.0±0.0 | 0.4±0.2 |

Table S3 The relative abundances (%) of top ten bacterial phyla in bedding of different padded time. Values at individual sites are mean values of three replicated samples (mean ± standard error).

Table S4 The relative abundances (%) of fungal phyla in bedding of different padded time. Values at individual sites are mean values of three replicated samples (mean ± standard error).

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Sample ID | Time (d) | Ascomycota | Basidiomycota | Zygomycota | Neocallimastigomycota | Unclassified |
| BA | 0 | 73.5±12.4 | 8.2±6.5 | 0.6±0.3 | 0.0±0.0 | 17.7±9.7 |
| BB | 1 | 82.5±4.4 | 8.5±4.5 | 0.0±0.0 | 0.0±0.0 | 8.9±1.4 |
| BC | 2 | 62.9±16.7 | 2.5±0.6 | 0.0±0.0 | 0.0±0.0 | 34.5±16.8 |
| BD | 5 | 75.9±7.0 | 0.2±0.0 | 0.0±0.0 | 0.0±0.0 | 23.8±7.0 |
| BE | 11 | 89.2±2.0 | 0.5±0.0 | 0.0±0.0 | 0.0±0.0 | 10.1±2.0 |
| BF | 20 | 89.8±1.9 | 1.0±0.1 | 0.0±0.0 | 0.0±0.0 | 9.2±1.8 |

Table S5 Pearson correlation coefficient (r) between dominant bacterial phyla and environmental variables for all samples.\*indicate significant correlation (\*\*\* indicates *P*<0.001; \*\*indicates *P*<0.01;\*indicates *P*<0.05).

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Proteobacteria | Firmicutes | Bacteroidetes | Chloroflexi | Actinobacteria | Parcubacteria | Synergistetes | Deinococcus-Thermus | Gemmatimonadetes | Acidobacteria | other |
| TOC | 0.203 | 0.650\*\* | -0.661\*\* | 0.147 | 0.221 | -0.255 | 0.554\* | -0.238 | 0.308 | -0.061 | -0.212 |
| TN | -0.283 | -0.316 | 0.082 | -0.121 | 0.394 | 0.006 | -0.817\*\* | -0.052 | 0.079 | 0.108 | -0.062 |
| C/N | 0.313 | 0.687\*\* | -0.534\* | 0.172 | -0.076 | 0.192 | 0.919\*\* | -0.143 | 0.171 | -0.137 | -0.118 |
| Temperature | 0.070 | -0.020 | -0.076 | 0.000 | 0.081 | -0.223 | -0.002 | -0.205 | -0.095 | 0.486\* | 0.183 |
| water | -0.541\*\* | -0.092 | 0.327 | 0.081 | 0.112 | 0.163 | -0.266 | 0.166 | 0.193 | -0.008 | 0.152 |
| pH | -0.029 | 0.375 | 0.327 | -0.177 | -0.492\* | -0.336 | 0.374 | 0.279 | -0.274 | -0.666\*\* | 0.263 |

Table S6 Pearson correlation coefficient (r) between dominant fungal phyla and environmental variables for all samples.\*indicate significant correlation (\*\*\* indicates *P*<0.001; \*\*indicates *P*<0.01;\*indicates *P*<0.05).

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Neocallimastigomycota | Ascomycota | Zygomycota | Basidiomycota | other |
| TOC | 0.134 | -0.078 | 0.382 | 0.537\* | -0.129 |
| TN | -0.536\* | -0.043 | 0.266 | -0.211 | 0.121 |
| C/N | 0.417 | -0.140 | 0.107 | 0.521\* | -0.185 |
| Temperature | 0.091 | -0.346 | 0.047 | 0.012 | 0.358 |
| water | -0.416 | 0.282 | 0.063 | -0.601\*\* | -0.069 |
| pH | 0.239 | 0.359 | -0.581\* | -0.118 | -0.321 |

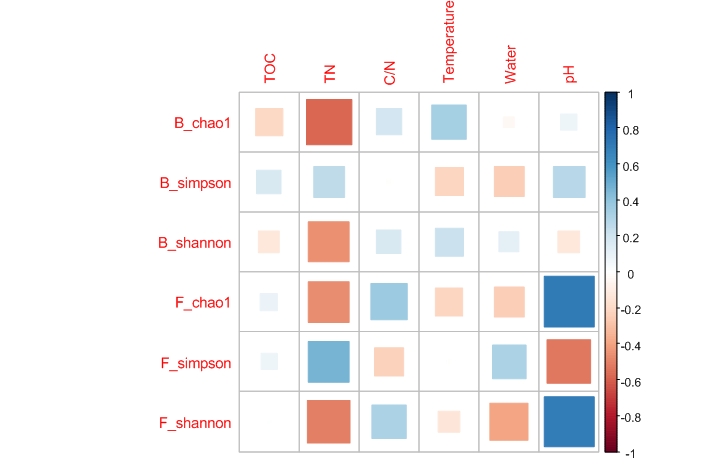


Figure S3. Pearson correlation between bacterial and fungal alpha diversity and environmental variables for all samples.

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Figure S4. Pearson correlation between bacterial and fungal abundance and environmental variables for all samples.