



# Variation in soil microbial communities following vegetation restoration in a Rare Earth Elements Mine area

**Zhaoyu Kong**

SCHOOL OF LIFE SCIENCES, NANCHANG UNIVERSITY

May 26, 2022



# Massive and intensive mining and leaching of REEs has led to severe ecological problems in Southern China over the last decades

Rare Earth Elements																		He
H												B	C	N	O	F	Ne	
Li	Be												Al	Si	P	S	Cl	Ar
Na	Mg												Ga	Ge	As	Se	Br	Kr
K	Ca	Sc	Ti	V	Cr	Mn	Fe	Co	Ni	Cu	Zn	Ga	Ge	As	Se	Br	Kr	
Rb	Sr	Y	Zr	Nb	Mo	Tc	Ru	Rh	Pd	Ag	Cd	In	Sn	Sb	Te	I	Xe	
Cs	Ba	*	Hf	Ta	W	Re	Os	Ir	Pt	Au	Hg	Tl	Pb	Bi	Po	At	Rn	
Fr	Ra	**	Rf	Db	Sg	Bh	Hs	Mt	Ds	Rg	Cn	Uut	Fl	Uup	Lv	Uus	Uuo	
		*	La	Ce	Pr	Nd	Pm	Sm	Eu	Gd	Tb	Dy	Ho	Er	Tm	Yb	Lu	
		**	Ac	Th	Pa	U	Np	Pu	Am	Cm	Bk	Cf	Es	Fm	Md	No	Lr	
			Light Rare Earth Element									Heavy Rare Earth Element						



Surface runoff & soil erosion



Water & soil pollution



Soil degradation & desertification

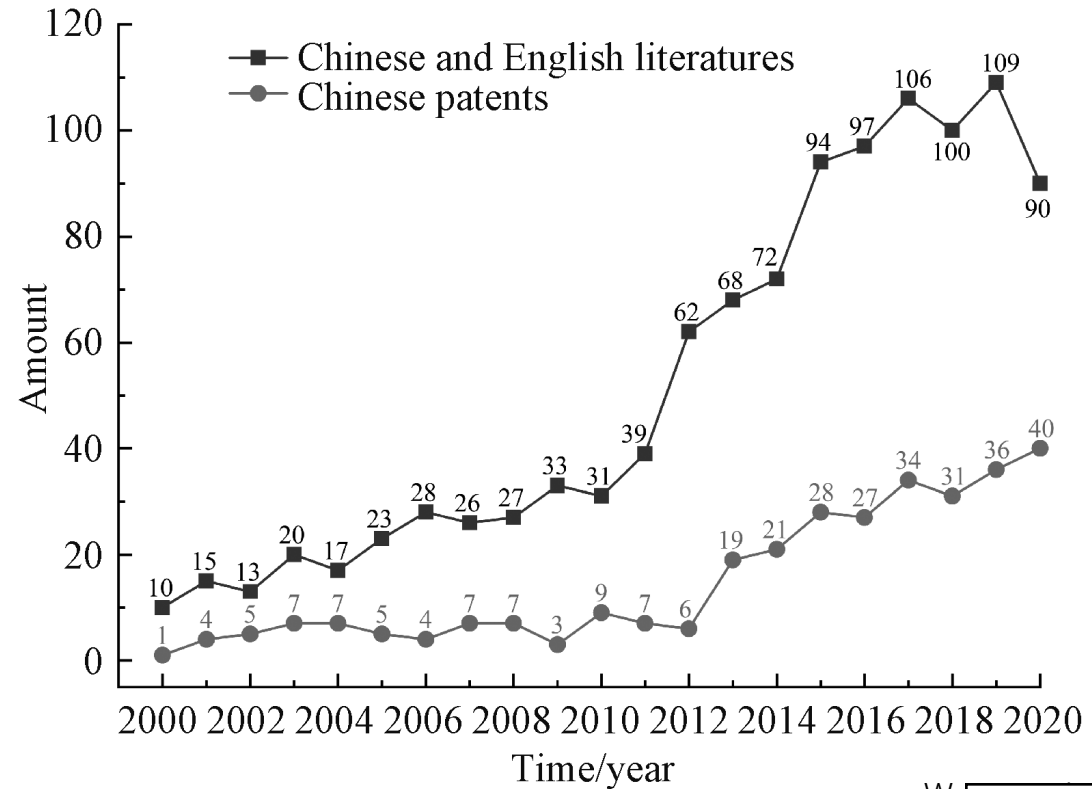
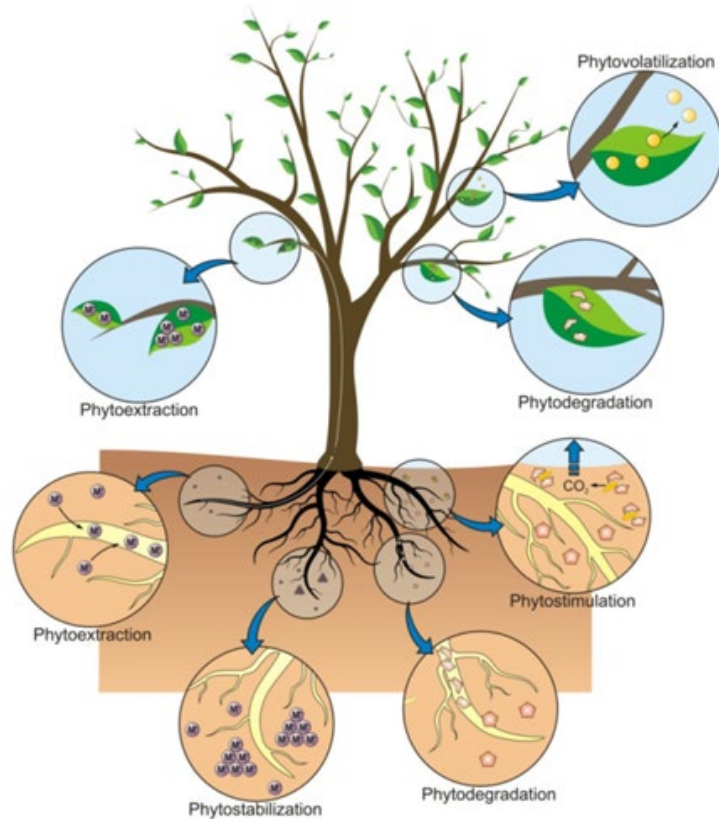


Geological



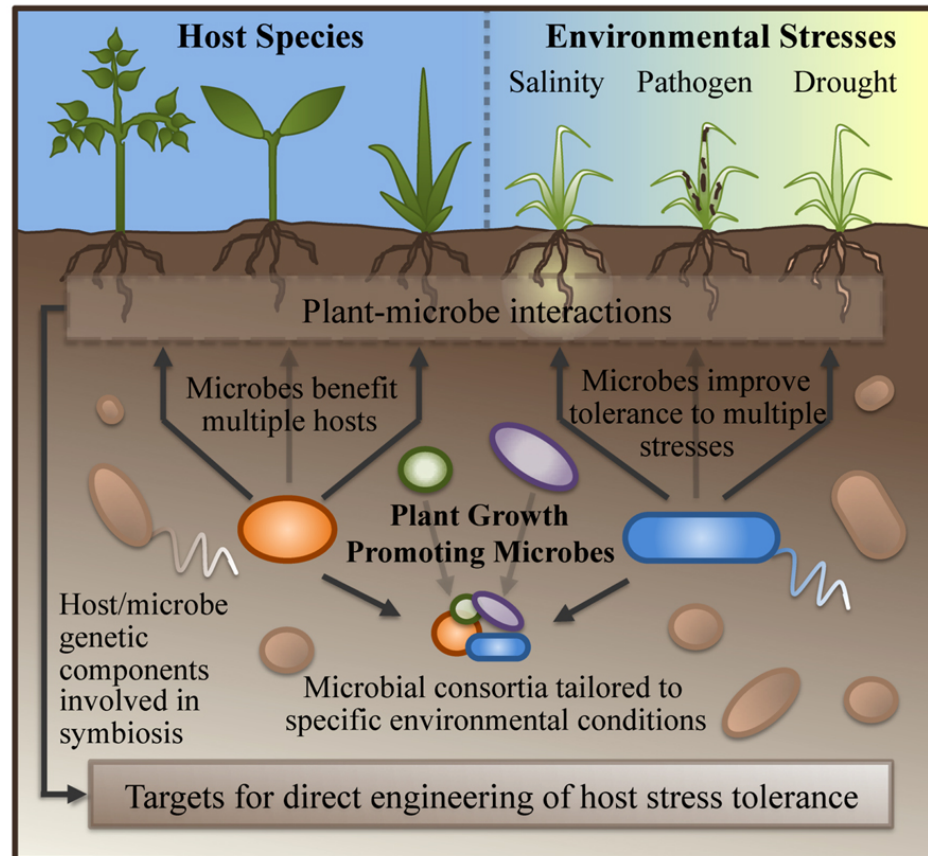


# Revegetation is a promising way to minimize the negative environmental impact of abandoned REEs mine tailings




In recent years, the REEs mining activities in Jiangxi Province are restricted, thus revegetation and phytoremediation has been widely used.

# Microbiological activities could contribute to successful revegetation



- Carbon fixation
- Nitrogen fixation
- P solubilization
- Siderophores
- Phytohormones
- Metal resistance

- 
- Plant growth and establishment
  - Plant tolerance
  - Soil development
  - Biogeological cycling

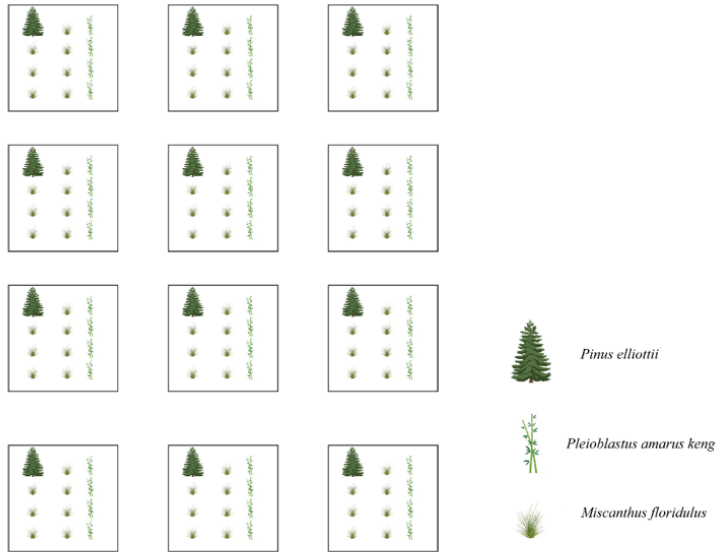
However, little is known about how soil microbial communities respond to the vegetation restoration in degraded REEs mine lands, although much research has emphasized their important roles in ecological restoration.





# A case study of revegetation management using arbor-shrub-grass in Gangxia mine tailings

*Pinus elliottii*- *Pleioblastus amarus* (Keng) keng- *Miscanthus floridulus* (Lab.) Warb. ex Schum. et Laut.



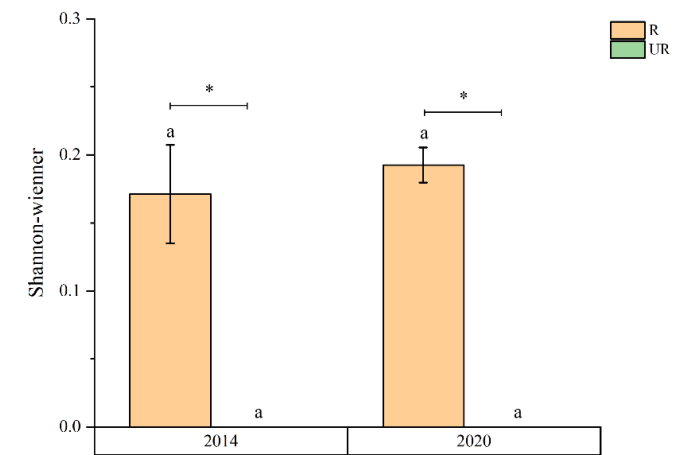
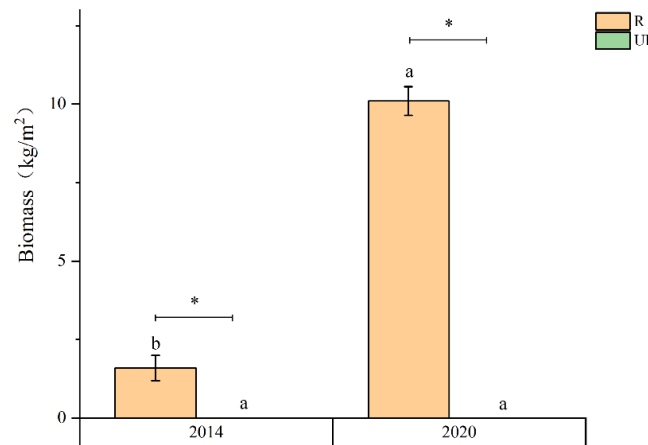
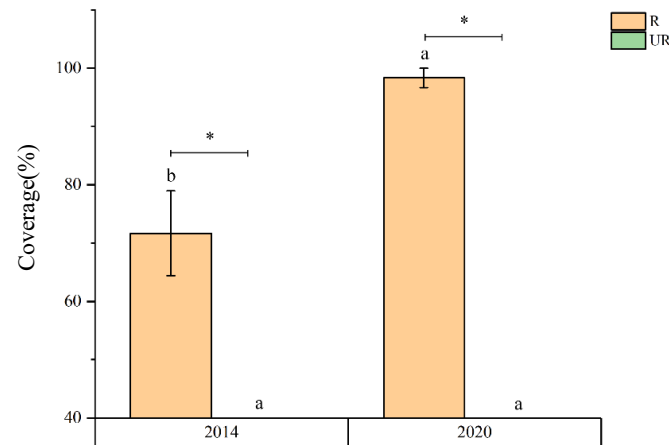
Planting design for revegetation management



Gangxia N25°16'37", E115°25'18"



# Biomass and diversity of plant community



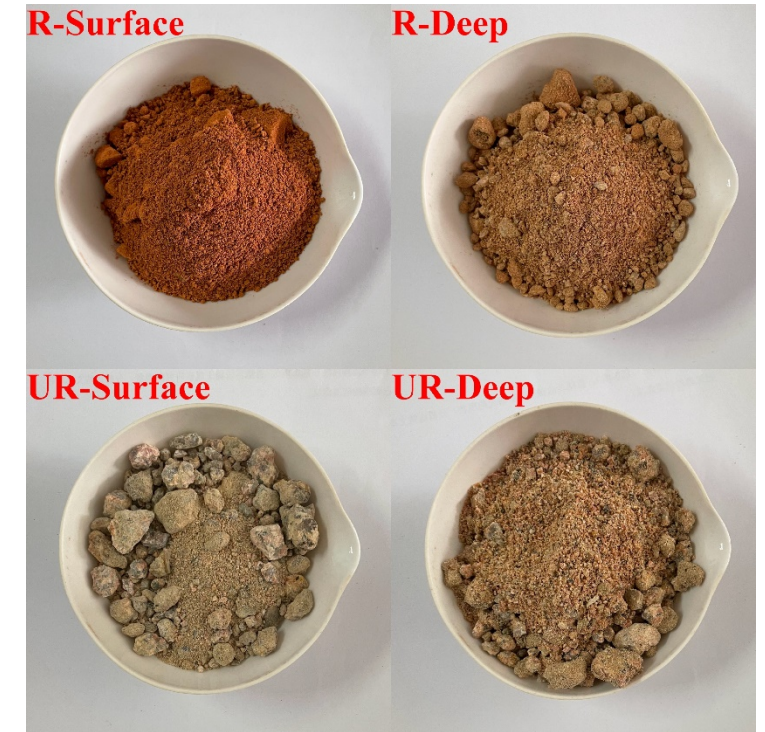
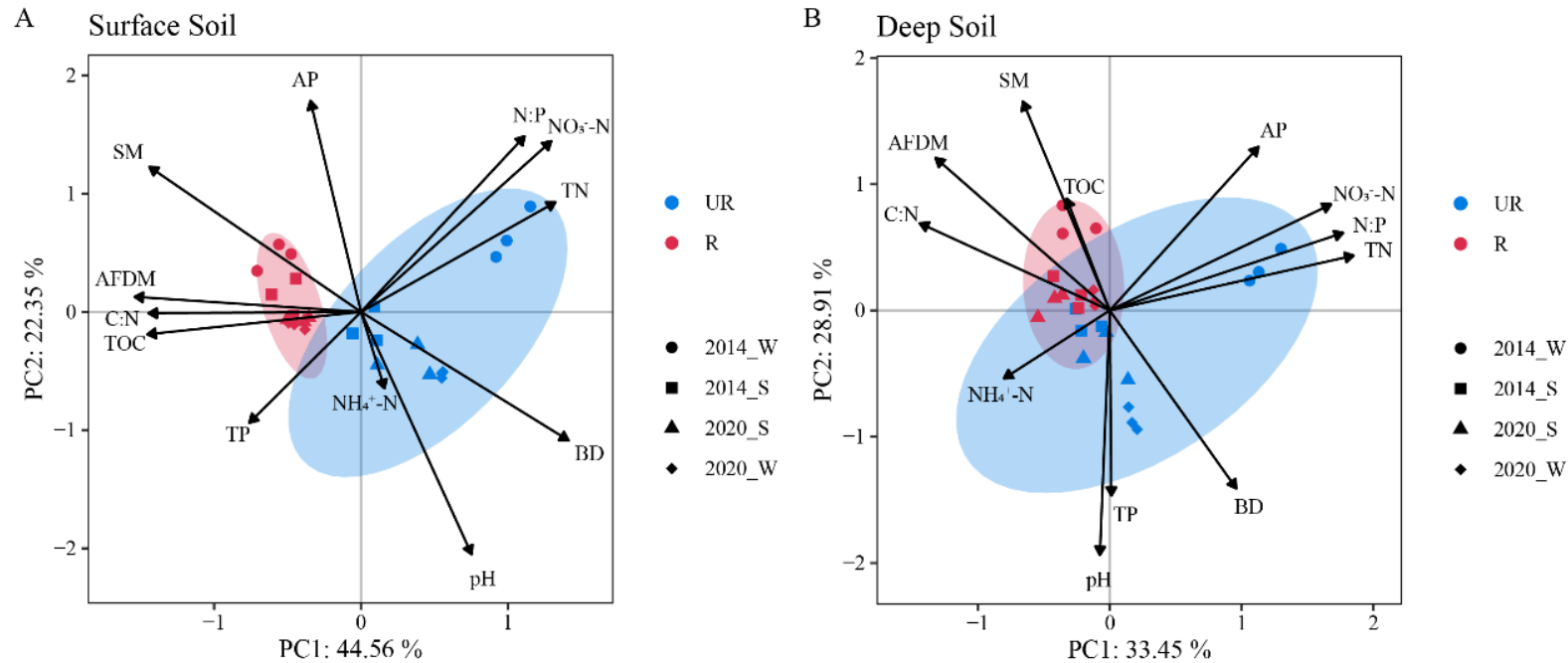
R: restored areas;  
UR: un-restored; unvegetated bare soils as control  
2014: 1 year after restoration;  
2020: 8 years after restoration  
 $P < 0.05$

**The un-vegetated area was not restored naturally even after 8 years; while the coverage, biomass and diversity of plant community in R were all greatly improved 8 years after restoration.**





# Soil physical and chemical properties

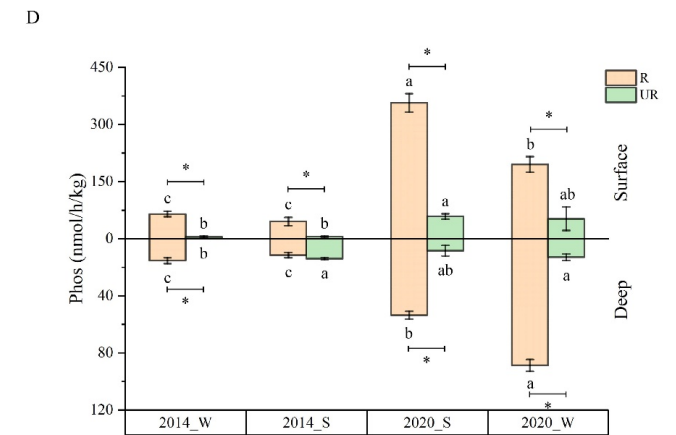
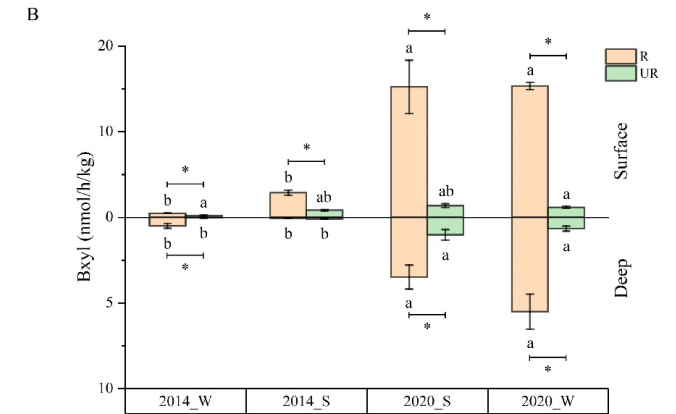
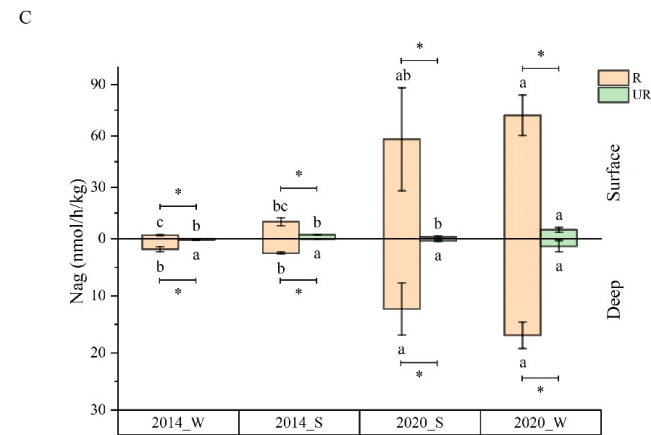
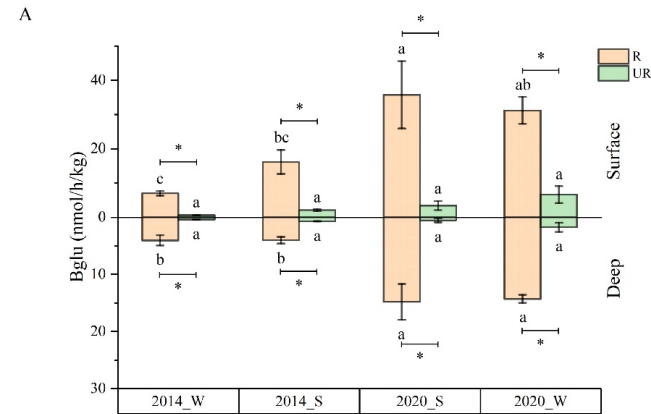
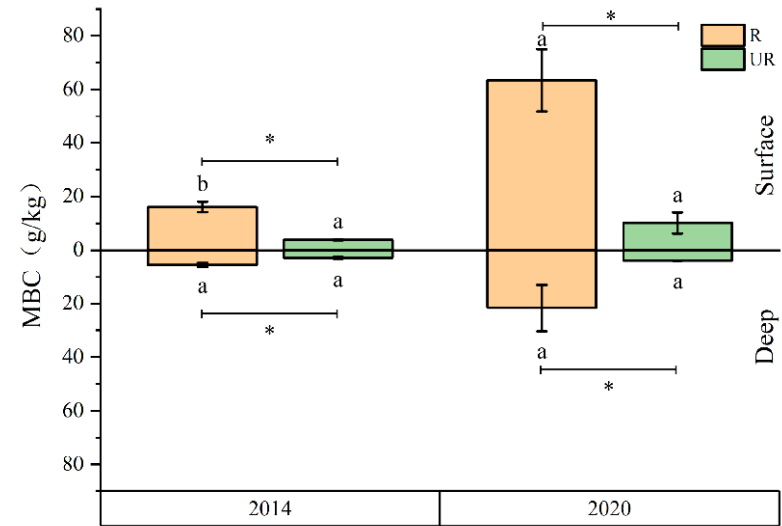


R: restored areas;  
 UR: un-restored; unvegetated bare soils as control  
 W: winter;  
 S: summer  
 Surface: 0-15 cm  
 Deep: 15-30 cm  
 $p < 0.05$

**The physical properties and organic matter content in R were significantly improved as compared with UR, particularly in surface soil.**



# Microbial biomass and activities

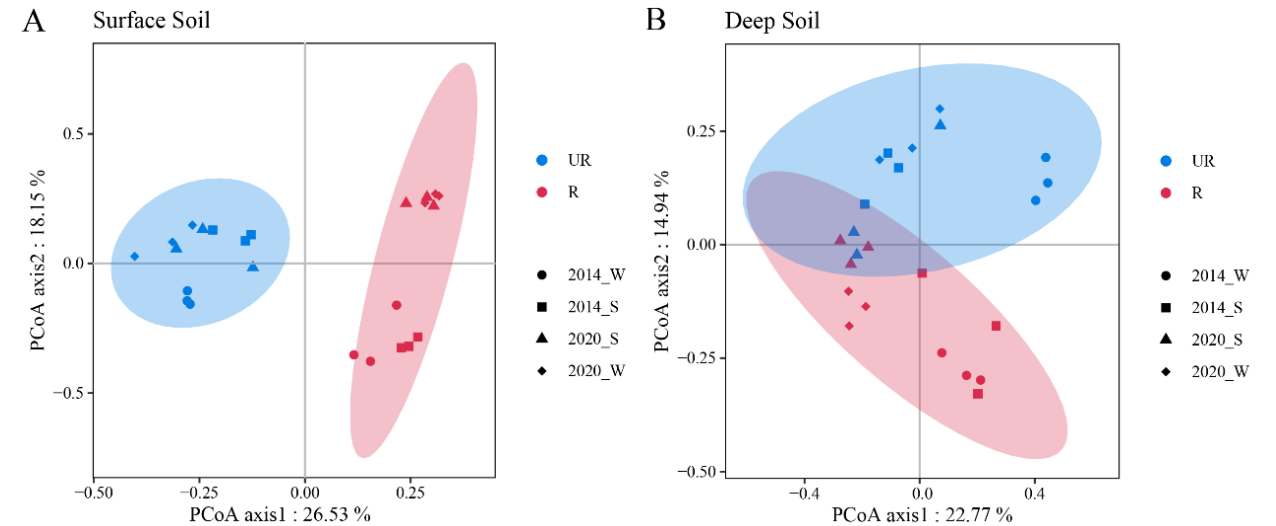
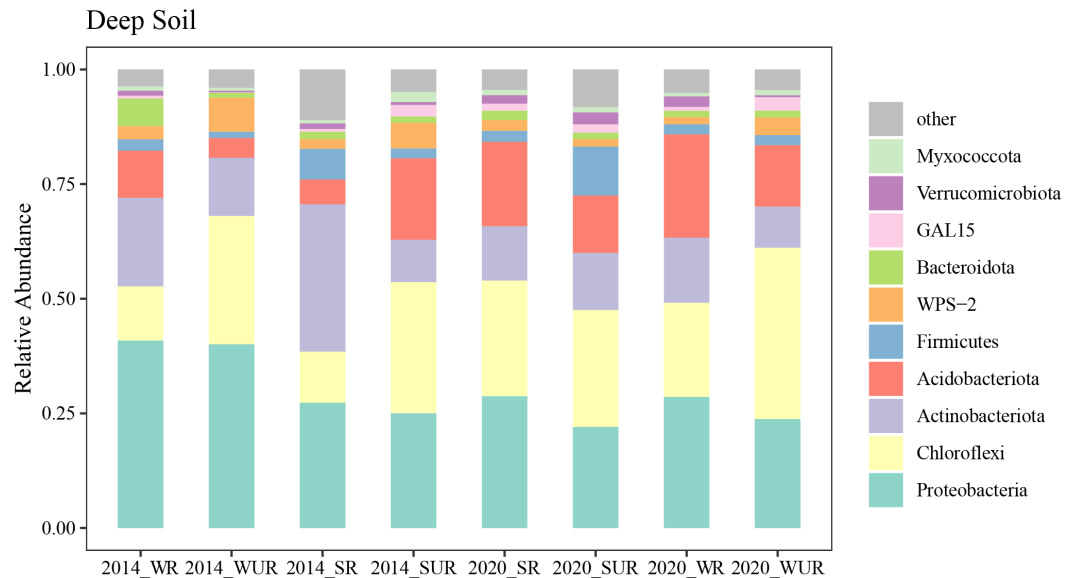
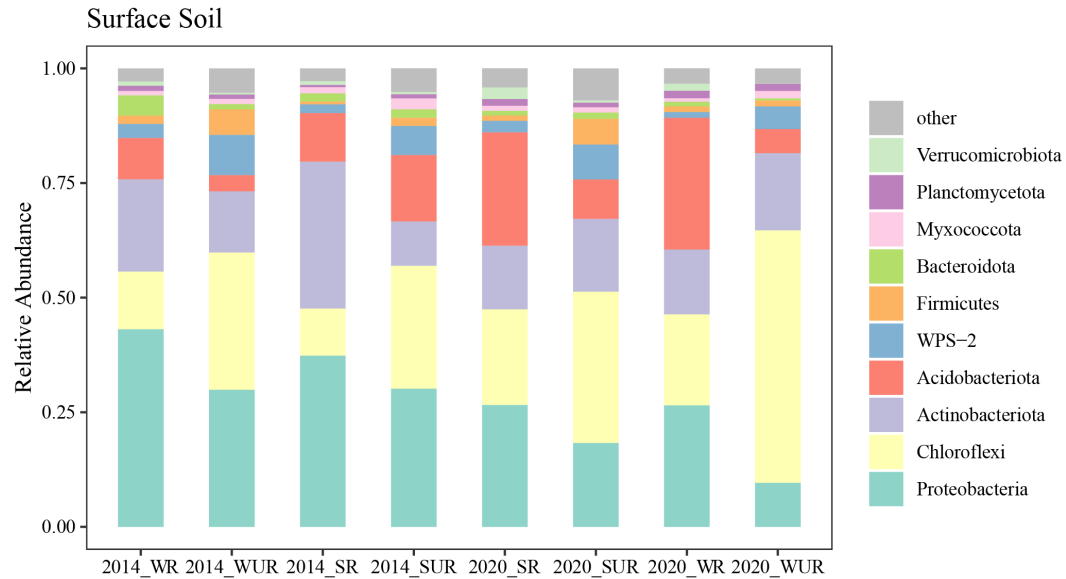


The microbial biomass and enzyme activities in R were significantly enhanced in both surface and deep soils as compared with UR ; moreover, microbial biomass and activities were also improved with time after restoration





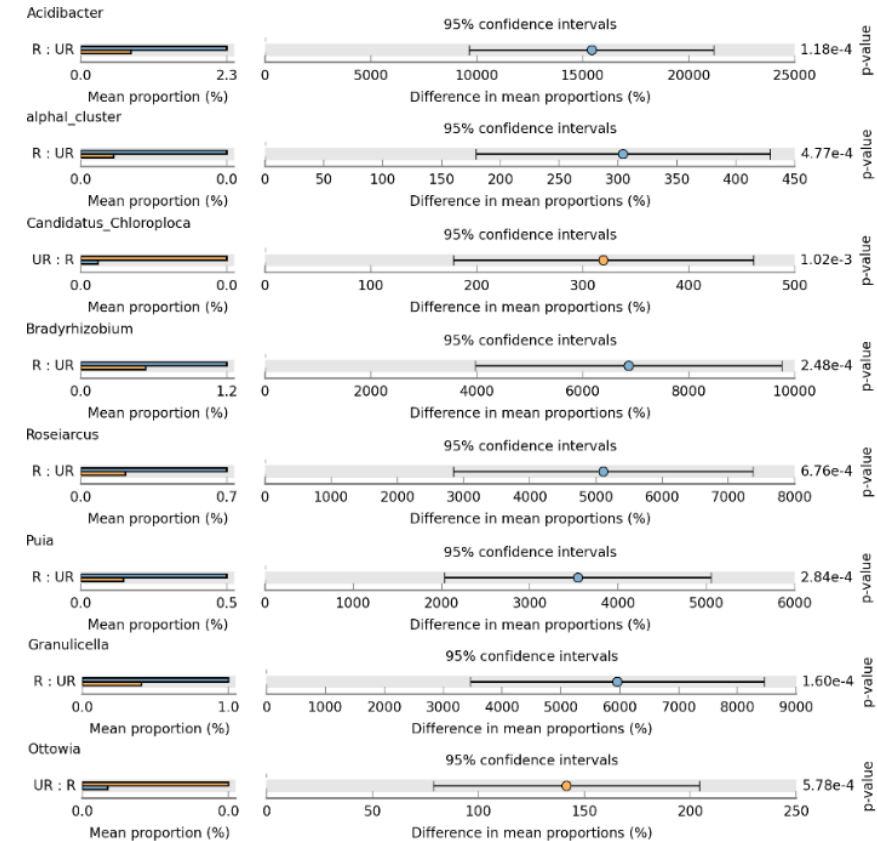
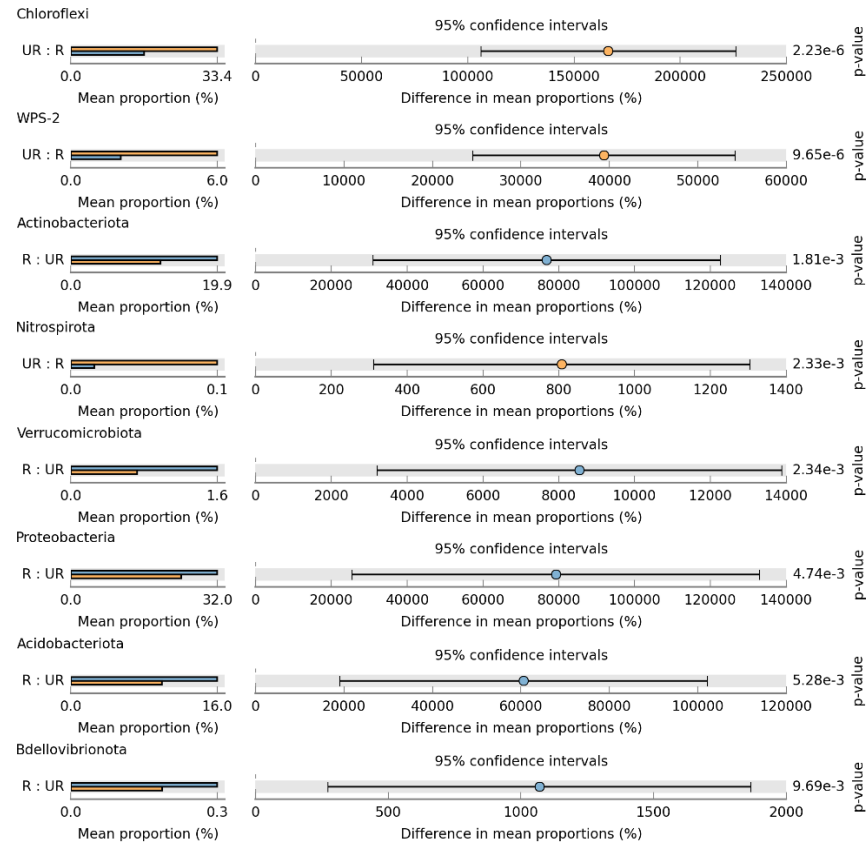
# Bacterial community composition and structure



**Vegetation restoration significantly increased the alpha-diversity of bacterial community only at some specific sampling time (data not shown), but the composition and structure of bacterial community in R was significantly different from UR ( $p < 0.05$ ), particularly in surface soil.**



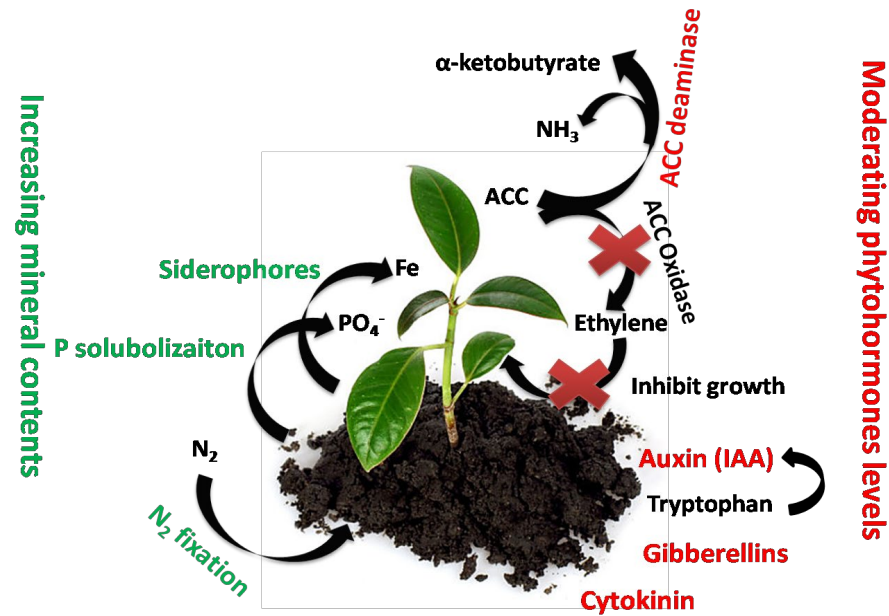
# Bacterial indicator taxa affected by vegetation restoration



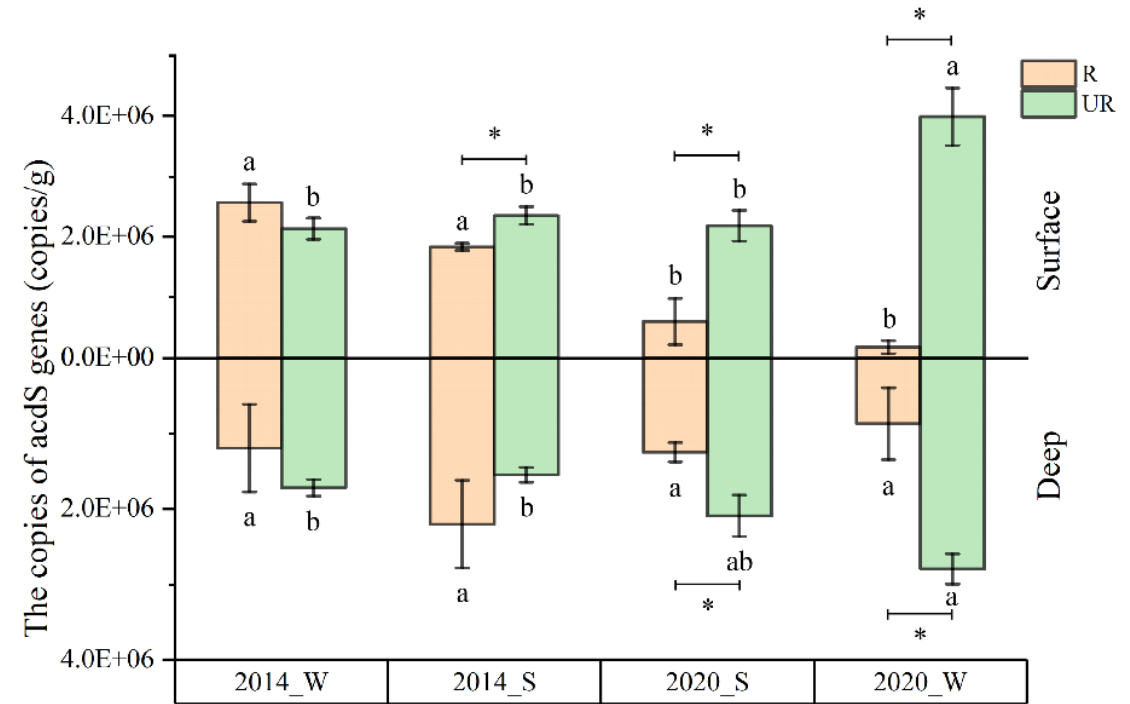
A number of bacterial phyla including Atinobacterita, Verrucomicrobiota, Proteobacteria, Acidobacteriota, Bdellovibrionota, and Bacteroidota and bacterial genera *Acidibacter*, *Cluster*, *Bradyrhizobium*, *Roseiarcus*, *Puic*, *Granulicella*, *Inquilinus*, *WD260\_gesome*, *Afipia*, *Acidicapsa*, *KF-JG30-B30\_ge*, *Caulobacter* were indicators for R, suggesting vegetation restoration affects specific taxa.



# The copies of *acdS* genes



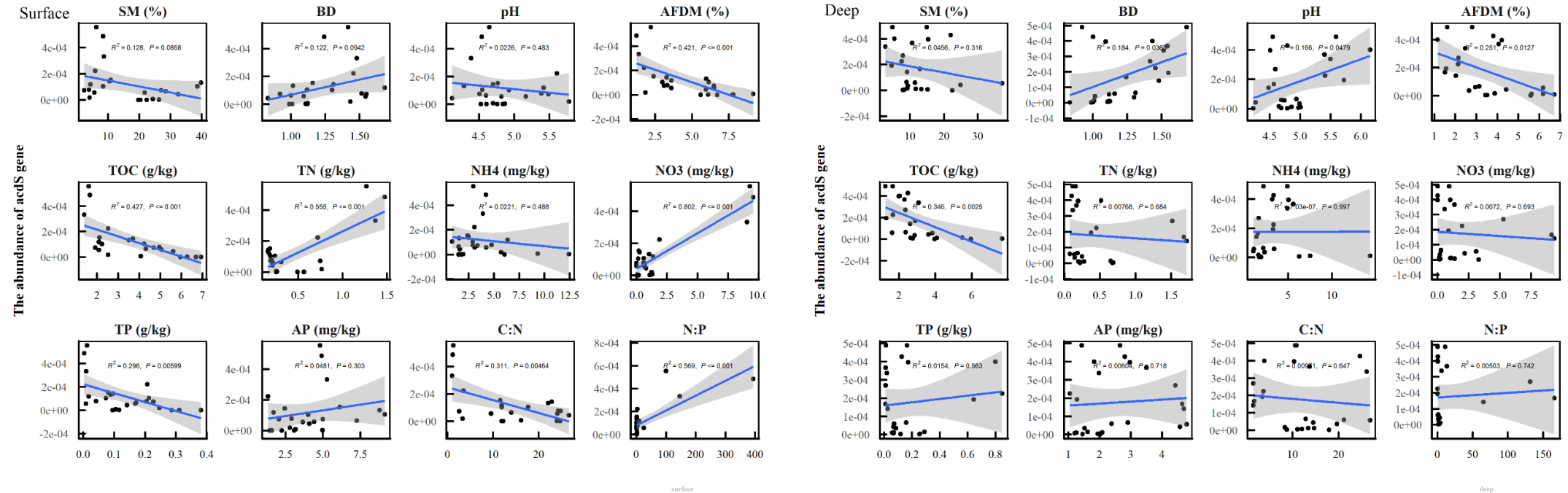
Kong & Glick, Adv. Microb. Physiol., 2017



As compared with UR, the abundance of *acdS* gene was significantly lower in R, particularly in 8 years after restoration; the abundance of *acdS* gene in surface soil was significantly decreased with time after restoration.



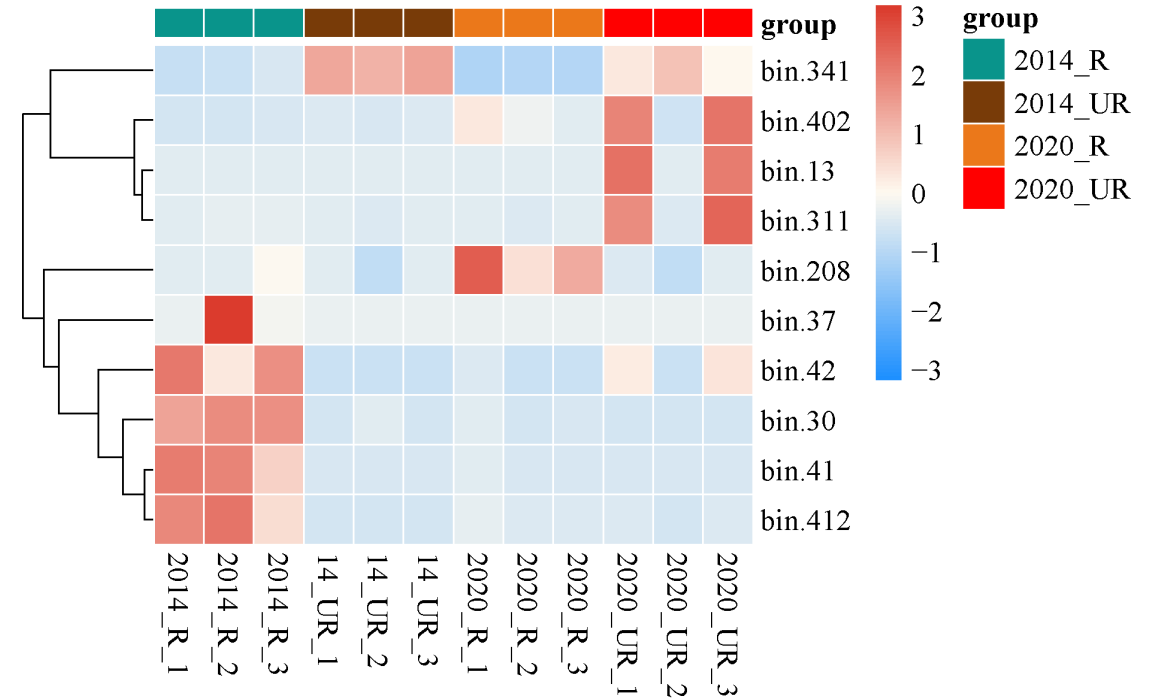
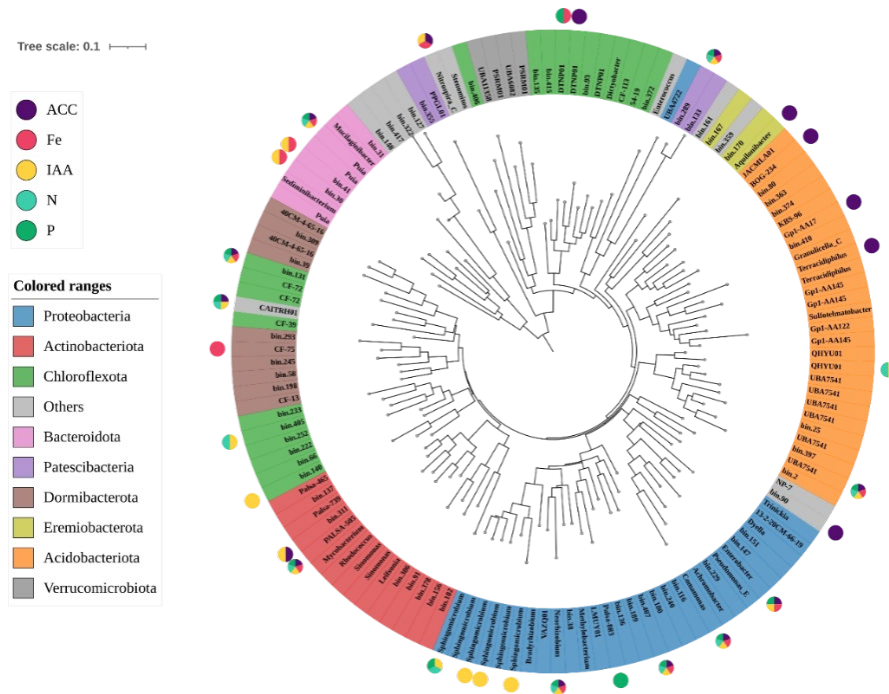
# Linkages between abundance of *acdS* gene and soil properties



The abundance of *acdS* gene was significantly and negatively correlated with TOC and AFDM contents in both surface and deep soils.



# Phylogenetic analysis of microbial genome bins



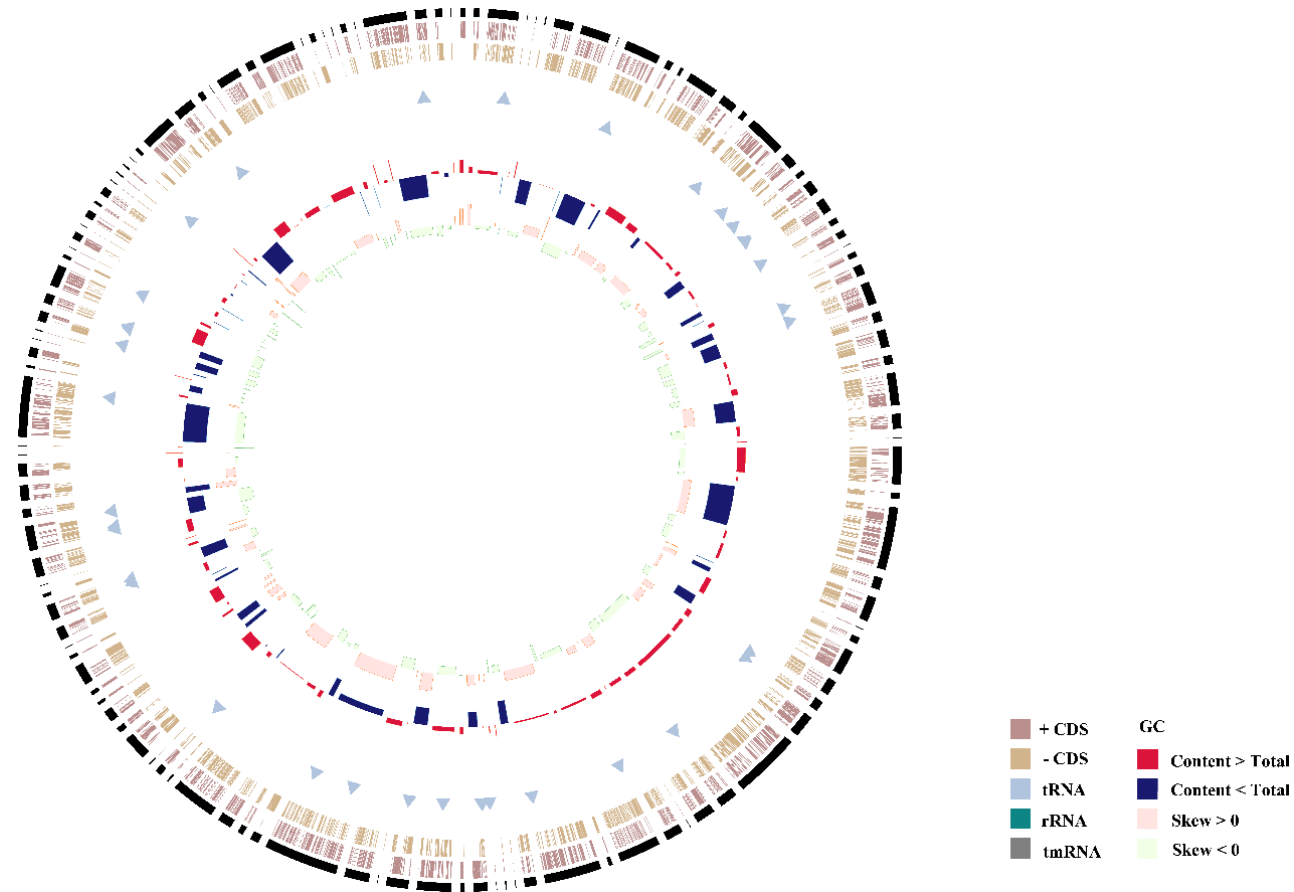
The assembly and binning process generated 142 microbial genome bins with more than 50% completeness and less than 5% contamination.

In total, 19 *acdS*-containing genome bins were detected; genes encoding other PGP traits (including phosphate-solubilization, production of IAA, siderophore, N-fixation) were also found in these genome bins; among them bin91 and bin311 were novel ACC deaminase-producing bacterial taxa.

The *acdS*-containing genome bins 42, 30, 41, 412 were enriched in R one year after restoration, but decreased with time after restoration.



# High-quality metagenome-assembled genome harboring sequences of *acdS* gene



The assembly and binning process generated 12 microbial genome bins with more than 90% completeness and less than 5% contamination (near-complete genomes).

Among them, bin 341 contained *acdS* gene (*Pseudomonas monteilii*). the genes involved in plant growth-promotion, metal-resistance and C, N mineralization were also found in bin 341.





# In summary

- **Vegetation restoration greatly improved physical structure, nutrient status, microbial biomass and activities of REEs mine tailings in both surface and deep soils;**
- **The composition and structure of bacterial community was significantly varied due to vegetation restoration; a number of bacterial phyla and genera were identified as indicators affected by vegetation restoration, suggesting vegetation restoration affects specific taxa;**
- **Vegetation restoration significantly decreased the abundance of *acdS* gene, particularly in 8 years after restoration; moreover, the abundance of *acdS* gene in surface soil was significantly decreased with time after restoration.**
- **A total of 19 *acdS*-containing genome bins were detected; other genes encoding PGP traits were also found in these genome bins; among them bin91 and bin311 were novel ACC deaminase-producing bacterial taxa; One near-complete genome bin 341 was reconstructed and the genes involved in plant growth-promoting, metal-resistance and C, N mineralization were also found in bin 341.**







# Thank you for your attention!

**Vegetation status 9 years after vegetation recovery in Gangxi  
REEs mine tailings**

**This photo was taken in May 202**

