

Supplementary data

Vegetative remediation mitigates secondary salinization of cultivation facility soil via crop nutrient absorption and regulation of soil microbial communities

Shumei Cai^a, Sixin Xu^a, Deshan Zhang^a, Zishi Fu^a, Hanlin Zhang^{a,*} & Haitao Zhu^{a,*}

*Corresponding Author:

Hanlin Zhang, S Institute of Eco-Environment Protection, Shanghai Academy of Agricultural Sciences, 1000 Jinqi Road, Shanghai 201403, P. R. China, Email: zhanghanlinchick@163.com;

Haitao Zhu, Institute of Eco-Environment Protection, Shanghai Academy of Agricultural Sciences, 1000 Jinqi Road, Shanghai 201403, P. R. China, Email: htzhu123@163.com.

CONTENTS

Fig. S1 qPCR standard curve for the 16S rRNA gene

Fig. S2 qPCR amplification curve for the 16S rRNA gene

Fig. S3 qPCR standard curve for the ITS gene

Fig. S4 qPCR amplification curve for the ITS gene

Fig. S5 Shoot and root nutrient contents of the three different crop species (** denotes statistically significant differences between crop varieties ($P < 0.01$, Duncan's test). The box plots show the medians, 25th and 75th percentiles. The whiskers extend to 1.5 times the interquartile range. CK, control; CM, Chinese milk vetch; SP, spinach; RY, ryegrass.)

Fig. S6 Correlations (Pearson's P -value) between crop nutrient accumulation and soil microbial abundance for Chinese milk vetch (A, B); spinach (C, D) and ryegrass (E, F). The shaded areas indicate the 95% confidence ranges derived from the models.

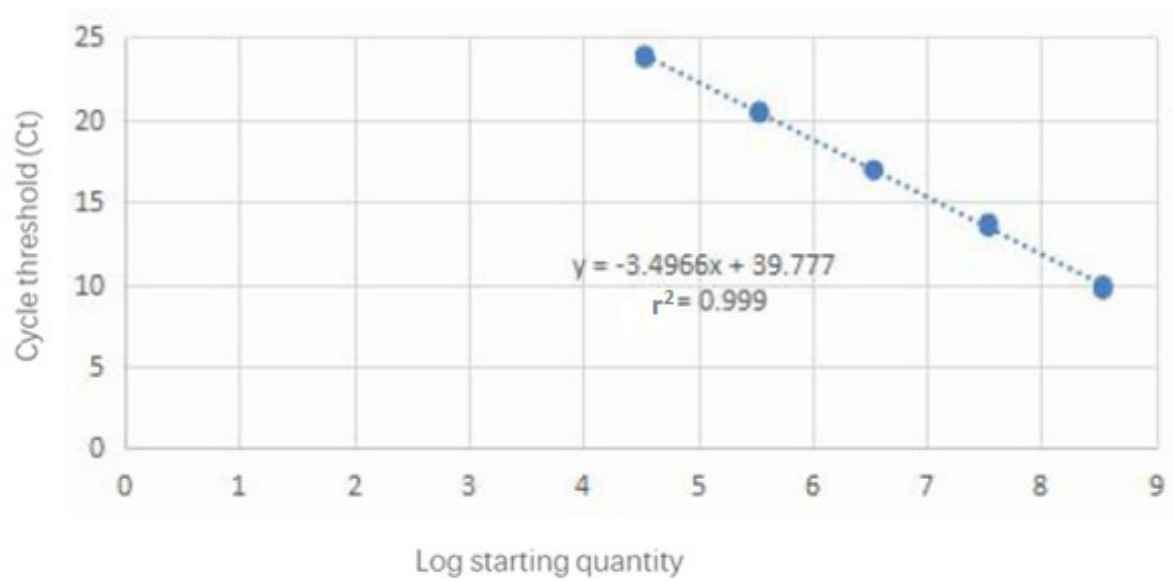


Figure S1. qPCR standard curve of 16S rRNA genes

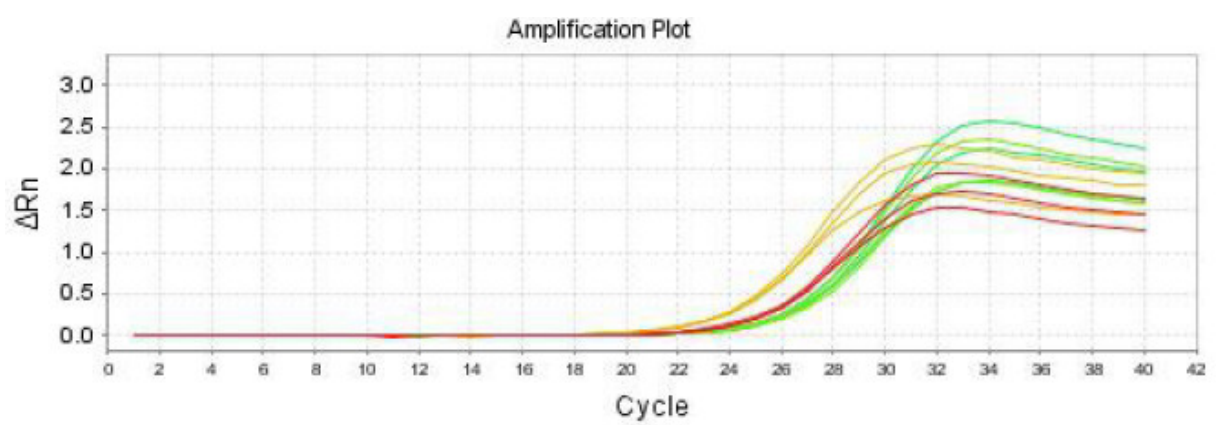


Figure S2. qPCR amplification curve of 16S rRNA genes

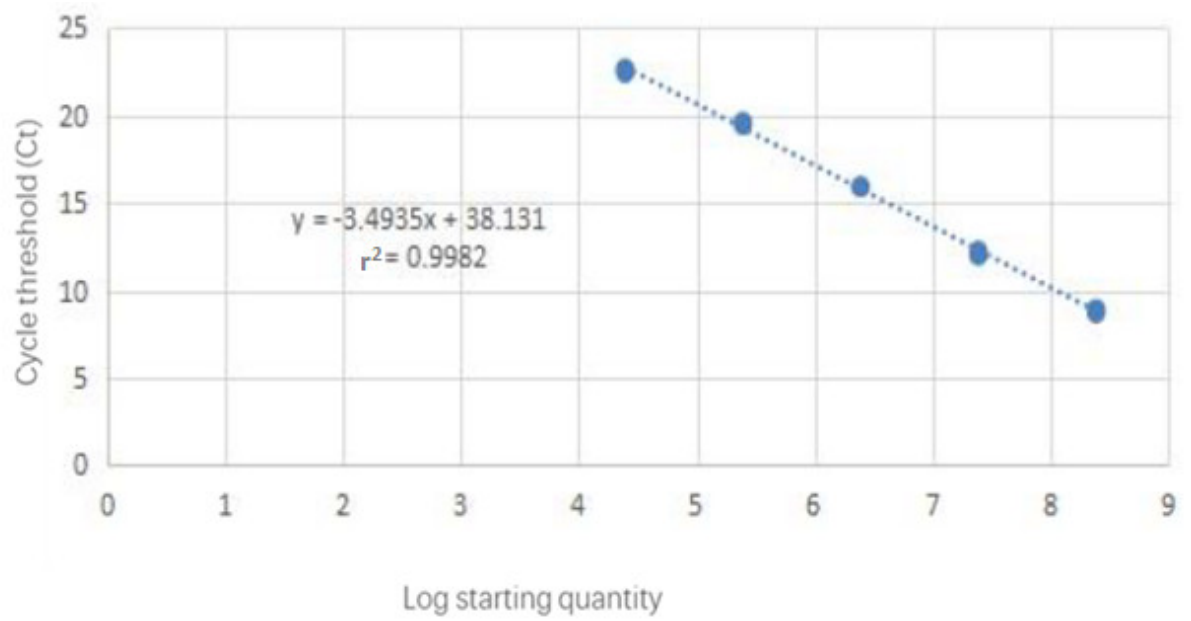


Figure S3. qPCR standard curve of ITS genes

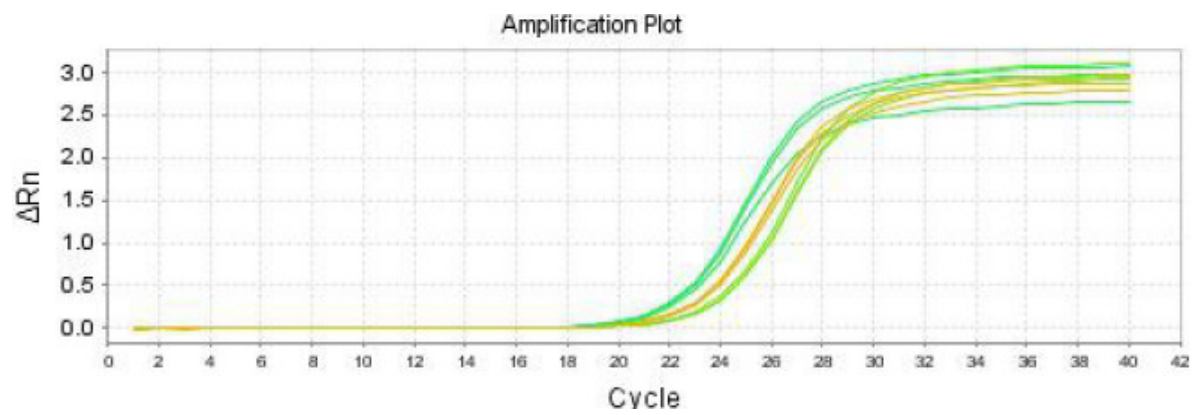


Figure S4. qPCR amplification curve of ITS genes

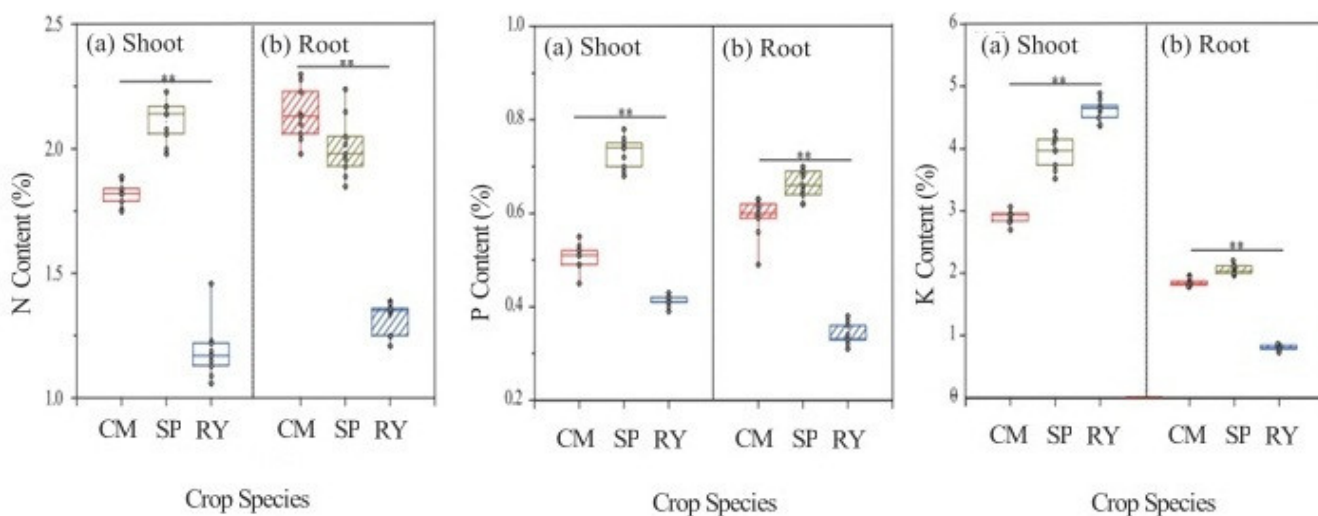


Figure S5. Shoot and root nutrient contents of the three different crop species

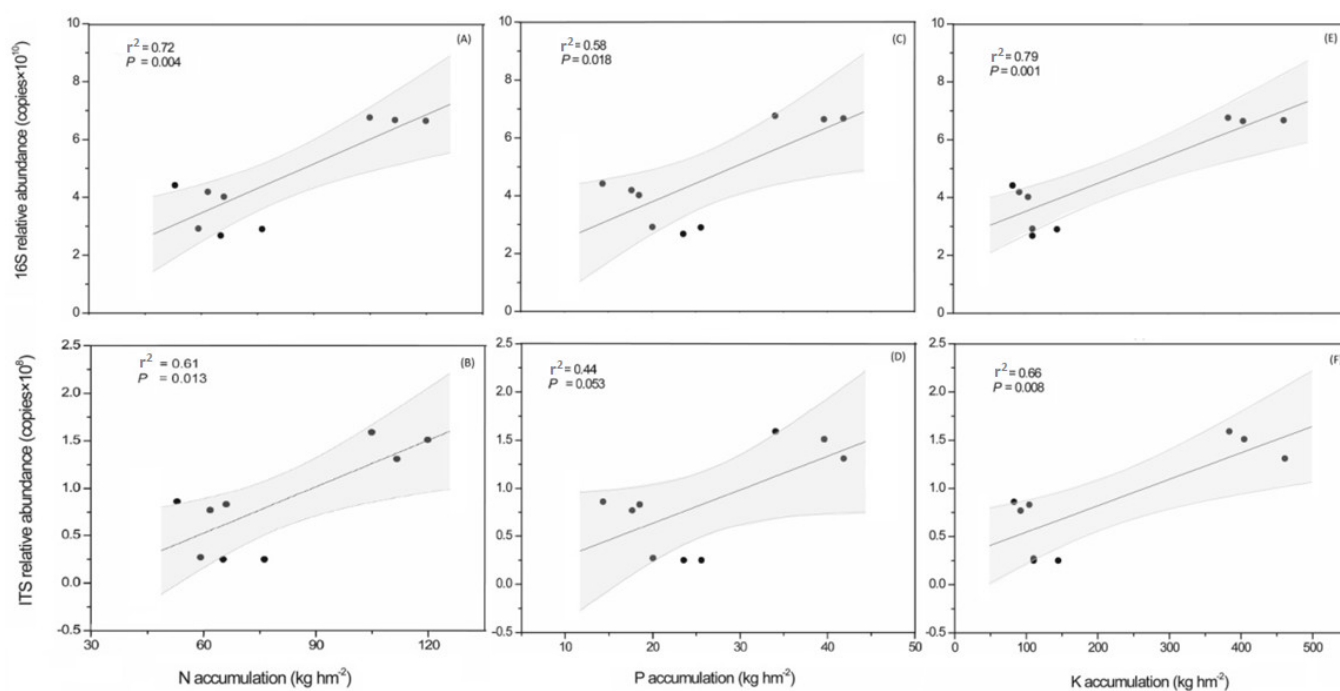


Figure S6. Correlations (Pearson's P-value) between crop nutrient accumulation and soil microbial abundance for Chinese milk vetch (A, B); spinach (C, D) and ryegrass (E, F)

Table S1. Biomass accumulation and root-to-shoot ratio of the bioremediation crops

	aboveground		belowground		root-shoot ratio	
	fresh biomass	dry biomass	fresh biomass	dry biomass	fresh biomass	dry biomass
	($\times 10^3$ kg hm ⁻²)	($\times 10^3$ kg hm ⁻²)	($\times 10^3$ kg hm ⁻²)	($\times 10^3$ kg hm ⁻²)		
CM	29.70c	3.07b	1.30b	0.20b	0.044a	0.064b
SP	33.63b	2.93b	1.18b	0.19b	0.035a	0.066b
RY	80.00a	8.93a	4.98a	0.49a	0.062a	0.055a

Table S2. Bacterial (16S rRNA) and fungal (ITS) α -diversity in soil samples

Treatments	16S rRNA				ITS			
	Shannon	Simpson	ACE	Chao1	Shannon	Simpson	ACE	Chao1
CK	6.36c	0.005a	2413.40c	2429.24b	2.58b	0.17b	198.41c	195.45c
CM	6.73a	0.003c	2703.31a	2715.60a	2.54b	0.19a	249.50a	249.20a
SP	6.56b	0.004b	2653.81b	2638.42a	2.66b	0.18b	224.17b	220.24b
RY	6.56b	0.005a	2712.96a	2714.70a	3.03a	0.09c	236.92ab	243.88a

Note: CK, control; CM, Chinese milk vetch; SP, spinach; RY, ryegrass. Different letters in the same column indicate a significant difference between treatments at the 0.05 level (n = 3).