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Data Article

Shotgun metagenomics sequencing data of root microbial community of Huanglongbing-infected *Citrus nobilis*

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ABSTRACT

Huanglongbing (HLB) is the most serious citrus disease in Vietnam. For the first time, this paper reported root microbial data of HLB-infected *Citrus nobilis* grown in Dak Lak Province, Vietnam, for further work toward controlling this disease. Roots of HLB-infected *C. nobilis* were collected, and the genomic DNA was isolated. The Illumina platform was used to sequence the shotgun metagenomic library, and bioinformatic tools were used to analyze sequenced data. We found that 4 kingdoms, 27 phyla, 57 classes, 124 orders, 246 families, 722 genera, and 1758 species of the root microbiome were identified from the sample. *Actinomycetota* was the predominant phylum (47.37 %), and biosynthesis was the primary function (57.38 %) of the microbiome.

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Specifications Table

Subject	Microbiology
Specific subject area	The root microbiome of diseased citrus
Data format	Raw (fastq.gz files), Filtered, and Analyzed
Type of data	Figures and Fastq files
Data collection	Root samples of HLB-infected *C. nobilis* L., which showed Huanglongbing symptoms in leaves, were collected from three positions in Dak Lak. The surface of the roots was sterilized and used to isolate the genomic DNA using DNeasy PowerSoil Pro kit. The shotgun metagenomic library was created using the NEBNext Ultra II DNA Library Prep Kit for Illumina. The DNBSeq-G99 machine was utilized to sequence the shotgun metagenomic library with the Illumina platform. Bcl2fastq 2.20 was used to demultiplex the raw data. Trimmomatic 0.39 and Cutadapt 2.10 were used to filter the sequence data. Kraken2 was used to assess taxonomic profiles, and the MetaCyc database was utilized to analyze functional characteristics.
Data source location	• Institution: Institute of Biotechnology and Environment, Tay Nguyen University • District/Province/Country: Buon Don/Dak Lak/ Vietnam • Latitude and longitude coordinates for collected samples: 12°42′59′′N, 107°57′36′′E; 12°43′00′′N, 107°57′32′′E; 12°43′04′′N, 107°57′33′′E
Data accessibility	Raw sequences (fastq.gz files) Repository name: Mendeley Data Data identification number: doi: 10.17632/cmvmnnmn4t.1 Direct URL to data: https://data.mendeley.com/datasets/cmvmnnmn4t/1

1. Value of the Data

- Data provided valuable taxonomic and functional profiles of the root microbiome of HLB-infected *C. nobilis* cultivated in Dak Lak, Vietnam.
- Data provided a valuable background of root microbial resources, especially new ones.
- Data could be valuable for further experiments concerning the application of the microbiome for green citrus production.

2. Background

Citrus is one of the main exporters of fruits in Vietnam. Of the citrus cultivars, *C. nobilis* L. was the main cultivar cultivated in the Dak Lak Province of the country. Currently, citrus plants in this province and Vietnam face the HLB disease caused by unculturable bacteria from the genus *Candidatus* Liberibacter. HLB is the most serious threat in the citrus industry worldwide [1]. Some ways to control HLB-infected citrus have been used, including using free HLB-infected citrus, cultivation techniques, and controlling citrus psyllid insect vectors [2–4]; however, this disease has not been cured. To our knowledge, data on the composition and functional profiles of the healthy *C. nobilis* root microbiome have been demonstrated [5]; however, the data on HLB-infected *C. nobilis* are still unknown. This work aimed to establish data on the root microbiome of HLB-infected *C. nobilis* using shotgun metagenomics to explore novel secondary metabolites further and apply microorganisms for green citrus production.

3. Data Description

In this experiment, 3190,632 reads were filtered from 32,926,765 raw reads and used to analyze the taxonomic and functional profiles. As shown in Tables S1–S7 and Fig. 1, we identified 4 kingdoms of root microorganisms, among them, bacteria accounted for (97.03 %), followed by

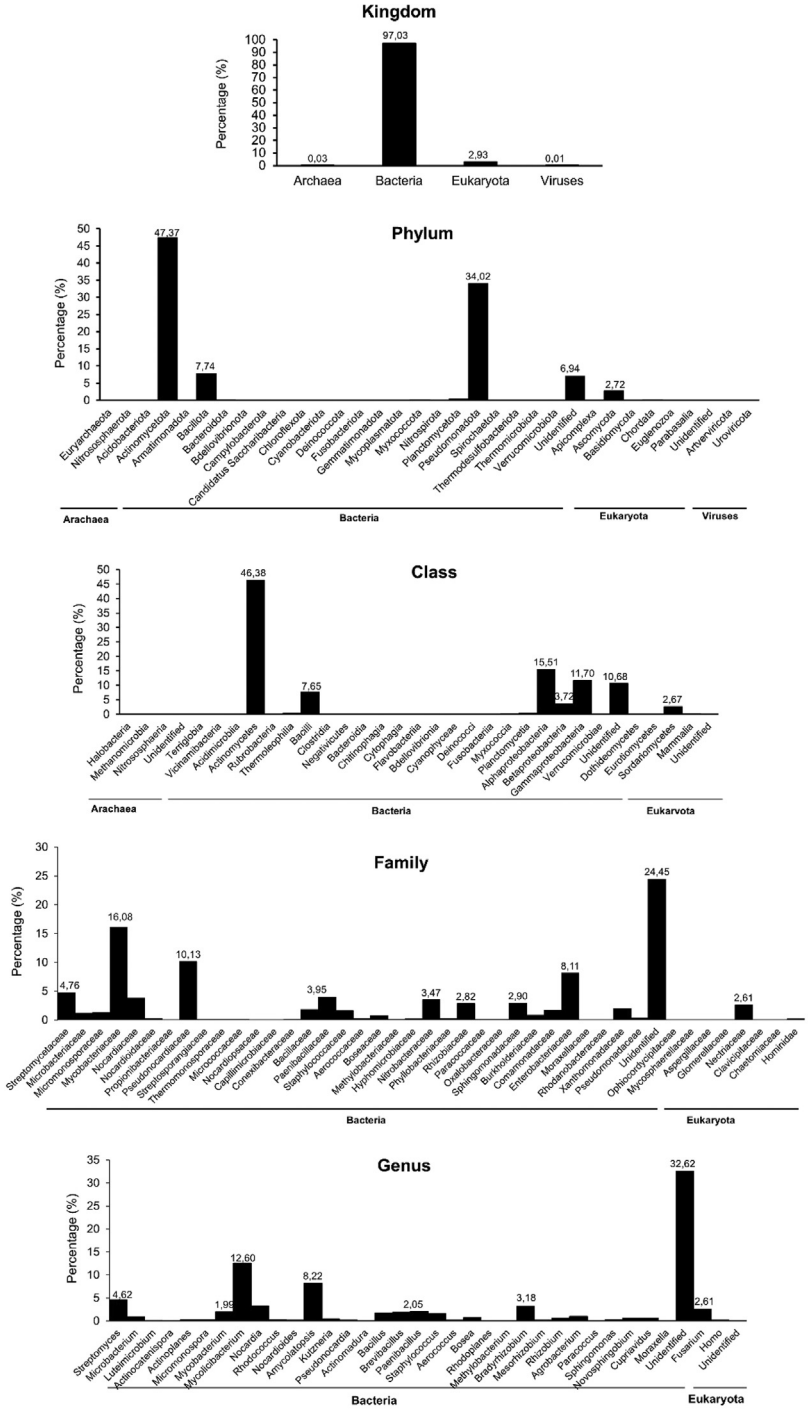

Fig. 1. Taxonomic profiles of the predominant microbiome of HLB-infected *Citrus nobilis* roots at levels of kingdom, phylum, class, family, and genus.

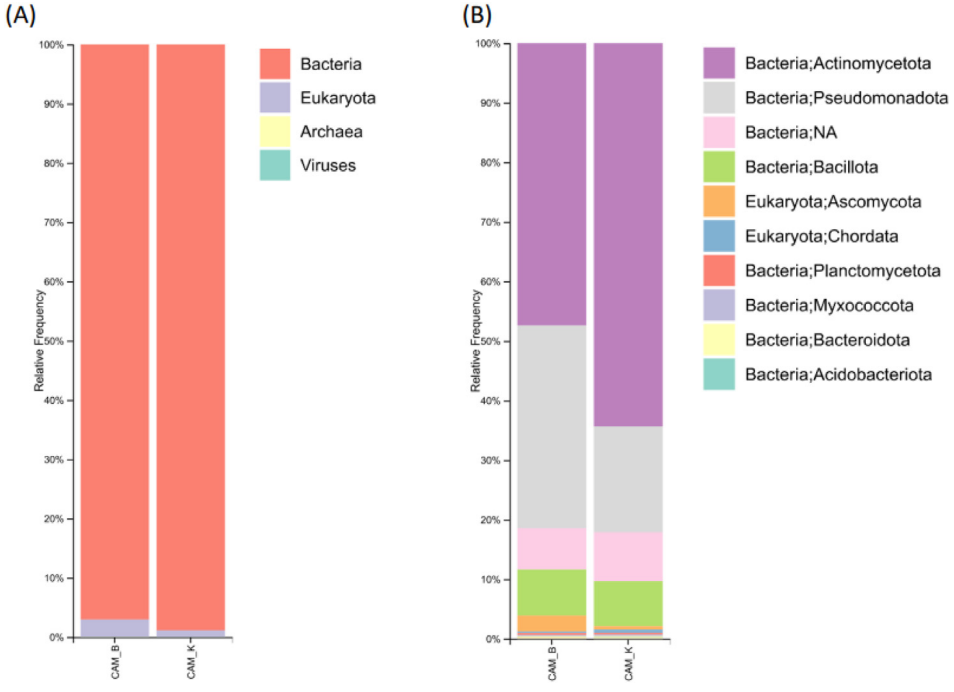

Fig. 2. Comparison of taxonomic profiles of the root microbiome of healthy and HLB-infected *Citrus nobilis* at kingdom (A) and phylum (B) levels. CAM_B, HLB-infected *Citrus nobilis* (this study); CAM_B, healthy *Citrus nobilis* (data referred from Tran et al., [5]. NA, unidentified phylum.

eukaryota (2.93 %), archaea (0.03 %), and viruses (0.006 %). Of the 27 identified phyla, *Actinomycetota* (47.37 %) was the main phylum, followed by *Pseudomonadota* (34.02 %). Among 57 classes, *Actinomycetes* (46.38 %), *Alphaproteobacteria* (15.51 %), *Gammaproteobacteria* (11.69 %), and *Bacilli* (7.65 %) were shown to be the predominant classes. Of 124 orders, *Mycobacteriales* (20.85 %), *Pseudonocardiales* (10.13 %), *Hyphomicrobiales* (9.91 %), *Enterobacterales* (8.60 %), and *Bacillales* (7.39 %) were the most dominant. *Mycobacteriaceae* (18.08 %), *Pseudonocardiaceae* (10.13 %), *Enterobacteriaceae* (8.11 %), *Streptomycetaceae* (4.74 %), *Paenibacillaceae* (3.95 %), and *Rhizobiaceae* (2.82 %) were the predominant of 246 identified families. Of 722 genera, *Mycolicibacterium* (12.60 %) was the primary genus, followed by *Amycolatopsis* (8.22 %), *Enterobacter* (4.88 %), *Streptomyces* (4.62 %), and *Bradyrhizobium* (3.18 %). Finally, 1758 species of the microbiome were identified from the sample; among them, *Mycolicibacterium rhodesiae* (4.92 %), *Mycolicibacterium mucogenicum* (2.58 %), and *Brevibacillus brevis* (1.81 %) were the most abundant. Moreover, *Candidatus* Liberibacter asiaticus (0.071 %), a causal agent of Huanglongbing [1], was identified from the microbiome. Total unidentified families and genera of the root microbiome were calculated to be 24.72 % and 32.35 %, respectively. Furthermore, we identified numerous bacterial genera and species belonging to *Actinomyces, Streptomyces, Bacillus, Brevibacillus, Paenibacillus, and Pseudomonas*, which were reported to play an important role in agricultural cultivation [6–12] and suppressing citrus Huanglongbing [13–15], from the microbiome. A comparison (Fig. 2) shows that taxonomic profiles of the root microbiome of healthy and HLB-infected *C. nobilis* cultivated in Dak Lak differed at kingdom and phylum levels. For example, the kingdom *bacteria* of healthy *C. nobilis* was more abundant than that of the HLB-infected *C. nobilis*. The phylum *Actinomycetota* of healthy *C. nobilis* was more predominant than that of the HLB-infected *C. nobilis*. Raw sequences (fastq.gz files) were deposited in Mendeley Data and can be downloaded at https://data.mendeley.com/datasets/cmvmnnmn4t/1.

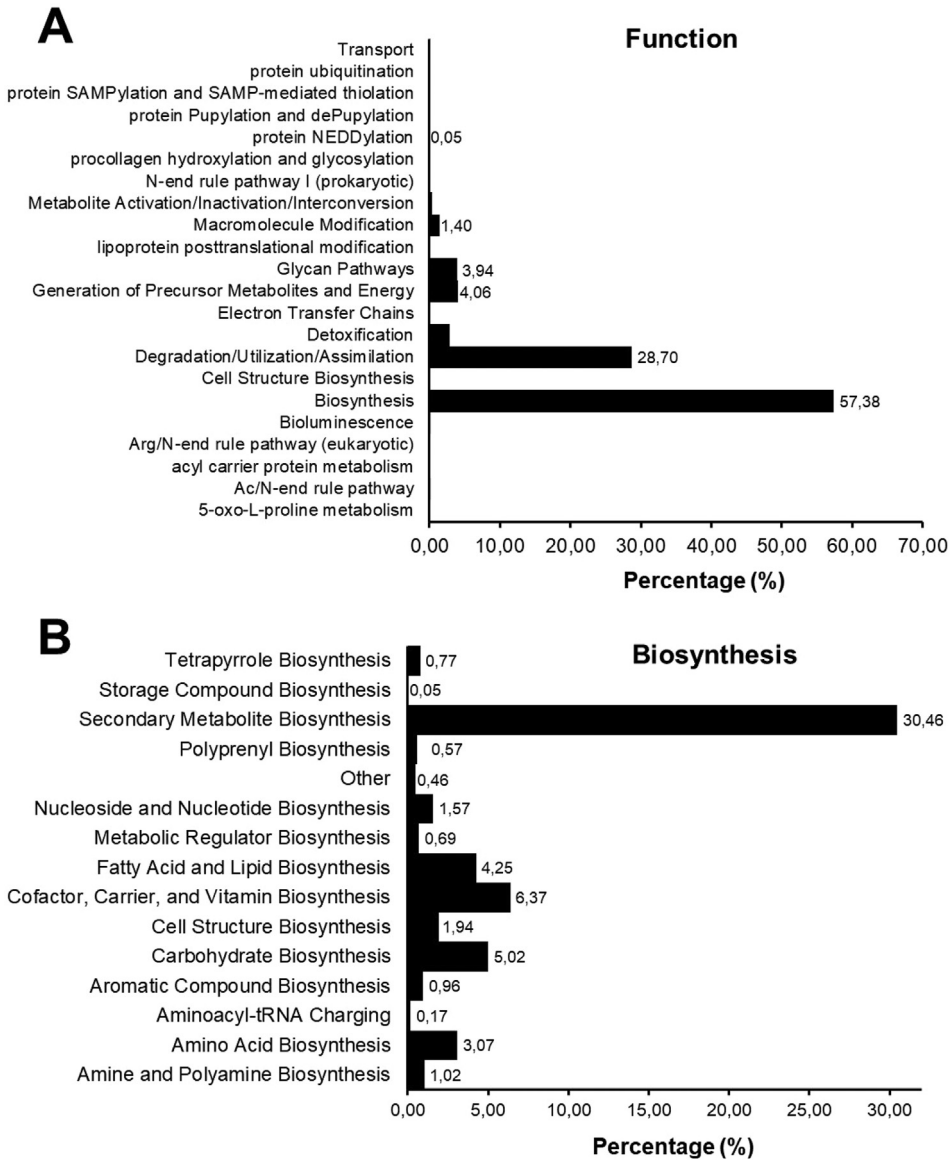

Fig. 3. Functional profiles of the root microbiome of HLB-infected *Citrus nobilis*.

As exhibited in Fig. 3A, biosynthesis (57.38 %) was found to be the primary function of the *C. nobilis* root microbiome, degradation/utilization/assimilation (28.7 %) was the second most abundant function, followed by generation of precursor metabolites and energy (4.06 %), and glycan pathways (3.94 %). Of the functions concerning biosynthesis, secondary metabolite biosynthesis (30.46 %) was the most predominant, followed by cofactor, prosthetic group, electron carrier, and vitamin biosynthesis (6.37 %); carbohydrate biosynthesis (5.02 %); fatty acid and lipid biosynthesis (4.25 %); amino acid biosynthesis (3.07 %); cell structure biosynthesis (1.94 %); and nucleoside and nucleotide biosynthesis (1.57 %) (Fig. 3B). Raw sequences (fastq.gz files) were deposited in Mendeley Data and can be downloaded at https://data.mendeley.com/datasets/cmvmnnmn4t/1.

Fig. 4. *Citrus nobilis* exhibiting Huanglongbing symptoms in leaves cultivated in Dak Lak, Vietnam.

4. Experimental Design, Materials and Methods

Three root samples (about 70 g each) of HLB-infected *C. nobilis* L., which showed Huanglongbing symptoms in leaves, were collected from three positions (12°42′59″N, 107°57′36″E; 12°43′00″N, 107°57′32″E; 12°43′04″N, 107°57′33″E) in Dak Lak. The leaves exhibited non-symmetrical mottling, thickened, expanded, corky midribs, and indications of zinc insufficiency, which included erect leaves about the shoot [4] (Fig. 4). The samples were combined to generate the representative sample. The root was washed with tap water, then treated with tween 80 for 10 min, and washed again with sterilized water. After that, the surface of the root was sterilized with 2 % sodium hypochlorite solution for 10 min and then 70 % ethanol for 1 min. Finally, the root was washed six times with sterilized distilled water [16]. DNeasy PowerSoil Pro kit (Qiagen, Germany) was used to isolate the genomic DNA from the sample. Using the NEBNext Ultra II DNA Library Prep Kit for Illumina (New England Biolabs, USA), the shotgun metagenomic library was created. The DNBSeq-G99 (MGI) machine was utilized to sequence the shotgun metagenomic library with the Illumina platform (2 × 150 PE). Bcl2fastq 2.20 was used to demultiplex the raw data [17]. Trimmomatic 0.39 [18] and Cutadapt 2.10 [19] were used to filter the sequence data. Kraken2 [20] was used to assess taxonomic profiles, while the MetaCyc database [21] was utilized to analyze functional characteristics.

Limitations

Not applicable.

Ethics Statement

The current work does not involve human subjects, animal experiments, or any data collected from social media platforms.

CRediT Author Statement

Dinh Minh Tran: Conceptualization, Methodology, Investigation, Formal analysis, Software, Data curation, Validation, Visualization, Writing, Review and Editing. **Thi Huyen Nguyen:** Investigation, Formal analysis. **Anh Dzung Nguyen:** Conceptualization, Sampling, Data curation, Validation, Visualization.

Data Availability

Endophytic microbiome diversity and functional profiles of Huanglongbing-infected citrus revealed by shotgun metagenomics sequencing data (Original data) (Mendeley Data).

Acknowledgments

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Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Supplementary Materials

Supplementary material associated with this article can be found, in the online version, at doi:10.1016/j.dib.2024.111061.

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