**Supplementary Tables**

**Supplementary Table 1.** Details ofsampling environmental conditions

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Sample ID** | **Sample type** | **Detection time** | **Ambient temperature** | **Humidity** | **Sunlight (LUX)** | **Soil temperature** | **Sampling zone** |
| LR-01 | Rock | 10:44 AM | 21.5 | 60 % | 256-260 | Nil | Outside cave |
| LS-01 | Soil | 256-261 | 18.5 |
| LR-05 | Rock | 11:55 AM | 23.3 | 63 % | 0 | Nil | Inside cave |
| LS-05 | Soil | 0 | 18.3 |

LR-01, LS-01: outside the cave; LR-05, LS-05: inside the cave

**Supplementary Table 2.** Pearson’s correlation test against predominant bacteria phylum with environmental factors

|  |
| --- |
| **Correlations** |
|  | **1** | **2** | **3** | **4** | **5** | **6** | **7** | **8** | **9** | **10** | **11** |
| 1 | **Planctomycetes** |   |   |   |   |   |   |   |   |   |   |   |
| 2 | **Proteobacteria** | 0.86 |   |   |   |   |   |   |   |   |   |   |
| 3 | **Acidobacteria** | -0.57 | -0.87 |   |   |   |   |   |   |   |   |   |
| 4 | **Actinobacteria** | -0.71 | -0.71 | 0.30 |   |   |   |   |   |   |   |   |
| 5 | **Nitrospirae** | 0.07 | -0.03 | 0.46 | -0.68 |   |   |   |   |   |   |   |
| 6 | **Chloroflexi** | -0.89 | -0.86 | 0.80 | 0.39 | 0.37 |   |   |   |   |   |   |
| 7 | **Gemmatimonadetes** | -0.83 | -0.86 | 0.86 | 0.32 | 0.46 | .99\*\* |   |   |   |   |   |
| 8 | **Cyanobacteria** | 0.77 | .98\* | -0.95 | -0.58 | -0.19 | -0.85 | -0.88 |   |   |   |   |
| 9 | **Temperature** | 0.13 | -0.38 | 0.52 | 0.28 | -0.08 | -0.06 | 0.03 | -0.46 |   |   |   |
| 10 | **Humidity** | -0.91 | -0.89 | 0.54 | 0.93 | -0.38 | 0.70 | 0.64 | -0.78 | 0.19 |   |   |
| 11 | **Sunlight** | 0.91 | 0.89 | -0.54 | -0.93 | 0.39 | -0.70 | -0.64 | 0.78 | -0.19 | -1.00\*\* |   |
| \*. Correlation is significant at the 0.05 level (2-tailed). |
| \*\*. Correlation is significant at the 0.01 level (2-tailed). |

**Supplementary Table 3.** KEGG pathway normalized OTU reads for rock and soil samples collected outside and inside the cave.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Super pathway** | **Sub pathway** | **LR-01** | **LS-01** | **LR-05** | **LS-05** |
| **Carbohydrate metabolism** | **Starch and sucrose metabolism** | 0.0051 | 0.0082 | 0.0040 | 0.0062 |
| **Galactose metabolism** | 0.0845 | 0.0731 | 0.0817 | 0.0809 |
| **Amino sugar and nucleotide sugar metabolism** | 0.0004 | 0.0010 | 0.0004 | 0.0005 |
| **Fructose and mannose metabolism** | 0.0003 | 0.0000 | 0.0000 | 0.0000 |
| **Pentose phosphate pathway** | 0.0288 | 0.0162 | 0.0245 | 0.0245 |
| **Citrate cycle (TCA cycle)** | 0.0420 | 0.0746 | 0.0685 | 0.0543 |
| **Ascorbate and aldarate metabolism** | 0.0808 | 0.0700 | 0.0802 | 0.0791 |
| **Amino acid metabolism** | **Arginine and proline metabolism** | 0.1093 | 0.0798 | 0.1075 | 0.1069 |
| **Phenylalanine metabolism** | 0.0006 | 0.0021 | 0.0041 | 0.0014 |
| **Glycine, serine and threonine metabolism** | 0.0499 | 0.0324 | 0.0368 | 0.0418 |
| **Other amino acid metabolism** | **Glutathione metabolism** | 0.0014 | 0.0061 | 0.0045 | 0.0044 |
| **Lipid metabolism** | **Glycerophospholipid metabolism** | 0.0047 | 0.0126 | 0.0037 | 0.0071 |
| **Xenobiotics biodegradation and metabolism** | **Bisphenol degradation** | 0.0382 | 0.0321 | 0.0299 | 0.0359 |
| **Benzoate degradation** | 0.0139 | 0.0163 | 0.0134 | 0.0136 |
| **Energy metabolism**  | **Photosynthesis - antenna proteins** | 0.0000 | 0.0000 | 0.0001 | 0.0000 |
| **Carbon fixation pathways in prokaryotes** | 0.0027 | 0.0071 | 0.0044 | 0.0035 |
| **Methane metabolism** | 0.0101 | 0.0135 | 0.0092 | 0.0054 |
| **Membrane transport** | **ABC transporters** | 0.0319 | 0.0507 | 0.0282 | 0.0216 |

LR-01, LS-01: outside the cave; LR-05, LS-05: inside the cave

**Supplementary Table 4.** Primer information list.

|  |  |  |
| --- | --- | --- |
| Primer type  | Primer name  | Basepair sequence  |
| Forward  | 341F | CCTACGGGNGGCWGCAG |
| Reverse  | 805R | GACTACHVGGGTATCTAATCC |

**Supplementary Figures**



**Supplementary Figure 1.** Heatmap analysis with dendrogram plot at the genus level for all samples



**Supplementary Figure 2.** Visualization of Pearson’s correlation statistical test with 31 Biolog EcoPlate™ carbon sources according to the functional KEGG pathway prediction data of the bacterial communities