

Research Application Summary

Rhizomicrobial Composition in Relation to Bacterial Wilt Outbreak

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Abstract

The rhizomicrobial composition of plants consists of various types of microbes, playing important roles in the growth and development of plants. The mechanism by which each microbe obtains energy and nutrients for its survival and reproduction is inter-connected, preventing the entry and colonization of pathogenic microbes. The type of microbe found around the plant rhizosphere is determined by the plant genotype, plant species, and the physical, chemical and biological properties of the soil. The chemical composition of the root exudates controls the type and kind of rhizomicrobials communities that will be present in the soil, which ranges from beneficial to pathogenic. Research has shown that beneficial microbes together with harmful ones are attracted to the plant rhizosphere by the help of root exudates. The beneficial microbiota protects the plant from being colonized by pathogenic microbiota whereas the pathogenic microbiota causes disease to the plants. Therefore, the types of microbiomes found in the rhizosphere of tomato plants and the mechanisms by which they suppress disease outbreak in a particular bacterial wilt in the tomato plants are discussed in this paper.

Key words: Bacterial wilt, disease suppression, soil microbiota

Résumé

La composition rhizo-microbienne des plantes est constituée de divers types de microbes, jouant des rôles importants dans la croissance et le développement des plantes. Le mécanisme par lequel chaque microbe obtient de l'énergie et des nutriments pour sa survie et sa reproduction est interconnecté, empêchant l'entrée et la colonisation de microbes pathogènes. Le type de microbes présents autour de la rhizosphère des plantes est déterminé par le génotype et l'espèce de la plante, ainsi que par les propriétés physiques, chimiques et biologiques du sol. La composition chimique des exsudats racinaires contrôle le type et la nature des communautés rhizo-microbiennes présentes dans le sol, allant des microbes bénéfiques aux microbes pathogènes. Des recherches ont montré que les microbes bénéfiques aussi bien que les microbes nuisibles sont attirés dans la rhizosphère des plantes par les exsudats racinaires. La flore microbienne bénéfique protège la plante contre la colonisation par la flore microbienne pathogène, tandis que celle provoque des maladies chez les plantes. Par conséquent, les types de microbiomes trouvés dans la rhizosphère des plants de tomates et les mécanismes par lesquels ils empêchent l'apparition de la maladie dans un flétrissement bactérien particulier dans les plants de tomates sont discutés dans cet article.

Mots clés : Flétrissement bactérien, suppression de la maladie, microbiote du sol

Introduction

Plants have developed a relationship with a vast population of different microbes around them in the soil, which interact together to improve the plant health. This interaction among different microbes allow for a healthy environment around the plant roots (also known as the rhizosphere), which prevents disease causing micro-organisms from colonizing the rhizosphere. The type of microbes found around the plant rhizosphere is dictated by the plant genotype, the species, physical, chemical and biological properties of the soil (Compant *et al.*, 2019). The soil microbiota is specific to the plant (Durán *et al.*, 2018), in that the root exudates' chemical composition defines the type and kind of microbes that will be found around the plant rhizosphere and in turn the exudates released by the plant roots is determined by the type and kind of microbes around the plant rhizosphere (Prashar *et al.*, 2014). This type of interaction between plant and rhizomicrobials is the primary mechanism for disease suppression through intervention thereby preventing disease outbreak (Durán *et al.*, 2018). The microbial community are found in the endosphere, phyllosphere and the rhizosphere (Lemanceau *et al.*, 2017), and as such are termed as the endophytes, epiphytes and rhizobiomes. These are found within, on the surface and around the plant, respectively. The endophytes in particular have been instrumental in the biocontrol of phytopathogens (Sharma *et al.*, 2017), and comprises of bacteria, fungi and archaea; bacteria and fungi being the most outstanding. These endophytic bacteria and fungi have a symbiotic relationship with the plants in which they inhabit by offering protection to the host plant while receiving nourishment from them (Omomowo and Babalola, 2019).

Ralstonia solanacearum is the causative agent of bacterial wilt disease in tomatoes leading to great losses in its cultivation on an economic scale (Mansfield *et al.*, 2012). It causes disease symptoms on more than 200 plant species in 54 different families. It gains access into the plant through the roots and takes over its vascular system, causing disease (Genin and Denny, 2012). The disease has posed a challenge in its control over the years due to the nature of the pathogen to survive in the soil for many years even in the absence of a suitable host (van Elsas *et al.*, 2012). The control of bacterial wilt in tomato has posed a challenge in the cultivation of tomato (*Solanum lycopersicon*) as it serves as a suitable host for the pathogen, being spread mostly through cultural practices and irrigation water (splashing). Research has suggested that the composition of soil microbes contributes to the development of plant resistance against pathogens. This review will highlight how suppressive soils and the rhizomicrobials can reduce the incidence of bacterial wilt in crops.

Suppressive soil. Soil is a network of diverse microbial communities interacting together (Philippot *et al.*, 2013). According to recent study results, the development of soils that are capable of suppressing disease in the event of an outbreak is because of the joining together of beneficial microbes; these are the epiphytes, endophytes and rhizobiomes around the rhizosphere of the plant (Berendsen *et al.*, 2018). These microbes improve the plant's resistance against pathogen attack through mutualistic associations by prompting the systemic resistance of the plant, increasing the hormonal level of the plant, synthesis of lytic enzymes and the generation of antibiotics and volatile compounds that restrain the attack of pathogens (Hopkins *et al.*, 2017). The rhizobiome serves important roles to the plant most of them being biochemical through nutrient provision and volatile organic compound secretion. An example is the enzyme 1-aminocyclopropane-1-carboxylate (ACC) deaminase (Rascovan *et al.*, 2016), released by strains of *Pseudomonas* spp, *Bacillus* spp. and *Arthrobacter* spp. Its function in the plant is that it lowers the level of stress

hormone (ethylene) thereby increasing the tolerance to stress. Another role of rhizobiome is that they are involved in the production of plant growth regulators (Singh *et al.*, 2020). Plant rhizobiome in most cases is dominated by individuals of four phyla of bacteria consisting of Proteobacteria, firmicutes, bacteroidetes and actinobacteria, amidst them, proteobacteria being the most prominent.

In other instances, some beneficial microbes are inoculated into soils to either improve resistance against *Ralstonia solanacearum* or enhance the diversification of microbes found in the soil (Hu *et al.*, 2016). In the case of plants, they attract beneficial microbes to prevent attack by pathogens. This technique is termed as disease suppression and is carried out by microbial communities that are ever present in the soil. A specific example is the phytophthora blight, a soil borne disease that colonizes sweet pepper as its host, is controlled by beneficial bacteria namely *Serratia* sp., *Bacillus cereus* and *Bacillus subtilis*, indirectly through increasing the population of antagonistic micro-organisms in the rhizosphere such as Comamonas, pontibacter, sporichthya, Burkholderia, Achromobacter and Ramlibacter, that significantly reduce the quantity of disease causing micro-organisms in the soil and improve the nutrient quantities present in the soil that are critical for plant health and growth such as the total nitrogen, organic carbon, phosphorus, potassium and ammonia nitrogen (Guo *et al.*, 2012).

Suppression of soil diseases by rhizomicrobials. Soils that are capable of suppressing disease are remarkable ecosystems. Recent research has supported findings on soils that are capable of supporting various pathogenic micro-organisms responsible for causing fusarium wilt in susceptible host plants, potato common scab (Rosenzweig *et al.*, 2012), damping-off disease (Hunter *et al.*, 2006), sugar beet wilt, and bacterial wilt. Additional research has supported the fact that the assortment of microbial community is important for perpetuating the soils' ability to subdue disease which in turn affects the conquest of pathogenic species (van Elsas *et al.*, 2012; Kwak *et al.*, 2018).

Results from a study conducted to assess the microbial composition and their interaction between soils with resistance and those showing no resistance revealed an increase in the heterogeneity of species found around the rhizosphere of resistant as compared to the soils that did not exhibit resistance. This includes microbes from the main genera *Bacillus*, *Roseiflexus*, among others whose population decreased as bacterial wilt disease increased, with the richness of *Bacillus* sp. in resistant soils being higher than that of the non-resistant soils. Increased heterogeneity in the microbial populations around the rhizosphere causes increased interplay amongst the microbials in the resistant soils and thus the formation of a more solid system that deters disease invasion and proliferation. Results from several studies have supported the fact that *Bacillus* sp. play important roles that are beneficial to plants, such as production of a broad assembly of bioactive molecules that impedes attacks by pathogens. The bioactive molecules includes surfactin, iturin and fengycin that have an antagonistic effect against *Ralstonia solanacearum* (Tahir *et al.*, 2017), *Rhizoctonia solani*, *Pythium aphanidermatum*, and *Podosphaera fusca* (Romero *et al.*, 2007).

Diversity of rhizomicrobials. The microbial community in the soil are varied, stretching across numerous types of microorganisms including bacteria, viruses, actinomycetes, fungi, algae, protozoa and nematodes (Geisen *et al.*, 2019), with bacteria leading in number, then actinomycetes, fungi, soil algae and protozoa, respectively in a descending manner, which play

an equally important role in the general health of the plant. Soils that exhibit resistance against disease proliferation have been shown to consist of microbes such as *Blastococcus*, *Agromyces*, *Thermoleophilum*, *Gemmatimonas*, *Trichoderma* and *Aspergillus*, where species of Actinobacteria (*Agromyces*, *Thermoleophilum* and *Blastococcus*) are involved in the production of antibiotics that deter pathogen activities in the soil (Zeng *et al.*, 2016). Others like *Trichoderma* spp. are involved in the production of antibiotics, activate systemic resistance in plants, facilitate uptake of nutrients among other functions beneficial to plants. For example, *T. harzianum* produces chemical compounds such as phosphatase that scavenges, mobilizes and acquires phosphate to enhance soil fertility and foster plant growth (Souza *et al.*, 2016). Therefore, the combination of different micro-organisms playing different roles in the rhizosphere improves disease suppressiveness.

Conclusion

Maintenance of healthy soil is crucial in ensuring growth of healthy plants as healthy soils ensure availability of essential nutrients needed for plant growth and development and the resistance of such plants to diseases, being soil borne and foliar. The resistance of plants to pathogen attack can be direct or indirect. Direct resistance occurs when the plant is able to suppress disease outbreak due to its vigorous growth and health while indirect resistance occurs when the beneficial microbes proliferate due to well-maintained soils and outcompete the harmful microbes thereby suppressing their activity. Healthy soils can be maintained or achieved by adding beneficial microbes to improve on the microbial diversity or through addition of specific treatments such as biochar with the aim of improving the soil health and consequently its quality as it increases the abundance of beneficial micro-organisms.

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References

- Berendsen, R. L., Vismans, G., Yu, K., Song, Y., de Jonge, R., Burgman, W. P., Burmølle, M., Herschend, J., Bakker, P. A. H. M. and Pieterse, C. M. J. 2018. Disease-induced assemblage of a plant-beneficial bacterial consortium. *The ISME Journal* 12 (6): 1496–1507. <https://doi.org/10.1038/s41396-018-0093-1>
- Compant, S., Samad, A., Faist, H. and Sessitsch, A. 2019. A review on the plant microbiome: Ecology, functions, and emerging trends in microbial application. *Journal of Advanced Research* 19: 29–37. <https://doi.org/10.1016/j.jare.2019.03.004>
- Durán, P., Tortella, G., Viscardi, S., Barra, P. J., Carrión, V. J., Mora, M. de la L. and Pozo, M. J. 2018. Microbial community composition in take-all suppressive soils. *Frontiers in Microbiology* 9. <https://doi.org/10.3389/fmicb.2018.02198>
- Geisen, S., Briones, M. J. I., Gan, H., Behan-Pelletier, V. M., Friman, V.-P., de Groot, G. A., Hannula, S. E., Lindo, Z., Philippot, L., Tiunov, A. V. and Wall, D. H. 2019. A methodological framework to embrace soil biodiversity. *Soil Biology and Biochemistry* 136: 107536. <https://doi.org/10.1016/j.soilbio.2019.107536>
- Genin, S. and Denny, T. P. 2012. Pathogenomics of the *Ralstonia solanacearum* Species

- Complex. *Annual Review of Phytopathology* 50 (1): 67–89. <https://doi.org/10.1146/annurev-phyto-081211-173000>
- Guo, W., Yin, H., Ye, Z., Zhao, X., Yuan, J. and Du, Y. 2012. A comparison study on the interactions of two oligosaccharides with tobacco cells by time-resolved fluorometric method. *Carbohydrate Polymers* 90 (1): 491–495. <https://doi.org/10.1016/j.carbpol.2012.05.070>
- Hopkins, S. R., Wojdak, J. M. and Belden, L. K. 2017. Defensive symbionts mediate host–parasite interactions at multiple scales. *Trends in Parasitology* 33 (1): 53–64. <https://doi.org/10.1016/j.pt.2016.10.003>
- Hu, J., Wei, Z., Friman, V.-P., Gu, S., Wang, X., Eisenhauer, N., Yang, T., Ma, J., Shen, Q., Xu, Y. and Jousset, A. 2016. Probiotic diversity enhances rhizosphere microbiome function and plant disease suppression. *MBio* 7 (6): e01790-16, [/mbio/7/6/e01790-16.atom](https://doi.org/10.1128/mBio.01790-16). <https://doi.org/10.1128/mBio.01790-16>
- Hunter, P. J., Petch, G. M., Calvo-Bado, L. A., Pettitt, T. R., Parsons, N. R., Morgan, J. A. W., and Whipps, J. M. 2006. Differences in microbial activity and microbial populations of peat associated with suppression of damping-off disease caused by *Pythium sylvaticum*. *Applied and Environmental Microbiology* 72 (10): 6452–6460. <https://doi.org/10.1128/AEM.00313-06>
- Kwak, M.-J., Kong, H. G., Choi, K., Kwon, S.-K., Song, J. Y., Lee, J., Lee, P. A., Choi, S. Y., Seo, M., Lee, H. J., Jung, E. J., Park, H., Roy, N., Kim, H., Lee, M. M., Rubin, E. M., Lee, S.-W. and Kim, J. F. 2018. Rhizosphere microbiome structure alters to enable wilt resistance in tomato. *Nature Biotechnology* 36 (11): 1100–1109. <https://doi.org/10.1038/nbt.4232>
- Lemanceau, P., Blouin, M., Muller, D. and Moënne-Loccoz, Y. 2017. Let the Core Microbiota Be Functional. *Trends in Plant Science* 22 (7): 583–595. <https://doi.org/10.1016/j.tplants.2017.04.008>
- Mansfield, J., Genin, S., Magori, S., Citovsky, V., Sriariyanum, M., Ronald, P., Dow, M., Verdier, V., Beer, S. V., Machado, M. A., Toth, I., Salmond, G. and Foster, G. D. 2012. Top 10 plant pathogenic bacteria in molecular plant pathology. *Molecular Plant Pathology* 13 (6): 614–629. <https://doi.org/10.1111/j.1364-3703.2012.00804.x>
- Olanrewaju, O. S., Ayangbenro, A. S., Glick, B. R. and Babalola, O. O. 2019. Plant health: Feedback effect of root exudates-rhizobiome interactions. *Applied Microbiology and Biotechnology*, 103 (3): 1155–1166. <https://doi.org/10.1007/s00253-018-9556-6>
- Omomowo, B. and Babalola, O. 2019. Bacterial and Fungal Endophytes: Tiny giants with immense beneficial potential for plant growth and sustainable agricultural productivity. *Microorganisms* 7 (11): 1-15. <https://doi.org/10.3390/microorganisms7110481>
- Philippot, L., Raaijmakers, J. M., Lemanceau, P. and van der Putten, W. H. 2013. Going back to the roots: The microbial ecology of the rhizosphere. *Nature Reviews. Microbiology* 11 (11): 789–799. <https://doi.org/10.1038/nrmicro3109>
- Prashar, P., Kapoor, N. and Sachdeva, S. 2014. Rhizosphere: Its structure, bacterial diversity and significance. *Reviews in Environmental Science and Bio/Technology* 13 (1): 63–77. <https://doi.org/10.1007/s11157-013-9317-z>
- Romero, D., de Vicente, A., Rakotoaly, R. H., Dufour, S. E., Veening, J.-W., Arrebola, E., Cazorla, F. M., Kuipers, O. P., Paquot, M. and Pérez-García, A. 2007. The iturin and fengycin families of lipopeptides are key factors in antagonism of *Bacillus subtilis* toward *Podosphaera fusca*. *Molecular Plant-Microbe Interactions: MPMI* 20 (4): 430–440. <https://doi.org/10.1094/MPMI-20-4-0430>
- Rosenzweig, N., Tiedje, J., Quensen, J., Meng, Q. and Hao, J. 2012. Microbial communities

- associated with potato common scab-suppressive soil determined by pyrosequencing analyses. *Plant Disease* 96: 718–725. <https://doi.org/10.1094/PDIS-07-11-0571>
- Sharma, I. P., Chandra, S., Kumar, N. and Chandra, D. 2017. PGPR: Heart of Soil and Their Role in Soil Fertility. pp. 51–67. In: Meena, V. S., Mishra, P. K., Bisht, J. K. and Pattanayak, A. (Eds.), *Agriculturally important microbes for sustainable agriculture: Volume I: Plant-soil-microbe nexus*. Springer. https://doi.org/10.1007/978-981-10-5589-8_3
- Singh, B. P., Singh, G., Kumar, K., Nayak, S. C. and Srinivasa, N. (Eds.). 2020. *Management of fungal pathogens in pulses: Current status and future challenges*. Springer International Publishing. <https://doi.org/10.1007/978-3-030-35947-8>
- Singh, D., Raina, T. K., Kumar, A., Singh, J. and Prasad, R. 2019. Plant microbiome: A reservoir of novel genes and metabolites. *Plant Gene* 18: 100177. <https://doi.org/10.1016/j.plgene.2019.100177>
- Souza, A. A., Leitão, V. O., Ramada, M. H., Mehdad, A., Georg, R. de C., Ulhôa, C. J. and Freitas, S. M. de. 2016. *Trichoderma harzianum* produces a new thermally stable acid phosphatase, with potential for biotechnological application. *PloS one* 11(3): e0150455. <https://doi.org/10.1371/journal.pone.0150455>
- Tahir, H. A. S., Gu, Q., Wu, H., Niu, Y., Huo, R. and Gao, X. 2017. *Bacillus volatiles* adversely affect the physiology and ultra-structure of *Ralstonia solanacearum* and induce systemic resistance in tobacco against bacterial wilt. *Scientific Reports* 7. <https://doi.org/10.1038/srep40481>
- Tian, T., Wu, X.-G., Duan, H.-M. and Zhang, L.-Q. 2010. The resistance-nodulation-division efflux pump EmhABC influences the production of 2,4-diacetylphloroglucinol in *Pseudomonas fluorescens* 2P24. *Microbiology* 156 (1): 39-48. <https://doi.org/10.1099/mic.0.031161-0>
- van Elsas, J. D., Chiurazzi, M., Mallon, C. A., Elhottova, D., Kristufek, V. and Salles, J. F. 2012. Microbial diversity determines the invasion of soil by a bacterial pathogen. *Proceedings of the National Academy of Sciences of the United States of America* 109 (4): 1159–1164. <https://doi.org/10.1073/pnas.1109326109>
- Zeng, Y., Baumbach, J., Barbosa, E. G. V., Azevedo, V., Zhang, C. and Koblí ek, M. 2016. Metagenomic evidence for the presence of phototrophic Gemmatimonadetes bacteria in diverse environments. *Environmental Microbiology Reports* 8 (1): 139–149. <https://doi.org/10.1111/1758-2229.12363>