**Physical disturbance reduces cyanobacterial relative abundance and substrate metabolism potential of biological soil crusts on a gold mine tailing of Central China**

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**Supplementary Method**

*1.* *Illumina MiSeq sequencing data processing*

Raw fastq files were demultiplexed, quality-filtered by Trimmomatic and merged by FLASH with the following criteria: (i) The reads were truncated at any site receiving an average quality score <20 over a 50 bp sliding window. (ii) Primers were exactly matched allowing 2 nucleotide mismatching, and reads containing ambiguous bases were removed. (iii) Sequences whose overlap longer than 10 bp were merged according to their overlap sequence.

*2. Bacterial network construct*

First, the experimental data used for constructing bacterial networks were generated by pyrosequencing of 16S rDNA genes. Since the sequence numbers of individual ASVs obtained varied significantly among different samples, the relative proportions of sequence numbers were used for subsequent Spearman correlation analysis. Second, a similarity matrix was obtained by taking the absolute values of the correlation matrix. This similarity matrix measures the degree of concordance between the abundance profiles of individual ASVs across different samples. Third, an appropriate threshold for defining network structure, st, is defined using the RMT-based network approach to obtain an adjacency matrix, which encodes the strength of the connection between each pair of nodes (Luo et al., 2007; Junker and Schreiber, 2011). Fourth, the submodules within a large module were detected by fast greedy modularity optimization (Clauset et al., 2004). Correlation coefficients greater than 0.5 with a corresponding of p-value less than 0.001 were considered statistically robust and were included to generate the networks.

Table S1 Biological soil crusts element composition.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Al (mg/g) | Mg (mg/g) | Fe (mg/g) | Mn(mg/g) | Ti (mg/g) | Ca (mg/g) | Na (mg/g) | S (mg/g) |
| DH | 19.84±0.45a | 21.46±0.57a | 82.83±15.04b | 2.16±0.05a | 1.05±0.05bc | 180.84±4.36a | 3.52±2.37a | 13.15±4.24a |
| DB | 18.04±0.62b | 18.05±0.23b | 83.18±0.23b | 2.16±0.05a | 1.13±0.03b | 174.17±1.46a | 2.45±0.38a | 15.57±0.10a |
| UB | 18.41±0.13b | 16.13±0.11c | 112.92±1.09a | 2.15±0.02a | 1.00±0.06c | 179.36±3.83a | 4.07±0.66a | 11.54±0.23a |
| U | 19.66±0.56a | 17.28±0.71b | 72.53±2.00b | 1.94±0.05b | 1.28±0.10a | 159.71±2.35b | 1.24±0.17a | 11.94±0.41a |

Values represent means ± standard errors (n =3). Significant differences (P < 0.05) are marked by different letters.

Table S2 Correlation between physiochemical properties and enzyme activity.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | S-NP | S-NPT | S-β-GC | S-α-GC | S-POD | S-SC | S-UE | S-PPO | NITS |
| TOC | 0.606\* | -0.467  | 0.592\* | 0.790\*\* | 0.569  | 0.424  | 0.736\*\* | 0.257  | 0.918\*\* |
| TK | -0.679\* | 0.187  | -0.536  | -0.709\*\* | -0.281  | -0.714\*\* | -0.864\*\* | -0.475  | -0.885\*\* |
| NO3--N | 0.530  | -0.442  | 0.552  | 0.876\*\* | 0.492  | 0.451  | 0.741\*\* | 0.325  | 0.954\*\* |
| Scytonemin | 0.438  | -0.551  | 0.554  | 0.905\*\* | 0.506  | 0.330  | 0.673\* | 0.146  | 0.942\*\* |
| Chl-a | 0.492  | -0.458  | 0.634\* | 0.897\*\* | 0.512  | 0.417  | 0.727\*\* | 0.245  | 0.963\*\* |
| NH4+-N | 0.732\*\* | -0.290  | 0.603\* | 0.778\*\* | 0.487  | 0.686\* | 0.911\*\* | 0.426  | 0.954\*\* |
| EPS | 0.213  | 0.492  | 0.542  | -0.255  | -0.158  | 0.338  | 0.102  | 0.452  | -0.186  |
| EC | -0.679\* | 0.187  | -0.536  | -0.709\*\* | -0.281  | -0.714\*\* | -0.864\*\* | -0.475  | -0.885\*\* |
| pH | -0.811\*\* | 0.048  | -0.601\* | -0.569  | -0.543  | -0.782\*\* | -0.924\*\* | -0.487  | -0.810\*\* |

Analysis method using Pearson.\*(p＜0.05); \*\*(p＜0.01)

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