# Plant pathogenesis: towards multidimensional understanding of the microbiome meta

Tianxing Lv<sup>1,2</sup>, Chengfang Zhan<sup>1,2</sup>, Qianqian Pan<sup>1,2</sup>, Haorong Xu<sup>1,2</sup>, Hongda Fang<sup>1,2</sup>, Mengcen Wang<sup>1,2,3</sup>, Haruna Matsumoto<sup>1,2</sup>

 <sup>1</sup> State Key Laboratory of Rice Biology & Ministry of Agricultural and Rural Affairs Laboratory of Molecular Biology of Crop Pathogens and Insects, Zhejiang University
<sup>2</sup> Key Laboratory of Biology of Crop Pathogens and Insects of Zhejiang Province, Institute of Pesticide and Environmental Toxicology, College of Agriculture and Biotechnology, Zhejiang University
<sup>3</sup> Global Education Program for AgriScience Frontiers, Graduate School of Agriculture, Hokkaido University



### **Highlights**

- The resident microbiota is a hidden game changer in plant health and disease.
- The invasive pathogen can hijack certain members of the resident microbiota to form partnerships within the reassembled community, which is currently conceptualized as the pathobiome.
- The pathobiome facilitates the pathological process of host plants, from the onset of the disease to its progression, by coordinating complex interactions at multiple scales.
- The pathobiome-targeted approach may pave a new way to address the increasing trends of plant diseases in the face of global change.

#### Introduction — The hidden player in plant diseases



- The disease-preventing members from the resident microbiota coined as soterobionts.
  - Some resident microbiota members even can be manipulated by the invasive pathogen to form the partnership along with the pathogenesis process. And the host pathogenesis-associated microbial consortia, presenting from disease onset and progression, is contemporarily conceptualized as pathobiome.
- We aim to highlight that the potentially negative impacts of the resident microbiota on plant health should not be overlooked, and further holistic insight into the microbiota-associated interaction and plant pathogenesis needs to be expanded by the characterization of the pathobiome as well.

#### Microbial intra- and inter-species signaling systematically affects plant pathogenesis

- A growing awareness of pathogenesis has evolved from the 'one pathogen-one disease' paradigm to the pathobiome concept.
- The onset and progression of plant disease are likely to be the result of interactions among/between multiple microbial taxa and their host plants.
- The mechanistic insight into the plant pathobiome-associated interactions is important for uncovering the process that governs the outcome of pathogen infection in the host plants.
- The mutualistic relationships among the invasive pathogen and the native potentially pathogenic microbial members are generally concealed within the complex intramicrobiome interaction from intraspecies to interspecies and interkingdom, which negatively affect the homeostasis of vegetative and reproductive organs, drive the infection outcome, and result in disease progression.



Quorum-sensing (QS) is the first identified bacterial intraspecies signaling system, which enables bacterial cells to chemically sense the density of the surrounding population and regulate variously physiological activities such as motility, biofilms, secondary metabolism, and virulence in a cell density-dependent manner.

- Quorum quenching (QQ) has been previously characterized as ubiquitous interspecies interaction employed by symbiotic bacteria to interfere with the QS of phytopathogenic bacteria.
- Establishment of the mutualistic relationships among the invasive pathogen and resident microbiota members highlight the ecological scale implication of the intraspecies communication on the plant pathogenesis.

#### Microbial interkingdom interaction in plant disease progression



- Bacterial-fungal interactions (BFIs) majorly including physical interactions and chemical interactions.
- The bacterium can physically attach to fungus and utilize fungus as an effective vector to facilitate its infection and expansion in the host plant.
- The pathogenic mycobiome can benefit from bacteriome through the formation of the multi-kingdom biofilm matrix, which functions as a physical barrier to protect against the host and antimicrobial insults and advancing the infection.



- The volatiles emitted by fungus might act as signaling molecules for attracting bacteria and further are likely to achieve co-infection of fungi and bacteria.
- The characterization of the microbial-derived signaling molecules, ranging from chemical small molecules to larger effectors, would be instrumental in revealing the landscape of BFIs-mediated plant disease progression.



- The potential pathobiome members collaborate to counteract the plant genetics-governed alliance.
- Effectors produced by different members of the plant pathobiome can rapidly evolve to overcome ETI by evading recognition of R proteins, leading to effector-triggered susceptibility (ETS).
- Effectors may target various plant factors encoded by susceptibility genes (S genes) to magnify the ETS of the host plants.

#### Multi-scale interactions underlying the pathobiome-responsible pathogenesis



- Conventional defense strategies based on plant innate immunity remain ineffective when confronted with highly virulent small molecule-based virulence systems employed by bacterial phytopathogens.
- The specific members of the plant pathobiome possibly promote their spread and disease epidemics via manipulating the host attraction to insect herbivore vectors.
- The plant pathobiome members may compromise defense against insect herbivores by influencing the cross-talk between the phytohormones jasmonic acid (JA) and salicylic.

#### **Triggers behind the plant pathobiome prevalence**



- The impacts of global change on the plant microbiome including the cascading effects on plant productivity, biodiversity, and ecosystem functioning.
- Climate change and anthropogenic activity can influence the composition and microbial community diversity of phyllosphere microbiome.
- In the water and soil, prevalence of antibiotics and microplastics may increase the abundance of potential pathogens, which are spatially co-located with an increased abundance of antibiotic resistance genes in the rhizosphere.
- The increased inputs of agrochemicals and fertilizers cause uncertain impacts on the structure and function of the resident microbiota in both rhizosphere and phyllosphere, and reversely allow the non-native potentially pathogenic microbes from the surrounding environment to colonize the below-to-above niches of host plants through a 'vacuum effect'.

#### **Conclusion and future perspectives**

- The involvement of the pathobiome in plant pathogenesis, suggesting the onset and progression of plant disease are not simply dominated by single pathogen but rather the pathobiome-coordinated interactions at multi-scale.
- Answering how these natural and human triggers influence the prevalence of plant pathobiome is positive to prevent the assembly of the plant pathobiome before they initiate the pathogenic actions.
- The further efforts are made in not only revealing the specific member in the pathobiome at the taxonomic level, but also molecular understanding of the mechanisms underpinning the assembly and multiple actions of the pathobiome to direct the infection towards disease.
- We aim to advance the current insight into the plant pathogenesis and also pave a new way to cope with the upward trends of plant disease by designing the pathobiome-targeted measure.

Tian-Xing Lv, Cheng-Fang Zhan, Qian-Qian Pan, Hao-Rong Xu, Hong-Da Fang, Meng-Cen Wang, and Haruna Matsumoto. 2023. Plant pathogenesis: toward multidimensional understanding of the microbiome. *iMeta* e129. https://doi.org/10.1002/imt2.129

## **iMeta:** Integrated meta-omics to change the understanding of the biology and environment

# WILEY



"*iMeta*" is an open-access Wiley partner journal launched by scientists of the Chinese Academy of Sciences. iMeta aims to promote metagenomics, microbiome, and bioinformatics research by publishing original research, methods, or protocols, and reviews. The goal is to publish high-quality papers (Top 10%, IF > 15) targeting a broad audience. Unique features include video submission, reproducible analysis, figure polishing, APC waiver, and promotion by social media with 500,000 followers. Three issues were released in <u>March</u>, <u>June</u>, and <u>September</u> 2022.



Society: <u>http://www.imeta.science</u>

Publisher: https://wileyonlinelibrary.com/journal/imeta

Submission: <u>https://mc.manuscriptcentral.com/imeta</u>

