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RESEARCH

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Comparative analysis on root exudate and rhizosphere soil bacterial assembly between tomatoes and peppers infected by *Ralstonia*

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Abstract

Background The rhizosphere environment regulated by root secretory activity and rhizosphere microbial interactions plays an essential role in resisting soil-borne diseases, while the host species is an important factor that affects the composition of root exudates and rhizosphere microbiomes. However, few studies have been done on the characteristics of root exudates and bacterial communities in terms of composition, diversity, and functional potential when host plants of different species are subjected to the same disease.

Results In this study, we examined the rhizosphere soil bacteria and root exudates of both healthy and diseased tomatoes and peppers employing metabolomics and amplicon techniques. Our findings indicated that variations existed in both root exudates and the bacterial community among different host species and health states. The diversities of both rhizosphere metabolites and bacterial communities were significantly reduced in different diseased plants. Although pepper and tomato resisted the invasion of *Ralstonia* by recruiting different potentially beneficial bacteria, their rhizosphere bacterial communities had the same functional potential. In comparison to diseased rhizosphere soil, healthy rhizosphere soil had many more functional pathways associated with disease suppression and plant growth.

Conclusions This study highlighted the crucial role of host plants in shaping the rhizosphere environment and revealed the variation characteristics of root exudates and rhizosphere bacteria of different host plants induced by the same disease.

Keywords Root exudate, Rhizosphere, Soil bacteria, Host species, Functional prediction

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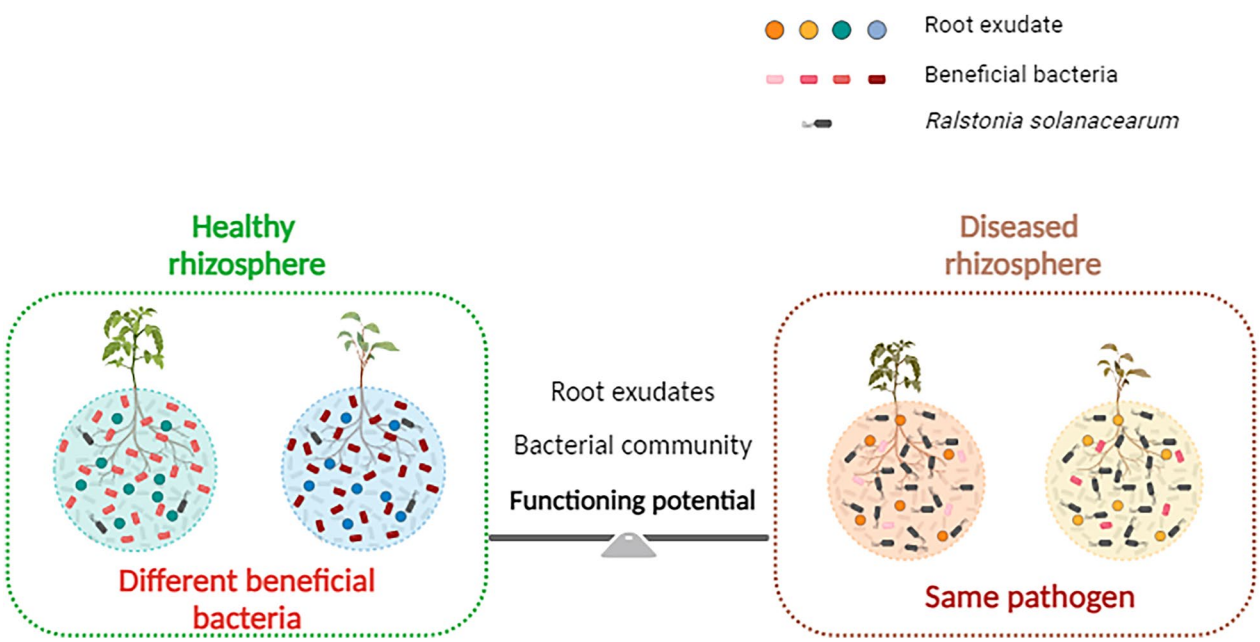
Graphical Abstract



Background

The plant rhizosphere is a unique environment primarily driven by the secretory activity of plant roots and soil microbiomes, in which complex biogeochemical cycles and dynamic biological interactions occur, playing an essential role in protecting host health and responding to biotic and abiotic stresses [1, 2]. A large proportion of photosynthetic carbon is exuded into the soil through plant roots to provide abundant resources for soil microbiomes, which move to the rhizosphere colonization through a chemotaxis response [3–5]. Host characteristics are important drivers of root exudate composition and rhizosphere microbial community assembly under controlled conditions, as supported by the observation that differences in root exudates from four species of plants in the same soil environment shaped different rhizosphere bacterial communities [6–8]. However, the rhizosphere environment regulated by host plants is dynamically changing in response to biotic and abiotic stresses [9, 10]. For instance, basil and tomato roots could secrete large amounts of rosmarinic acid and caffeic acid [11, 12], respectively, to directly inhibit the growth of pathogens when facing disease stress. In addition, previous studies have discovered that the composition and diversity of rhizosphere microbiomes differed among species of angiosperm plants and that the responses of specific bacterial taxa to drought stress were affected by host species [13]. The findings of this collection of studies implied that diverse rhizosphere environments regulated by different host plants exhibit unique mechanisms for resisting the same external stresses. Therefore, it is crucial to investigate the traits of root metabolic patterns and soil microbial community structure when different host-regulated rhizosphere microdomains are subjected to the same disease stress.

Host plant-associated rhizosphere microbial communities are the first line of immune defense against soil-borne pathogens that endanger the root system [14, 15]. Plants can recruit and select beneficial microbiomes by releasing specific root exudates and signaling molecules, a process that is largely influenced by host characteristics and the soil environment [1, 16–18]. *Bacillus*, *Pseudomonas*, *Sphingomonas*, and *Streptomyces* have all been found to be recruited by the rhizosphere to resist the same pathogen invasion through multiple functional mechanisms, including inducing systemic resistance, producing plant hormones, competing for resources, and improving plant adaptability [3, 19–21]. However, we still have little insight into the assembly and functional potential of rhizosphere soil bacterial communities induced by the same disease in different host plants.

More than 200 plants, including tomatoes and peppers, are susceptible to being infected by the soil-borne pathogen *Ralstonia solanacearum*, causing bacterial wilt

[22]. Here, diseased and healthy plants are collected in greenhouses where tomatoes and peppers are grown. Untargeted metabolomics and amplicon sequencing were used to explore the rhizosphere characteristics of different host plants infected by *Ralstonia*. We attempted to address (1) whether the composition, structure, and diversity of exudates and soil bacteria are consistent among different hosts with different health states; and (2) whether the recruitment of potentially beneficial bacteria and the functional potential characteristics among different hosts facing the same disease are consistent.

Methods

Sample preparation

All samples were obtained from plastic greenhouses in the Pukou District of Nanjing City, Jiangsu Province, China. The sampling site is situated in a subtropical monsoon climate zone with annual mean temperatures of 15.7 °C and annual mean precipitation of 1106.5 mm. The following were the chemical properties of the soil at the sampling site: pH 6.53, SOM 20.84 g kg^{-1}, TN 1.35 g kg^{-1}, TP 0.71 g kg^{-1}, TK 12.65 g kg^{-1}, AN 136.19 mg kg^{-1}, AP 75.06 mg kg^{-1}, and AK 120.06 mg kg^{-1}. In July 2021, tomato (Hezuo-903) and pepper (Sujiao-5) seedlings were transplanted to two adjacent vegetable greenhouses with continuous cropping obstacles, and samples were taken in October at the maturity stage. At each site, samples identified as diseased plants had typical symptoms of bacterial wilt, including the young tissue at the top of the plant wilting, leaves remaining green, dark brown at the base of the stem, and white bacterial fluid flowing from the base of the stem when pressed [23]. Plants adjacent to diseased plants and without typical bacterial wilt symptoms were collected as healthy plant samples. A total of 32 plant samples were obtained (2 species (tomato/pepper) × 2 (healthy/diseased) × 8 repetitions).

At adjacent plots at the tomato and pepper sites, eight replicates of both healthy and diseased plants were obtained. The roots of selected plants (healthy and diseased) were carefully excavated, then the loose soil linked to the roots was shaken off with violence, and the soil that was tightly adhered to the roots was carefully brushed off as rhizosphere soil. And bulk soil was collected 20 cm away from the root. After carefully rinsing the plant roots with ultrapure water, the plants were placed into a brown bottle containing 200 ml of ultrapure water for the collection of root exudates. About 24 h later, the plants were taken out of the bottles, and the solutions were temporarily stored at 4 °C. In total, 64 soil samples (2 species × 2 (healthy/diseased) × 2(bulk soil/rhizosphere soil) × 8 repetitions) and 32 root exudate samples were obtained (2 species × 2 (healthy/diseased) × 8 repetitions). Until further experimentation, all soil samples were kept at − 40 °C.

Rhizosphere metabolome detection

Untargeted metabolomic approach we utilized was based on UHPLC-MS/MS to investigate the effects of pathogens on the root exudate composition of different species of plants. Specifically, extraction of the root exudate from the solution is as follows: the extraction process of the root exudate from the solution involves several steps. First, filter out the impurities from the solution, followed by full extraction with ethyl acetate, then evaporation on a vacuum rotary evaporator, and finally dissolved in 2 mL of methanol.

Vanquish UHPLC system and Orbitrap Q Exactive™ HF mass spectrometer (Thermo Fisher, Germany) were combined for UHPLC-MS/MS. Specifically, exudates were injected at an average speed of 0.2 mL min^{-1} into a Hypesil Gold column. Eluent A was 0.1% formic acid (FA) in the positive polarity and 5 mM ammonium acetate in the negative polarity, respectively, and Eluent B was methanol in both modes. Compound Discoverer 3.1 was employed for handling the raw data. Afterwards, the intensity of the peaks was normalized to the total spectral intensity. Finally, the compounds were annotated and classified by KEGG [24] and HMDB [25].

DNA extraction and amplicon sequencing

Following the manufacturer's instructions, DNA was taken out from 500mg rhizosphere and bulk soil employing the FastDNA™ SPIN Kit for Soil (MP Biomedicals, Santa Ana, CA). The bacterial sequences were identified by amplification of the 16S rRNA gene's V4–V5 region utilizing the primers 515F-907R [26]. The following reaction process was applied for the PCR reactions, which utilized 15 μL of Phusion® High-Fidelity PCR Master Mix: Denaturation at 98 °C for 1 min, followed by 30 cycles at this temperature for ten seconds, annealing at 50 °C for 1 min, extension at 72 °C for 1 min, and holding at 72 °C for 5 min. The amplified PCR products were sequenced on the Illumina MiSeq platform.

QIIME2 (version 2020.8, https://qiime2.org/) [27] was employed for analyzing raw sequencing data. FastQC was used to assess the quality of the original sequences, and then the sequences were uploaded for quality control and categorization annotation. The 16S rRNA gene sequences were annotated by Silva database version 138 (https://qiime2.org/2022.11/data-resources/).

Statistical analyses

The R Studio (version 4.1.2) was employed to carry out all statistical analyses. The *adonis* function was implemented to execute a PERMANOVA using 999 permutations

to ascertain the influence of various parameters on the community dissimilarity. Employing the "vegan" R package, the beta diversity and the alpha diversity indices (Shannon and Simpson indexes) for various treatments were investigated. All correlation analyses in the text use the spearman correlation, which was calculated by the *rcorr* function in the R package "Hmisc". The "EdgeR" package was utilized to investigate the compounds that were enriched in both healthy and diseased rhizosphere soils. The intersection of enriched compounds of different species was analyzed using the *intersect* function, and the Venn diagram was drawn with the "VennDiagram" package. The two-tailed test was applied to evaluate variations in bacterial genera' abundance and enrichment. The KEGG ortholog functional profiles of bacterial communities were predicted by PICRUSt2 using the 16S rRNA sequences. Furthermore, the KEGG Database was consulted to identify pathways. Graphical abstract was drawn on the BioRender (https://www.biorender.com/).

Results

Composition and diversity of root exudates

Using untargeted metabolomics, 1325 distinct compounds were identified in root exudates. Then, we classified rhizosphere metabolites into 10 groups based on the HMDB database annotation at the Super Class level [25] (Additional file 1: Fig. S1). Depending on the number and relative abundance of compounds, lipids and organic acids were predominant in all treatments (Fig. 1A, Additional file 1: Fig. S1). For both pepper and tomato, the relative abundance of lipids and lipid-like compounds in diseased rhizosphere soil exceeded that in healthy soil (Fig. 1A).

Principal coordinate analysis showed that the structure of root exudate was significant differences between healthy and diseased plants, as well as between different plant species (Fig. 1B, Additional file 1: Table S1). PERMANOVA analysis confirmed that species ($F_{species}=19.15$, $P<0.001$) had more effect on the composition of root exudates than the pathogen ($F_{pathogen}=13.27$, $P<0.001$, Fig. 1B). Additionally, the diversity of diseased plant root exudates was significantly lower compared to that of healthy plants, both in pepper and tomato (Fig. 1C, D). Differential compound analysis showed that PHR and PDR were significantly enriched with 103 and 219 compounds, respectively ($P<0.05$, Fig. 1E), and THR and TDR were significantly enriched with 115 and 244 compounds, respectively ($P<0.05$, Fig. 1F). In the healthy rhizosphere soil of various host plants, only 10 identical compounds were enriched, but 92 identical compounds were enriched in the diseased rhizosphere soil of various host plants, of which 28 were lipids and lipid-like molecules (Fig. 1G). Although species and pathogens can cause variations in overall exudation patterns, the results revealed that two Solanaceae plants infected with the same disease were enriched with a higher number of the same compounds and reduced the diversity of exudates.

Soil microbial community composition in rhizosphere

In total, 7,593,358 16S rRNA reads were provided from 64 samples, which were classified as 33,830 bacterial ASVs. *Proteobacteria*, *Actinobacteria*, *Chlorofexi*, *Bacteroidetes*, *Acidobacteria*, *Firmicutes*, *Myxococcota*, *Planctomycetes*, and *Verrucomicrobia* were largely dominant among the bacteria (Fig. 2A, Additional file 1: Table. S2). Our results also implied that the variance of pepper and tomato at the phylum level corresponded between treatments and that there was a much higher relative abundance of *Proteobacteria* in the soil of diseased plants than in healthy plants.

Then, we conducted a two-tailed test for genera with relative abundance greater than 1% to reveal the significantly enriched bacterial genera in the healthy rhizosphere and diseased rhizosphere of pepper and tomato, respectively. The results showed that *Ralstonia*, a typical pathogen of bacterial wilt, was significantly enriched in TDR and PDR, with a relative abundance of 22.73% and 31.98%, respectively (Fig. 2B, C). However, THR and PHR were enriched with different bacterial genera. *Bacillus*, *Rhodanobacter*, *Pseudolabrys*, *Gemmatimonas*, *Sphingomonas*, and *JG30–KF–AS9* were significantly enriched in THR, and *Chitinophaga*, *Streptomyces*, *Devosia*, and *Bacillus* were significantly enriched in PHR (Fig. 2B, C). Meanwhile, correlation analysis uncovered a significant negative correlation between the relative abundance of *Ralstonia* and bacterial genera, which were notably enriched in the PHR and THR, respectively (Additional file 1: Fig. S2). These results suggested that different Solanaceae plants will accumulate different microbial genera in the rhizosphere to prevent plant diseases when facing the invasion of the same diseases.

Soil microbial community structure and diversity in rhizosphere

Principal coordinate analysis showed significant differences in bacterial community structure between the healthy and diseased plants in rhizosphere, but not in bulk soil. PERMANOVA analysis confirmed that compartments had the greatest impact on bacterial communities ($F_{compartment}=28.83$, $P<0.001$), followed by plant species ($F_{plant\ species}=18.51$, $P<0.001$), and the pathogen ($F_{pathogen}=3.90$, $P=0.002$, Fig. 3A, Additional file 1: Table S3). Additionally, as shown by beta dispersion, the bacterial communities in the diseased plants were more variable in comparison to the healthy plants (Fig. 3B). Further correlation analysis displayed a significant

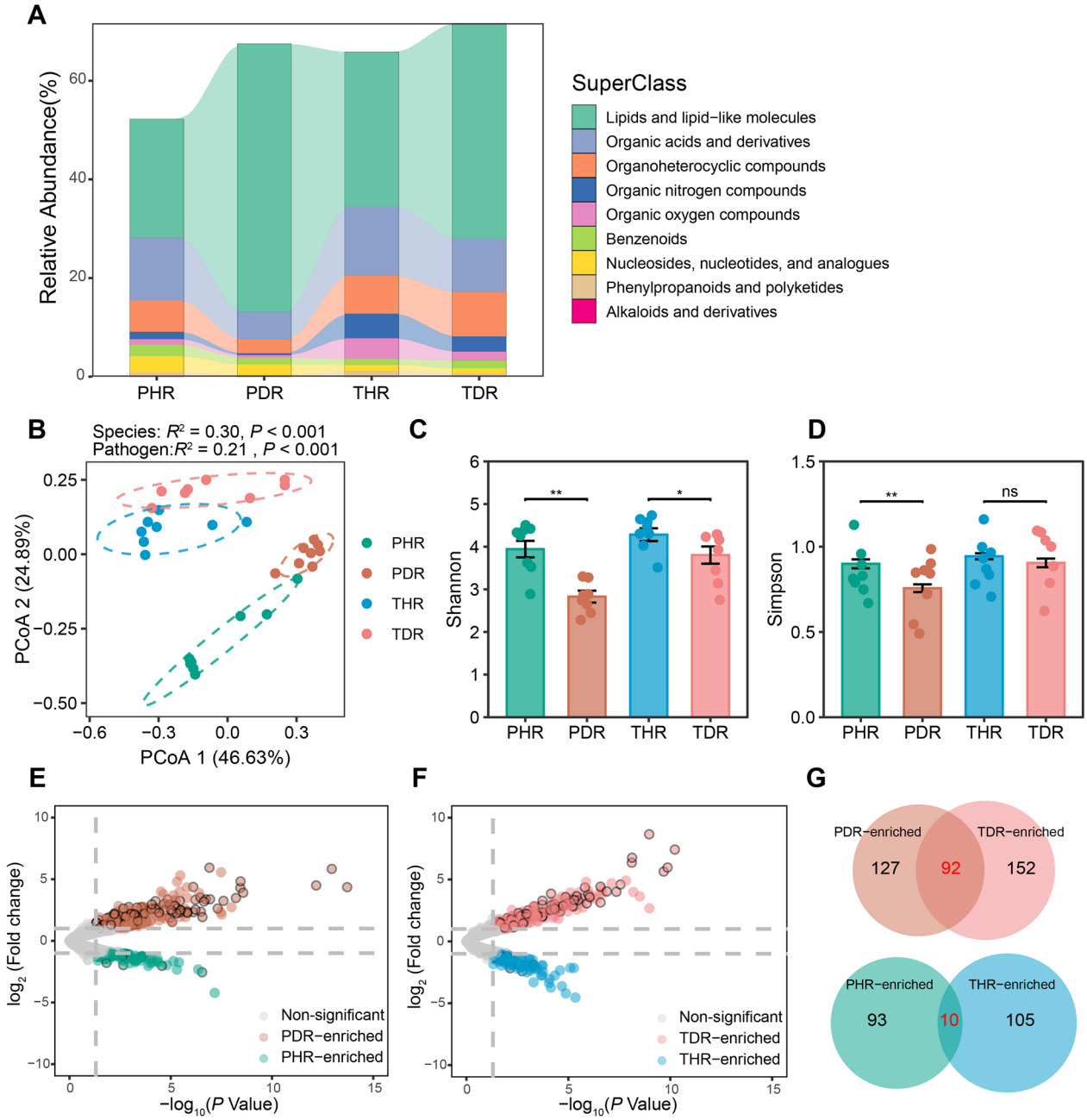


Fig. 1 Composition and diversity of root exudates. **A** The distribution of compounds in the tomato and pepper root exudates at the Superclass level. **B** PCoA combined with PERMANOVA shows the influence of species and pathogen on the root exudates. **C**, **D** The alpha diversities of root exudates in different treatments. "ns" (non-significant); *($P < 0.05$); **($P < 0.01$); ***($P < 0.001$). **E** Enrichment of root exudates in healthy and diseased peppers (FDR-corrected $P < 0.05$). Black border represents the intersection of significantly enriched root exudates in peppers and tomatoes with the same state. **F** Enrichment of root exudates in healthy and diseased tomatoes (FDR-corrected $P < 0.05$). Black border represents the intersection of significantly enriched root exudates in peppers and tomatoes with the same state. **G** Intersection of significantly enriched root exudates in peppers and tomatoes with the same state. *THR* rhizosphere of healthy tomato, *TDR* rhizosphere of diseased tomato, *PHR* rhizosphere of healthy pepper, *PDR* rhizosphere of diseased pepper

positive association between the variance of the bacterial community on the first axis and the relative abundance of *Ralstonia* (Fig. 3C). That suggested that higher pathogen abundance may drive the variation of community structure.

Bacterial alpha diversity in peppers and tomatoes, including Shannon and Simpson, displayed similar

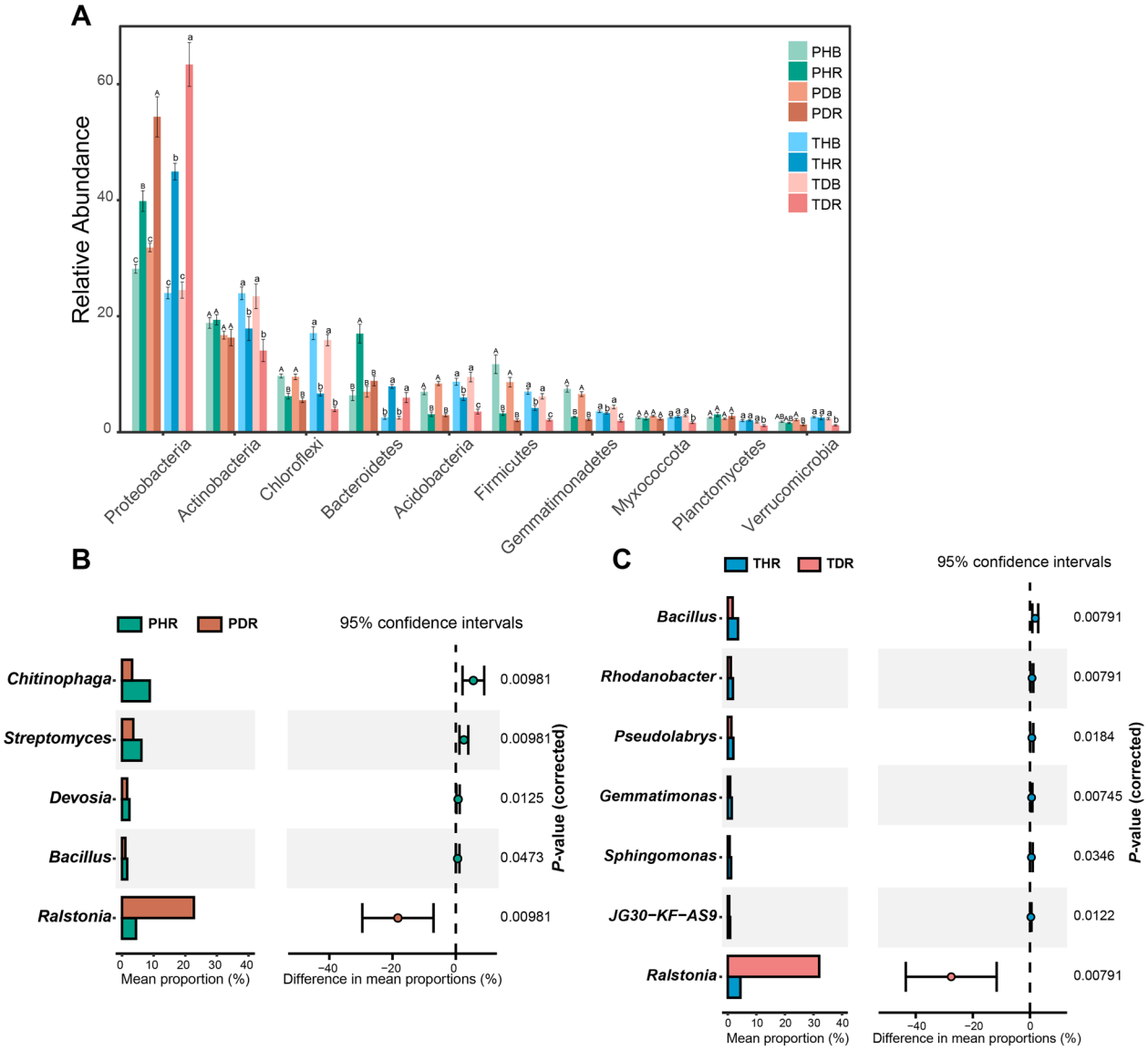


Fig. 2 Composition of the pepper and tomato bacterial communities. **A** The relative abundance of the top 10 bacterial phyla in different treatments of tomato and pepper. Bacterial phyla relative abundance differences between pepper treatments are indicated by capitalized letters, and differences between tomato treatments are shown with lowercase letters ($P < 0.05$). **B** The two-tailed test revealed significantly different bacterial genera (relative abundance > 1%) in PHR and PDR, and the *P*-value was corrected using Bonferroni. **C** The two-tailed test revealed significantly different bacterial genera (relative abundance > 1%) in THR and TDR, and the *P*-value was corrected using Bonferroni. *PHB* bulk of healthy pepper, *PHR* rhizosphere of healthy pepper, *PDB* bulk of diseased pepper, *PDR* rhizosphere of diseased pepper, *THB* bulk of healthy tomato, *THR* rhizosphere of healthy tomato, *TDB* bulk of diseased tomato, *TDR* rhizosphere of diseased tomato

patterns of change. Healthy plants showed higher bacterial diversity in rhizosphere soil than diseased plants, while all plant rhizospheres had significantly higher bacterial diversity than bulk soil (Fig. 3D, Additional file 1: Fig. S3A). In addition, the correlation analysis found that bacterial alpha diversity was negatively correlated with the relative abundance of the *Ralstonia* (Fig. 3E, Additional file 1: Fig. S3B). These results implied that the community structure and diversity of different Solanaceae plants had the same changing pattern after infection with the same disease. The enrichment of pathogens in the rhizosphere changed the community structure and reduced the alpha diversity.

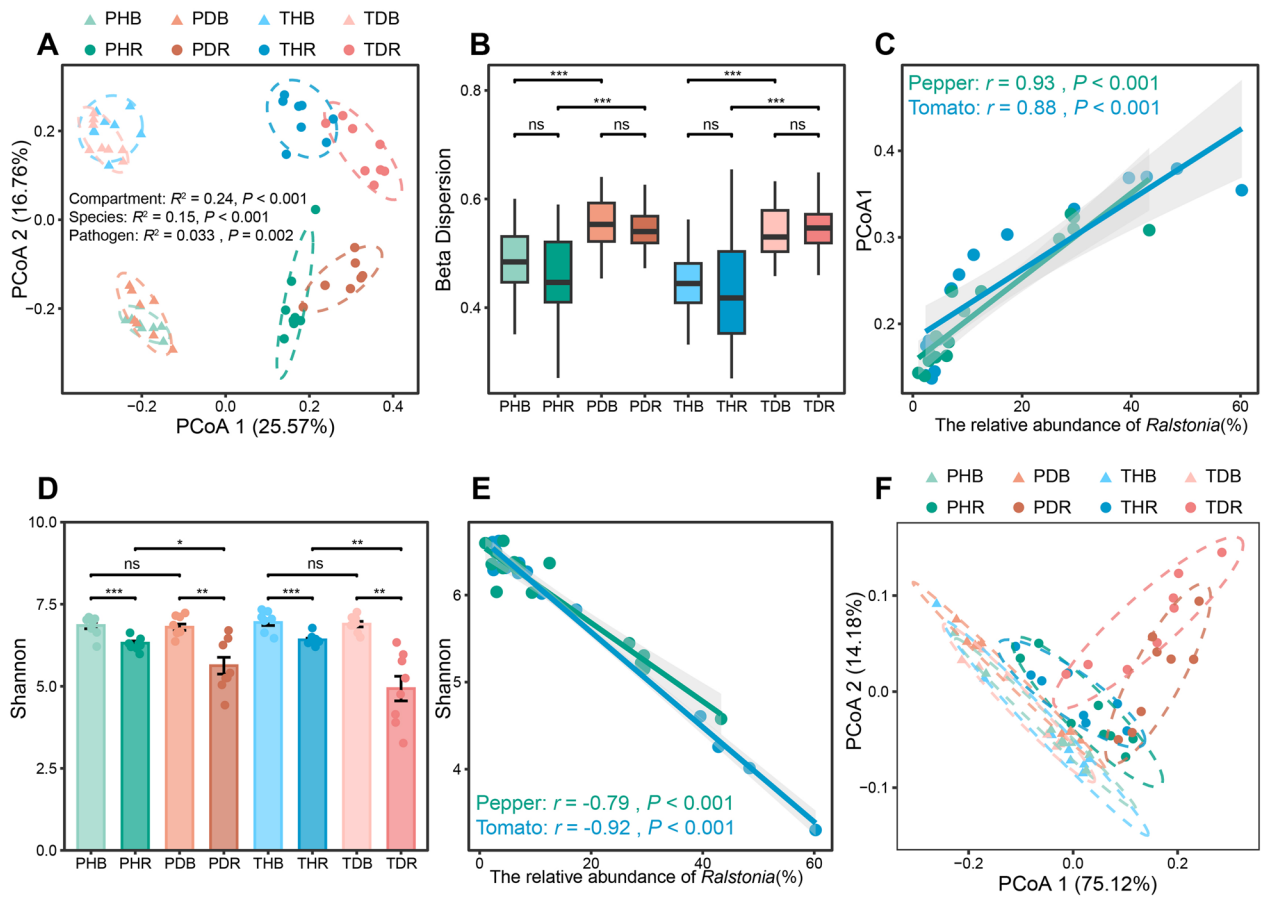


Fig. 3 Bacterial community structure and diversity. **A** Principal coordinate analysis combined with PERMANOVA displays how compartment, species, and pathogen impact the structure of the bacterial community. The symbols of the triangle and circle represent bulk and rhizosphere, respectively. **B** Analysis of the beta dispersion based on the bray distance. "ns" represents no significant difference between treatments. "ns" (non-significant); *(P < 0.05); **(P < 0.01); ***(P < 0.001). **C** The correlation between the first column of PCoA and the relative abundance of *Ralstonia*. **D** Shannon diversity of bacterial communities among species, compartments, and plant states. **E** The correlation between alpha diversity index and the relative abundance of *Ralstonia*. **F** The influence of compartment, species, and pathogen on the KO functional categories. The symbols of the triangle and circle represent bulk and rhizosphere, respectively. *PHB* bulk of healthy pepper, *PHR* rhizosphere of healthy pepper, *PDB* bulk of diseased pepper, *PDR* rhizosphere of diseased pepper, *THB* bulk of healthy tomato, *THR* rhizosphere of healthy tomato, *TDB* bulk of diseased tomato, *TDR* rhizosphere of diseased tomato

Soil microbial functioning potential in rhizosphere

Further, PICRUSt2 was implemented to predict the functioning potential of soil bacterial communities in peppers and tomatoes. As shown by principal coordinate analysis and pairwise comparison analysis, the functional potential of healthy and diseased rhizosphere soils was significantly different, but not between species, especially between THR and PHR (Fig. 3F, Additional file 1: Table S4). This suggested that when different solanaceous plants encountered the same pathogen invasion, although they had enriched different microbial genera to resist diseases, their functional potential was similar.

Additional investigation on the KEGG pathway enrichment of KO functional categories showed the existence of 15 and 12 significantly enriched pathways in HR and DR correspondingly (P < 0.001, Fig. 4). Pathways associated with genetic information replication, repair, and Protein export, such as "DNA replication", "Homologous recombination", "Mismatch repair", and "Protein export" all showed significantly higher relative abundance in the HR than DR. "Pentose phosphate pathway", "Peptidoglycan biosynthesis", "Photosynthesis", "Phenazine biosynthesis", and "Lysine biosynthesis", those biosynthetic pathways were significantly enriched in the HR. The metabolism of cysteine, methionine, purine, and pyrimidine was also enriched in the HR. Conversely, the degradation pathways of aminobenzoate, benzoate, caprolactam, dioxin, polycyclic aromatic hydrocarbon, xylene, and other toxic

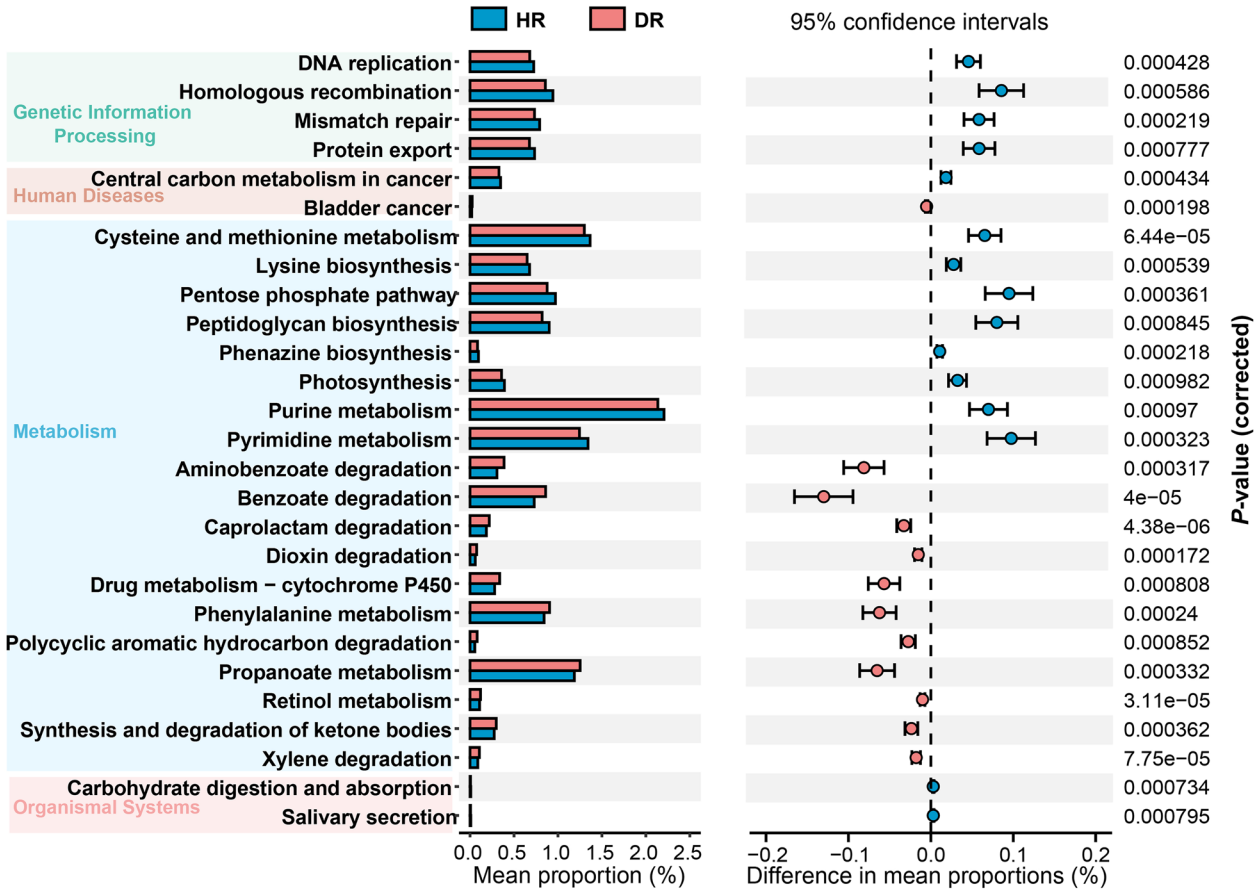


Fig. 4 The two-tailed test revealed significantly different KEGG pathway in HR and DR ($P < 0.001$), and the *P*-value was corrected using Bonferroni. HR and DR represent healthy rhizosphere and diseased rhizosphere, respectively

substances were significantly enriched in DR. The relative abundance of metabolic pathways, including "Drug metabolism—cytochrome P450", "Phenylalanine metabolism", "Propanoate metabolism", "Retinol metabolism", "Synthesis and degradation of ketone bodies", were notably higher in the DR than HR (Fig. 4).

Discussion

The dominant influences of plant species on root exudates and rhizosphere bacterial composition

In this study, we used metabolomics and amplicons to investigate the characteristics of root secretory activities and rhizosphere microbial community assembly and function of host plants of different species under the same disease stress. Our results revealed that the composition of root exudates and bacterial communities was regulated by host species and disease stress (Figs. 1B and 3A). Host-driven root secretory activity shapes unique rhizosphere microbiomes, while pathogen invasion drives the assembly and variation of microbial communities, which further affects the composition and release of root exudates [28–30]. Previous studies have demonstrated through a split root experiment that rhizosphere microorganisms could induce systemic signals to affect the composition of root exudates [31]. Additionally, we identified that the host species and plant compartment, respectively, could more effectively account for variations in root exudate and the bacterial community. (Additional file 1: Tables S1 and S3). This is consistent with previous findings that the rhizosphere environment is primarily influenced by host selection (host species and plant compartment) [17, 32].

Disease-induced convergence of composition of root exudates in pepper and tomato

Metabolomics was used to investigate the changes in both the composition and diversity of root exudates induced by disease in pepper and tomato. Lipids and lipid-like compounds composed the majority of the root exudates of pepper and tomato (Fig. 1A). Lipids, which are constituents of primarily cell membranes, play a crucial role as "chemical language" in rhizosphere microbial

colonization and interaction [33, 34]. Root exudates are food resources for microorganisms, and microorganisms have different resource preferences [35]. Previous studies have also shown an interaction between changes in root exudate composition and substrate preference of microbial metabolites, such as rhizosphere bacteria preferentially utilizing plant-secreted aromatic organic acids [36, 37]. And the differential analysis showed that the rhizospheres of the two plants infected with the same pathogen significantly enriched more of the same compounds (Fig. 1G). Therefore, the accumulation of pathogenic bacteria in the diseased rhizosphere may lead to the homogeneity of resources.

Differences in enrichment of potentially beneficial bacteria in healthy tomato and pepper

Our results found that many potentially beneficial bacteria were enriched at THR, such as *Bacillus*, *Rhodanobacter*, *Pseudolabrys*, *Gemmatimonas*, *Sphingomonas*, and *JG30-KF-AS9*, and at PHR, such as *Chitinophaga*, *Streptomyces*, *Devosia*, and *Bacillus* (Fig. 2B, C). Plants could use the strategy of "crying for help" to recruit beneficial microbiomes to cooperate with them to resist pathogen invasion [38]. Numerous studies have demonstrated that these potentially beneficial bacteria were crucial for regulating host growth and protecting plant health [39, 40]. For example, *Bacillus* promotes plant health by stimulating plant-beneficial *Pseudomonas* through metabolic interaction [41], while *Streptomyces* prevents soil-borne diseases by producing antibacterial compounds [42]. The metabolic synchronization between microbial resource consumption and plant secretory traits may lead to variation in potential beneficial microbiome recruitment among different plant species [17, 43, 44]. The difference analysis also showed that diseased plants dominated by pathogenic bacteria were enriched with a larger number of same compounds. Furthermore, our results revealed that regardless of species, bacterial diversity in the diseased rhizosphere decreased significantly compared to that in the healthy rhizosphere (Fig. 3D), while recent studies have also shown that highly diverse microbial communities showed better resistance to plant disease due to intense resource and niche competition [37, 45].

Same functional potential in the pepper and tomato rhizosphere against *Ralstonia*

The same functional potential of THR and PHR was found by PICRUSt2, suggesting that different Solanaceous plants had the same functional potential to resist the same disease stress, despite the different composition of rhizosphere microbiomes and root exudates (Fig. 3F). Previous studies pointed out that different taxonomic compositions may lead to convergence in functional structure [46, 47]. More specifically, in similar environments, the microbial community function was similar, but the composition of the microbial communities that driving a function may differ [48]. The reason may be functional redundancy in the soil microbial system, in other words, the microbiomes with different taxonomic compositions perform the same function [49]. Thus, which species performs a function in a specific environment requires specific analysis.

Moreover, we found that some pathways were differentially enriched in HR and DR, which were related to rhizosphere health and plant growth (Fig. 4). For instance, by up-regulating the "pentose phosphate pathway," plants were better able to adapt to salt stress by activating secondary metabolites and endogenous antioxidant enzymes [50]. Phenazine derivatives produced by *Pseudomonas* in rhizosphere soil had strong antibacterial activity [51], while methionine and cysteine could inhibit the growth of *Fusarium oxysporum* [52]. These functions were significantly enriched in HR to ensure plant health through direct or indirect disease suppression. Conversely, some pathways related to toxin degradation and secondary metabolism were significantly enriched in DR, because soil-borne diseases were usually accompanied by the accumulation of toxic substances [36, 53], such as allelopathic substances [54, 55].

Conclusions

In this study, metabolomics and amplicon techniques were employed to investigate the root exudates and rhizosphere bacterial communities of pepper and tomato. We discovered that despite both host species and pathogens could shape unique rhizosphere environments, the structure and diversity of root exudates and bacterial communities followed a similar pattern of variation when different species were subjected to the same disease stress. More importantly, we revealed that variations in the taxonomic composition of rhizosphere bacteria in pepper and tomato responding to the same disease stress led to a convergence in functional potential. In conclusion, our study revealed the responses of plant secretory activity and rhizosphere bacterial community assembly and function when plants of different species face the same biotic stress, emphasizing the importance of the host plant in shaping the rhizosphere environment.

Abbreviations

PHB	Bulk of healthy pepper
PHR	Rhizosphere of healthy pepper
PDB	Bulk of diseased pepper
PDR	Rhizosphere of diseased pepper
THB	Bulk of healthy tomato
THR	Rhizosphere of healthy tomato
TDB	Bulk of diseased tomato

TDR	Rhizosphere of diseased tomato
UHPLC–MS/MS	Ultra high-performance liquid chromatography–tandem mass spectrometry
PERMANOVA	Permutational multivariate analysis of variance
HMDB	Human Metabolome Database
PICRUSt2	Phylogenetic Investigation of Communities by Reconstruction of Unobserved States 2
HR	Healthy rhizosphere
DR	Diseased rhizosphere
KEGG	Kyoto Encyclopedia of Genes and Genomes
KO	KEGG oethology

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s40538-024-00561-5.

Additional file 1: Figure S1. Number of compounds in root exudate at the Superclass level. **Figure S2.** Shows the correlation between the relative abundance of differential bacterial genera. **Figure S3.** The Simpson index of rhizosphere bacteria. **Table S1.** Pairwise differences in root exudates composition between treatments were assessed. **Table S2.** The relative abundance of the top 10 bacterial phyla in different treatments of tomato and pepper. **Table S3.** Pairwise differences in bacterial community composition between treatments were assessed. **Table S4.** Pairwise differences in KO functional categories between treatments were assessed.

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Author contributions
ZL and MY conceived and planed the experiments. MY, MW, ML, GL, YB, CP, and KL performed the experiments, consulted literature and did the data analysis. MY and MW wrote the paper. All authors discussed the results and commented on the manuscript. All authors read and approved the final manuscript.

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Availability of data and materials
The raw data are available at https://github.com/MengyuanYan/data_yanmengyuan.

Declarations

Ethics approval and consent to participate
Not applicable.

Consent for publication
Not applicable.

Competing interests
The authors declare that they have no competing interests.

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