**Supporting Online Materials**

**Table S1.** Summary of environmental parameters analyzed by two-tailed T-test.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Environmental parameters | | Alpine meadow | Alpine steppe meadow | *FDR* |
| Vegetation properties | Plant biomass | 23.23±8.25 | 36.31±7.89 | 0.005 |
| Plant diversity | 4.10±1.29 | 7.08±1.15 | 0.004 |
| Plant species | 10.20±1.32 | 11.60±1.58 | 0.063 |
| Soil properties | Moisture (%) | 0.20±0.03 | 0.18±0.03 | 0.100 |
| pH | 7.54±0.10 | 7.70±0.05 | 0.000 |
| Total nitrogen (g/100g) | 0.39±0.04 | 0.26±0.02 | 0.000 |
| Total phosphorus (g/100g) | 0.058±0.004 | 0.045±0.002 | 0.000 |
| Total Sulfur (g/100g) | 0.072±0.02 | 0.045±0.004 | 0.004 |
| NH4+-N (mg/kg) | 5.55±1.80 | 4.98±1.42 | 0.777 |
| NO3--N (mg/kg) | 37.30±11.28 | 38.11±8.47 | 0.858 |
| Soil organic carbon (g/100g) | 4.04±0.45 | 2.51±0.28 | 0.000 |
| Available nitrogen (mg/kg) | 277.55±40.64 | 207.40±33.26 | 0.004 |
| Rapidly available Phosphorus (mg/kg) | 28.25±5.38 | 8.65±2.69 | 0.000 |

Data present the mean value and standard deviation.

**Table S2.** The number of soil microbial OTUs and relative abundance in two meadow sites

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Domain | Phylum | OTU number | | |  |  | Relative abundance | | |
| Total (%) | AM | ASM | *FDR* |  | AM | ASM | *FDR* |
| Archaea | *Crenarchaeota* | 109 (0.53) | 25.70±6.68 | 28.20±5.92 | 0.411 |  | 0.021±0.004 | 0.023±0.05 | 0.120 |
| *Euryarchaeota* | 24 (0.12) | 1.00±1.15 | 2.00±1.41 | 0.164 |  | 0.001±0.000 | 0.001±0.000 | 0.357 |
| Bacteria | *Proteobacteria* | 6257 (30.14) | 980.00±159.79 | 1157.80±94.34 | 0.014 |  | 0.286±0.024 | 0.262±0.027 | 0.088 |
| *α-* | 2719 (13.10) | 498.60±80.20 | 541.20±47.13 | 0.212 |  | 0.181±0.017 | 0.153±0.021 | 0.009 |
| *β-* | 592 (2.85) | 108.30±24.99 | 121.10±15.48 | 0.222 |  | 0.029±0.003 | 0.024±0.002 | 0.003 |
| *δ-* | 1571 (7.57) | 194.70±37.91 | 265.70±28.76 | 0.000 |  | 0.029±0.003 | 0.037±0.005 | 0.000 |
| *γ-* | 1293 (6.23) | 172.60±25.59 | 222.00±23.56 | 0.000 |  | 0.045±0.007 | 0.048±0.010 | 0.577 |
| *Acidobacteria* | 3135 (15.10) | 650.20±117.67 | 781.00±79.06 | 0.016 |  | 0.251±0.024 | 0.267±0.012 | 0.119 |
| *Actinobacteria* | 2757 (13.28) | 607.60±90.63 | 669.20±71.95 | 0.165 |  | 0.207±0.045 | 0.170±0.027 | 0.077 |
| *Planctomycetes* | 2429 (11.70) | 389.60±63.68 | 487.30±40.03 | 0.003 |  | 0.050±0.006 | 0.063±0.004 | 0.000 |
| *Bacteroidetes* | 1600 (7.71) | 303.10±59.87 | 332.90±40.57 | 0.235 |  | 0.057±0.012 | 0.056±0.007 | 0.841 |
| *Verrucomicrobia* | 1146 (5.52) | 199.50±41.12 | 227.20±35.29 | 0.170 |  | 0.046±0.008 | 0.050±0.011 | 0.412 |
| *Chloroflexi* | 1033 (4.98) | 166.00±23.07 | 238.40±20.46 | 0.000 |  | 0.025±0.003 | 0.035±0.003 | 0.000 |
| *Firmicutes* | 1011 (4.87) | 159.50±23.47 | 203.90±20.70 | 0.000 |  | 0.023±0.002 | 0.031±0.004 | 0.000 |
| *Gemmatimonadetes* | 401 (1.93) | 85.70±16.74 | 84.50±9.81 | 0.847 |  | 0.019±0.003 | 0.018±0.003 | 0.420 |
| *Armatimonadetes* | 227 (1.09) | 25.80±6.18 | 51.00±6.43 | 0.000 |  | 0.002±0.001 | 0.005±0.001 | 0.000 |
| others | 634 (3.05) | 87.00±11.25 | 111.00±11.44 | 0.000 |  | 0.114±0.002 | 0.020±0.004 | 0.005 |
| total | 20763 (100) | 3680.70±559.64 | 4374.40±301.34 | 0.007 |  |  |  |  |

Data present the mean value and standard deviation.

**Table S3.** The number of OTUs and relative abundance of phylum Acidobacteria in two meadow sites

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Subgroups | OTU number | | |  | | |  | Relative abundance (%) | | |
| AM | ASM | *P=value* | |  | AM | | | ASM | *P-value* | |
| Subgroup 3 | 16±.29 | 24.70±1.37 | 0.000 | |  | 0.20±0.05 | | | 0.36±0.09 | 0.000 | |
| Subgroup 4 | 218.90±12.66 | 247.30±10.03 | 0.096 | |  | 9.21±2.43 | | | 10.47±0.74 | 0.135 | |
| Subgroup 6 | 238.90±17.60 | 288.80±10.42 | 0.025 | |  | 9.44±1.53 | | | 10.13±0.81 | 0.224 | |
| Subgroup 7 | 28.50±2.41 | 37.90±2.11 | 0.009 | |  | 0.80±0.19 | | | 1.05±0.15 | 0.004 | |
| Subgroup 10 | 28.60±2.34 | 38.80±1.95 | 0.004 | |  | 0.60±0.19 | | | 0.88±0.27 | 0.016 | |
| Subgroup 16 | 68.10±3.25 | 88.80±3.06 | 0.000 | |  | 2.77±0.64 | | | 2.82±0.24 | 0.829 | |
| Subgroup 17 | 23.80±1.27 | 25.10±0.97 | 0.427 | |  | 0.76±0.17 | | | 0.54±0.13 | 0.004 | |

Data present the mean value and standard deviation.

**Table S4.** Dissimilarity report of the overall microbial community structure with three different statistical approaches between Alpine meadow and Alpine steppe meadow .

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | MRPP | | Anosim | | Adonis | |
| δ | *P* | R | *P* | R2 | *P* |
| OTUs | 0.558 | 0.001 | 0.535 | 0.001 | 0.187 | 0.002 |

**Table S5.** Topological properties of OTUs network analysis in the two alpine meadow sites.

|  |  |  |  |
| --- | --- | --- | --- |
| Network indexes | | ASM | AM |
| Empirical networks | Threshold | 0.890 | 0.890 |
| Total nodes (n) | 828 | 613 |
| Total links | 1588 | 945 |
| Modularity (no. of modules) | 0.744(129) | 0.741(128) |
| R square of power-law | 0.959 | 0.909 |
| Average degree (avgK) | 3.836 | 3.083 |
| Average clustering coefficient(avgCC)) | 0.190 | 0.162 |
| Average path distance(GD) | 2.559 | 0.782 |
| Geodesic efficiency(E) | 0.070 | 0.028 |
| Harmonic geodesic distance(HD) | 14.346 | 35.097 |
| Density (D) | 0.005 | 0.005 |
| Transitivity (Trans) | 0.499 | 0.495 |
| Random networks | Avg clustering coefficient ±SD | 0.017±0.004 | 0.018±0.003 |
| Avg path length±SD | 3.285±0.150 | 3.651±0.098 |
| Avg modularity±SD | 0.593±0.006 | 0.515±0.004 |

**Fig. S1.** The difference of using carbon sources based on Biolog micro- plate analysis between alpine steppe meadow and alpine meadow were tested by two-tailed unpaired t-test. \*: *P* < 0.05; \*\*: *P* < 0.01.

a

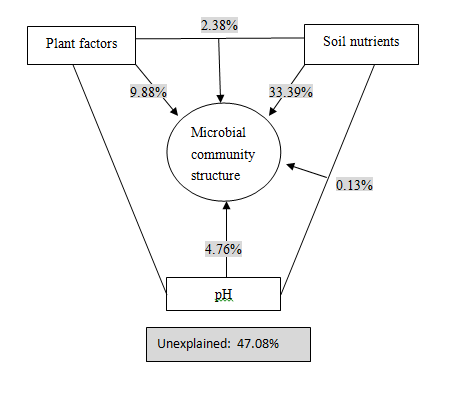


b

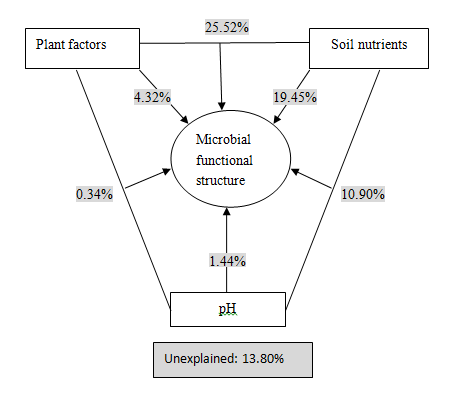


**Fig. S2.** Canonical correspondence analysis (CCA) of (a) high-throughput sequencing data and (b) functional genes involved in C and N cycling with environmental factors. Ts, total sulfur, Tp, total phosphorus, Soc, soil organic carbon, Available N, available nitrogen, Mo, soil moisture.

a



b



**Fig. S3.** Variation partitioning analysis (VPA) of (a) high-throughput sequencing data and (b) functional genes involved in C and N cycling with environmental factors. Plant factors included plant diversity and plant biomass. Soil nutrients included total nitrogen, total phosphorus, NH4+-N, NO3--N, soil organic carbon, alkaline hydrolysis nitrogen, and rapidly available phosphorus.