

UC Riverside

Journal of Citrus Pathology

Title

Announcement of the International Citrus Microbiome (Phytobiome) Consortium.

Permalink

<https://escholarship.org/uc/item/5xp3v2rc>

Journal

Journal of Citrus Pathology, 2(1)

Authors

Wang, N.
Jin, T.
Trivedi, P.
[et al.](#)

Publication Date

2015

DOI

10.5070/C421027940

Copyright Information

Copyright 2015 by the author(s). This work is made available under the terms of a Creative Commons Attribution License, available at <https://creativecommons.org/licenses/by/4.0/>

Peer reviewed

Letter to the Editor

Announcement of the International Citrus Microbiome (Phytobiome) Consortium.

N. Wang^{1*}, T. Jin², P. Trivedi³, J. C. Setubal⁴, J. Tang⁵, M. A. Machado⁶, E. Triplett⁷,
H. D. Coletta-Filho⁸, J. Cubero⁹, X. Deng¹⁰, X. Wang¹¹, C. Zhou¹¹, V. Ancona¹², Z. Lu¹³, M. Dutt¹⁴,
J. Borneman¹⁵, P. E. Rolshausen¹⁵, C. Roper¹⁵, G. Vidalakis¹⁵, N. Capote¹⁶, V. Catara¹⁷, G. Pietersen¹⁸,
A. M. Al-Sadi¹⁹, A. K. Srivastava²⁰, J. H. Graham¹⁴, J. Leveau²¹, S. R. Ghimire²², C. Vernière²³,
and Y. Zhang¹

¹ Citrus Research and Education Center, Department of Microbiology and Cell Science, IFAS, University of Florida, Lake Alfred, FL, USA; ² BGI-Shenzhen, Shenzhen, China; ³ Department of Soil Biology and Genomics, University of Western Sydney, Australia; ⁴ Department of Biochemistry, Institute of Chemistry, University of São Paulo, São Paulo, Brazil; ⁵ Guangxi University, Guangxi, China; ⁶ Laboratório de Biotecnologia, Centro de Citricultura Sylvio Moreira, IAC, Cordeirópolis, São Paulo, Brazil; ⁷ Department of Microbiology and Cell Science, IFAS, University of Florida, USA; ⁸ Instituto Agrônomo – IAC Centro de Citricultura Sylvio Moreira – CCSM, Brazil; ⁹ Departamento de Protección Vegetal, INIA, Madrid, Spain; ¹⁰ Department of Plant Pathology, South China Agricultural University, Guangzhou, Guangdong, China; ¹¹ National Citrus Engineering Research Center, Citrus Research Institute, Southwest University, Chongqing, China; ¹² Texas A&M University-Kingsville Citrus Center, Texas, USA; ¹³ National Navel Orange Engineering Research Center, Gannan Normal University, Ganzhou, Jiangxi, China; ¹⁴ Citrus Research and Education Center, IFAS, University of Florida, Lake Alfred, FL, USA; ¹⁵ University of California, Riverside, USA; ¹⁶ IFAPA Centro Las Torres-Tomejil Alcalá del Río, Sevilla, Spain; ¹⁷ Dipartimento di Agricoltura, Alimentazione e Ambiente, University of Catania, Via Santa Sofia 100, 95123 Catania, Italy; ¹⁸ ARC-Plant Protection Research Institute c/o Dept. of Microbiology and Plant Pathology, University of Pretoria, 0002 Pretoria, South Africa; ¹⁹ Department of Crop Sciences, Sultan Qaboos University, Oman; ²⁰ Central Citrus Research Institute, Nagpur, Maharashtra, India; ²¹ Department of Plant Pathology, University of California, Davis, CA, USA; ²² International Livestock Research Institute, Kenya; ²³ CIRAD, La Réunion, France.

*Correspondence to: nianwang@ufl.edu

Citation: Wang N, Jin T, Trivedi P, Setubal JC, Tang J, Machado MA, Triplett E, Coletta-Filho HD, Cubero J, Deng X, et al. 2015. Announcement of the International Citrus Microbiome (Phytobiome) Consortium. *J Cit Pathol.* iocv_journalcitruspathology_27940.

Plants host rich and diverse microbial communities near, on, and inside their tissues. The microbial communities associated with plants are known as the plant microbiome or phytobiome, which is comprised of a diverse array of microorganisms such as bacteria, archaea, fungi, oomycetes, viruses, and nematodes, that are associated with different plant habitats including the rhizosphere, phyllosphere, and endosphere (Fig. 1) (Turner et al. 2013; Berg et al. 2014; Lebeis 2014; Schlaeppli and Bulgarelli 2015). The phytobiome is an emerging field of research aimed at generating a systems-level understanding of plant-microbe interactions which influence plant health and plant productivity. The study of phytobiomes is currently in its infancy, and most research focuses on profiling plant microbiomes in different hosts and environments.

Recent advances in cultivation-independent next generation sequencing techniques have provided valuable tools to investigate plant microbiomes, enabling thorough descriptions of these plant-associated microorganisms. The latest approaches overcome the limitation of culturing since only a small portion of microbes can be cultivated. The microorganisms in the rhizosphere, phyllosphere, and endosphere of various plants, including the model plant *Arabidopsis* and crop plants such as maize, rice, wheat, sugar beet, lettuce, and pea, have been characterized (Guttman et al. 2014). These studies have significantly advanced our understanding of the

composition and structure of plant microbiomes. In general, the phyllosphere microbiomes are of a higher variability and lower diversity than the belowground (soil and the rhizosphere) microbiomes, and the endophytic microbiomes have higher diversity than the epiphytic microbiomes. Together these studies indicate that abiotic factors as well as plant-microbe, microbe-microbe, and plant-plant interactions contribute to plant microbiome composition and structure.

The interactions between the microbiome and plant are highly complex and dynamic. The interactions among plant and microbes can be beneficial (mutualistic), neutral (commensalism), or detrimental (parasitic). Consequently, the plant microbiome dramatically affects plant health and productivity (Turner et al. 2013; Berg et al. 2014; Schlaeppli and Bulgarelli 2015). The plant microbiome is known to induce or prime plant defenses against a broad range of pathogens and insect herbivores. The plant microbiome also plays essential roles in disease-suppressive soils. Additionally, the plant microbiome is a crucial player in global biogeochemical cycles, participating significantly in biochemical cycling of the products of photosynthesis (Turner et al. 2013). Therefore, manipulation of plant microbiomes is believed to have the potential to interfere with plant disease development, promote plant production, and ease chemical inputs, leading to more sustainable agricultural practices (Turner et al. 2013).

The citrus microbiome remains largely unexplored. Although the productive lifetime of citrus trees is usually less than 50 years, they can live for more than a century. The long lifespan of citrus likely leads to fluctuation in microbiome composition, which adapts to the changing environment and citrus physiology over time. Citrus is grown worldwide. More than 140 countries produce citrus, with most grown in subtropical regions. The worldwide distribution of citrus and the wide variations in soil, temperature, rainfall, pH, citrus varieties, different disease challenges (e.g., citrus Huanglongbing), and production practices almost certainly leads to a wide range of microorganisms comprising the citrus microbiome. Consequently, we aim to investigate the citrus microbiome at the global scale.

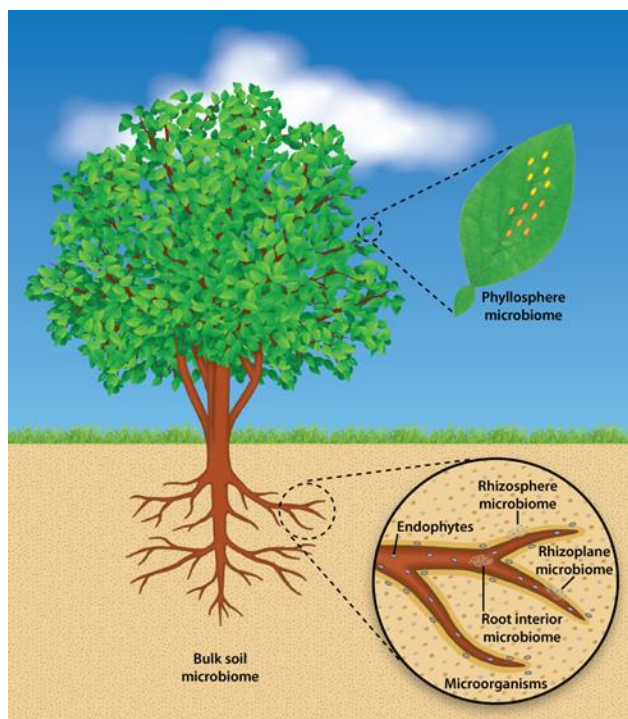


Figure 1. Model of the plant microbiome (phytobiome). The plant microbiome consists of microorganisms (e.g., bacteria and fungi) in the phyllosphere (above-ground portions of plants); the rhizosphere (the area surrounding the plant root), the rhizoplane (the root-soil interface), and the endosphere (internal compartments).

For this purpose we have formed the International Citrus Microbiome (Phytobiome) Consortium. The consortium will endeavor to synergize colleagues from all citrus-producing countries. It will be comprised of expertise in microbiology, bioinformatics, citrus, biogeography, and soil, all working together to understand the citrus microbiome from a systems biology perspective. We have proposed the following objectives for the International Citrus Microbiome (Phytobiome) Consortium:

1. Profile citrus microbiomes in different countries.

2. Determine the effect of citrus age on the citrus microbiome.
3. Investigate the effect of different rootstocks and scions on the citrus microbiome.
4. Study the effect of different biotic (diseases) and abiotic stresses (e.g., drought) on the citrus microbiome.
5. Determine the effect of different citrus management strategies (herbicides, mulching, fertilizing, etc) on the citrus microbiome.
6. Functionally characterize the citrus microbiome using RNA-Seq, proteomics and metabolomics approaches.
7. Isolate and characterize beneficial microbes.
8. Manipulate the citrus microbiomes to improve plant production and health.

Currently, the International Citrus Microbiome (Phytobiome) Consortium consists of colleagues from USA, China, Brazil, Spain, Australia, South Africa, India, Italy, Oman, Kenya, and France. We welcome colleagues to join the consortium, and to collectively contribute to this important area of research.

Acknowledgments

The International Citrus Microbiome (Phytobiome) Consortium is partly supported by the Florida Citrus Research and Development Foundation and IFAS University of Florida.

References

- Berg G, Grube M, Schlöter M, Smalla K. 2014. Unraveling the plant microbiome: looking back and future perspectives. *Front Microbiol.* 5:148.
- Guttman DS, McHardy AC, Schulze-Lefert P. 2014. Microbial genome-enabled insights into plant-microorganism interactions. *Nat Rev Genet.* 15:797-813.
- Lebeis SL. 2014. The potential for give and take in plant-microbiome relationships. *Front Plant Sci.* 5:287.
- Schlaeppli K, Bulgarelli D. 2015. The plant microbiome at work. *Mol Plant Microbe Interact.* 28:212-217.
- Turner TR, James EK, Poole PS. 2013. The plant microbiome. *Genome Biol.* 14:209.