



Soil-borne legacy facilitates the dissemination of antibiotic resistance genes in soil–plant continua

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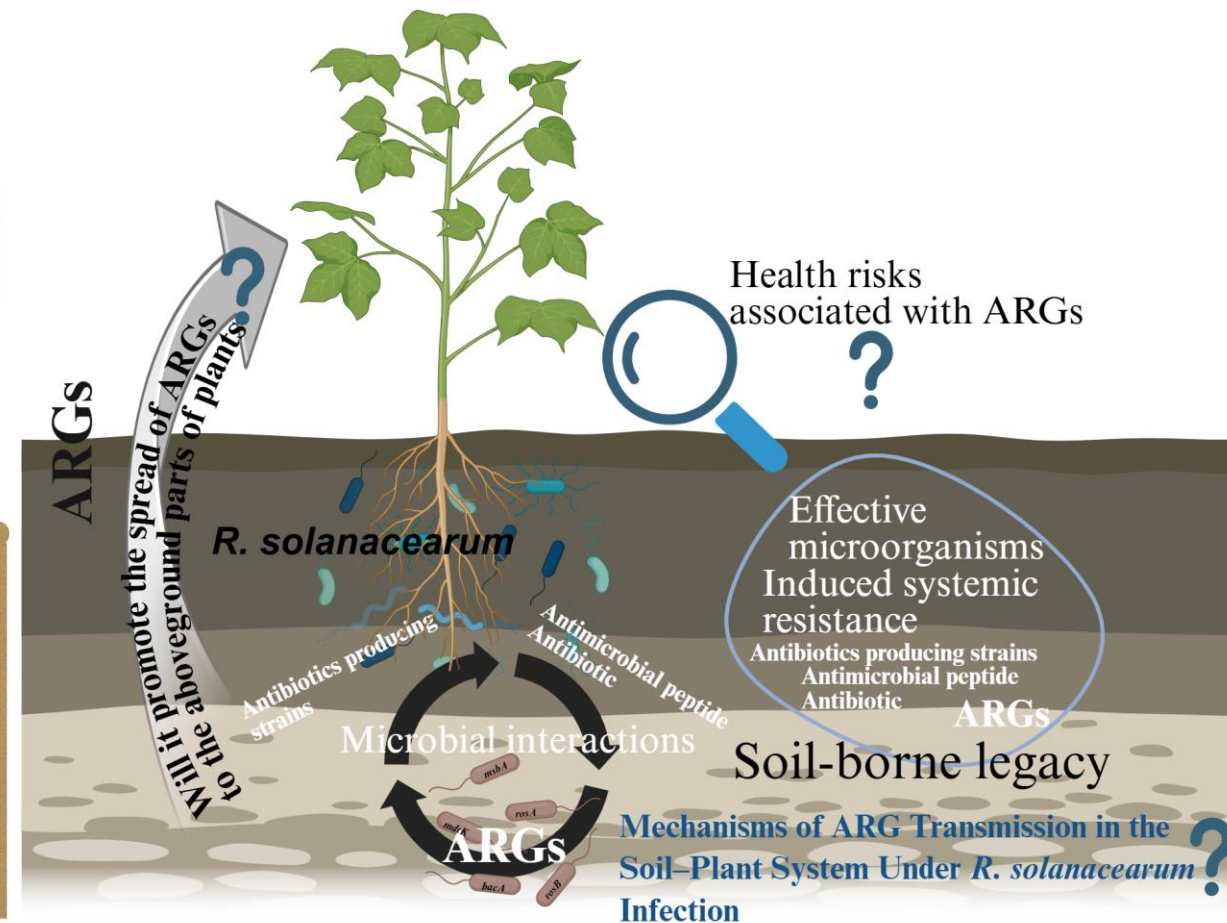
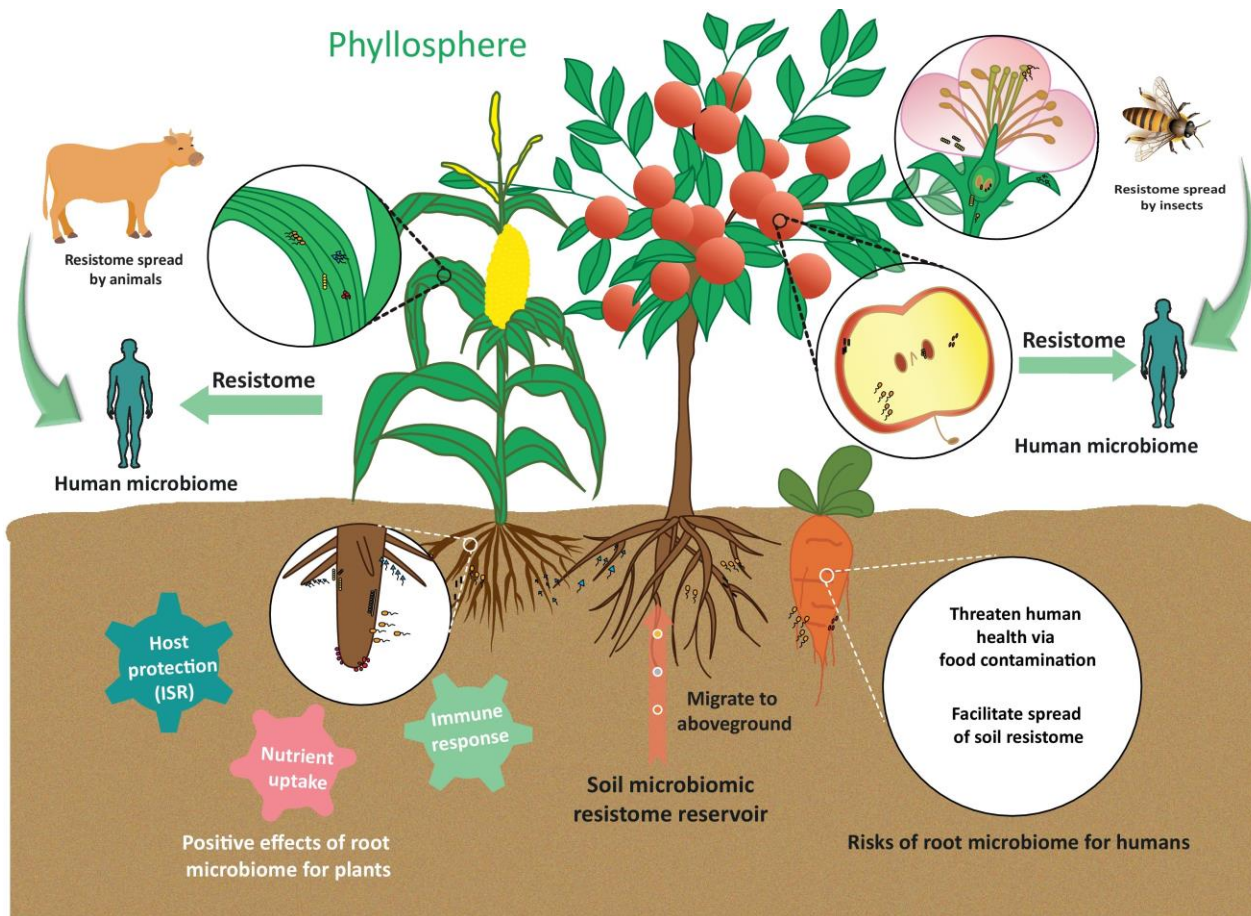


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Introduction

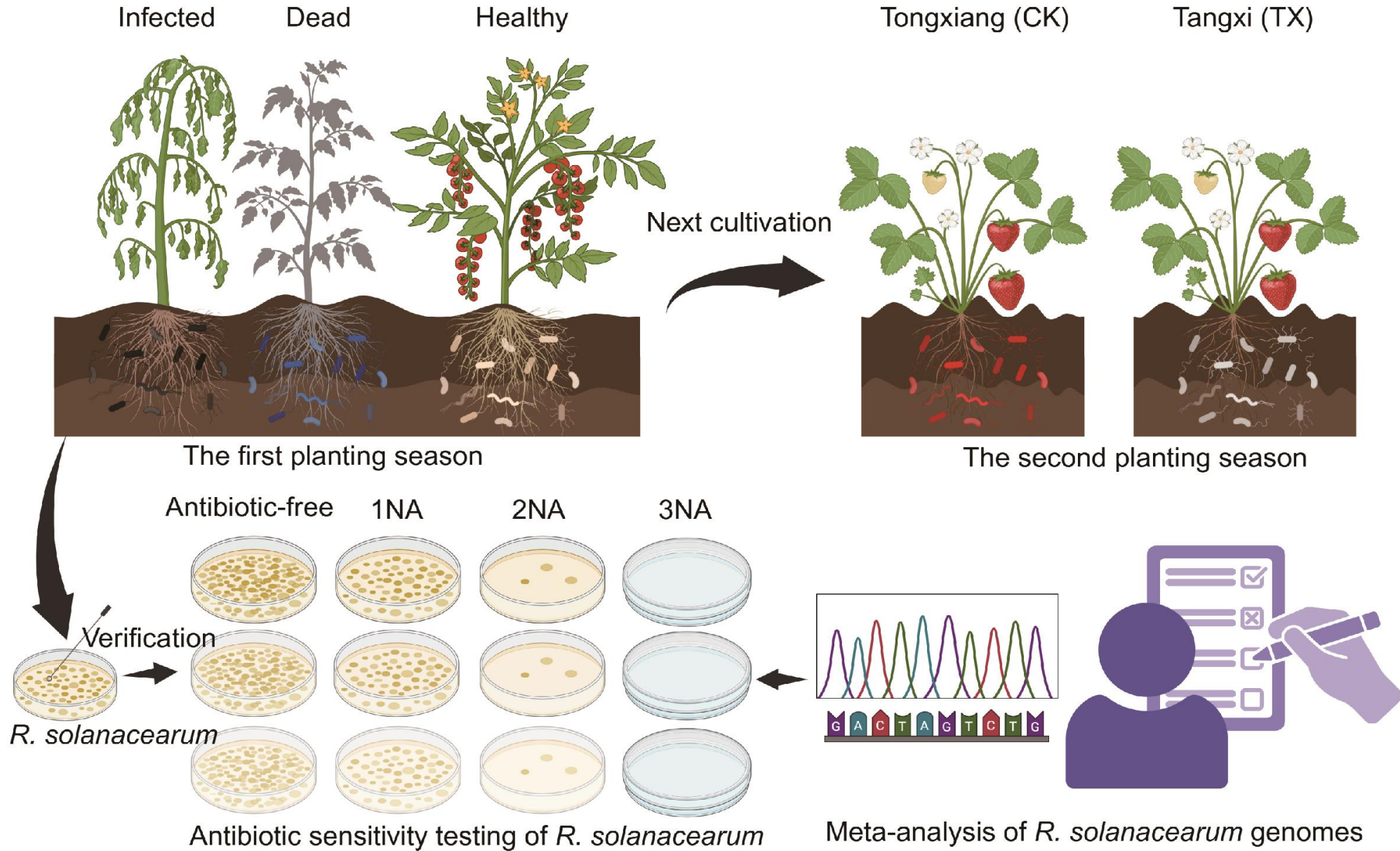


The soil-plant microbiome and resistome.

Key drivers of ARG transmission in the soil-plant continuum during plant pathogen infection.

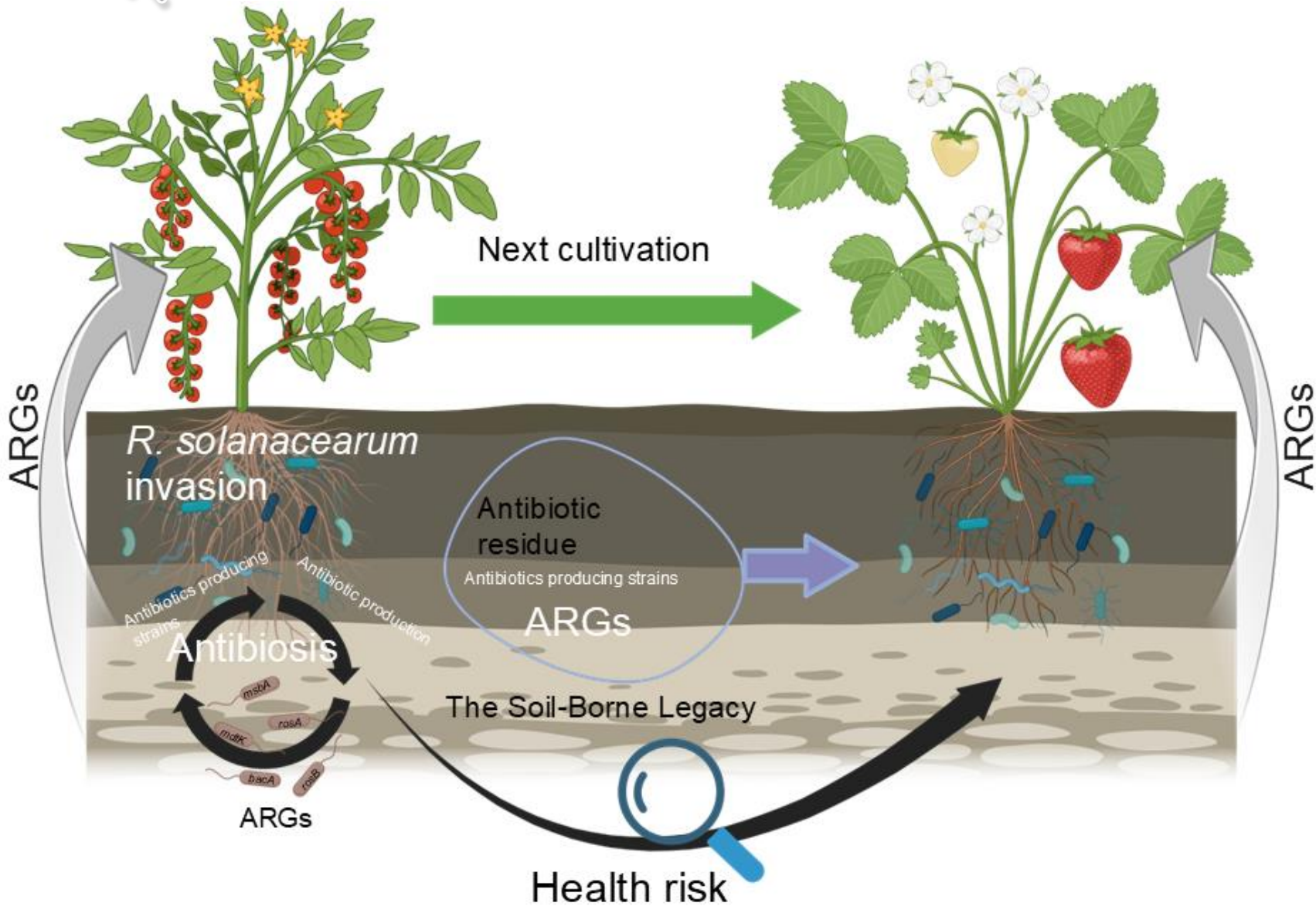


Experimental design



Experimental flowchart

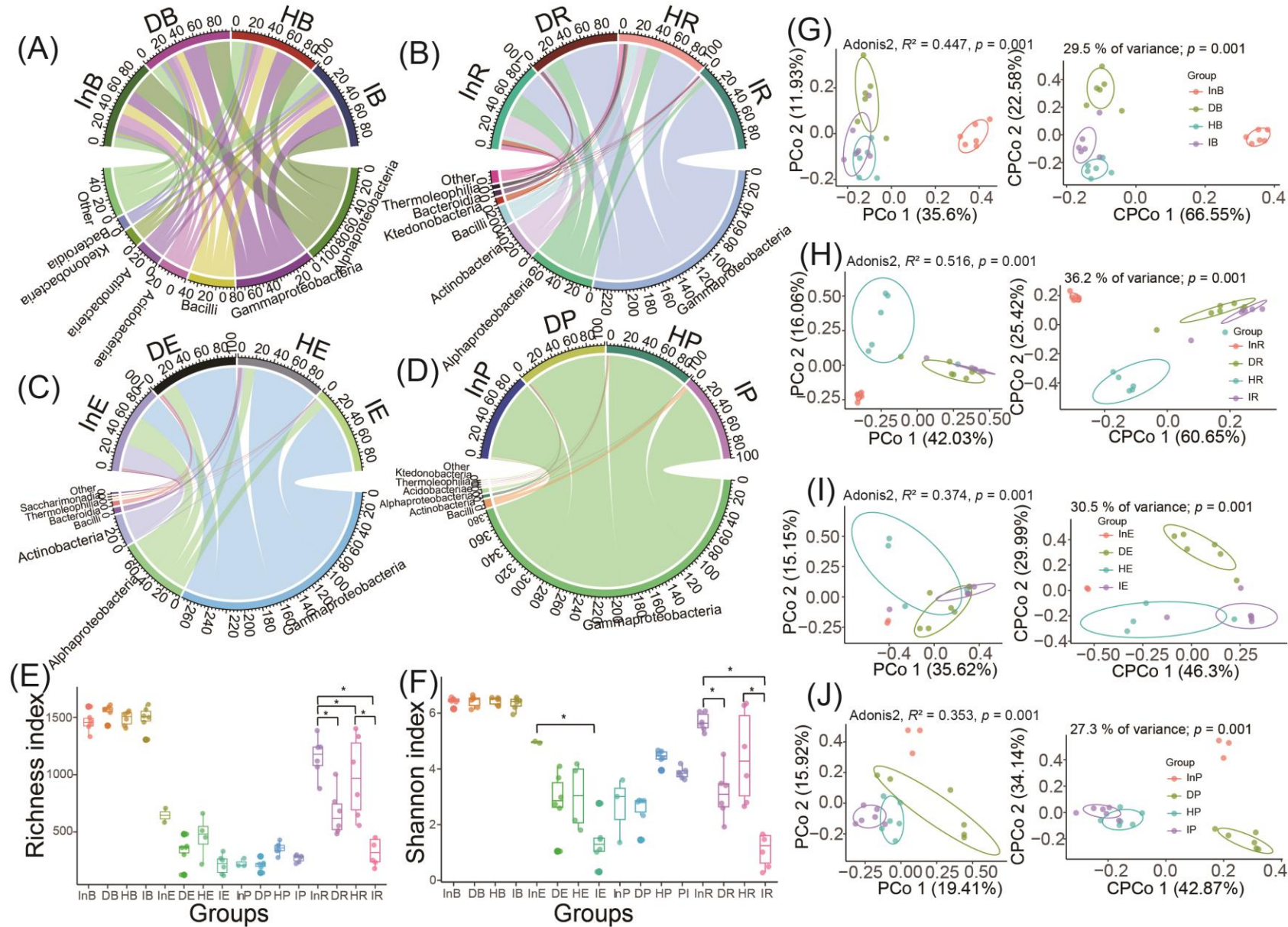
Highlights



The graphical abstract of this research

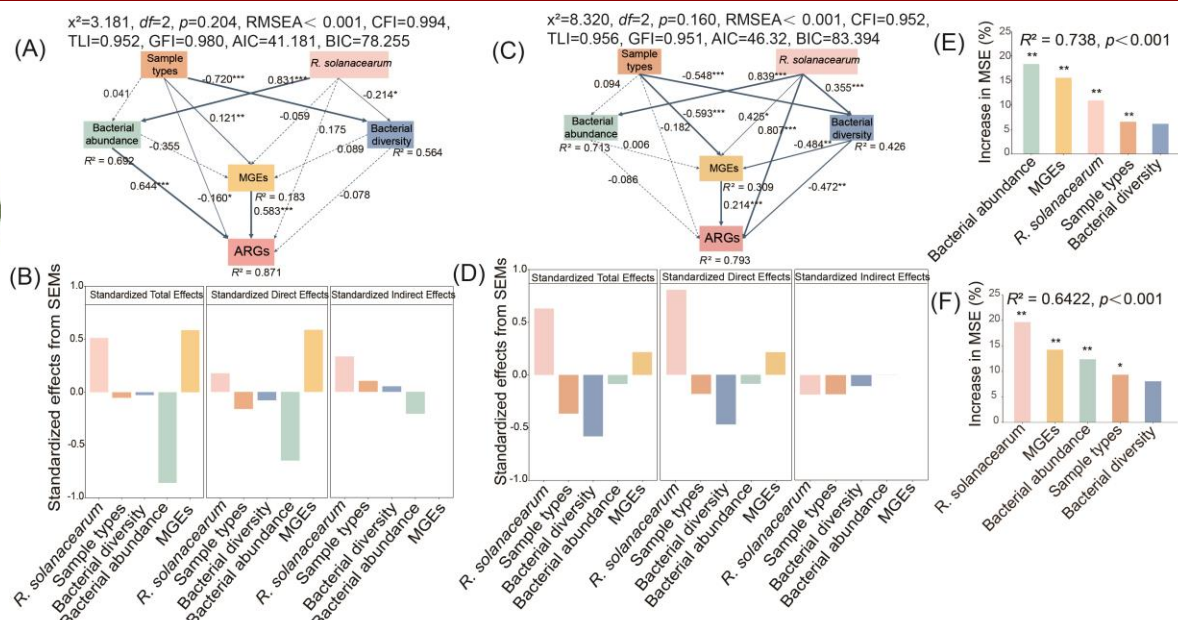
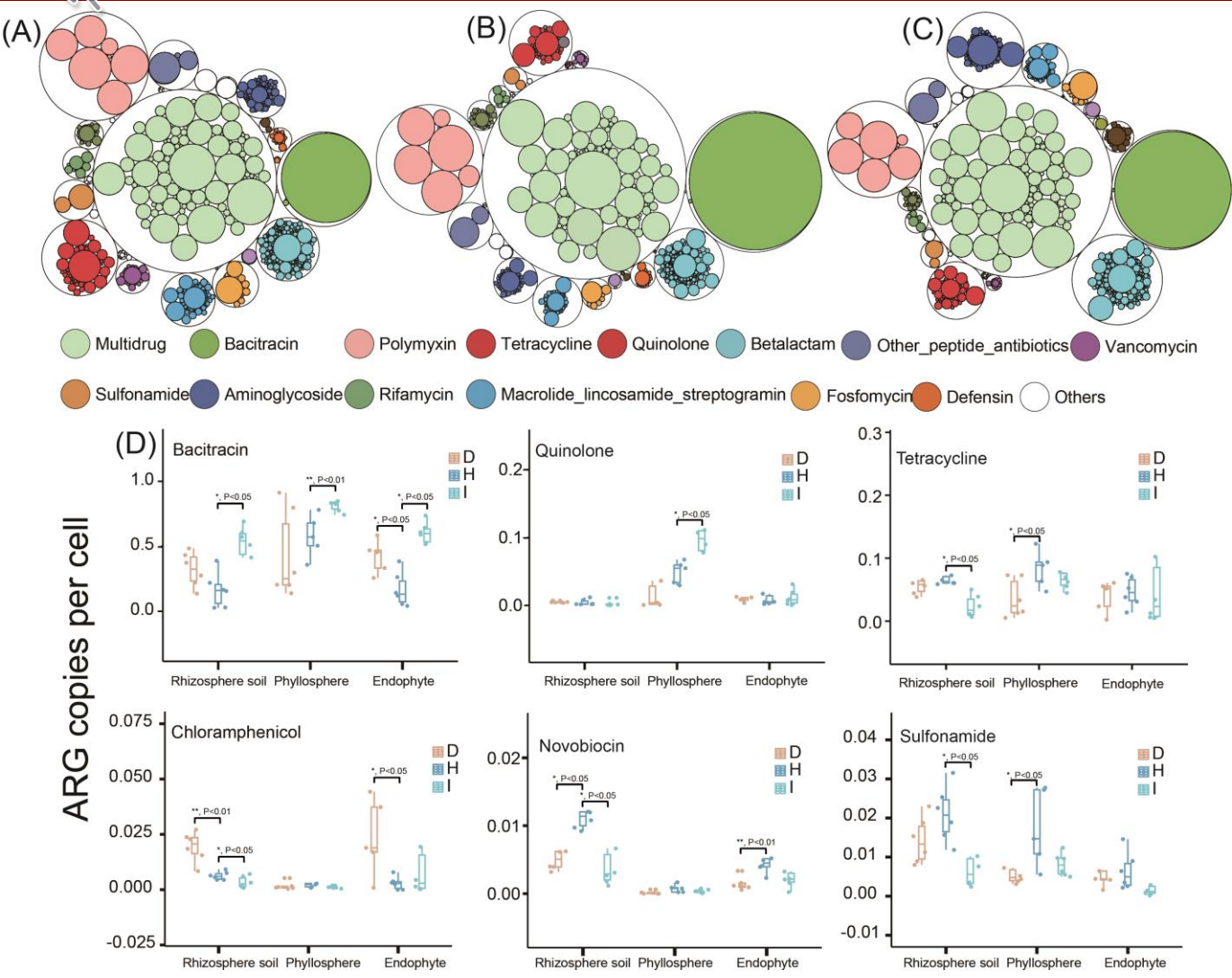
- ❑ Soil-borne diseases, such as bacterial wilt, substantially accelerate the dissemination and accumulation of ARGs throughout the soil-plant continuum;
- ❑ Soil-borne legacy can facilitate cross-crop transmission of ARGs, thereby posing sustained risks to the health and safety of subsequent plantings;
- ❑ ARGs show strong co-occurrence patterns with MGEs and VFGs, highlighting a potential risk of horizontal transfer to human-associated pathogens.

Shifts in the bacterial community under *R. solanacearum* invasion

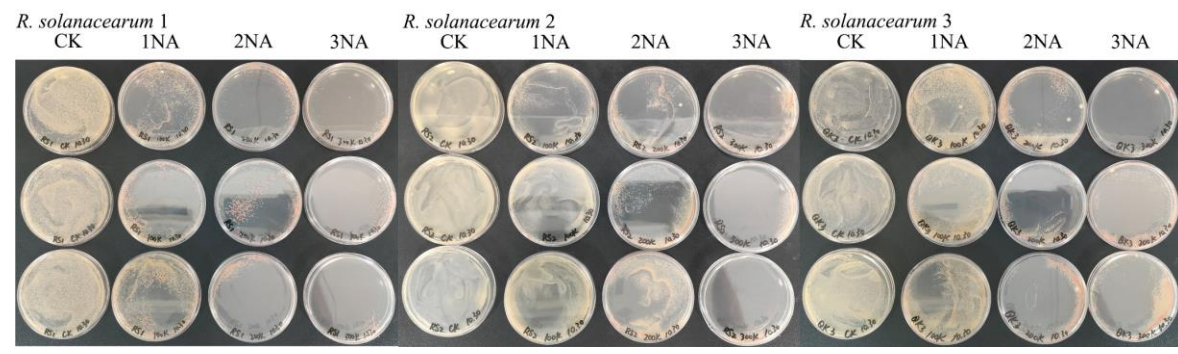


Response of bacterial communities to *R. solanacearum* infestation in the soil–tomato continuum.

Resistome reshaping across the soil–tomato continuum



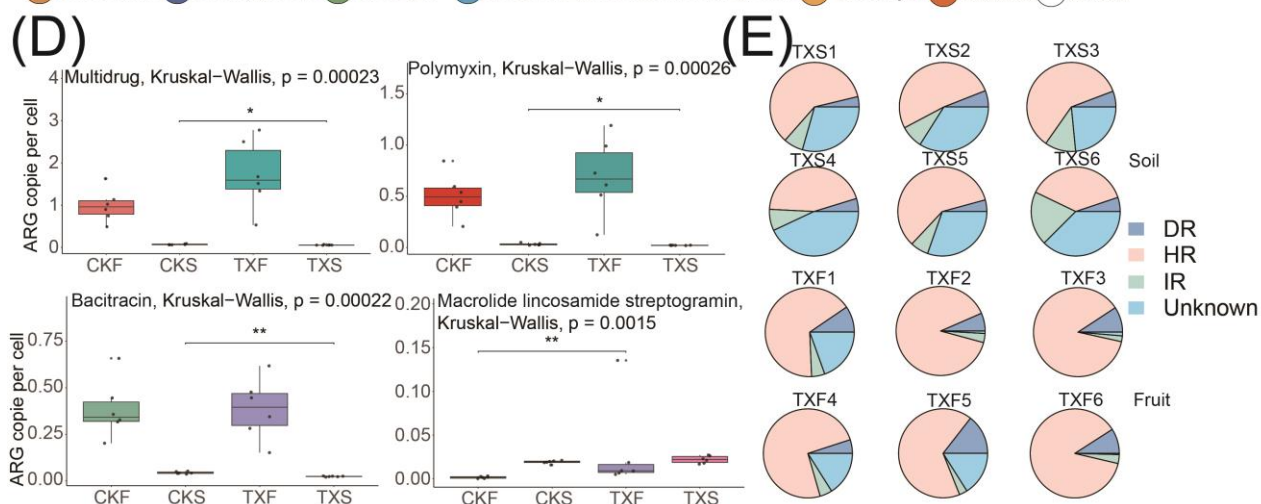
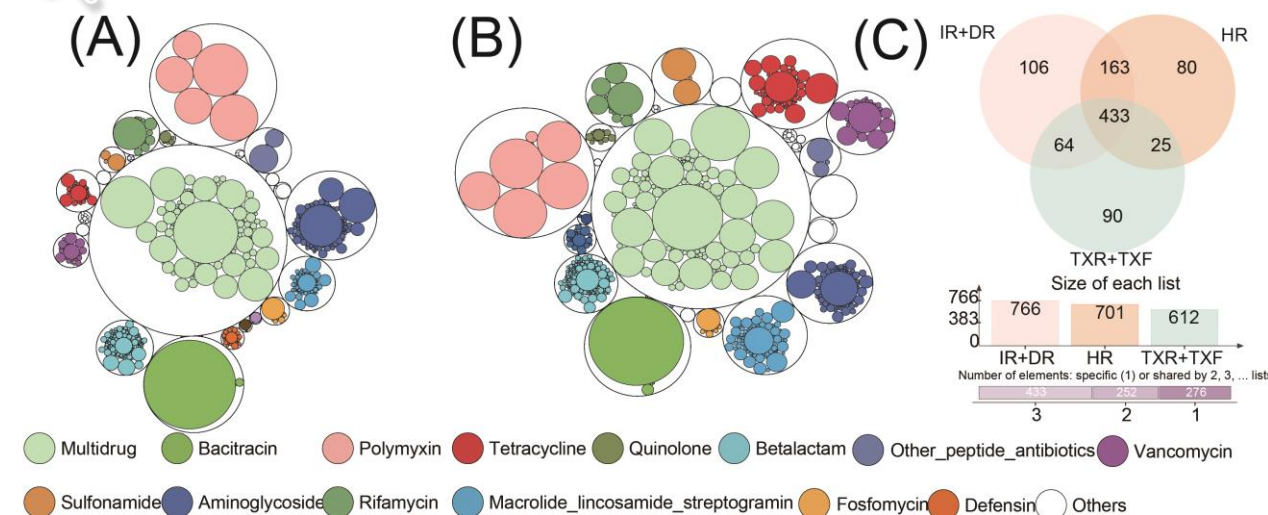
Potential drivers of ARG variation in the soil–plant continuum identified by metagenomic and HT-qPCR analyses.



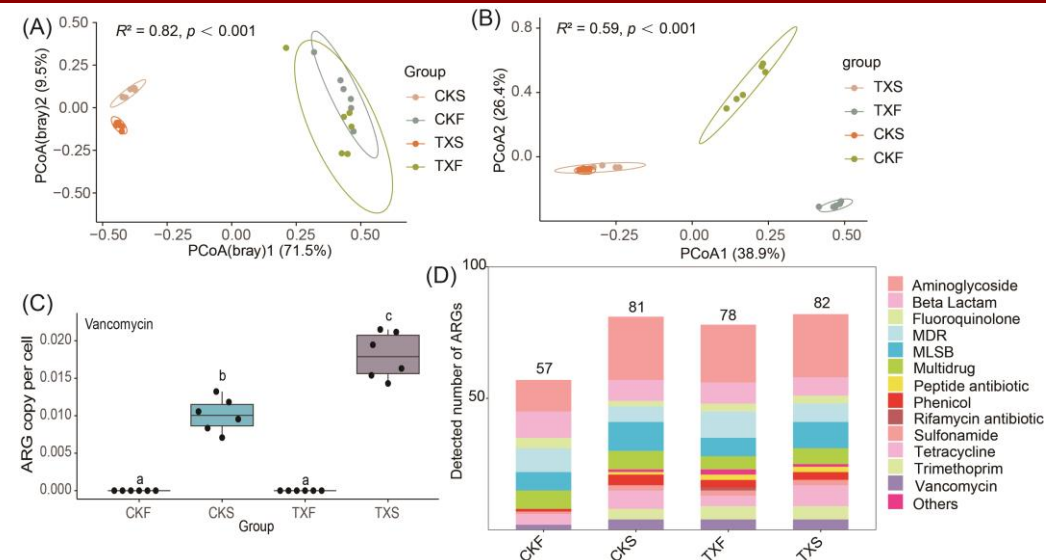
Response of bacterial communities to *R. solanacearum* infestation in the soil–tomato continua.

Antibiotic susceptibility test results for *R. solanacearum*.

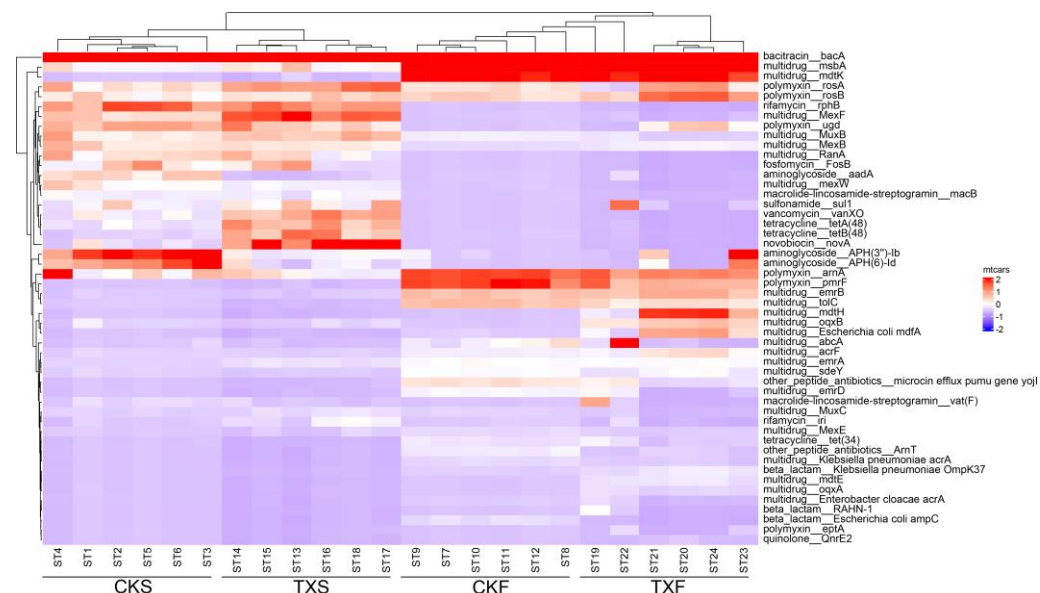
Soil-borne legacy and cross-crop ARG dissemination



Distribution, composition, and potential sources of ARGs in soil-strawberry continua across distinct ecological niches.



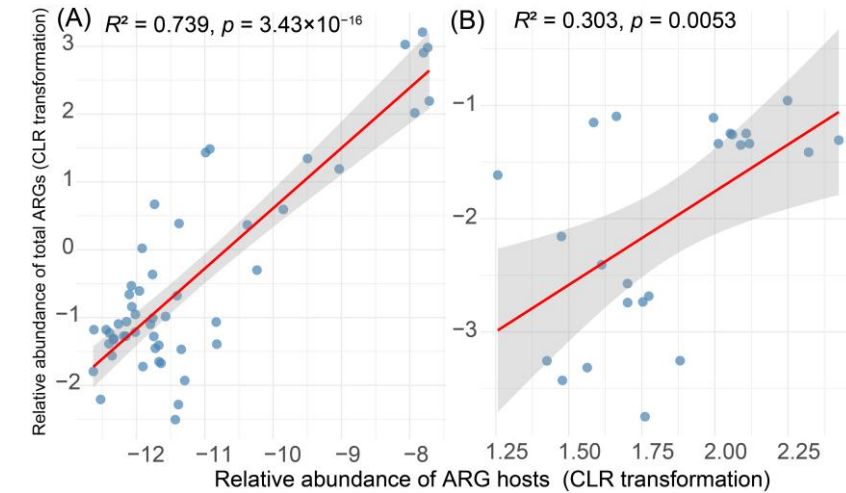
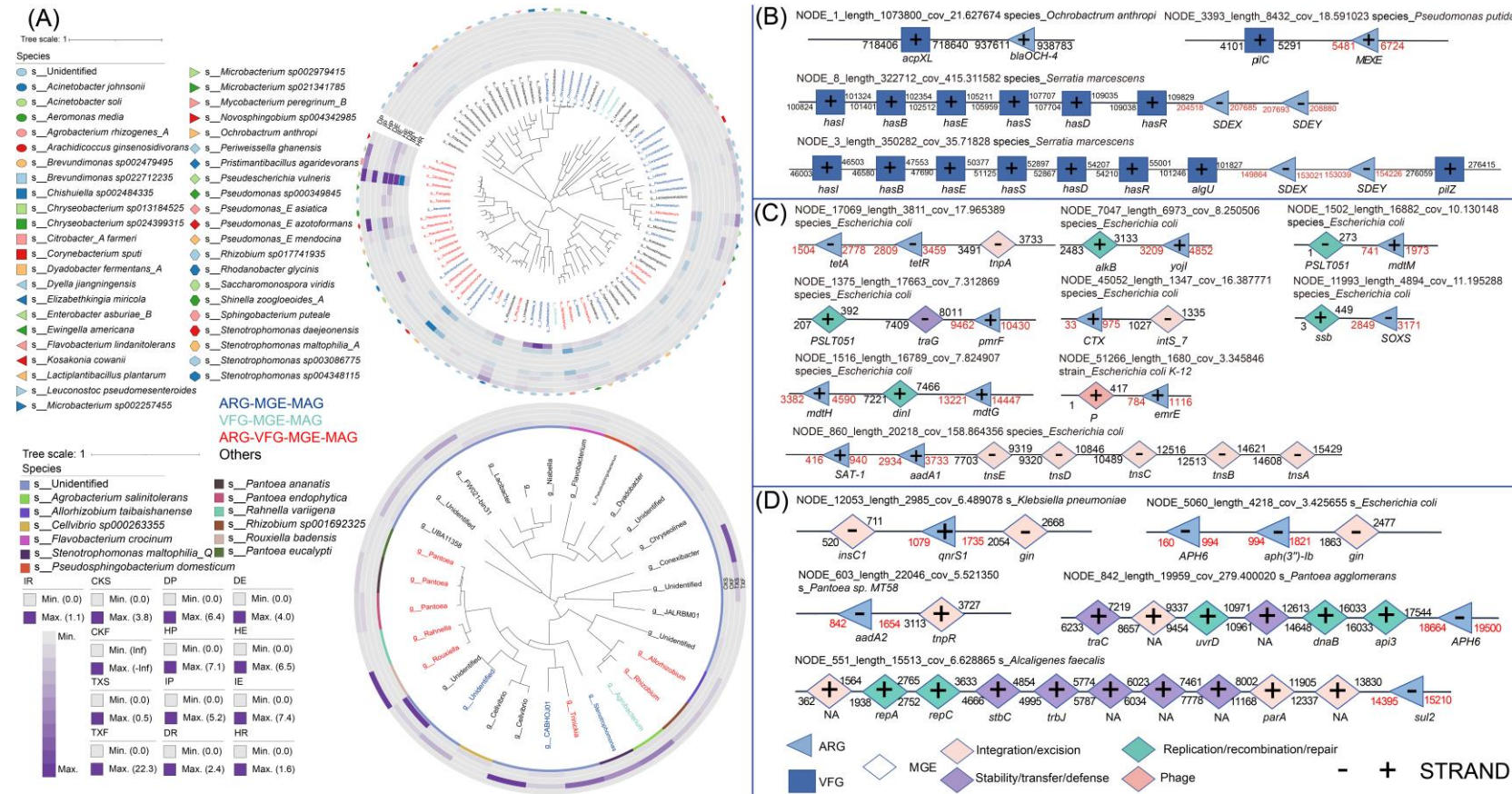
Distribution and composition of ARGs in the soil-strawberry continuum.



Heatmap illustrating the top 50 most abundant ARG subtypes in the soil-strawberry continuum.



Mobilization of ARGs and public health risks



Linear regression analysis of the relationship between ARG relative abundance and ARG-host relative abundance in the soil–tomato (A) and soil–strawberry (B) continua.

Microbial hosts carrying ARGs, MGEs, and VFGs in soil–tomato and soil–strawberry continua.



Integrative perspective

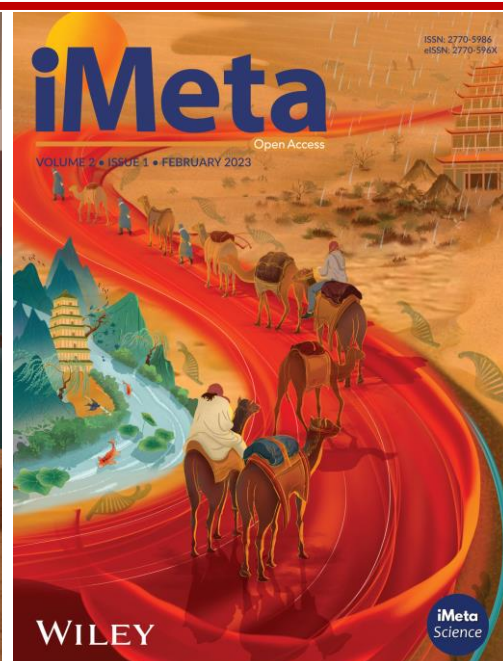
- ❑ Core discovery: *R. solanacearum* acts as a cryptic driver that, even during asymptomatic colonization, continuously promotes the cross-generational spread of resistance genes throughout the soil–crop continuum, creating a complex network of dissemination.
- ❑ Current limitations: Existing techniques still face substantial constraints in accurately identifying ARG hosts, resolving long-term ecological dynamics, and achieving absolute quantification.
- ❑ Future perspectives: Future research should integrate cutting-edge technologies to precisely resolve ARG transmission mechanisms. Long-term monitoring coupled with a unified assessment framework will be essential for translating fundamental insights into effective risk-management strategies.
- ❑ Github website: <https://github.com/XiaoRhywings/Soil-borne-legacy-spreads-antibiotic-resistance>

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