**Bacterial community in saline farmland soil on the Tibetan Plateau: Responding to salinization while resisting extreme environments**

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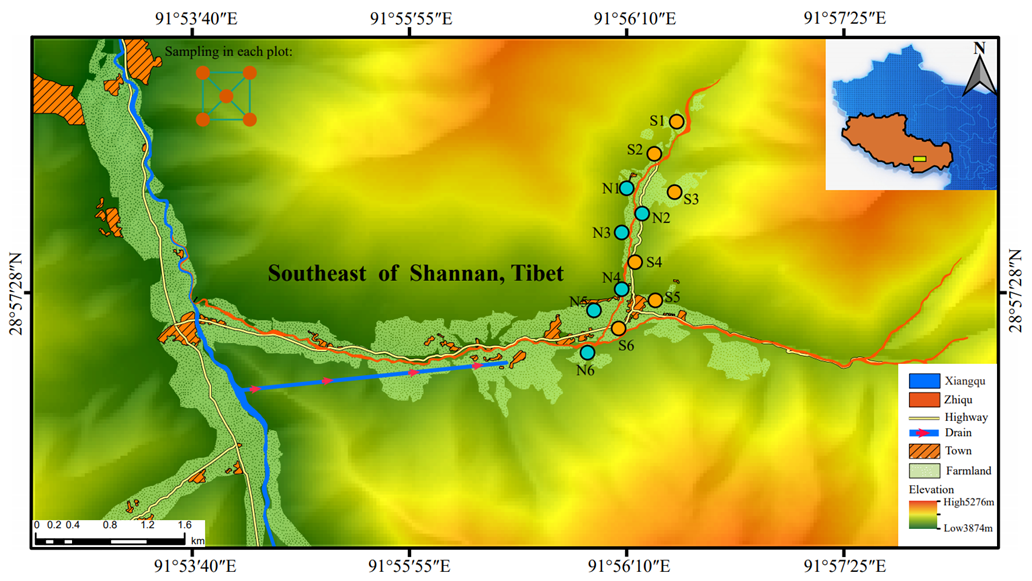
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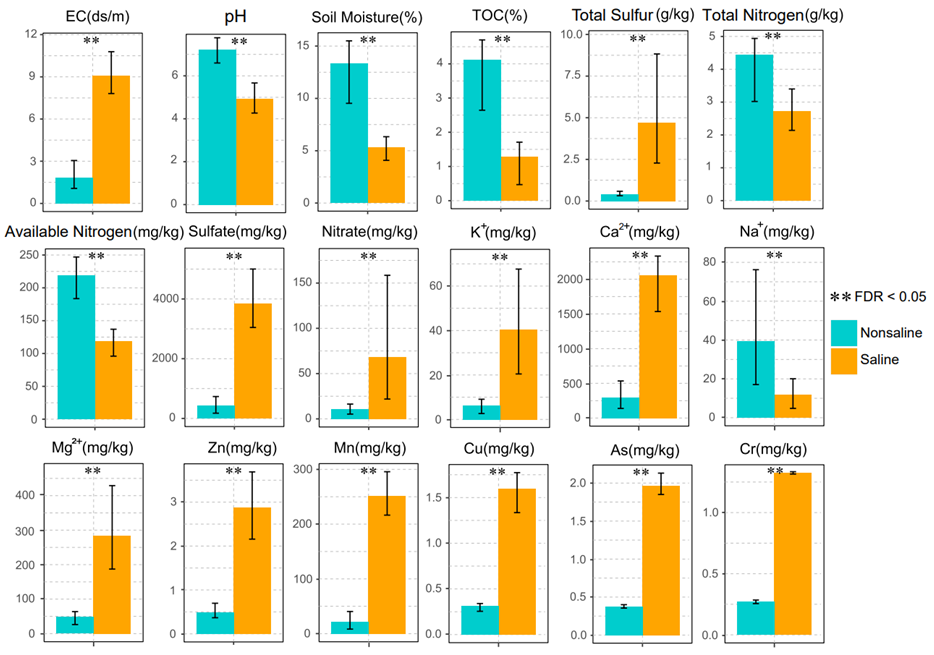
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# Supplementary Materials

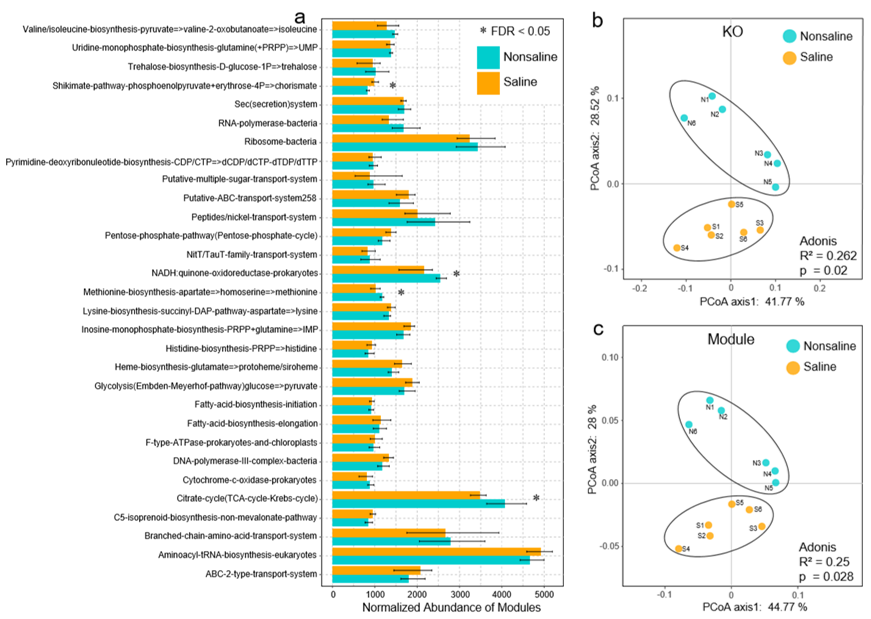
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**Figure S1. Sampling sites on the Tibetan Plateau.**

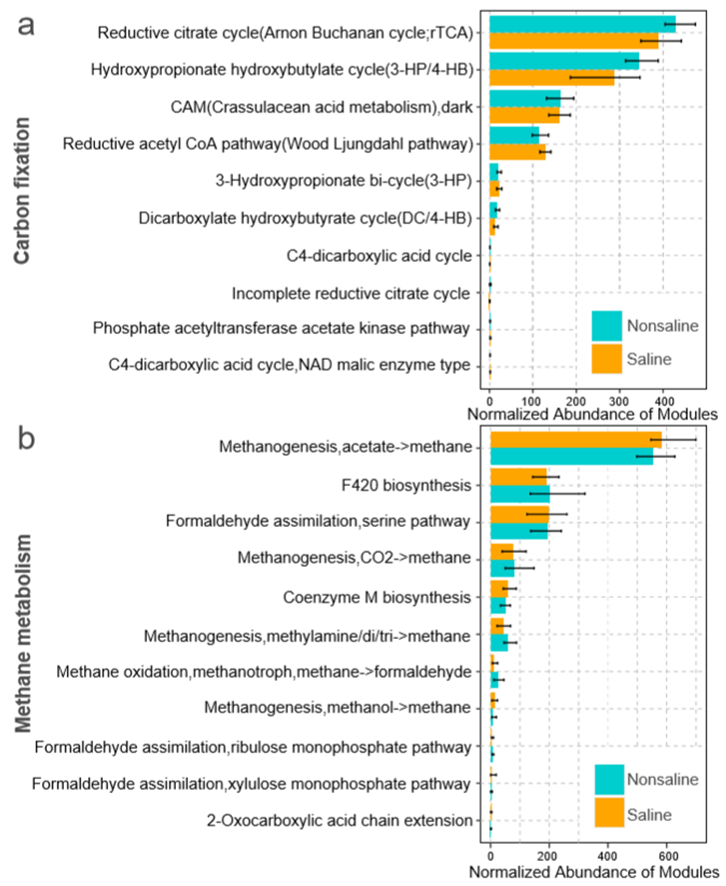
The orange dots represent sampling sites of saline soil, and cyan dots represent sampling sites of nonsaline soil.



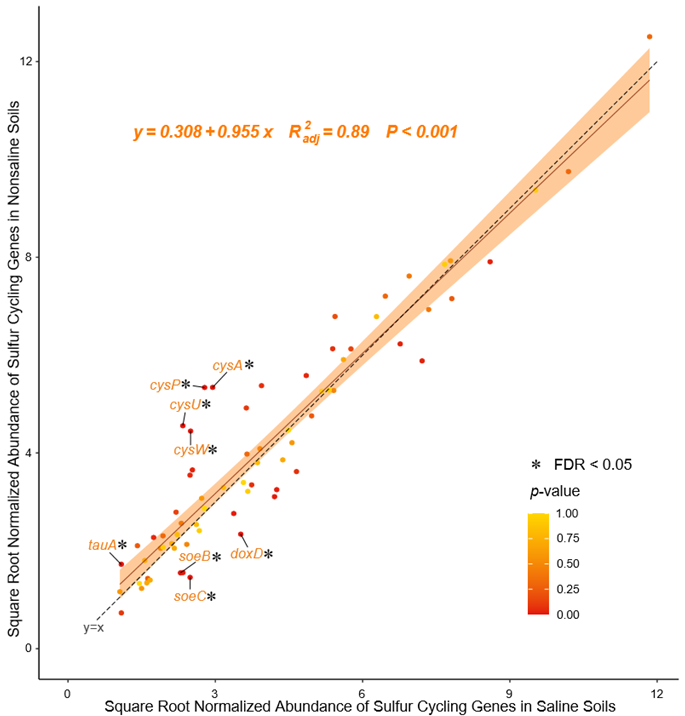
**Figure S2. physicochemical parameters in saline and nonsaline soil on the Tibetan Plateau.**



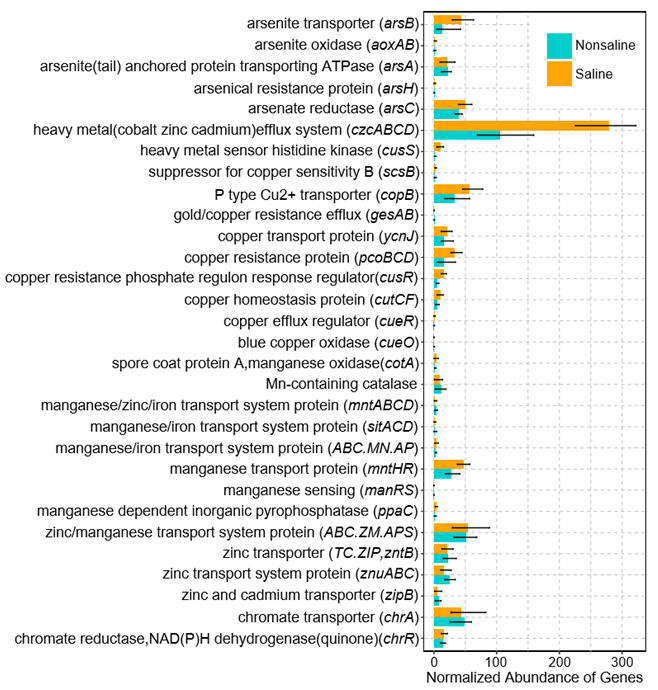
**Figure S3. The difference and principal coordinate analysis (PCoA) of bacterial community functions in saline and nonsaline soil on the Tibetan Plateau.** a. The normalized abundance of top30 functional modules in two types of soil samples from the Tibetan Plateau at module level. Significant difference (FDR < 0.05) genes are marked with “\*”. The total number of reads is normalized to 100000. b. PCoA of microbial community functions at KO level. c. PCoA of microbial community functions at KEGG module level. The Significant differences (ADONIS, P < 0.05) of functions in the two types of soil samples from the Tibetan Plateau were tested.



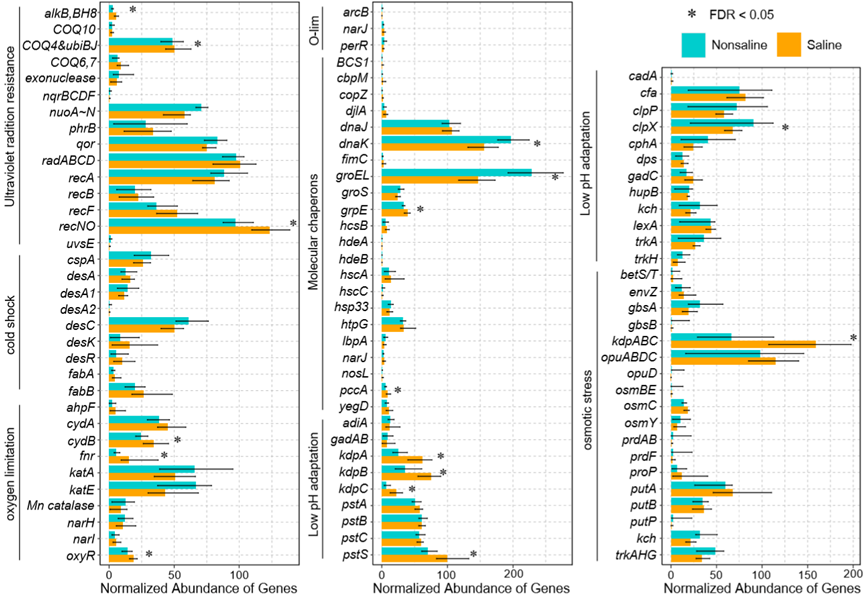
**Figure S4. Normalized abundance of functional pathways of carbon fixation (a) and methane metabolism (b) of bacterial community in saline and nonsaline soil on the Tibetan Plateau.** Bar plots show the normalized abundances of carbon cycling modules. The total number of reads is normalized to 100000.



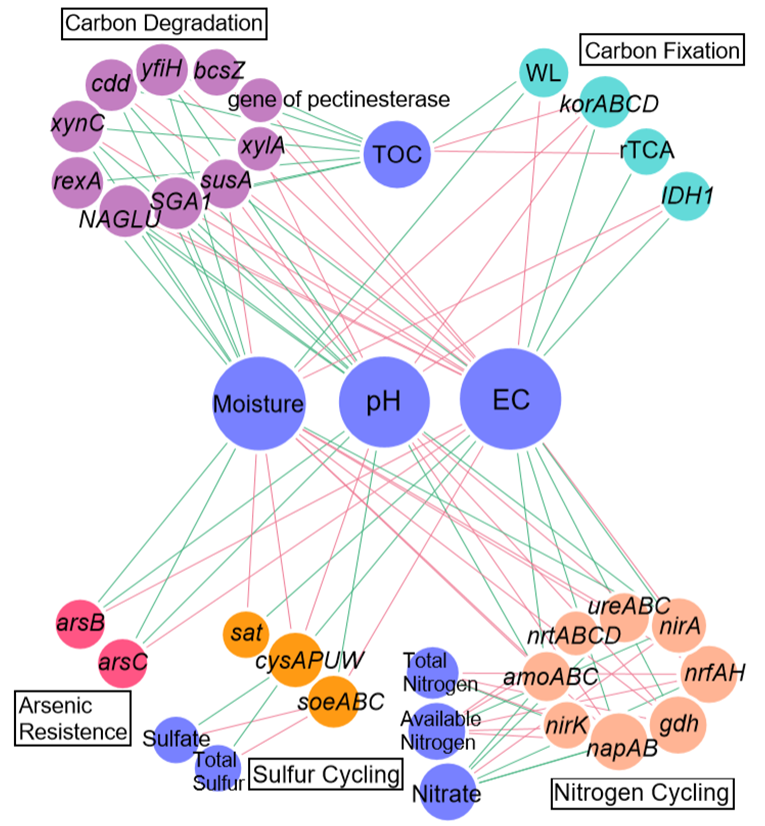
**Figure S5. The ratio of sulfur cycling genes in saline and nonsaline soil on the Tibetan Plateau.** The black dotted line equation: “y = x”, indicates that the horizontal and vertical axes are equal. Genes of Significant difference (FDR < 0.05) are marked with text in orange and connected with short lines. The total number of reads is normalized to 100000.



**Figure S6.** **The normalized abundance of heavy metal(loid)s resistance genes in saline and nonsaline soil on the Tibetan Plateau.** Bar plots show the normalized abundances of mental resistance genes.The total number of reads is normalized to 100000.



**Figure S7. The normalized abundance of environmental stress response genes in saline and nonsaline soil on the Tibetan Plateau.** Bar plots show the normalized abundances of environmental stress resistance genes. Significant difference (FDR < 0.05) genes are marked with “\*”. The total number of reads is normalized to 100000.



**Figure S8. The network of carbon, nitrogen and sulfur cycling genes and arsenic resistance genes with environmental factors in saline and nonsaline soil on the Tibetan Plateau.**

The significantly strong correlation (|r|>0.6, *p*-value < 0.05) between functional genes and physicochemical parameters were used to construct a network. The red and green lines mean positive and negative correlation between two nodes. The size of each node is proportion of the number of connections (i.e., degree). The thickness of each connection between two nodes (i.e., edge) is proportion of the Spearman’s correlation coeﬃcient (i.e., weight), ranging from |0.6| to |1|. WL: Wood–Ljungdahl pathway. rTCA: reductive citrate cycle.

**Table S1. The quality of whole-genome shotgun data of bacterial community in saline and nonsaline soils of Tibetan Plateau.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Samples** | **Clean reads** | **Clean base(bp)** | **Percent in raw reads(%)** | **Percent in raw bases(%)** |
| S1 | 47225924 | 7.08E+09 | 99.44756 | 99.39406 |
| S2 | 43152670 | 6.47E+09 | 99.11633 | 99.05117 |
| S3 | 50480934 | 7.57E+09 | 99.59716 | 99.54808 |
| S4 | 39621138 | 5.94E+09 | 99.45815 | 99.3844 |
| S5 | 59838390 | 8.97E+09 | 99.57736 | 99.52632 |
| S6 | 43471276 | 6.52E+09 | 99.26592 | 99.19434 |
| N1 | 55238666 | 8.28E+09 | 99.5666 | 99.51223 |
| N2 | 62112944 | 9.31E+09 | 99.47834 | 99.42098 |
| N3 | 66759060 | 1E+10 | 99.6198 | 99.5683 |
| N4 | 44842584 | 6.72E+09 | 99.37352 | 99.31624 |
| N5 | 43635626 | 6.54E+09 | 99.41396 | 99.35688 |
| N6 | 42532714 | 6.38E+09 | 99.44296 | 99.38223 |

**Table S2. The assembly of whole-genome shotgun data of bacterial community in saline and nonsaline soils of Tibetan Plateau.**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Samples** | **Contigs** | **Contigs bases(bp)** | **N50**  **(bp)** | **N90**  **(bp)** | **Max**  **(bp)** | **Min**  **(bp)** |
| S1 | 247170 | 1.65E+08 | 681 | 346 | 62138 | 300 |
| S2 | 664171 | 3.98E+08 | 588 | 341 | 106047 | 300 |
| S3 | 560395 | 3.88E+08 | 720 | 349 | 115026 | 300 |
| S4 | 567654 | 3.7E+08 | 668 | 346 | 68168 | 300 |
| S5 | 656432 | 4.26E+08 | 673 | 346 | 171693 | 300 |
| S6 | 311586 | 1.94E+08 | 632 | 344 | 86932 | 300 |
| N1 | 242951 | 1.09E+08 | 445 | 325 | 4689 | 300 |
| N2 | 298994 | 1.31E+08 | 431 | 322 | 18250 | 300 |
| N3 | 503193 | 2.58E+08 | 507 | 333 | 39120 | 300 |
| N4 | 378385 | 1.95E+08 | 518 | 335 | 9810 | 300 |
| N5 | 472496 | 2.73E+08 | 581 | 340 | 41898 | 300 |
| N6 | 377628 | 1.71E+08 | 446 | 324 | 10643 | 300 |

**Table S3. The alpha diversity of bacterial community in saline and nonsaline soils of Tibetan Plateau.**

|  |  |
| --- | --- |
| **Samples** | **Shannon index** |
| S1 | 5.60745 |
| S2 | 5.660981 |
| S3 | 5.421845 |
| S4 | 4.999145 |
| S5 | 5.393344 |
| S6 | 5.495674 |
| N1 | 5.297761 |
| N2 | 5.40852 |
| N3 | 5.392616 |
| N4 | 5.367385 |
| N5 | 5.369099 |
| N6 | 5.280454 |

**Table S4. The topology structure characteristics of network of bacteria and environmental factors.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Module** | **All node** | **All link** | **Positive link** | **Negative link** | **Color** |
| 0 | 22 | 440 | 440 | 0 | Red |
| 1  2  Environmental Factors | 42  36  9 | 598  738  219 | 594  736  108 | 4  2  111 | Lavender  Green  Blue |

Average Degree：27.266

Average Weighted Degree：20.397

Average Clustering Coefficient：0.632

Diameter：4

Radius：3

Average Path Length：1.961

Density：0.252

**Table S5. Genera in different modules in network of genus and environmental factors.**

|  |  |  |  |
| --- | --- | --- | --- |
| **Module** | | **Genus** | |
| 0 | *Gemmatirosa*  *Bradyrhizobium*  *unclassified\_f\_\_Acidobacteriaceae*  *Rhodanobacter*  *Candidatus\_Koribacter*  *Pseudolabrys*  *Burkholderia*  *Ktedonobacter*  *Rudaea*  *unclassified\_o\_\_Rhodospirillales*  *Acidobacterium* | | *Opitutus*  *Thermogemmatispora*  *Edaphobacter*  *Candidatus\_Nitrosotalea*  *Chthoniobacter*  *Mizugakiibacter*  *Dyella*  *Silvibacterium*  *Sphaerobacter*  *Granulicella*  *Dokdonella* |
| 1 | *Gemmatimonas*  *unclassified\_c\_\_Betaproteobacteria*  *unclassified\_p\_\_Acidobacteria*  *unclassified\_d\_\_Bacteria*  *Pyrinomonas*  *Candidatus\_Solibacter*  *unclassified\_p\_\_Chloroflexi*  *unclassified\_p\_\_Candidatus\_Rokubacteria*  *Nitrospira*  *Pedosphaera*  *unclassified\_c\_\_Gammaproteobacteria*  *Rhodoplanes*  *Haliangium*  *Pseudomonas*  *Sorangium*  *Candidatus\_Entotheonella*  *Mesorhizobium*  *Steroidobacter*  *Variovorax*  *Rhizobacter*  *Polaromonas* | | *Myxococcus*  *Nitrososphaera*  *Anaeromyxobacter*  *Reyranella*  *unclassified\_c\_\_Deltaproteobacteria*  *Bryobacter*  *Microvirga*  *Massilia*  *Dongia*  *Geobacter*  *Methylobacterium*  *Labilithrix*  *Methylibium*  *Cystobacter*  *Chloracidobacterium*  *Paenibacillus*  *Cupriavidus*  *Rhizobium*  *Azospirillum*  *Herbaspirillum*  *Janthinobacterium* |
| 2 | *Sphingomonas*  *Streptomyces*  *Nocardioides*  *Arthrobacter*  *Mycobacterium*  *unclassified\_f\_\_Geodermatophilaceae*  *Leifsonia*  *Solirubrobacter*  *unclassified\_c\_\_Actinobacteria*  *Frankia*  *Conexibacter*  *Blastococcus*  *Pseudonocardia*  *Amycolatopsis*  *unclassified\_o\_\_Solirubrobacterales*  *Actinoplanes*  *Gaiella*  *Marmoricola* | | *Phenylobacterium*  *Lysobacter*  *Modestobacter*  *Phycicoccus*  *Devosia*  *Singulisphaera*  *Rhodococcus*  *Microbacterium*  *Gemmata*  *Mucilaginibacter*  *Altererythrobacter*  *Nocardia*  *Geodermatophilus*  *Rubrobacter*  *Caulobacter*  *Flavobacterium*  *Kribbella*  *Aeromicrobium* |