

Supplementary Materials

Seasonal comparison of bacterial communities in rhizosphere of alpine cushion plants in the Himalayan Hengduan Mountains

Shuai Chang ^{a, b}, Jianguo Chen ^a, Jianqiang Su ^{c*} & Yang Yang ^{a*} & Hang Sun ^{a*}

^a Key Laboratory for Plant Diversity and Biogeography of East Asia, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming 650201, China

^b University of Chinese Academy of Sciences, Beijing 100049, China

^c Key Laboratory of Urban Environment and Health, Institute of Urban Environment, Chinese Academy of Sciences, Xiamen 361021, China

*** Correspondence:**

Hang Sun, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming, China, sunhang@mail.kib.ac.cn;

Yang Yang, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming, China, yangyang@mail.kib.ac.cn;

Jianqiang Su, Institute of Urban Environment, Chinese Academy of Sciences, Xiamen, China, jqsu@iue.ac.cn.

The *Supplementary Materials* contains **2** figures and **4** tables.

Contents

Figure S1	1
Figure S2	2
Table S1	3
Table S2	4
Table S3	5
Table S4	6



(a)



(b)

Figure S1. *Chionocharis hookeri* (a) and *Arenaria polytrichoides* (b) cushions occurring at 4780m elevation in the Sino-Himalayas.

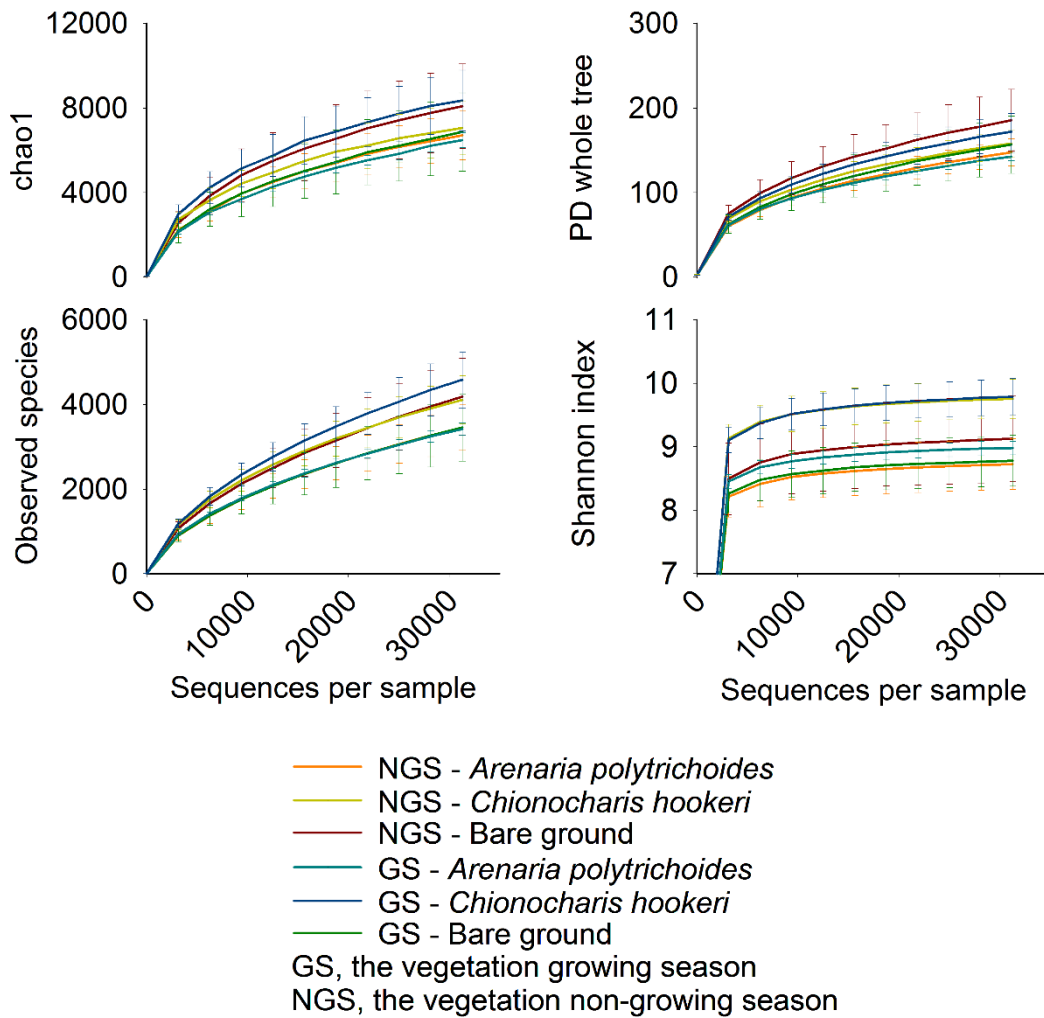


Figure S2. Rarefaction curves for alpha diversities of bacterial communities in the sequencing depth of 31290 reads. PD whole tree, chao1, observed species and Shannon indices were calculated with QIIME (1.7).

Table S1. Main information about the soil samples and sequencing datasets

Sample ID ¹	Barcodes	Tags Number	Data production ² (bp)	Effective Reads Number	OTUs
NGS-B1	AACCAACC	44974	6248804	42395	6024
NGS-B2	AACCAAGG	48633	6815747	46047	5349
NGS-B3	AACCATCG	52522	7316053	52069	3422
NGS-B4	AACCATGC	98724	13750775	93761	8047
NGS-A1	AACCGCAT	55934	7840761	54074	5574
NGS-A2	AACCGCTA	51780	7155382	50941	3651
NGS-A3	AACCGGAA	31783	4413605	31290	3083
NGS-A4	AACCGGTT	51466	7248564	50008	4778
NGS-C1	AACCTACG	44730	6374115	43311	5419
NGS-C2	AACCTAGC	45054	6428873	43768	4897
NGS-C3	AACCTTCC	38384	5501272	37484	3420
NGS-C4	AACCTTGG	38065	5433070	36270	4806
GS-B1	AACGAACG	58090	8042489	55900	4874
GS-B2	AACGAAGC	37701	5234262	35639	5063
GS-B3	AACGATCC	38234	5307182	37844	3007
GS-B4	AACGATGG	41090	5704012	40514	3186
GS-A1	AACCATCG	46465	6509035	45763	4337
GS-A2	AACCATGC	47930	6764899	47191	3896
GS-A3	AACCGCAT	50295	7020316	49426	4393
GS-A4	AACCGCTA	53635	7553831	52403	4446
GS-C1	AACCGGAA	49561	6988657	47870	6065
GS-C2	AACCGGTT	48125	6745817	44983	6672
GS-C3	AACCTACG	37283	5263844	36282	4275
GS-C4	AACCTAGC	36827	5222373	36109	4263

¹ A = *Arenaria polytrichoides*; C = *Chionocharis hookeri*; B = bare ground; GS, the vegetation growing season; NGS, the vegetation non-growing season; numbers behind letters mean the repetitions.

² Data production = the total length of all tags within the sample.

Table S2. Primary scripts used during the sequence processing

Scripts
add_qiime_labels.py
count_seqs.py
pick_de_novo_otus.py
filter_otus_from_otu_table.py
parallel_identify_chimeric_seqs.py
filter_fasta.py
make_otu_table.py
convert_biom.py
filter_alignment.py
make_phylogeny.py
make_otu_heatmap_html.py
make_otu_network.py
summarize_taxa_through_plots.py
print_biom_table_summary.py
alpha_rarefaction.py
beta_diversity_through_plots.py
jackknifed_beta_diversity.py
make_bootstrapped_tree.py
compare_categories.py
shared_phylotypes.py
summarize_otu_by_cat.py
otu_category_significance.py
compare_alpha_diversity.py
compare_distance_matrices.py
make_distance_boxplots.py

Table S3. Spearman's correlation coefficient among the bacterial phyla and the microhabitats and the seasons

Abiotic factors Bacterial phyla	Microhabitats ¹	Seasons ²
Proteobacteria	0.871**	-0.048
Actinobacteria	0.434*	-0.301
Acidobacteria	-0.038	0.277
Chloroflexi	-0.677**	0.325
AD3	-0.690**	0.506*
Bacteroidetes	0.421*	-0.590**
Verrucomicrobia	0.102	0.265
WPS2	-0.817**	0.120
Planctomycetes	-0.562**	-0.217
Gemmatimonadetes	-0.741**	-0.157
Cyanobacteria	-0.306	-0.530**
TM7	0.460*	-0.421*
Firmicutes	-0.306	0.169

¹ The rhizosphere of the cushion plants and the bare ground;

² The vegetation growing season and the vegetation non-growing season.

Table S4. Average relative abundances of phyla detected in soils at the study site

Taxa detected	Average Relative Abundances ¹					
	GS-A	NGS-A	GS-C	NGS-C	GS-B	NGS-B
k__Bacteria;Other	0.015424	0.020963	0.022867	0.024665	0.037628	0.045406
k__Bacteria;p__AD3	0.011857	0.003763	0.023682	0.001095	0.170376	0.032648
k__Bacteria;p__Acidobacteria	0.172673	0.162583	0.125343	0.107407	0.149862	0.133556
k__Bacteria;p__Actinobacteria	0.283714	0.335121	0.362018	0.358911	0.165354	0.308879
k__Bacteria;p__Armatimonadetes	0.000443	0.000307	0.000271	0.000260	0.000434	0.000550
k__Bacteria;p__BRC1	0.000005	0.000005	0.000028	0.000019	0.000000	0.000016
k__Bacteria;p__Bacteroidetes	0.016889	0.022256	0.014694	0.039323	0.004601	0.016430
k__Bacteria;p__Caldithrix	0.000000	0.000000	0.000014	0.000007	0.000006	0.000000
k__Bacteria;p__Chlamydiae	0.001816	0.001355	0.001624	0.001748	0.000452	0.000398
k__Bacteria;p__Chlorobi	0.000432	0.000244	0.000264	0.000398	0.000289	0.000690
k__Bacteria;p__Chloroflexi	0.071490	0.041464	0.072872	0.053882	0.134008	0.106258
k__Bacteria;p__Cyanobacteria	0.002050	0.003941	0.001326	0.002842	0.003026	0.012973
k__Bacteria;p__Elusimicrobia	0.002600	0.001939	0.001260	0.001102	0.000716	0.001006
k__Bacteria;p__FCPU426	0.000113	0.000055	0.000014	0.000000	0.000056	0.000180
k__Bacteria;p__Fibrobacteres	0.000037	0.000081	0.000061	0.000191	0.000000	0.000046
k__Bacteria;p__Firmicutes	0.001568	0.000879	0.006523	0.005472	0.002490	0.000690
k__Bacteria;p__Fusobacteria	0.000015	0.000008	0.000014	0.000000	0.000000	0.000000
k__Bacteria;p__GAL15	0.000011	0.000000	0.000110	0.000000	0.000399	0.000055
k__Bacteria;p__GN02	0.000179	0.000083	0.000206	0.000718	0.000030	0.000414
k__Bacteria;p__GOUTA4	0.000000	0.000000	0.000054	0.000034	0.000000	0.000000
k__Bacteria;p__Gemmatimonadetes	0.007029	0.008834	0.006848	0.007686	0.018250	0.025958
k__Bacteria;p__MVP-21	0.000000	0.000000	0.000000	0.000013	0.000000	0.000000

k__Bacteria;p__NKB19	0.000000	0.000000	0.000000	0.000027	0.000000	0.000000
k__Bacteria;p__Nitrospirae	0.000986	0.000412	0.004903	0.001507	0.003646	0.002351
k__Bacteria;p__OD1	0.001727	0.000848	0.000907	0.000957	0.000265	0.000902
k__Bacteria;p__OP3	0.000381	0.000220	0.000250	0.000195	0.000039	0.000025
k__Bacteria;p__OP8	0.000000	0.000000	0.000028	0.000000	0.000000	0.000000
k__Bacteria;p__OP9	0.000005	0.000000	0.000007	0.000000	0.000117	0.000320
k__Bacteria;p__Planctomycetes	0.012657	0.016478	0.006341	0.009265	0.013993	0.018101
k__Bacteria;p__Proteobacteria	0.370274	0.359314	0.321553	0.341177	0.244857	0.235930
k__Bacteria;p__TM6	0.000295	0.000206	0.000233	0.000112	0.000084	0.000037
k__Bacteria;p__TM7	0.002990	0.002932	0.004556	0.010496	0.001035	0.003472
k__Bacteria;p__Tenericutes	0.001438	0.001720	0.000872	0.000173	0.000027	0.000962
k__Bacteria;p__Thermi	0.000000	0.000000	0.000000	0.000012	0.000061	0.000165
k__Bacteria;p__Verrucomicrobia	0.014528	0.008583	0.017048	0.029230	0.018877	0.010006
k__Bacteria;p__WPS-2	0.006284	0.005300	0.002637	0.000393	0.028783	0.041144
k__Bacteria;p__WS2	0.000032	0.000029	0.000110	0.000196	0.000116	0.000000
k__Bacteria;p__WS3	0.000032	0.000061	0.000426	0.000383	0.000016	0.000049
k__Bacteria;p__WYO	0.000025	0.000018	0.000035	0.000104	0.000107	0.000383

¹A = *Arenaria polytrichoides*; C = *Chionocharis hookeri*; B = bare ground; GS, the vegetation growing season; NGS, the vegetation non-growing season.