

Olive Tree and Its Vascular Pathogens

Subjects: Plant Sciences

Contributor: Manuel Anguita-Maeso, Juan A. Navas-Cortés, Blanca B. Landa

Vascular pathogens are the causal agents of some of the most devastating plant diseases in the world, which can cause, under specific conditions, the destruction of entire crops, such as their impact on olive trees. These plant pathogens activate a range of physiological and immune reactions in the host plant following infection, which may trigger the proliferation of a specific microbiome to combat them by, among others, inhibiting their growth and/or competing for space.

Keywords: microbiome ; endophytes ; xylem

1. Introduction

Plant microbiome research has been expanding over the last years due to its key determinant role in plant health and crop productivity ^[1], as is revealed by the increase in the number of scientific publications listed in Web of Science (WoS) and Scopus databases. Nowadays, it is generally accepted that plants live in association with a rich diversity of microorganisms. The sum of these microbial cells formed by multi-kingdom microbial communities (bacteria, fungi, viruses, etc.) that colonize both below- and aboveground plant organs in a particular environment is called plant-associated microbiota and refers to the taxonomy and abundance of microbial community members in a given environment. On the other hand, the totality of genomes of this microbiota is called the plant microbiome and it is often used to define the microbial behaviors or functions determined by a microbiota ^[2].

A better knowledge of the plant microbiome will result in developing alternatives to solve some of the environmental issues and challenges worldwide caused by excess use of chemicals for pest control by enhancing crop production and soil health ^[3] and by developing biological control alternatives for managing plant diseases ^{[4][5]}. Plant-associated beneficial microbiomes can confer fitness advantages to the host plant because these microorganisms can directly impact plant growth and health by producing phytohormones, improving nutrient acquisition and phosphate solubilization and tolerance to biotic and abiotic stresses. Additionally, they can act indirectly by activating a series of host physiological and immune responses that may trigger the multiplication of a specific microbiome to cope with the pathogen infection. This beneficial elicited microbiome can compete for plant resources and niche space or inhibit the growth of plant pathogens via the production of antibiotics, fungal cell wall-degrading enzymes or siderophores, among others ^{[6][7][8]}.

Several authors have described the importance and ecological interpretations of the cross-kingdom co-occurrence networks in the plant microbiome ^{[9][10]}. Network analyses have identified the existence of interactions among the myriad of endophytes present in natural communities and other potential higher-order interactions ^[11]. Thus, this analysis has contributed to the discovery of hub or keystone microbial taxa in the plant microbiome. In fact, leaves of *Arabidopsis thaliana*, a fungal species, *Dioszegia* sp., and an oomycete, *Albugo* sp., were detected as hubs in the networks and experimentally validated as keystone species ^[12]; whereas in the wild rice seed microbiome, two fungal species were identified to be hub species in the cross-kingdom network ^[13]. This data analysis tool can be used to determine the existence of aggregation or exclusion interactions in xylem-associated microbiomes and reveal keystone microbial players in the xylem of olive trees to fight against vascular pathogens to contribute to the production of olive plants that are more resilient to these pathogens.

2. Olive Tree and Its Vascular Pathogens

Olive (*Olea europaea* subsp. *europaea* L.) is one of the most relevant tree species within the Mediterranean Basin due to its cultural and economic importance, without underestimating the noteworthy environmental attributes related to its ability to survive in poor, shallow and dry soils, and its contribution to the control of soil erosion and increase in soil nutrient retention ^{[14][15]}. In addition, olive orchards are important agroforestry habitats, playing essential roles in maintaining ecosystem diversity ^[16]. Hence, olive cultivation comprises relevant economic, environmental and socio-cultural values representing an agricultural system that should remain integral to the Mediterranean Basin. However, the health status of

olive trees is being threatened by a remarkable increase in diseases caused by xylem-inhabiting pathogens, such as the plant pathogenic bacterium *Xylella fastidiosa* and the soilborne fungus *Verticillium dahliae*. Both pathogens are global threats to olive production which can adversely affect olive growth and production, causing substantial economic losses and severe environmental impact ^{[17][18][19][20][21]}.

The life cycle of *V. dahliae*, the causal agent of Verticillium wilt, is mainly characterized by its growth confined within the xylem vessels during the pathogenic phase and its ability to survive for many years as dormant microsclerotia in soil or within plant debris ^{[17][22]}. *Verticillium dahliae* infects the olive plants through the root system; then, the pathogen colonizes the xylem vessels and impairs the sap flow through mycelial proliferation, the formation of occlusions and tyloses that ultimately may cause the death of the tree ^{[17][23]}. The implementation of an integrated management strategy is the best option for controlling this disease, combining the use of resistant olive cultivars, or tolerant ones grafted onto resistant rootstocks, with adequate irrigation management and agricultural practices that prevent the spread of inoculum of the pathogen ^{[17][24][25][26][27][28]}.

On the other hand, *X. fastidiosa* is a quarantine plant pathogenic bacterium in the European Union (EU) and was ranked first on the list of the 20 priority pests within the EU territory (Commission Delegated Regulation (EU) 2019/1702). *X. fastidiosa* is transmitted by sap-feeding insect vectors and has been described as the causal agent of Olive Quick Decline Syndrome (OQDS). This disease is characterized by rapid dieback of shoots, twigs and branches, followed by the death of the tree ^[29]. Sap-feeding insect vectors inoculate the pathogen into xylem vessels from infected to healthy trees. Once inside, the aggregation of bacterial cells and biofilm formation block the sap flow in the xylem causing the plant to dry out and die ^[30]. *Xylella fastidiosa* is taxonomically divided into three major subspecies (*fastidiosa*, *multiplex* and *pauca*) ^[31], although two additional subspecies have been proposed (*morus* and *sandyi*). Only isolates belonging to the subspecies *pauca* are currently considered a threat to olive production worldwide. As previously indicated for *V. dahliae*, currently, there is no efficient control measure for the management of *X. fastidiosa* once the plant is infected. Consequently, the use of preventive strategies focused on the early detection and eradication of infected host plants, the control of the vectors and restrictions on plant material movements are currently the only available tools for the management of the diseases caused by this harmful bacterium ^{[32][33][34]}.

The establishment of a pathogen lifestyle in a microorganism depends on its interactions with the host microbiome and the host immune system ^[35]. The xylem-associated microorganisms are involved in several biotic and abiotic processes within the plant host, including the acquisition of nutrients and increase of plant tolerance to abiotic stresses, without overlooking their role in the defense of the plant against vascular pathogens. In this context, acquiring and maintaining a beneficial xylem-associated microbiota capable of adapting more rapidly to a changing environment could be a selective advantage for the olive tree to fight against vascular pathogens ^{[36][37]}.

References

1. Berendsen, R.L.; Pieterse, C.M.J.; Bakker, P.A.H.M. The rhizosphere microbiome and plant health. *Trends Plant Sci.* 2012, 17, 478–486.
2. Schlaeppi, K.; Bulgarelli, D. The Plant Microbiome at Work. *Mol. Plant Microbe Interact.* 2015, 28, 212–217.
3. Chaparro, J.M.; Sheflin, A.M.; Manter, D.K.; Vivanco, J.M. Manipulating the soil microbiome to increase soil health and plant fertility. *Biol. Fertil. Soils* 2012, 48, 489–499.
4. Weller, D.M.; Raaijmakers, J.M.; Gardener, B.B.M.; Thomashow, L.S. Microbial populations responsible for specific soil suppressiveness to plant pathogens. *Annu. Rev. Phytopathol.* 2002, 40, 309–348.
5. Anguita-Maeso, M.; Trapero-Casas, J.L.; Olivares-García, C.; Ruano-Rosa, D.; Palomo-Ríos, E.; Jiménez-Díaz, R.M.; Navas-Cortés, J.A.; Landa, B.B. *Verticillium dahliae* inoculation and in vitro propagation modify the xylem microbiome and disease reaction to *Verticillium* wilt in a wild olive genotype. *Front. Plant Sci.* 2021, 12, 250.
6. Carrión, V.J.; Perez-Jaramillo, J.; Cordovez, V.; Tracanna, V.; de Hollander, M.; Ruiz-Buck, D.; Mendes, L.W.; van Ijcken, W.F.J.; Gomez-Exposito, R.; Elsayed, S.S.; et al. Pathogen-induced activation of disease-suppressive functions in the endophytic root microbiome. *Science* (80) 2019, 366, 606–612.
7. Song, C.; Zhu, F.; Carrión, V.J.; Cordovez, V. Beyond Plant Microbiome Composition: Exploiting Microbial Functions and Plant Traits via Integrated Approaches. *Front. Bioeng. Biotechnol.* 2020, 8, 896.
8. Trivedi, P.; Leach, J.E.; Tringe, S.G.; Sa, T.; Singh, B.K. Plant–microbiome interactions: From community assembly to plant health. *Nat. Rev. Microbiol.* 2020, 18, 607–621.

9. Van der Heijden, M.G.A.; Hartmann, M. Networking in the Plant Microbiome. *PLoS Biol.* 2016, 14, e1002378.
10. Lee, K.K.; Kim, H.; Lee, Y.-H. Cross-kingdom co-occurrence networks in the plant microbiome: Importance and ecological interpretations. *Front. Microbiol.* 2022, 13, 953300.
11. Enespa; Chandra, P. Tool and techniques study to plant microbiome current understanding and future needs: An overview. *Commun. Integr. Biol.* 2022, 15, 209–225.
12. Agler, M.T.; Ruhe, J.; Kroll, S.; Morhenn, C.; Kim, S.-T.; Weigel, D.; Kemen, E.M. Microbial Hub Taxa Link Host and Abiotic Factors to Plant Microbiome Variation. *PLoS Biol.* 2016, 14, e1002352.
13. Kim, H.; Lee, K.K.; Jeon, J.; Harris, W.A.; Lee, Y.-H. Domestication of *Oryza* species eco-evolutionarily shapes bacterial and fungal communities in rice seed. *Microbiome* 2020, 8, 20.
14. Allen, H.D.; Randall, R.E.; Amable, G.S.; Devereux, B.J. The impact of changing olive cultivation practices on the ground flora of olive groves in the Messara and Psiloritis regions, Crete, Greece. *Land Degrad. Dev.* 2006, 17, 249–273.
15. Gómez, J.A.; Infante-Amate, J.; De Molina, G.M.; Vanwalleghem, T.; Taguas, V.E.; Lorite, I. Olive Cultivation, its Impact on Soil Erosion and its Progression into Yield Impacts in Southern Spain in the Past as a Key to a Future of Increasing Climate Uncertainty. *Agriculture* 2014, 4, 170–198.
16. Tschulin, T.; Neokosmidis, L.; Petanidou, T.; Settele, J. Influence of landscape context on the abundance and diversity of bees in Mediterranean olive groves. *Bull. Entomol. Res.* 2011, 101, 557–564.
17. Jiménez-Díaz, R.M.; Cirulli, M.; Bubici, G.; del Mar Jiménez-Gasco, M.; Antoniou, P.P.; Tjamos, E.C. Verticillium Wilt, a major threat to olive production: Current status and future prospects for its management. *Plant Dis.* 2011, 96, 304–329.
18. Saponari, M.; Giampetruzzi, A.; Loconsole, G.; Boscia, D.; Saldarelli, P. *Xylella fastidiosa* in olive in Apulia: Where we stand. *Phytopathology* 2018, 109, 175–186.
19. Almeida, R.P.P.; De La Fuente, L.; Koebnik, R.; Lopes, J.R.S.; Parnell, S.; Scherm, H. Addressing the New Global Threat of *Xylella fastidiosa*. *Phytopathology* 2019, 109, 172–174.
20. Landa, B.B.; Pérez, A.G.; Luaces, P.; Montes-Borrego, M.; Navas-Cortés, J.A.; Sanz, C. Insights into the effect of *Verticillium dahliae* defoliating-pathotype infection on the content of phenolic and volatile compounds related to the sensory properties of virgin olive oil. *Front. Plant Sci.* 2019, 10, 232.
21. Schneider, K.; van der Werf, W.; Cendoya, M.; Mourits, M.; Navas-Cortés, J.A.; Vicent, A.; Oude Lansink, A. Impact of *Xylella fastidiosa* subspecies *pauca* in European olives. *Proc. Natl. Acad. Sci. USA* 2020, 117, 9250–9259.
22. Berlanger, I.; Powelson, M.L. Verticillium wilt. *Plant Health Instr.* 2000, 151, 109–110.
23. Báidez, A.G.; Gómez, P.; Del Río, J.A.; Ortuño, A. Dysfunctionality of the xylem in *Olea europaea* L. Plants associated with the infection process by *Verticillium dahliae* Kleb. Role of phenolic compounds in plant defense mechanism. *J. Agric. Food Chem.* 2007, 55, 3373–3377.
24. López-Escudero, F.J.; Mercado-Blanco, J.; Roca, J.M.; Valverde-Corredor, A.; Blanco-López, M.Á. Verticillium wilt of olive in the Guadalquivir Valley (southern Spain): Relations with some agronomical factors and spread of *Verticillium dahliae*. *Phytopathol. Mediterr.* 2010, 49, 370–380.
25. Bubici, G.; Cirulli, M. Control of Verticillium wilt of olive by resistant rootstocks. *Plant Soil* 2012, 352, 363–376.
26. Jiménez-Fernández, D.; Trapero-Casas, J.L.; Landa, B.B.; Navas-Cortés, J.A.; Bubici, G.; Cirulli, M.; Jiménez-Díaz, R.M. Characterization of resistance against the olive-defoliating *Verticillium dahliae* pathotype in selected clones of wild olive. *Plant Pathol.* 2016, 65, 1279–1291.
27. Montes-Osuna, N.; Mercado-Blanco, J. Verticillium Wilt of Olive and Its Control: What Did We Learn during the Last Decade? *Plants* 2020, 9, 735.
28. Ostos, E.; Garcia-Lopez, M.T.; Porras, R.; Lopez-Escudero, F.J.; Trapero-Casas, A.; Michailides, T.J.; Moral, J. Effect of cultivar resistance and soil management on spatial–temporal development of Verticillium wilt of olive: A long-term study. *Front. Plant Sci.* 2020, 11, 1595.
29. Saponari, M.; Boscia, D.; Altamura, G.; Loconsole, G.; Zicca, S.; D'Attoma, G.; Morelli, M.; Palmisano, F.; Saponari, A.; Tavano, D.; et al. Isolation and pathogenicity of *Xylella fastidiosa* associated to the olive quick decline syndrome in southern Italy. *Sci. Rep.* 2017, 7, 17723.
30. Bucci, E.M. *Xylella fastidiosa*, a new plant pathogen that threatens global farming: Ecology, molecular biology, search for remedies. *Biochem. Biophys. Res. Commun.* 2018, 502, 173–182.
31. Schaad, N.W.; Postnikova, E.; Lacy, G.; Fatmi, M.; Chang, C.-J. *Xylella fastidiosa* subspecies: *X. fastidiosa* subsp. *piercei*, subsp. nov., *X. fastidiosa* subsp. *multiplex* subsp. nov., and *X. fastidiosa* subsp. *pauca* subsp. nov. *Syst. Appl. Microbiol.* 2004, 27, 763.

32. EFSA. Effectiveness of in planta control measures for *Xylella fastidiosa*. EFSA J. 2019, 17, e05666.
33. Di Serio, F.; Bodino, N.; Cavalieri, V.; Demichelis, S.; Di Carolo, M.; Dongiovanni, C.; Fumarola, G.; Gilioli, G.; Guerrieri, E.; Picciotti, U.; et al. Collection of data and information on biology and control of vectors of *Xylella fastidiosa*. EFSA Support. Publ. 2019, 16, 1628E.
34. Morelli, M.; García-Madero, J.M.; Jos, Á.; Saldarelli, P.; Dongiovanni, C.; Kovacova, M.; Saponari, M.; Baños Arjona, A.; Hackl, E.; Webb, S.; et al. *Xylella fastidiosa* in Olive: A Review of Control Attempts and Current Management. Microorganisms 2021, 9, 1771.
35. Landa, B.B.; Saponari, M.; Feitosa-Junior, O.R.; Giampetruzzi, A.; Vieira, F.J.D.; Mor, E.; Robatzek, S. *Xylella fastidiosa*'s relationships: The bacterium, the host plants and the plant microbiome. New Phytol. 2022, 234, 1598–1605.
36. Doty, S.L. Functional importance of the plant microbiome: Implications for agriculture, forestry and bioenergy. Funct. Importance Plant Microbiome. Implic. Agric. For. Bioenergy 2017, 178, 1–111.
37. Rabiey, M.; Hailey, L.E.; Roy, S.R.; Grenz, K.; Al-Zadjali, M.A.S.; Barrett, G.A.; Jackson, R.W. Endophytes vs tree pathogens and pests: Can they be used as biological control agents to improve tree health? Eur. J. Plant Pathol. 2019, 155, 711–729.

Retrieved from <https://encyclopedia.pub/entry/history/show/94581>