

Tomato microbiome under long-term organic and conventional farming

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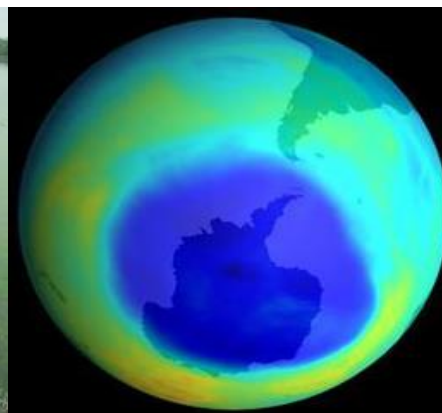
Introduction



Soil compaction



Eutrophication of water



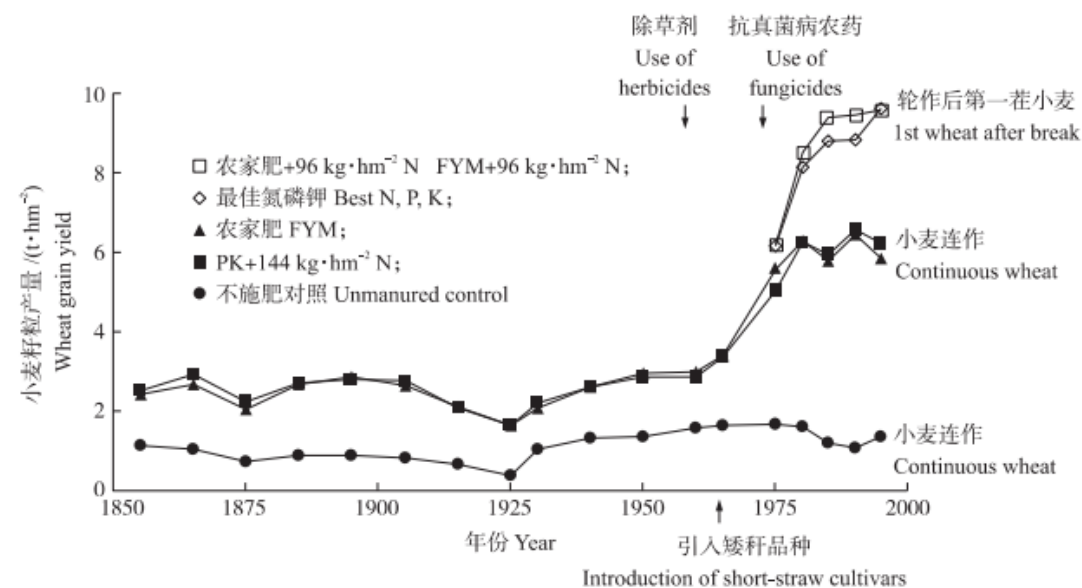
Ozone Hole



Biodiversity decline

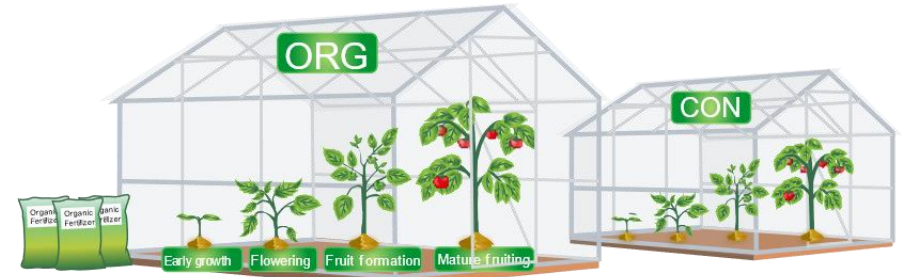
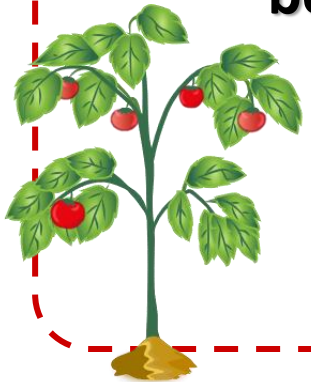
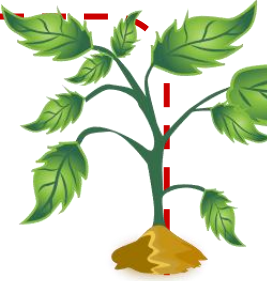


Long-term trail in Rothamsted-
Experimental-Station, UK

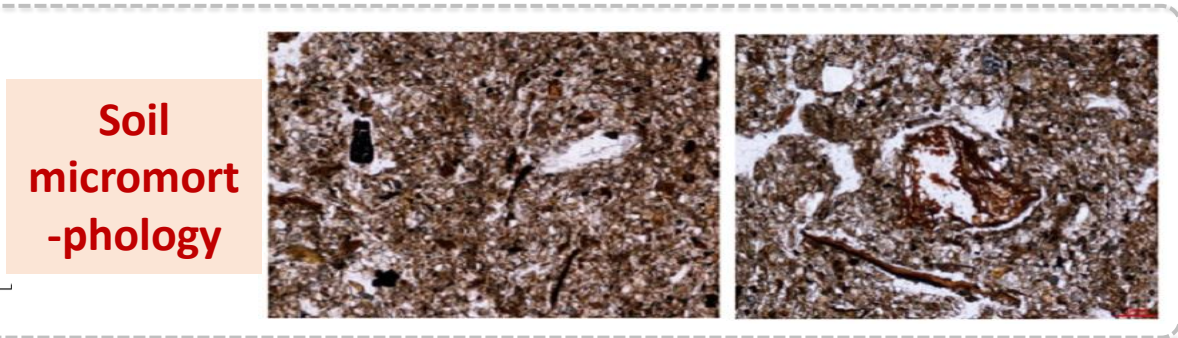
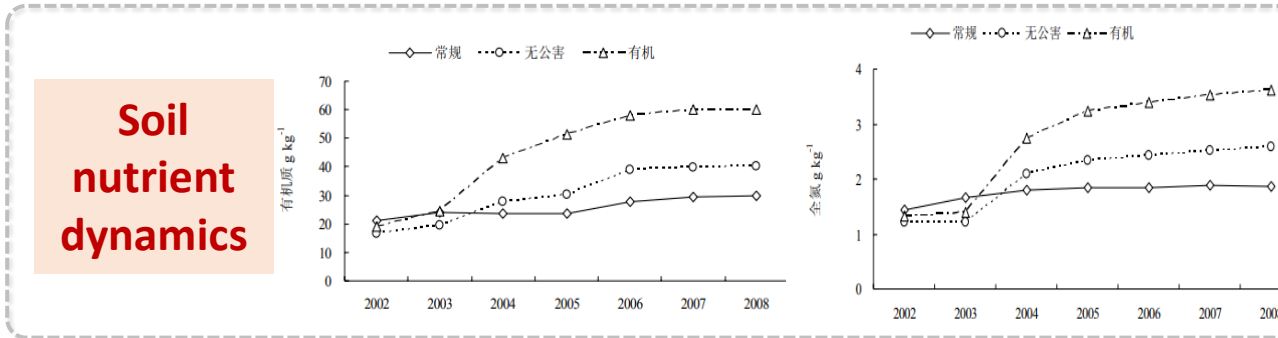
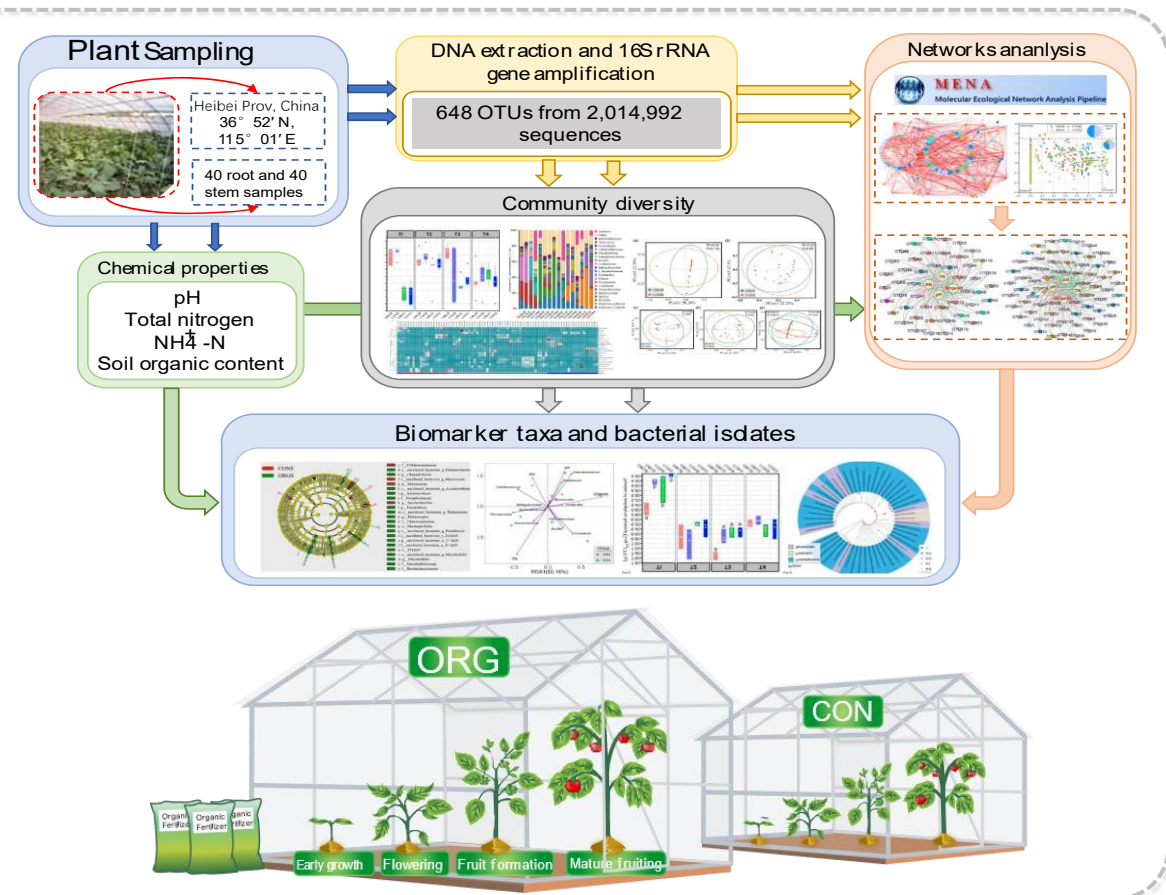
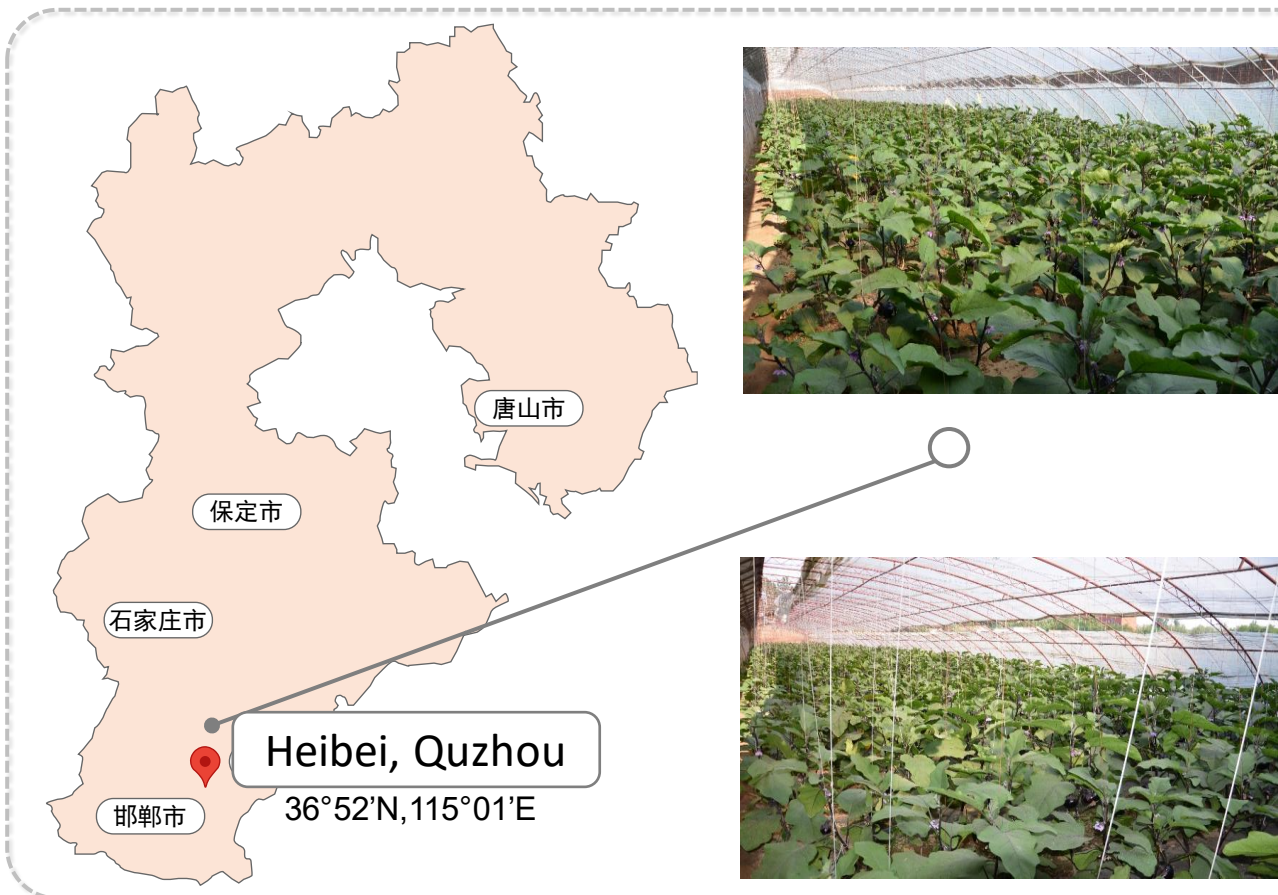


Principal Objective

- ❖ Assess how host (compartment niche) and environmental factors (organic farming or conventional farming) interactively shape tomato endophytic microbiome assemblies and concurrence patterns based on long-term field trials since 2002.
- ❖ Isolate the potential beneficial tomato microbiomes as candidate for agricultural inoculants. This study will help to provide comprehensive insight into the tomato endophytic bacterial communities cultivated in a greenhouse agroecosystem and provide useful information for using the beneficial microbiome into agricultural production.



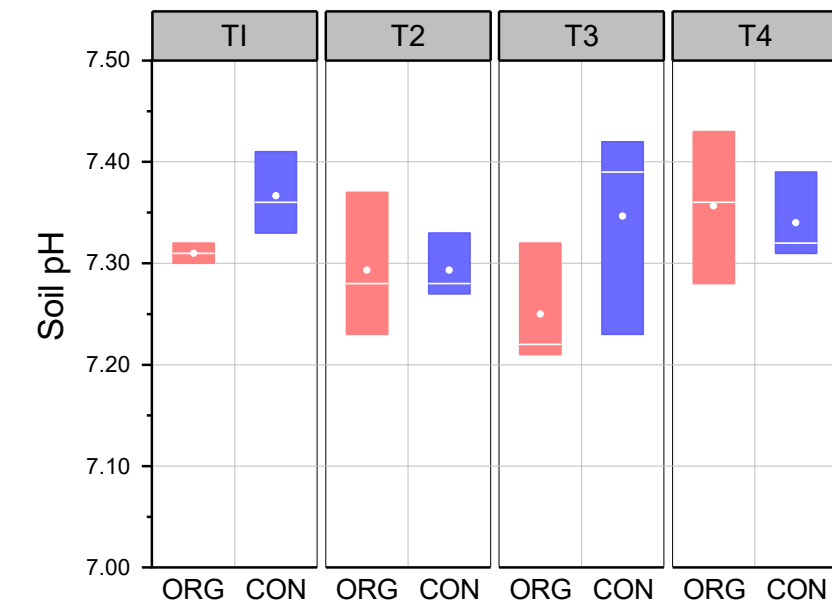
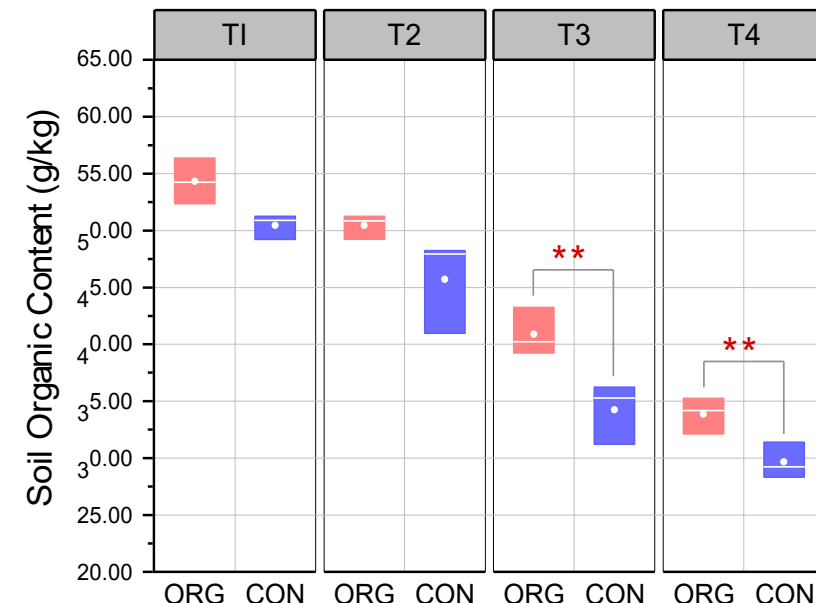
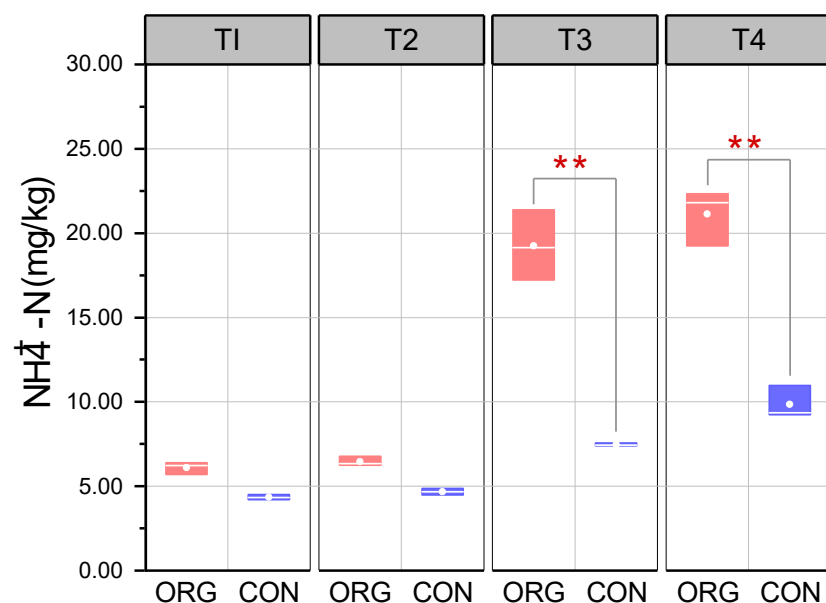
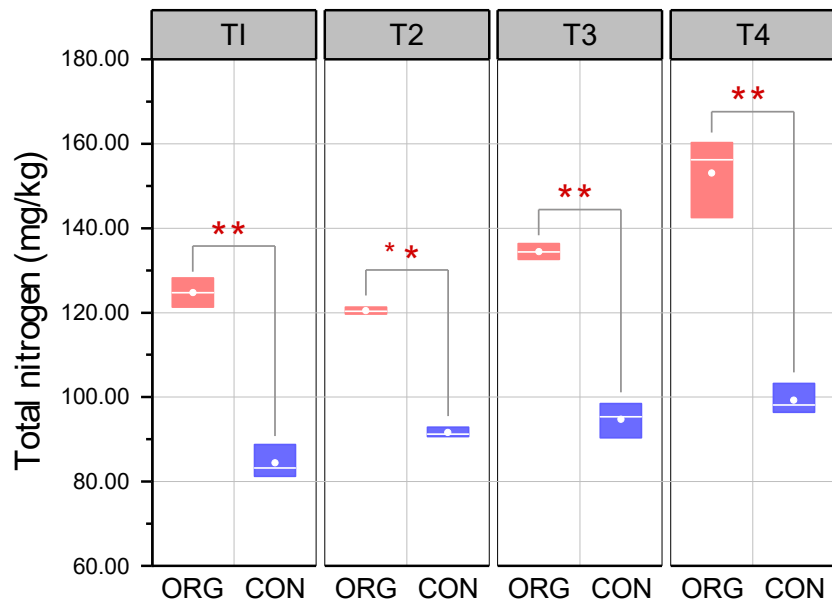
Experimental Design



Soil nutrient dynamics

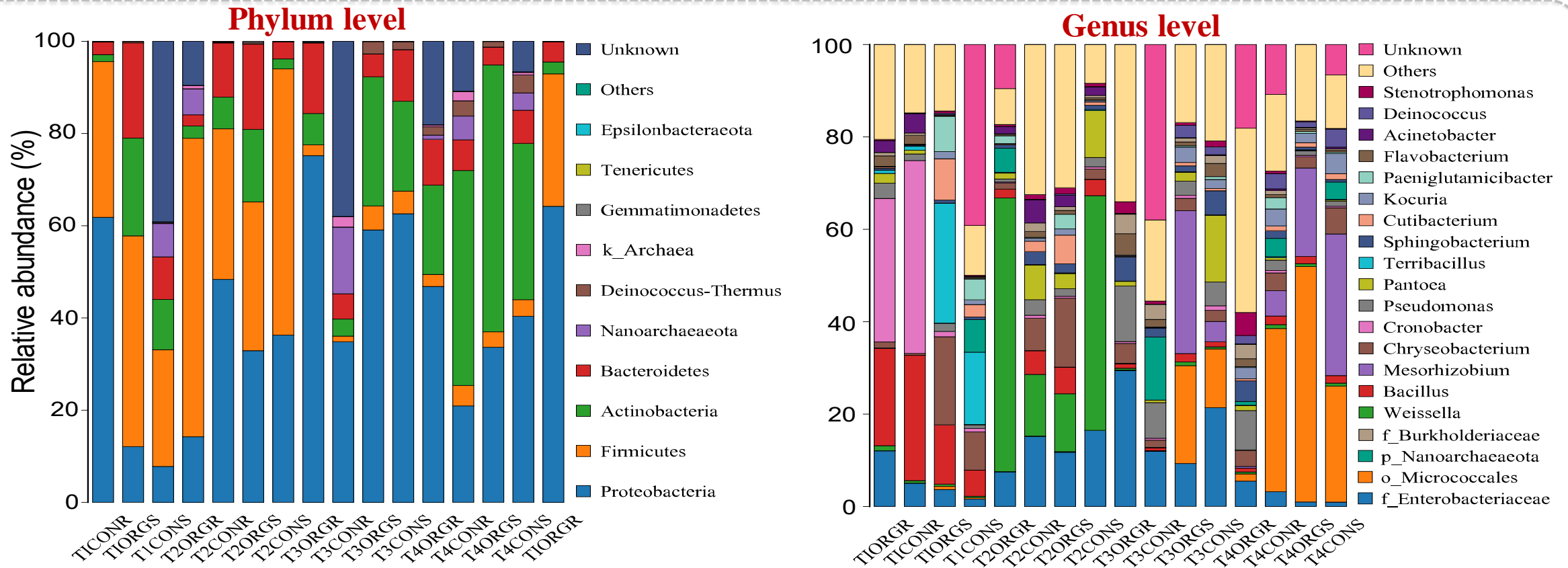
Soil micromorphology

Shifts of Soil Chemical Parameters



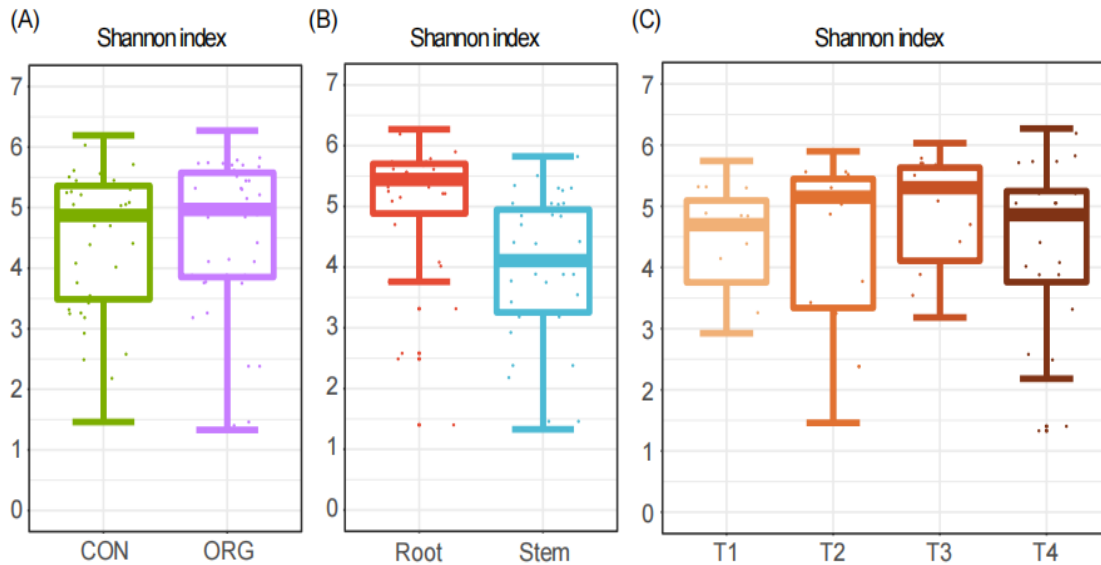
- The total nitrogen concentration was higher in the organic greenhouse than that of conventional greenhouse (Student's *t*-test, $P < 0.001$).
- The dynamic trend of $\text{NH}_4^+\text{-N}$ was similar to that of TN, but only at T3 and T4, ORG and CON treatments showed significant differences (Student's *t*-test, $P < 0.01$).
- Soil organic matter content in ORG treatment was higher than that in CON treatment, and the difference was also significant only in T3 and T4 stages (Student's *t*-test, $P < 0.01$).

Changes of taxonomy of tomato bacteria

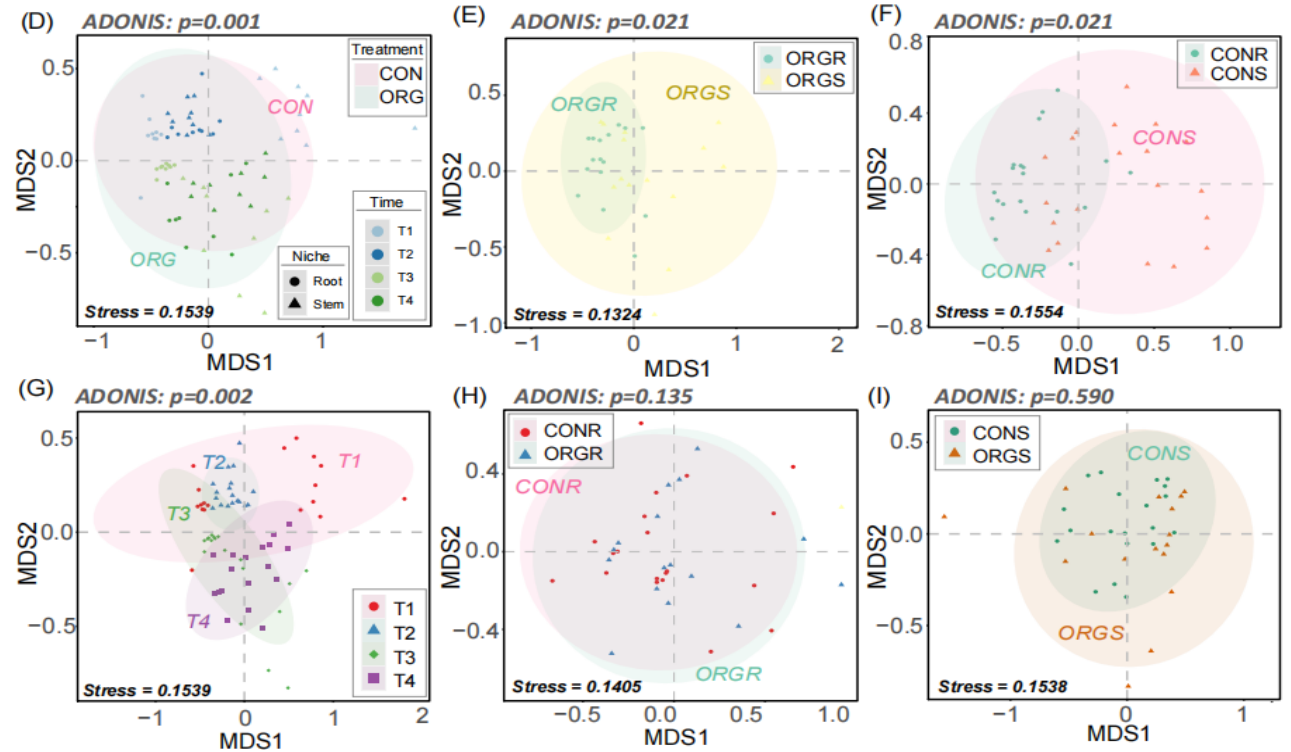


- *Proteobacteria* was the most abundant ($40.63\% \pm 2.68$), followed by *Firmicutes* ($21.76\% \pm 1.66$), *Actinobacteria* ($20.3\% \pm 3.62$) and *Bacteroidetes* ($8.7\% \pm 4.45$)
- With the growth of tomato, the abundance of *Firmicutes* in root microbial community decreased, while that of *Proteobacteria* increased significantly.
- Similar phenomenon occurred in stem endophytic bacterial communities: the relative abundance of *Arthrobacter.sp*, *Rhizobium.sp* gradually increased, while the *Bacillus.sp* decreased dramatically at the late crop season.

Diversity index difference

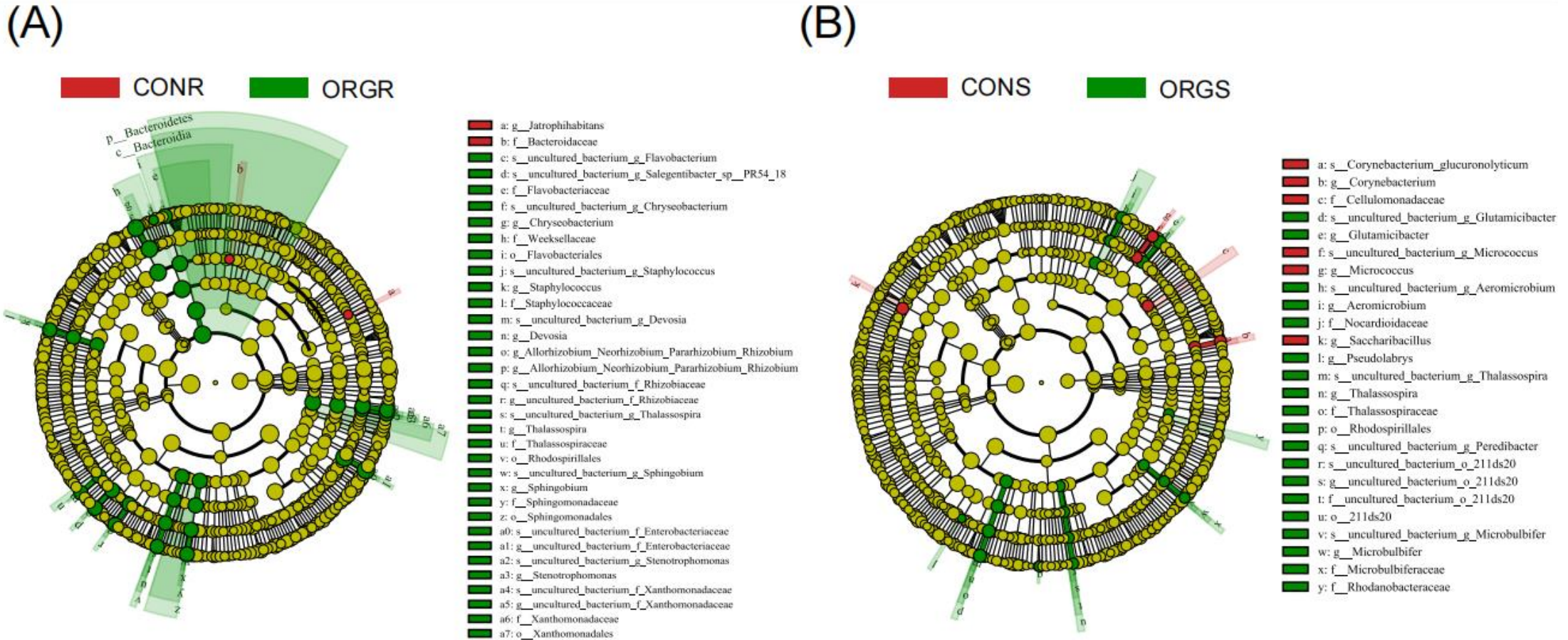


- The Shannon index of microbial community in ORG treatment was higher than that in CON, and that in root was higher than that in stem
- There were no significant differences in Shannon index of microbial communities among agricultural manipulation, compartment-niche and key growth stages of tomato.



- Compartment niche was the main reason for the variation of microbial communities, and the microbial communities in root and stem niches were significantly different between organic and conventional greenhouse.
- The microbial communities were also significantly different in different growth stages of tomato.
- Organic treatments did not significantly affect the microbial communities in the roots or stems.

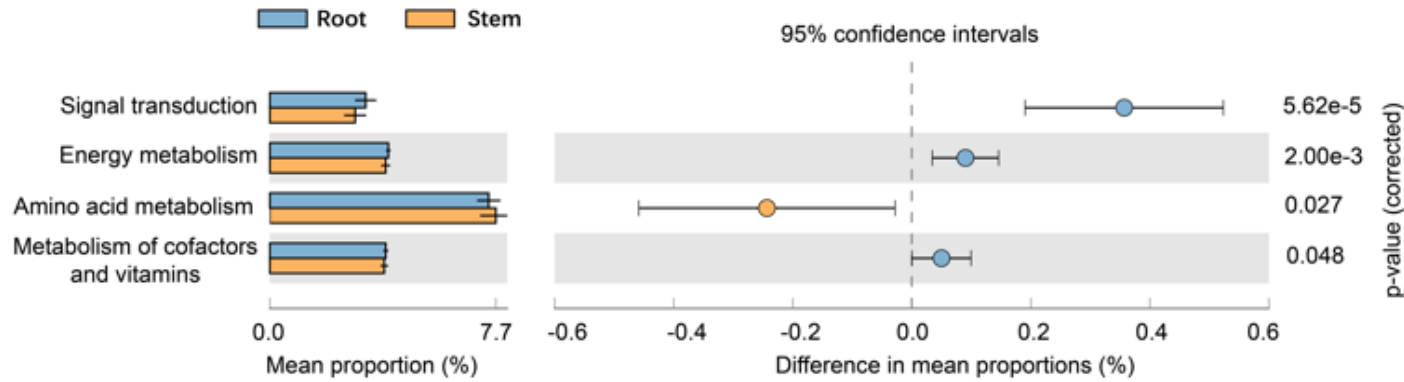
Biomarker taxa



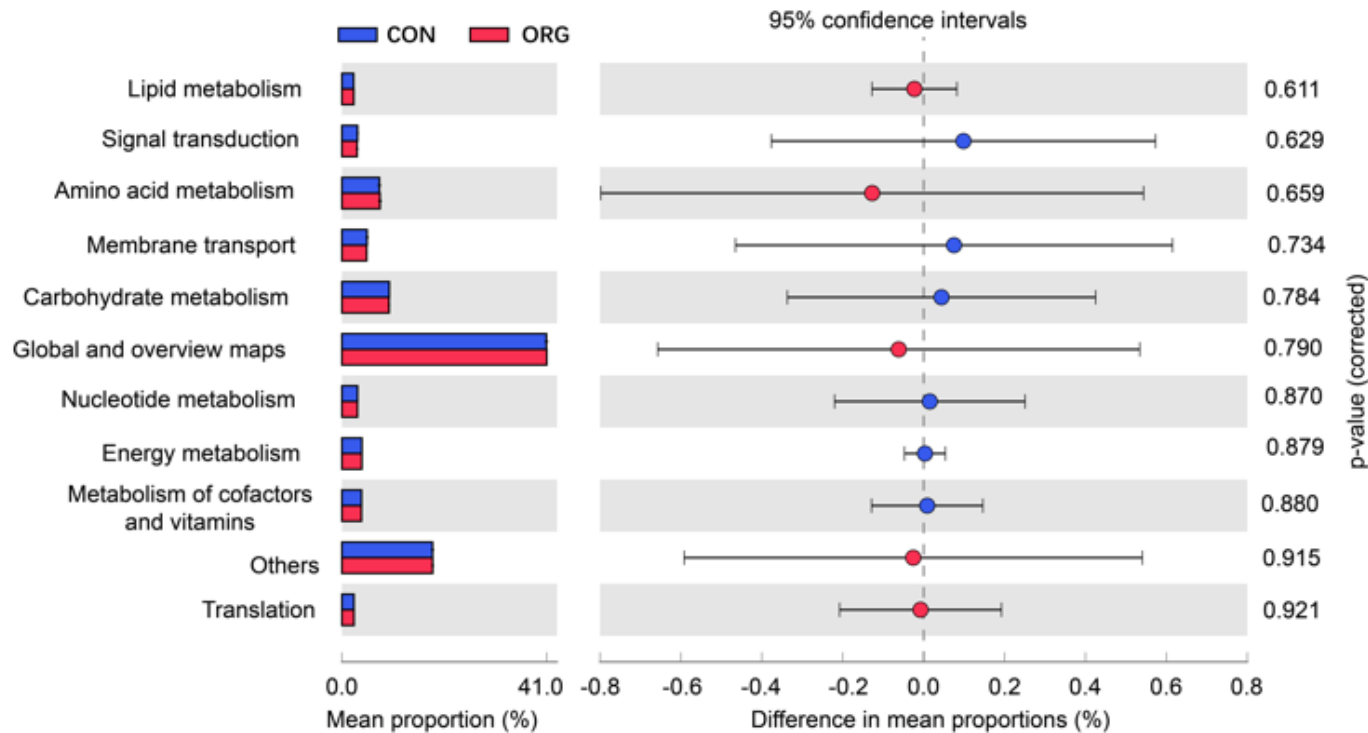
- *Flavobacterium*, *Sphingomonadales*, *Xanthomonadaceae* and *Rhizobium* enriched in the organic tomato root, while *Bacteriodes* contained in the conventional tomato root.
- *Enterobacteriaceae* enriched in organic stem, and *Corynebacterium* enriched in the conventional stem.

Potential function of bacterial microbiome

(C)

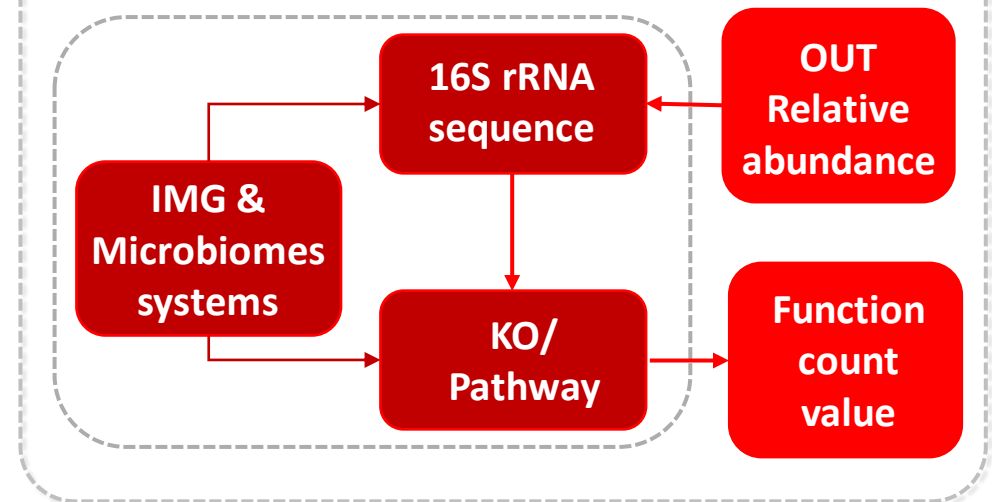


(D)

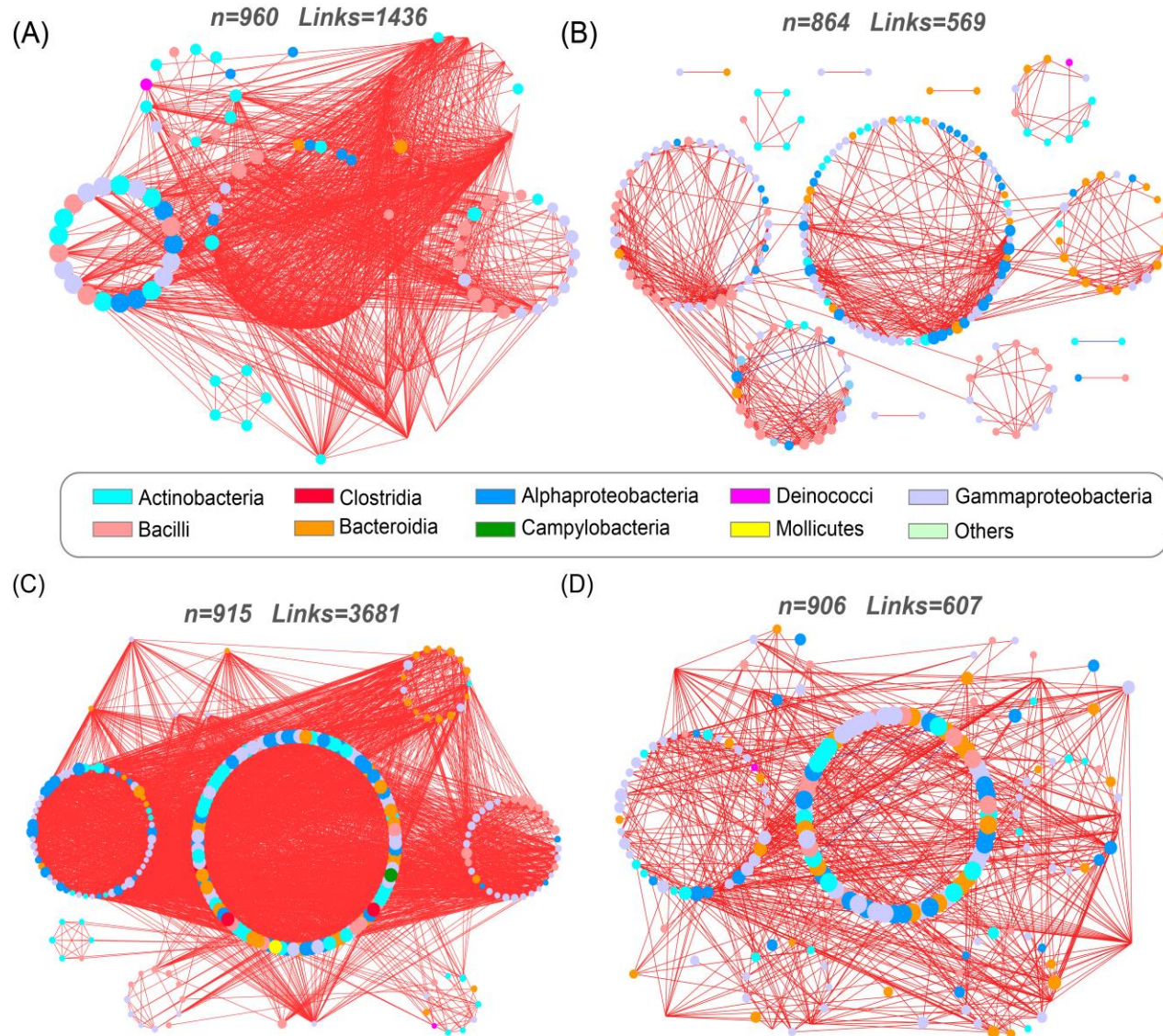


➤ Signal Transduction, energy metabolism, amino acid metabolism and Metabolism of cofactors and vitamins were observed to have significant differences in the roots and stems. The abundance of amino acid metabolism was higher in stems than in roots.

➤ There was little difference was observed in the potential function of tomato microbiota between CON and ORG treatments.

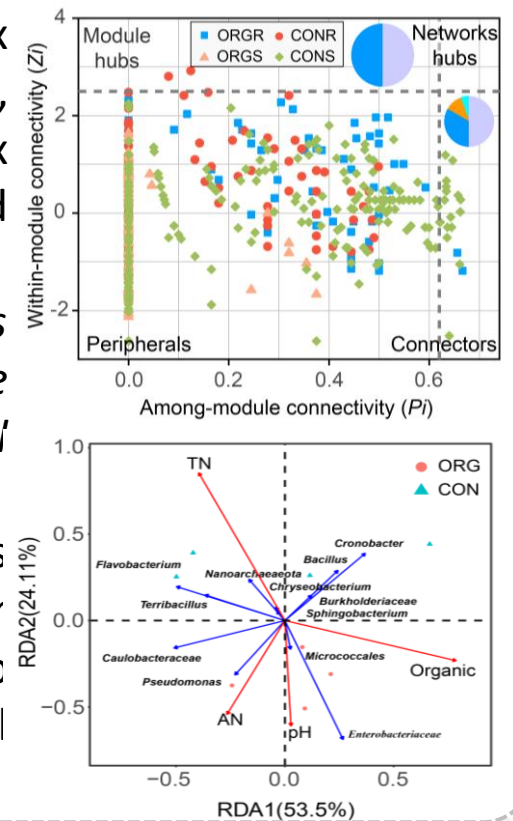


Network associations and microbial hubs

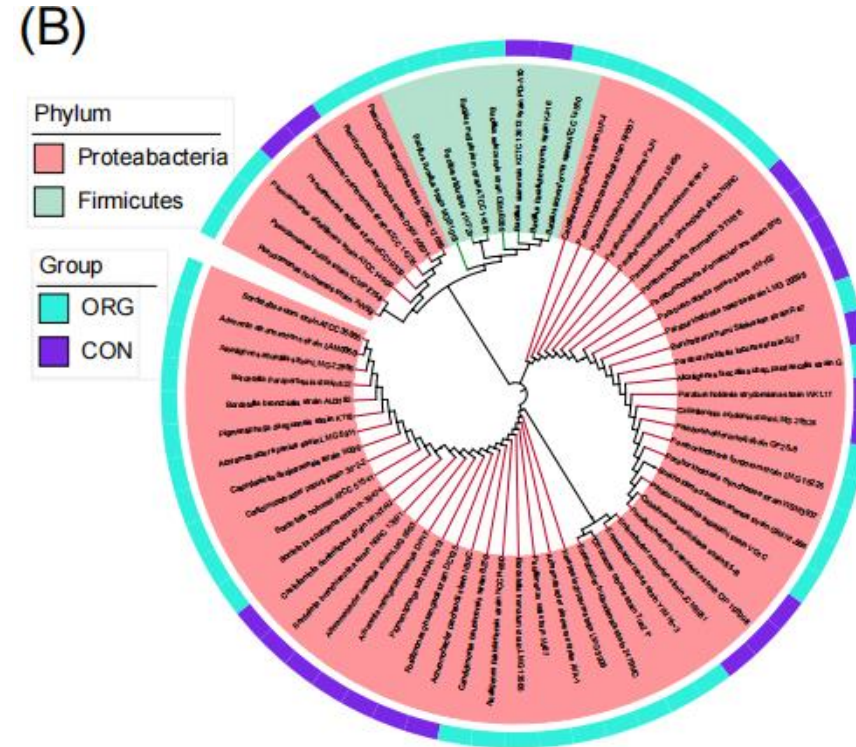
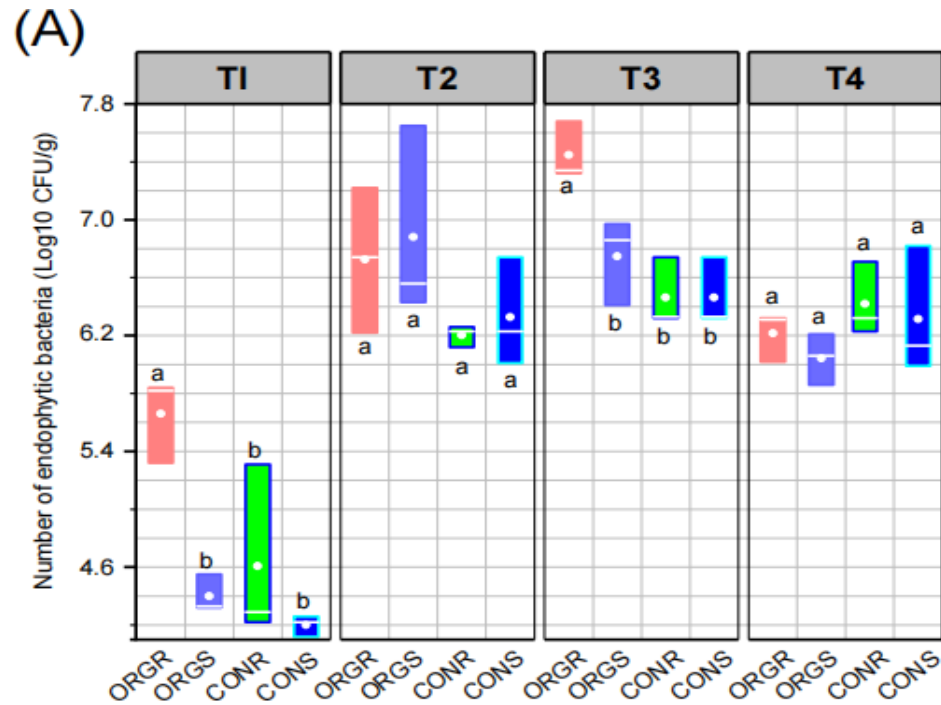


Treatment	Nodes	Links	avgK	avgCC	Modularity
ORGR	915	3681	30.172	3.19	0.855
CONR	960	1436	19.415	4.99	0.911
ORGS	906	607	6.215	2.71	0.883
CONS	864	569	5.893	3.05	0.872

- Root formed a more complex microbial network than stem, ORG formed a more complex microbial network compared with CON
- *Proteobacteria, Bacteroidetes and Actinobacteria* are considered as the key microbial groups in this ecosystem.
- soil total nitrogen (TN) was considered as the major driver which led to a tomato endophytic bacterial community shift.



Cultivable isolation Endophytic bacterial diversity



- A total of 663 bacteria were isolated by cultural-dependent method, but after 16S sequence alignment to remove redundancy, we obtained 60 bacteria from different genus.
- the number of endophytic bacterial increased with plant growing, ranging from 4.21 to 7.45 (log10 CFU/g. FW), reaching peak in the fruiting phase.
- Organic agricultural practice and conventional practice nearly almost have no influence for number of endophytic bacterial, and the isolated number of bacteria were more in roots than that in stems.
- *Bacteroidetes* and *Proteobacteria* were dominant endophytic bacterial phylum, specifically, *Bacillus* is more prevalent in the organic farming greenhouse than that in the conventional farming greenhouse

Conclusion

- Long-term organic manipulation exerted limited influence on the variations of bacterial communities under long-term trail, while compartment niche was the main driver force for the shifts of endophytic bacterial communities.
- Organic greenhouse tomato bacterial had more complex co-occurrence networks than conventional greenhouse tomato bacterial, and root bacterial had more complex co-occurrence networks than stem bacterial, respectively.
- Cultivable method results found that *Proteobacteria* and *Firmicutes* are dominant phylum in the endophytes, and *Bacillus* were more prevalent in the organic farming greenhouse.

Zeyu Zhang, Yang Sean Xiao, Yabin Zhan, Zengqiang Zhang, Youzhou Liu, *et al.* 2022. Tomato microbiome under long-term organic and conventional farming. *iMeta* e48.
<https://doi.org/10.1002/imt2.48>



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 Society: <http://www.imeta.science>
Publisher: <https://onlinelibrary.wiley.com/journal/2770596x>

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