

Figure S1. Difference in bacterial, fungal alpha diversity (Simpson analysis) among the treatments. (The data are presented as the mean \pm SD of three independent replicates. CK, CNa, S, and SNa represent control check soil, additive NaCl soil, HU2014 soil, and inoculating HU2014 soil with the addition of NaCl, respectively.) Asterisk indicates significant differences ($P < 0.05$) between treatments.

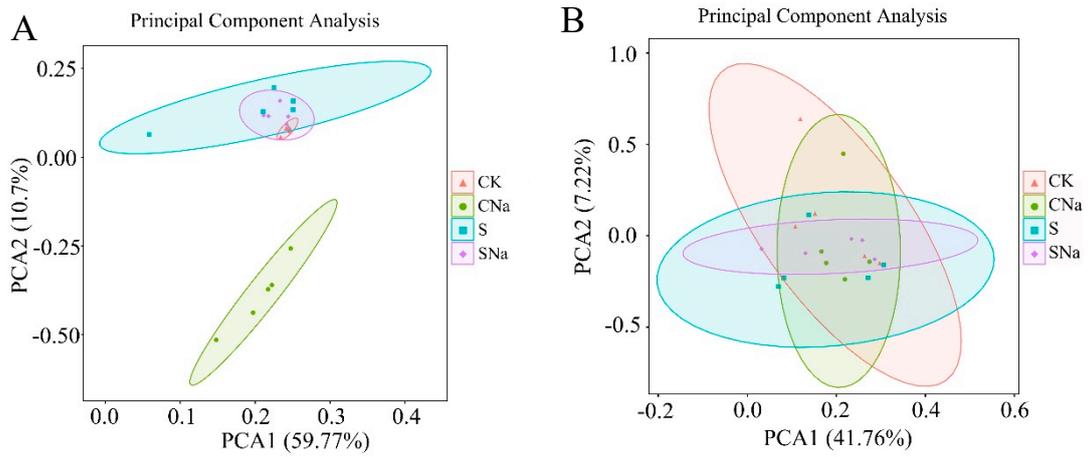


Figure S2. Principal component analysis of the Bray-Curtis distance for soil bacterial and fungal communities. CK, CNa, S, and SNa represent control check soil, additive NaCl soil, HU2014 soil, and inoculating HU2014 soil with the addition of NaCl, respectively.

Table S1. The results of showing the effects of additive NaCl, inoculation, and their interactions on soil properties.

T	TSS (%)	NH ₄ ⁺ -N (mg/kg)	NO ₃ ⁻ -N (mg/kg)	Olsen-P (mg/kg)	pH	SOC (mg/kg)	TN (g/kg)	TP (g/kg)
CK	0.04±0.00d	39.25±1.99a	36.36±3.32c	167.11±3.29d	8.31±0.01a	50.45±0.22a	1.33±0.01c	1.09±0.04b
CNa	0.29±0.02b	31.03±0.62c	42.33±1.12b	172.51±4.78c	7.78±0.00c	50.52±0.08a	1.28±0.03d	1.10±0.07b
S	0.09±0.01c	32.88±1.40bc	46.29±3.28b	206.42±2.80b	7.98±0.00b	50.83±0.48a	1.50±0.04a	1.23±0.09a
SNa	0.35±0.01a	33.53±1.07b	63.55±4.10a	225.58±2.67a	7.97±0.01b	50.76±0.26a	1.38±0.02b	1.25±0.10a

CK, CNa, S, and SNa represent control check soil, additive NaCl soil, HU2014 soil, and inoculating HU2014 soil with the addition of NaCl, respectively. Values are the means (\pm SD) of five replicate soil samples. Different lowercase letters within a row indicate significant differences ($P < 0.05$) between different treatments with the Tukey test. T: treatment; TSS: Total soluble salt; NH₄⁺, NH₄⁺-N content; NO₃⁻, NO₃⁻-N content; Olsen-P content; SOC, soil organic-carbon content; TN, total nitrogen content; TP, total phosphorus content.

Table S2. The effects of HU2014 inoculation and NaCl addition on relative abundances of bacterial taxa of top 10 (phylum level).

Taxa	CK (RA%)	CNa (RA%)	S (RA%)	SNa (RA%)	Total (RA%)	p_value
Proteobacteria	36.93±0.94b	43.96±2.94a	41.46±4.00a	44.48±1.29a	41.71	0.02
Acidobacteriota	18.36±0.63a	14.65±1.63b	12.31±2.05c	13.31±0.48bc	14.66	0.01
Actinobacteriota	8.93±1.01ab	9.00±0.45ab	11.53±5.34a	6.67±0.14b	9.03	0.01
Bacteroidota	5.13±0.49c	5.65±0.47c	6.62±0.74b	7.63±0.37a	6.26	0.00
Gemmatimonadota	6.36±0.74ab	6.09±0.45ab	5.41±0.92b	6.60±0.37a	6.11	0.11
Firmicutes	4.45±0.36a	4.14±0.70a	6.25±2.65a	5.63±0.83a	5.12	0.08
Planctomycetota	4.70±0.43a	3.64±0.76b	3.83±0.65ab	4.02±0.44ab	4.04	0.13
Chloroflexi	3.91±0.29a	3.29±0.34b	3.19±0.41b	3.04±0.16b	3.36	0.02
Myxococcota	3.54±0.15a	2.49±0.46bc	2.97±0.48b	2.22±0.16c	2.80	0.01
Verrucomicrobiota	2.51±0.19a	1.89±0.17b	2.00±0.42b	2.14±0.23ab	2.13	0.03

CK, CNa, S, and SNa represent control check soil, additive NaCl soil, HU2014 soil, and inoculating HU2014 soil with the addition of NaCl, respectively. Values are the means (\pm SD) of five replicate soil samples. Different lowercase letters within a row indicate significant differences ($P < 0.05$) between different treatments with the Tukey test.

Table S3. The effects of HU2014 inoculation and NaCl addition on relative abundances of fungal taxa of top 6 (phylum level).

Taxa	CK (RA%)	CNa (RA%)	S (RA%)	SNa(RA%)	Total (RA%)	P value
Ascomycota	73.38±8.44a	73.69±6.06a	70.17±15.86a	64.18±16.13a	70.36	0.70
Fungi_unclassified	3.88±0.73b	15.13±5.88a	10.75±11.63ab	9.43±3.38ab	9.79	0.02
Basidiomycota	6.79±7.81a	2.84±0.79a	10.72±14.93a	13.72±19.93a	8.52	0.84
Zygomycota	7.01±2.51a	6.30±3.04a	4.59±2.57a	7.97±2.98a	6.47	0.37
Chytridiomycota	5.24±8.50a	0.93±0.56a	2.12±1.73a	3.29±0.77a	2.89	0.06
Olpidiomycota	3.25±2.28a	1.02±1.09a	1.58±0.93a	1.10±0.78a	1.74	0.15

CK, CNa, S, and SNa represent control check soil, additive NaCl soil, HU2014 soil, and inoculating HU2014 soil with the addition of NaCl, respectively. Values are the means (\pm SD) of five replicate soil samples. Different lowercase letters within a row indicate significant differences ($P < 0.05$) between different treatments with the Tukey test.