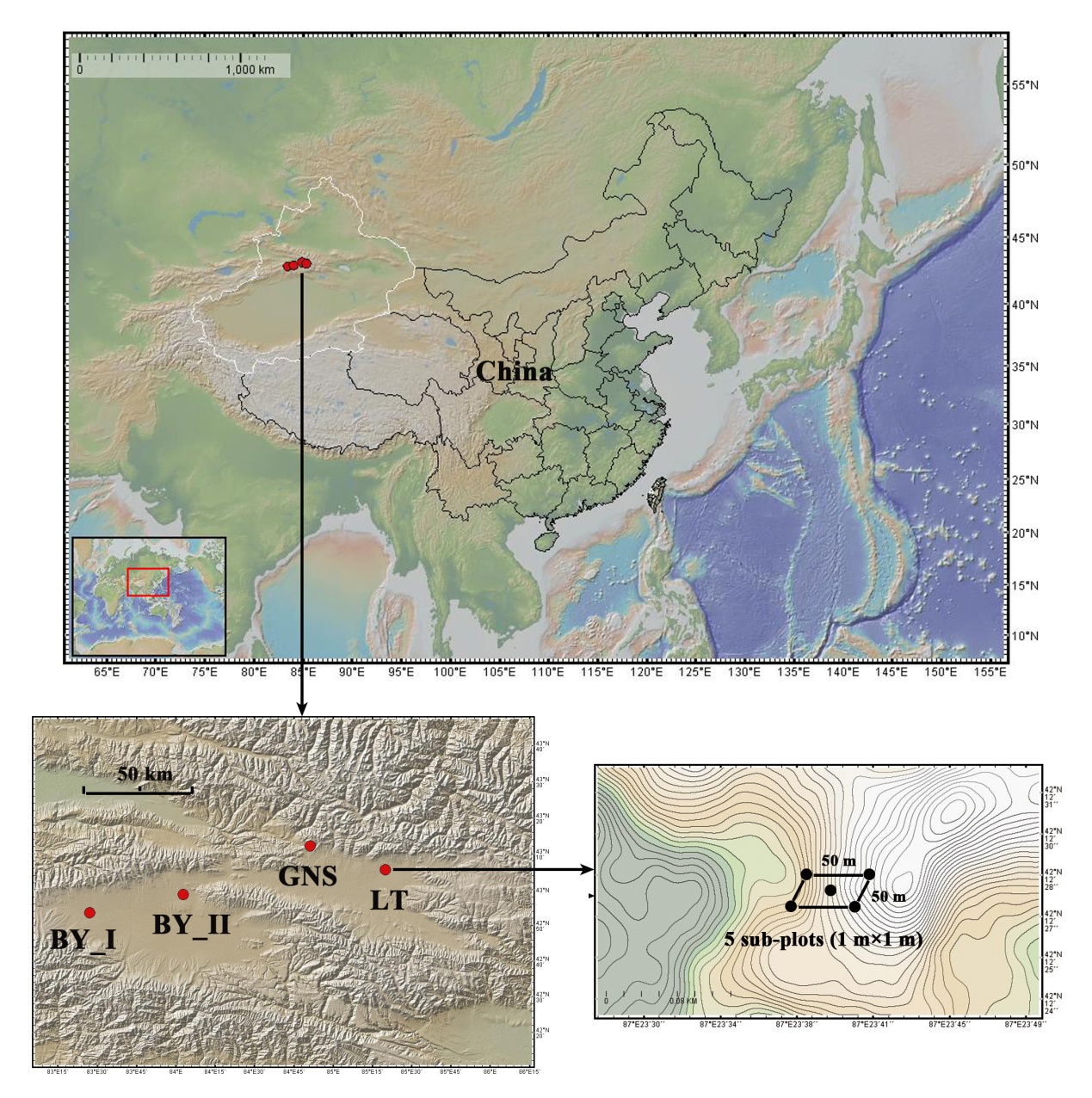
**Figure S1.** Study area and sampling sites (red dots). A total of 4 sampling sites were selected across alpine grasslands of Xinjiang in northern China. Individual plots within a sampling site are shown (black dots). MAP was generated using GeoMapApp, version 3.4.1. (http:// www.geomapapp.org/).

****

**Table S1.** Environmental and soil physicochemical characteristics of the sampling sites (given are the mean value and standard error, SE).

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Site abbr.** | **MAP (mm)** | **MAT (oC)** | **Altitude (m)** | **TOC (%)** | **TN (%)** | **TP (%)** | **pH** | **Moisture (%)** |
| BY\_I | 280.00±0.00a | -3.42±0.00a | 2664.00±0.00a | 4.58±0.16a | 0.55±0.01a | 0.06±0.00a | 7.96±0.03a | 0.41±0.03a |
| BY\_II | 261.00±0.00b | -3.57±0.00b | 2488.00±0.00b | 3.76±0.06b | 0.48±0.01ab | 0.06±0.00a | 8.23±0.05b | 0.33±0.00a |
| GNS | 301.00±0.00c | -4.41±0.00c | 3062.00±0.00c | 7.79±0.29c | 0.87±0.11c | 0.13±0.00b | 5.50±0.15c | 0.89±0.02b |
| LT | 262.00±0.00d | -2.28±0.00d | 2654.00±0.00d | 2.83±0.11d | 0.38±0.01bd | 0.09±0.00c | 8.15±0.09ab | 0.18±0.01c |

Different letters indicate statistical differences at a *P* value of < 0.05 (ANOVA) among sites by Tukey tests.

**Table S2.** The number of bacterial and fungal reads and OTUs, and all functional genes in each site across alpine grasslands of Xinjiang in northern China. Given OTU and gene number are the mean value and standard error (SE).

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Site abbr. | Samples | *16S rRNA* | | *ITS2* | | *Functional genes* |
| No. Reads | No. OTUs | No. Reads | No. OTUs | No. genes |
|  |  |  |  |  |  |  |
| BY\_I | 5 | 182,986 | 1989 ± 28a | 53,101 | 169 ± 23a | 335 ± 4.83a |
| BY\_II | 5 | 152,934 | 1965 ± 13a | 87,581 | 211 ± 20ab | 315 ± 13.31a |
| GNS | 5 | 177,583 | 1578 ± 12b | 30,495 | 193 ± 24ac | 324 ± 9.38a |
| LT | 5 | 173,981 | 1992 ± 43a | 69,576 | 238 ± 13bc | 305 ± 22.98a |

Different letters indicate statistical differences at a *P* value of < 0.05 (ANOVA) among sites by Tukey tests.

**Table S3.** Spearman **c**orrelation between alpha diversity (Shannon index) of phylogenetic groups or microbial functional genes (groups) and environmental variables.

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | MAP | MAT | Altitude | TOC | TN | TP | C/N | N/P | pH | SM | PR |
| Phylogenetic groups |  |  |  |  |  |  |  |  |  |  |  |
| Bacteria | - 0.37 | 0.39 | - 0.34 | - **0.62\*\*** | - 0.31 | - 0.26 | - 0.32 | - 0.23 | **0.75\*\*** | - **0.70\*\*** | - 0.27 |
| Fungi | - 0.14 | 0.32 | 0.14 | - 0.08 | 0.03 | **0.49\*** | - 0.39 | - **0.60\*\*** | 0.11 | - 0.11 | - **0.47\*** |
|  | | | | | | | | | | | |
| Functional genes | 0.13 | 0.13 | - 0.26 | 0.09 | - 0.16 | - 0.33 | 0.19 | 0.33 | 0.08 | 0.11 | 0.29 |
| Functional groups |  | | | | | | | | | | |
|  | | | | | | | | | | | |
| C degradation | 0.07 | 0.10 | - 0.18 | 0.28 | - 0.11 | - 0.28 | 0.30 | 0.35 | 0.12 | 0.11 | 0.35 |
| C fixation | 0.12 | 0.10 | - 0.20 | 0.25 | - 0.13 | - 0.22 | 0.19 | 0.33 | 0.11 | 0.14 | 0.38 |
| Methane metabolism | 0.25 | 0.11 | - 0.34 | 0.20 | - 0.20 | - 0.33 | 0.26 | 0.38 | 0.09 | 0.19 | 0.35 |
| Anammox | 0.33 | 0.20 | - 0.21 | 0.09 | - 0.21 | - 0.31 | 0.23 | 0.16 | 0.18 | 0.20 | 0.22 |
| Ammonification | 0.13 | 0.21 | - 0.08 | 0.11 | - 0.23 | - 0.13 | 0.22 | 0.07 | 0.18 | 0.16 | 0.20 |
| Nitrogen assimilation | 0.22 | 0.10 | - 0.20 | 0.13 | - 0.09 | - 0.17 | 0.28 | 0.09 | 0.20 | 0.19 | 0.28 |
| Assimilatory N reduction | 0.17 | 0.07 | - 0.19 | 0.02 | - 0.25 | - 0.30 | 0.20 | 0.23 | 0.06 | 0.14 | 0.32 |
| Denitrification | 0.18 | 0.09 | - 0.21 | 0.05 | - 0.26 | - 0.35 | 0.15 | 0.19 | 0.10 | 0.12 | 0.29 |
| Dissimilatory N reduction | 0.13 | 0.14 | - 0.19 | 0.08 | - 0.25 | - 0.35 | 0.18 | 0.21 | 0.06 | 0.15 | 0.33 |
| Nitrification | 0.20 | 0.09 | - 0.14 | 0.02 | - 0.21 | - 0.33 | 0.15 | 0.18 | 0.09 | 0.12 | 0.27 |
| Nitrogen fixation | 0.20 | 0.11 | - 0.16 | 0.09 | - 0.29 | - 0.32 | 0.21 | 0.15 | 0.04 | 0.09 | 0.30 |
| Adenylysulfate reductase | 0.18 | 0.06 | - 0.22 | 0.13 | - 0.24 | - 0.21 | 0.33 | 0.14 | 0.12 | 0.20 | 0.26 |
| DMSP degradation | 0.26 | 0.13 | - 0.12 | 0.18 | - 0.19 | - 0.25 | 0.31 | 0.17 | 0.10 | 0.22 | 0.29 |
| Sulfide oxidation | 0.22 | 0.11 | - 0.21 | 0.25 | - 0.16 | - 0.30 | 0.26 | 0.11 | 0.14 | 0.25 | 0.32 |
| Sulfide reduction | 0.19 | 0.14 | - 0.24 | 0.06 | - 0.11 | - 0.20 | 0.20 | 0.08 | 0.16 | 0.20 | 0.26 |

Table S3 (Continue)

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | MAP | MAT | Altitude | TOC | TN | TP | C/N | N/P | pH | SM | PR |
| Sulfur oxidation | 0.18 | 0.15 | - 0.26 | 0.12 | - 0.13 | - 0.22 | 0.19 | 0.11 | 0.19 | 0.19 | 0.24 |
| Phytic acid hydrolysis | 0.20 | 0.12 | - 0.18 | 0.14 | - 0.14 | - 0.23 | 0.15 | 0.12 | 0.10 | 0.22 | 0.29 |
| Polyphosphate degradation | 0.16 | 0.10 | - 0.17 | 0.16 | - 0.19 | - 0.25 | 0.15 | 0.18 | 0.12 | 0.23 | 0.27 |
| Polyphosphate synthesis | 0.13 | 0.09 | - 0.17 | 0.08 | - 0.11 | - 0.25 | 0.08 | 0.20 | 0.05 | 0.10 | 0.19 |
| Aromatics | 0.24 | 0.12 | - 0.20 | 0.09 | - 0.14 | - 0.19 | 0.07 | 0.23 | 0.05 | 0.16 | 0.15 |
| Chlorinated solvents | 0.29 | 0.14 | - 0.14 | 0.12 | - 0.18 | - 0.20 | 0.10 | 0.27 | 0.09 | 0.11 | 0.33 |
| Herbicides related compound | 0.21 | 0.11 | - 0.19 | 0.14 | - 0.22 | - 0.16 | 0.14 | 0.22 | 0.13 | 0.11 | 0.22 |
| Pesticides related compound | 0.20 | 0.13 | - 0.18 | 0.16 | - 0.21 | - 0.19 | 0.13 | 0.24 | 0.22 | 0.15 | 0.30 |
| Other hydrocarbons | 0.19 | 0.16 | - 0.20 | 0.15 | - 0.19 | - 0.18 | 0.14 | 0.23 | 0.22 | 0.19 | 0.29 |
| Arsenic | 0.18 | 0.18 | - 0.29 | 0.17 | - 0.20 | - 0.22 | 0.15 | 0.20 | 0.08 | 0.14 | 0.26 |
| Mercury | 0.22 | 0.12 | - 0.24 | 0.07 | - 0.12 | - 0.14 | 0.09 | 0.25 | 0.12 | 0.18 | 0.33 |
| Tellurium | 0.20 | 0.10 | - 0.21 | 0.10 | - 0.17 | - 0.15 | 0.12 | 0.22 | 0.09 | 0.16 | 0.29 |
| Chromium | 0.23 | 0.14 | - 0.21 | 0.15 | - 0.10 | - 0.19 | 0.11 | 0.21 | 0.13 | 0.12 | 0.30 |
| Copper | 0.15 | 0.18 | - 0.18 | 0.19 | - 0.11 | - 0.22 | 0.13 | 0.23 | 0.16 | 0.16 | 0.31 |
| Silicon | 0.24 | 0.20 | - 0.19 | 0.17 | - 0.13 | - 0.25 | 0.16 | 0.24 | 0.18 | 0.16 | 0.30 |

Asterisk represent significance of correlation (\**P* < 0.05; \*\**P* < 0.01). Abbreviations: MAP, mean annual precipitation (mm); MAT, mean annual temperature (oC); TOC, total organic carbon (%); TN, total nitrogen (%); TP, total phosphorus (%); C/N, carbon/nitrogen; N/P, nitrogen/phosphorus; SM, soil moisture (%), PR, plant richness.

**Table S4.** Significance tests of the functional gene differences in microbial communities among four sampling sites.The top 100 most abundant functional genes, normalized signal intensities determined by GeoChip 5.0, were selected (given are the mean value and standard error, SE).

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Gene** | **Gene category** | **Subcagegory** | **BY\_I** | | **BY\_II** | | **GNS** | | **LT** | | ***P* (ANOVA)** |
| **Mean** | **SE** | **Mean** | **SE** | **Mean** | **SE** | **Mean** | **SE** |
| *amyA* | Carbon cycling | Carbon degradation | 3043.10a | 46.05 | 2949.29a | 169.76 | 2988.56a | 99.97 | 2796.41a | 238.49 | 0.715 |
| *chitinase* | Carbon cycling | Carbon degradation | 727.58a | 10.42 | 705.91a | 40.15 | 713.09a | 23.99 | 664.61a | 61.76 | 0.702 |
| *acetylglucosaminidase* | Carbon cycling | Carbon degradation | 479.69a | 8.36 | 466.65a | 30.27 | 484.24a | 18.20 | 443.66a | 42.36 | 0.737 |
| *ara* | Carbon cycling | Carbon degradation | 448.27a | 5.91 | 435.68a | 22.78 | 439.23a | 12.93 | 410.68a | 36.51 | 0.685 |
| *xylanase* | Carbon cycling | Carbon degradation | 395.96a | 4.76 | 382.24a | 23.47 | 390.77a | 14.58 | 360.96a | 31.63 | 0.666 |
| *cellobiase* | Carbon cycling | Carbon degradation | 366.28a | 5.49 | 348.67a | 22.64 | 360.66a | 13.67 | 324.47a | 33.42 | 0.541 |
| *phenol oxidase* | Carbon cycling | Carbon degradation | 358.99a | 5.03 | 345.71a | 22.85 | 353.54a | 13.24 | 323.53a | 33.30 | 0.667 |
| *xyla* | Carbon cycling | Carbon degradation | 269.68a | 3.86 | 265.48a | 15.87 | 266.00a | 8.04 | 249.10a | 22.10 | 0.748 |
| *cutinase* | Carbon cycling | Carbon degradation | 243.18a | 2.61 | 241.62a | 7.74 | 241.16a | 4.88 | 230.16a | 13.70 | 0.679 |
| *endochitinase* | Carbon cycling | Carbon degradation | 237.20a | 3.88 | 230.03a | 13.01 | 232.69a | 7.73 | 217.37a | 19.20 | 0.706 |
| *mannanase* | Carbon cycling | Carbon degradation | 207.15a | 2.70 | 198.74a | 11.42 | 201.26a | 6.98 | 191.21a | 16.97 | 0.777 |
| *endoglucanase* | Carbon cycling | Carbon degradation | 185.01a | 2.18 | 182.22a | 8.81 | 183.88a | 5.11 | 174.30a | 12.76 | 0.793 |
| *RgaE* | Carbon cycling | Carbon degradation | 179.45a | 2.79 | 178.39a | 9.32 | 182.18a | 5.46 | 168.45a | 14.30 | 0.730 |
| *pme* | Carbon cycling | Carbon degradation | 165.97a | 3.24 | 160.82a | 10.84 | 166.33a | 5.39 | 152.57a | 13.56 | 0.699 |
| *vana* | Carbon cycling | Carbon degradation | 162.91a | 1.73 | 159.01a | 6.54 | 163.99a | 3.44 | 152.65a | 10.56 | 0.611 |
| *pectinase (pectate lyase)* | Carbon cycling | Carbon degradation | 162.79a | 3.24 | 157.65a | 9.59 | 160.51a | 6.33 | 153.40a | 12.90 | 0.886 |
| *rgl* | Carbon cycling | Carbon degradation | 161.41a | 2.29 | 155.91a | 8.23 | 159.59a | 4.29 | 149.02a | 11.69 | 0.671 |
| *glucoamylase* | Carbon cycling | Carbon degradation | 155.56a | 4.77 | 154.76a | 12.07 | 158.37a | 5.89 | 144.82a | 16.20 | 0.825 |
| *cda* | Carbon cycling | Carbon degradation | 146.17a | 3.43 | 142.43a | 9.43 | 143.64a | 5.58 | 133.66a | 12.54 | 0.748 |
| *alginase* | Carbon cycling | Carbon degradation | 129.51a | 1.21 | 122.89a | 6.11 | 130.51a | 4.74 | 119.77a | 10.64 | 0.614 |
| *exoglucanase* | Carbon cycling | Carbon degradation | 128.41a | 2.47 | 127.52a | 6.74 | 129.64a | 4.11 | 118.88a | 11.06 | 0.685 |

Table S4 (Continue)

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Gene** | **Gene category** | **Subcagegory** | **BY\_I** | | **BY\_II** | | **GNS** | | **LT** | | ***P* (ANOVA)** |
| **Mean** | **SE** | **Mean** | **SE** | **Mean** | **SE** | **Mean** | **SE** |
| *pula* | Carbon cycling | Carbon degradation | 111.70a | 2.43 | 108.08a | 7.26 | 110.70a | 4.55 | 102.45a | 10.20 | 0.772 |
| *pec Cdeg* | Carbon cycling | Carbon degradation | 89.49a | 1.51 | 87.25a | 4.97 | 86.83a | 2.26 | 82.28a | 5.91 | 0.658 |
| *limeh* | Carbon cycling | Carbon degradation | 84.26a | 0.40 | 81.27a | 3.13 | 83.24a | 1.83 | 79.26a | 5.30 | 0.706 |
| *fthfs* | Carbon cycling | Carbon fixation | 473.75a | 9.87 | 457.34a | 32.87 | 474.70a | 19.51 | 429.97a | 48.90 | 0.726 |
| *tktA* | Carbon cycling | Carbon fixation | 466.06a | 4.73 | 454.04a | 22.08 | 464.44a | 11.50 | 431.58a | 32.01 | 0.621 |
| *rubisco* | Carbon cycling | Carbon fixation | 300.01a | 6.63 | 292.99a | 17.28 | 293.12a | 10.25 | 272.13a | 25.56 | 0.668 |
| *CsoS1 CcmK* | Carbon cycling | Carbon fixation | 297.15a | 3.89 | 282.50a | 19.92 | 293.62a | 12.85 | 267.14a | 26.07 | 0.636 |
| *GAPDH Calvin* | Carbon cycling | Carbon fixation | 286.27a | 4.99 | 281.20a | 18.13 | 285.23a | 12.86 | 262.02a | 25.20 | 0.725 |
| *FBPase* | Carbon cycling | Carbon fixation | 277.87a | 3.18 | 271.48a | 14.85 | 276.17a | 7.84 | 255.03a | 21.08 | 0.630 |
| *TIM* | Carbon cycling | Carbon fixation | 228.41a | 3.69 | 219.26a | 11.87 | 230.42a | 6.64 | 210.83a | 17.24 | 0.591 |
| *PRI* | Carbon cycling | Carbon fixation | 189.88a | 2.59 | 186.19a | 10.32 | 192.65a | 6.08 | 175.06a | 14.98 | 0.602 |
| *pgk* | Carbon cycling | Carbon fixation | 180.41a | 1.89 | 176.05a | 8.41 | 178.79a | 4.10 | 165.93a | 13.27 | 0.605 |
| *ccmL* | Carbon cycling | Carbon fixation | 166.07a | 3.01 | 161.93a | 11.38 | 167.02a | 5.30 | 151.04a | 15.22 | 0.663 |
| *FBP aldolase* | Carbon cycling | Carbon fixation | 139.06a | 2.04 | 133.77a | 7.36 | 137.87a | 5.51 | 125.88a | 11.06 | 0.581 |
| *PRK* | Carbon cycling | Carbon fixation | 100.76a | 1.45 | 98.49a | 5.90 | 98.17a | 3.97 | 93.58a | 9.02 | 0.846 |
| *mcra* | Carbon cycling | Methane | 149.24a | 2.73 | 141.70a | 11.23 | 144.16a | 7.70 | 133.62a | 14.02 | 0.731 |
| *urec* | Nitrogen cycling | Ammonification | 419.62a | 5.83 | 409.27a | 20.72 | 423.38a | 11.35 | 391.43a | 31.20 | 0.673 |
| *nasa* | Nitrogen cycling | Assimilatory N reduction | 106.16a | 1.75 | 103.19a | 6.25 | 104.81a | 4.02 | 99.22a | 8.08 | 0.830 |
| *nirb* | Nitrogen cycling | Assimilatory N reduction | 84.44a | 1.37 | 84.79a | 4.71 | 87.69a | 2.33 | 81.13a | 6.39 | 0.748 |
| *narg* | Nitrogen cycling | Denitrification | 742.52a | 6.88 | 733.83a | 28.98 | 745.62a | 16.46 | 699.81a | 44.92 | 0.651 |
| *nosz* | Nitrogen cycling | Denitrification | 518.43a | 9.97 | 504.79a | 30.45 | 520.34a | 18.07 | 477.22a | 45.21 | 0.466 |
| nirs | Nitrogen cycling | Denitrification | 398.27a | 8.40 | 392.17a | 24.24 | 399.02a | 14.00 | 369.90a | 36.33 | 0.795 |

Table S4 (Continue)

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Gene** | **Gene category** | **Subcagegory** | **BY\_I** | | **BY\_II** | | **GNS** | | **LT** | | ***P* (ANOVA)** |
| **Mean** | **SE** | **Mean** | **SE** | **Mean** | **SE** | **Mean** | **SE** |
| *nirk* | Nitrogen cycling | Denitrification | 359.04a | 7.11 | 350.74a | 22.01 | 351.76a | 12.92 | 332.38a | 30.55 | 0.814 |
| *norb* | Nitrogen cycling | Denitrification | 82.93a | 0.93 | 81.05a | 3.82 | 84.46a | 2.41 | 75.49a | 5.34 | 0.331 |
| *napa* | Nitrogen cycling | Dissimilatory N reduction | 136.84a | 3.07 | 131.45a | 8.94 | 131.44a | 4.79 | 122.10a | 12.33 | 0.644 |
| *nrfa* | Nitrogen cycling | Dissimilatory N reduction | 96.86a | 1.48 | 93.16a | 6.73 | 93.71a | 4.65 | 87.18a | 9.23 | 0.739 |
| *nitrate reductase* | Nitrogen cycling | N Assimilation | 82.23a | 1.37 | 80.63a | 3.59 | 79.21a | 2.97 | 75.80a | 6.53 | 0.718 |
| *nifh* | Nitrogen cycling | Nitrogen fixation | 734.30a | 16.30 | 702.54a | 54.55 | 729.83a | 34.79 | 656.04a | 75.14 | 0.680 |
| *arsc* | Metal Homeostasis | Arsenic | 617.81a | 9.94 | 603.02a | 37.83 | 607.07a | 18.87 | 567.79a | 52.81 | 0.754 |
| *aoxb* | Metal Homeostasis | Arsenic | 171.91a | 1.63 | 167.84a | 8.08 | 175.30a | 5.75 | 158.77a | 11.81 | 0.488 |
| *terc* | Metal Homeostasis | Tellurium | 572.50a | 8.75 | 552.90a | 33.83 | 571.81a | 18.04 | 519.88a | 46.97 | 0.595 |
| *tehb* | Metal Homeostasis | Tellurium | 149.87a | 2.32 | 141.62a | 10.80 | 148.86a | 5.54 | 135.43a | 14.49 | 0.684 |
| *mer* | Metal Homeostasis | Mercury | 495.75a | 6.09 | 484.47a | 24.17 | 492.15a | 11.93 | 460.18a | 35.65 | 0.685 |
| *poba* | Organic Remediation | Aromatics | 249.31a | 2.81 | 244.07a | 10.70 | 247.90a | 5.82 | 234.83a | 15.59 | 0.737 |
| *bphF1* | Organic Remediation | Aromatics | 200.62a | 3.36 | 192.99a | 11.04 | 199.72a | 5.83 | 185.50a | 16.52 | 0.723 |
| *catechol* | Organic Remediation | Aromatics | 188.56a | 2.61 | 186.98a | 7.04 | 182.76a | 4.89 | 180.37a | 9.53 | 0.802 |
| *pcag* | Organic Remediation | Aromatics | 182.48a | 1.15 | 179.33a | 7.25 | 181.70a | 4.14 | 171.10a | 11.23 | 0.655 |
| *arylest* | Organic Remediation | Aromatics | 182.55a | 3.34 | 177.50a | 11.99 | 181.47a | 6.84 | 167.42a | 16.07 | 0.746 |
| *catechol b* | Organic Remediation | Aromatics | 177.48a | 2.42 | 177.98a | 6.94 | 179.19a | 3.84 | 167.42a | 10.76 | 0.599 |
| *badh* | Organic Remediation | Aromatics | 177.52a | 2.30 | 172.83a | 9.23 | 174.42a | 5.66 | 164.08a | 13.41 | 0.728 |
| *one ring 23diox* | Organic Remediation | Aromatics | 171.13a | 3.90 | 169.25a | 7.97 | 172.80a | 4.39 | 161.98a | 14.01 | 0.819 |
| *mdlc* | Organic Remediation | Aromatics | 166.02a | 2.01 | 163.81a | 5.29 | 162.94a | 3.01 | 158.26a | 8.51 | 0.771 |
| *tfda* | Organic Remediation | Aromatics | 147.82a | 1.53 | 143.14a | 5.63 | 147.30a | 3.99 | 136.31a | 11.83 | 0.627 |
| *cmci* | Organic Remediation | Aromatics | 148.04a | 0.92 | 143.24a | 6.51 | 146.28a | 2.90 | 134.42a | 10.06 | 0.436 |

Table S4 (Continue)

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Gene** | **Gene category** | **Subcagegory** | **BY\_I** | | **BY\_II** | | **GNS** | | **LT** | | ***P* (ANOVA)** |
| **Mean** | **SE** | **Mean** | **SE** | **Mean** | **SE** | **Mean** | **SE** |
| *nitrilase* | Organic Remediation | Aromatics | 133.65a | 2.74 | 130.96a | 8.04 | 131.97a | 4.94 | 124.21a | 10.80 | 0.810 |
| *xylj* | Organic Remediation | Aromatics | 128.70a | 0.44 | 124.68a | 4.04 | 128.87a | 2.07 | 122.59a | 5.82 | 0.567 |
| *bphd* | Organic Remediation | Aromatics | 125.49a | 1.89 | 121.54a | 5.70 | 127.75a | 3.58 | 116.30a | 8.96 | 0.522 |
| *xylg* | Organic Remediation | Aromatics | 119.99a | 1.41 | 116.74a | 4.40 | 120.19a | 3.16 | 114.84a | 6.52 | 0.778 |
| *nhh* | Organic Remediation | Aromatics | 116.96a | 0.42 | 115.09a | 3.99 | 118.26a | 2.87 | 109.97a | 6.81 | 0.538 |
| *bphc* | Organic Remediation | Aromatics | 113.78a | 1.14 | 109.98a | 5.52 | 111.71a | 3.62 | 105.54a | 8.61 | 0.746 |
| *catb* | Organic Remediation | Aromatics | 111.20a | 1.56 | 109.01a | 5.00 | 110.45a | 3.52 | 102.06a | 8.00 | 0.581 |
| *mult ring 12DiOx* | Organic Remediation | Aromatics | 104.57a | 1.18 | 101.05a | 3.73 | 99.33a | 2.06 | 97.33a | 6.64 | 0.629 |
| *one ring 12diox* | Organic Remediation | Aromatics | 97.65a | 0.51 | 94.81a | 3.93 | 96.14a | 3.37 | 91.05a | 8.10 | 0.794 |
| *nagg* | Organic Remediation | Aromatics | 96.40a | 1.35 | 91.51a | 5.93 | 95.87a | 3.18 | 87.74a | 7.51 | 0.600 |
| *dehh109* | Organic Remediation | Chlorinated solvents | 167.68a | 2.53 | 161.60a | 7.37 | 163.79a | 5.53 | 153.43a | 10.62 | 0.560 |
| *exaa(moxf)* | Organic Remediation | Chlorinated solvents | 146.70a | 1.52 | 141.86a | 6.33 | 145.18a | 4.03 | 133.17a | 10.69 | 0.488 |
| *rd* | Organic Remediation | Chlorinated solvents | 84.36a | 3.08 | 84.82a | 7.96 | 86.17a | 5.55 | 79.70a | 9.89 | 0.924 |
| *phn* | Organic Remediation | Herbicides related compound | 240.08a | 3.43 | 235.14a | 11.96 | 239.68a | 6.99 | 221.42a | 18.57 | 0.651 |
| *pcpe* | Organic Remediation | Herbicides related compound | 158.80a | 2.15 | 157.54a | 7.40 | 159.68a | 3.74 | 144.65a | 11.59 | 0.435 |
| *atza* | Organic Remediation | Herbicides related compound | 102.46a | 4.08 | 99.68a | 8.20 | 101.81a | 5.05 | 90.60a | 10.97 | 0.671 |
| *atzb* | Organic Remediation | Herbicides related compound | 98.39a | 0.61 | 95.33a | 4.30 | 98.27a | 1.94 | 89.13a | 7.22 | 0.415 |
| *alkb* | Organic Remediation | Other hydrocarbons | 300.28a | 3.04 | 290.26a | 14.43 | 301.10a | 8.68 | 275.78a | 22.58 | 0.569 |
| *chnb* | Organic Remediation | Other hydrocarbons | 146.90a | 3.23 | 144.66a | 6.04 | 144.34a | 4.29 | 136.44a | 10.62 | 0.708 |
| *alkk* | Organic Remediation | Others | 116.89a | 1.08 | 110.34a | 6.78 | 119.06a | 3.96 | 105.11a | 9.77 | 0.410 |
| *linb* | Organic Remediation | Pesticides related compound | 230.13a | 2.53 | 224.96a | 12.00 | 230.31a | 7.14 | 212.02a | 15.96 | 0.596 |
| *phytase* | Phosphorus cycling | Phytic acid hydrolysis | 151.07a | 3.32 | 145.24a | 9.27 | 147.62a | 4.13 | 139.18a | 10.75 | 0.730 |

Table S4 (Continue)

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Gene** | **Gene category** | **Subcagegory** | **BY\_I** | | **BY\_II** | | **GNS** | | **LT** | | ***P* (ANOVA)** |
| **Mean** | **SE** | **Mean** | **SE** | **Mean** | **SE** | **Mean** | **SE** |
| *ppx* | Phosphorus cycling | Polyphosphate degradation | 880.76a | 10.17 | 853.42a | 46.54 | 881.21a | 28.62 | 803.68a | 70.33 | 0.588 |
| *ppk* | Phosphorus cycling | Polyphosphate synthesis | 309.14a | 4.88 | 302.88a | 18.75 | 311.07a | 9.74 | 289.46a | 24.61 | 0.786 |
| *aps apra* | Sulfur cycling | Adenylylsulfate reductase | 162.14a | 2.80 | 158.38a | 9.65 | 165.68a | 5.64 | 149.30a | 13.68 | 0.612 |
| *cysI* | Sulfur cycling | Other | 209.89a | 1.66 | 197.48a | 10.64 | 208.61a | 5.32 | 190.72a | 18.75 | 0.576 |
| *cysJ* | Sulfur cycling | Reduction | 293.87a | 4.40 | 288.27a | 13.23 | 295.52a | 8.04 | 275.30a | 19.18 | 0.664 |
| *fccab* | Sulfur cycling | Sulfide oxidation | 96.98a | 1.94 | 93.33a | 4.55 | 95.66a | 3.29 | 87.34a | 7.43 | 0.510 |
| *sqr* | Sulfur cycling | Sulfide oxidation | 85.09a | 1.43 | 80.10a | 4.42 | 83.52a | 2.38 | 78.91a | 6.29 | 0.688 |
| *dsra* | Sulfur cycling | Sulfite reduction | 706.53a | 11.72 | 685.57a | 51.20 | 699.72a | 33.25 | 637.57a | 70.44 | 0.729 |
| *dsrB* | Sulfur cycling | Sulfite reduction | 508.00a | 7.26 | 489.07a | 35.04 | 498.83a | 19.59 | 462.86a | 44.41 | 0.743 |
| *Sir* | Sulfur cycling | Sulfite reduction | 156.55a | 1.53 | 150.53a | 9.12 | 154.88a | 5.56 | 143.24a | 11.25 | 0.636 |
| *soxY* | Sulfur cycling | Sulfur oxidation | 180.25a | 1.56 | 174.83a | 6.68 | 179.27a | 4.42 | 168.95a | 11.01 | 0.646 |
| *B lactamase A* | Virulence | Antibiotic resistance | 145.17a | 2.80 | 138.31a | 8.45 | 143.61a | 4.23 | 133.37a | 10.58 | 0.654 |
| *b lactamase* | Virulence | Antibiotic resistance | 101.75a | 0.85 | 98.01a | 3.28 | 105.64a | 2.64 | 93.45a | 7.72 | 0.282 |

Same letters indicate statistical differences at a *P* value of > 0.05 (ANOVA) among sites by Tukey tests.

**Table S5.** Significance tests of the differences in functional groups (subcategory) of the microbial communities among four sampling sites.We selected 30 most abundant groups, normalized signal intensities determined by GeoChip 5.0. (given are the mean value and standard error, SE).

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Subcagegory** | **BY\_I** | | **BY\_II** | | **GNS** | | **LT** | | ***P* (ANOVA)** |
| **Mean** | **SE** | **Mean** | **SE** | **Mean** | **SE** | **Mean** | **SE** |
| Carbon degradation | 9807.53a | 142.85 | 9512.77a | 548.87 | 9676.44a | 318.87 | 9008.30a | 795.00 | 0.711 |
| Carbon fixation | 3549.65a | 54.55 | 3444.14a | 207.33 | 3533.38a | 122.57 | 3241.76a | 297.11 | 0.664 |
| Methane metabolism | 265.71a | 4.80 | 253.79a | 19.34 | 265.95a | 12.16 | 238.96a | 26.92 | 0.679 |
| Denitrification | 2101.20a | 32.16 | 2062.57a | 109.38 | 2101.21a | 63.64 | 1954.80a | 162.20 | 0.726 |
| Nitrogen fixation | 734.30a | 16.30 | 702.54a | 54.55 | 729.83a | 34.79 | 656.04a | 75.14 | 0.680 |
| Ammonification | 612.43a | 8.49 | 592.99a | 32.31 | 610.41a | 19.40 | 565.20a | 49.26 | 0.696 |
| Assimilatory N reduction | 299.37a | 3.60 | 293.08a | 15.12 | 301.59a | 9.33 | 281.97a | 21.52 | 0.761 |
| Dissimilatory N reduction | 233.70a | 4.17 | 224.61a | 15.57 | 225.14a | 9.20 | 209.28a | 21.56 | 0.681 |
| Nitrogen assimilation | 82.23a | 1.37 | 80.63a | 3.59 | 79.21a | 2.97 | 75.80a | 6.53 | 0.718 |
| Nitrification | 63.76a | 1.30 | 61.88a | 5.15 | 62.58a | 2.85 | 57.51a | 5.95 | 0.745 |
| Arsenic | 917.58a | 13.18 | 897.88a | 54.45 | 910.85a | 29.13 | 844.49a | 76.34 | 0.722 |
| Tellurium | 722.37a | 11.01 | 694.52a | 44.55 | 720.67a | 23.58 | 655.31a | 61.42 | 0.618 |
| Mercury | 582.62a | 6.44 | 568.98a | 27.09 | 579.09a | 13.79 | 541.54a | 41.31 | 0.676 |
| Copper | 31.28a | 0.28 | 29.13a | 1.65 | 30.71a | 1.33 | 28.09a | 2.49 | 0.515 |
| Chromium | 28.83a | 0.76 | 29.46a | 1.31 | 29.70a | 0.79 | 28.08a | 1.70 | 0.781 |
| Aromatics | 4298.57a | 45.47 | 4183.02a | 194.33 | 4257.05a | 115.96 | 3998.10a | 299 | 0.691 |
| Herbicides related compound | 731.95a | 10.07 | 716.04a | 36.48 | 728.63a | 20.54 | 668.13a | 57.71 | 0.582 |
| Other hydrocarbons | 600.48a | 8.23 | 585.29a | 28.30 | 596.73a | 17.54 | 553.86a | 46.00 | 0.659 |
| Chlorinated solvents | 465.48a | 6.56 | 452.87a | 24.21 | 462.77a | 16.45 | 427.95a | 35.77 | 0.664 |
| Pesticides related compound | 299.04a | 3.46 | 293.93a | 14.38 | 299.97a | 8.00 | 276.58a | 20.78 | 0.588 |
| Polyphosphate degradation | 880.76a | 10.17 | 853.42a | 46.54 | 881.21a | 28.62 | 803.68a | 70.33 | 0.588 |
| Polyphosphate synthesis | 309.14a | 4.88 | 302.88a | 18.75 | 311.07a | 9.74 | 289.46a | 24.61 | 0.786 |
| Phytic acid hydrolysis | 151.07a | 3.32 | 145.24a | 9.27 | 147.62a | 4.13 | 139.18a | 10.75 | 0.730 |
| Sulfite reduction | 1371.07a | 19.81 | 1325.18a | 95.27 | 1353.43a | 58.25 | 1243.67a | 126.05 | 0.726 |
| Sulfur oxidation | 330.53a | 3.45 | 322.62a | 13.79 | 329.13a | 9.22 | 308.62a | 21.38 | 0.662 |
| Sulfide reduction | 293.87a | 4.40 | 288.27a | 13.23 | 295.52a | 8.04 | 275.30a | 19.18 | 0.664 |
| Adenylysulfate reductase | 230.18a | 3.08 | 224.09a | 13.91 | 233.61a | 8.42 | 211.05a | 19.93 | 0.631 |
| Sulfide oxidation | 182.07a | 3.29 | 173.43a | 8.92 | 179.18a | 5.64 | 166.25a | 13.70 | 0.606 |
| DMSP degradation | 63.93a | 0.91 | 61.70a | 4.33 | 63.63a | 1.85 | 57.11a | 5.79 | 0.565 |
| Antibiotic resistance | 353.81a | 4.68 | 339.24a | 17.01 | 352.89a | 9.34 | 322.34a | 27.18 | 0.530 |

Same letters indicate statistical differences at a *P* value of > 0.05 (ANOVA) among sites by Tukey tests.

**Table S6.** The correlation between bacterial and fungal communities, and functional gene groups (Bray-Curits distance) for all pairwise samples. The correlation (*r*) and significance (*P*) were determined by Mantel tests based on 9,999 permutations.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Bacteria** | | **Fungi** | |
|  | ***r*** | ***P*** | ***r*** | ***P*** |
| **Metal Homeostasis** |  |  |  |  |
| Arsenic | 0.019 | 0.331 | 0.136 | 0.230 |
| Chromium | 0.012 | 0.381 | 0.038 | 0.381 |
| Copper | 0.080 | 0.258 | 0.146 | 0.202 |
| Mercury | 0.002 | 0.345 | 0.139 | 0.232 |
| Silicon | -0.022 | 0.401 | 0.154 | 0.198 |
| Tellurium | 0.056 | 0.290 | 0.170 | 0.176 |
| **Organic Remediation** |  |  |  |  |
| Aromatics | 0.037 | 0.300 | 0.156 | 0.198 |
| Chlorinated solvents | 0.050 | 0.283 | 0.168 | 0.185 |
| halogenated compounds | 0.084 | 0.234 | 0.107 | 0.227 |
| Herbicides related compound | 0.040 | 0.282 | 0.171 | 0.183 |
| Other Hydrocarbons | 0.048 | 0.281 | 0.183 | 0.170 |
| Pesticides related compound | 0.040 | 0.300 | 0.160 | 0.199 |
| Polycyclic aromatics | -0.073 | 0.569 | 0.059 | 0.339 |
| **Secondary metabolism** |  |  |  |  |
| Pigments | 0.054 | 0.287 | 0.197 | 0.135 |
| **Virulence** |  |  |  |  |
| Antibiotic resistance | 0.065 | 0.274 | 0.166 | 0.196 |
| Degradation | 0.044 | 0.287 | 0.152 | 0.211 |
| **Others** | 0.053 | 0.306 | 0.175 | 0.158 |

**Table S7.** Summary statistics for the distance-decay relationships based on the bacterial and fungal communities, and functional genes across alpine grasslands of Xinjiang in northern China.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | *n* | Intercept | Slope (*z*) | *Avg similarity* | Mantel *r* | *P* |
| Bacteria | 399 | -0.41 | -0.157 | -0.93 | -0.47 | < 0.001 |
| Fungi | 399 | -0.73 | -0.214 | -1.44 | -0.34 | < 0.001 |
| Functional genes | 399 | -0.08 | -0.008 | -0.10 | -0.02 | 0.28 |

Statistics result of bacterial, fungal communities and microbial functional genes from ordinary least squares regressions of log-transformed bacterial OTU similarity against log-transformed geographical distance. n is the corresponding number of similarity pairs. To account for zero similarity values, logarithmic transformations were of the form log(*X*+1). The Mantel statistic *r* estimates the correlation between OTU similarity matrices and geographical distance matrices. *P*-values are based on 9,999 randomized pairings of OTU similarity and geographical distance.