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Changing of a Single Core Gene, tssM, of Type VI Secretion System of Xanthomonas perforans Influences Virulence, Epiphytic Survival, and Transmission during Pathogenesis on Tomato

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Editorial

In eukaryotes, protein phosphatases play a vital role in the control of different cellular activities. Colletotrichum gloeosporioides, an ascomycete, is the cause of anthracnose disease in a number of key crops and plants. CgPPZ1, a protein phosphate gene and a homolog of yeast PPZ1, was discovered in C. gloeosporioides in this investigation. CgPpz1 was found to be critical for vegetative growth and asexual development, conidial germination, and plant infection after targeted gene deletion. CgPpz1 was found to be located in the cytoplasm during cytological tests. Osmotic stresses, cell wall stressors, and oxidative stressors were all hypersensitive in the Cgppz1 mutant. Our findings suggest that CgPpz1 is involved in the fungal development and pathogenicity of C. gloeosporioides, as well as the numerous stress responses that occur [1].

Xanthomonas perforans is a seedborne hemibiotrophic pathogen that infects the tomato phyllosphere. While most investigations on the molecular basis of pathogenesis have focused on apoplastic expansion, variables relevant during asymptomatic colonisation in the early stages of disease development are little known. The tssM gene of the type VI secretion system cluster i3* (T6SS-i3*) plays an important role during initial asymptomatic epiphytic colonisation at various phases during the pathogen's life cycle, according to this study. When dip inoculating 4- to 5-week-old tomato plants, a mutation in a key gene, tssM of T6SS-i3*, conferred stronger pathogen aggressiveness, as seen by higher overall disease severity, higher in planta growth, and shorter latent infection period compared to the wild-type [2]. The role of tssM in aggressiveness was demonstrated during vertical transmission from seed to seedling, with wild-type seedlings demonstrating lower disease severity and in planta populations on seedlings than mutants. When examined in an experimental system that mimicked transplant house high-humidity conditions, the presence of functioning TssM resulted in enhanced epiphytic fitness as well as greater pathogen dissemination potential. We discovered that one mechanism by which TssM promotes epiphytic fitness is through increased osmotolerance. These findings suggest that a functional TssM plays a significant role in the pathogen's ability to gain an ecological advantage. TssM prolongs the hemibiotrophic pathogen's relationship with the host, reducing disease severity while allowing successful diffusion [3].

The pears (Pyrus spp.) are one of China's most popular fruits, but their supply is under threat from deadly illnesses. In this paper, we describe two cases of stem canker and twig dieback disease on pear plants in Guangxi and Jiangsu provinces, which resulted in the death of pear seedlings (about 10% of total plants). The fungus Neofusicoccum parvum was identified as the disease's causal agent in these two locations using a combination of morphological and molecular diagnostics, as well as a pathogenicity test [4]. The isolates were classified into two clades: the CY-2 isolate and the other four isolates, ZL-4, BM-9, BM-10, and BM-12, may have split into two N. parvum groupings. For further examination, two representative isolates (CY-2 and ZL-4) were chosen. The best temperature for in vitro infection on pear trees of these two isolates was around 25°C, according to our findings [5]. In vitro, both CY-2 and ZL-4 could infect many sand pear cultivars as well as other horticultural plants, however CY-2 was more virulent on certain pear varieties, including Nanyue, Lvyun, Qiushui, and Ningmenghuang. Additionally, the efficacy of fungicides against these two isolates was assessed, with carbendazim and flusilazole proving to be the most efficient fungicides in preventing the growth of these fungal infections. These findings, taken together, characterise the N. parvum species and offer viable solutions for the disease's future management [6].

Physiological saline solution was used to wash the germs away from the surface of the leaves or cones. The extract was used in different dilutions of a bacterial, fungal, and yeast culture medium. Sequential sprouting on agar plates yielded pure microorganism cultures. The Biolog microbiological ID system was used to identify all of the bacteria species (Hayward, CA) [7]. There are now 2,700 bacterium types in the database. Microscopic observations and the physical appearance of the colonies on the dishes were used to identify the fungi on a generic level. The fact that they have been identified is simply a hint. Bacillus species (megatherium, idriensis, indicus, endophyticus, licheniformis) and Pantotea species (aglomerans, dispersa) were the most commonly identified in the bacterial population in both years [8]. Fungi have a lot more variation, which is probably due to the diametrically opposite weather conditions in 2015 and 2016. In both years, just two fungi from the genera Penicillium and Rhizopus were found out of a total of eight. Yeasts were only found on hop leaves on rare occasions. Bacteria were discovered in both dried hops and hop pellets. This proves that post-harvest hops processing, kiln drying, and pelletization are not sterilising methods [9].

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Conflict of Interest

No potential conflicts of interest relevant to this article were reported.

References

1. Dulla G (2005) A closer look at Pseudomonas syringae as a leaf colonist. Asm News 71:469-475.
2. Borruso L, Bani A, Ventura M, Panzacchi P, Antonelli L, et al. (2017) Do Aerial Nitrogen Depositions Affect Fungal and Bacterial Communities of Oak Leaves? Front. Microbiol 35.
3. Zhao Y, Liu C, Qian G, Yin F, Zhou Y, et al. (2012) Functions of the RpfCxoc/RpfGxoc two-component system of Bacterial leaf spot oryzae. Acta Microbiol 52:449-456.
4. Larena I, Melgarejo P (2009) Detection and quantification of biocontrol agents. Detection and quantification of biocontrol agents 43:359-362.
5. Enya J (2015) Study on the composition of microbial flora on tomato leaves and screening of biological control agents. J Gen Plant Pathol 81:476-477.
6. Li L, Xiao B, Huang X, Tang D (2015) Identification of a small RNA associated with HR response in Brassicaceae black rot fungus. Genomics Appl Biol 7:1443-1450.
7. An SQ, Tang JL, Dow JM (2017) Probing the role of cyclic di-GMP signaling systems in disease using Chinese radish. In c-di-GMP Signaling 205-212.
8. Abdel-Gawad KM, Abdel-Mallek AY, Hussein NA, Abdel-Rahim IR(2021) Diversity of mycobiota associated with onion *(Allium cepa L.)* cultivated in Assiut, with a newly recorded fungal species to Egypt. J Microbiol Biotechnol Food Sci 2021: 1145-1171.
9. Liu X, Zhang A, Huang Y, Liu Ping, Han Yu, et al. (2020) Study on the paar gene function of Vibrio var. Disease Surveillance 35:294-300.