

Nowadays, viticulture worldwide is confronted with heavy economic losses caused by Grapevine Trunk Diseases (GTDs). Fungi have been described as the main cause of grapevine trunk diseases. Among these fungi, *Fomitiporia mediterranea*, is considered as the main white wood rotting Basidiomycota associated with GTDs. Bacteria diversity is very high in the wood of grapevine but little information is available about their functions and their interactions with fungi inhabiting the wood. We therefore isolated bacterial strains from different anatomical parts (i.e. trunk and cordon) and different type of tissues (i.e. necrotic or not) of GTD-symptomatic grapevines. Two hundred thirty seven bacterial strains were isolated from grapevine-wood samples and, based on their 16S rRNA genes, assigned to bacterial species, OTUs belonging to *Xanthomonadaceae* were the dominant taxonomic groups, at the family level. Fifty nine bacterial strains representing the various OTUs were screened for their ability to degrade the three main components of wood, i.e. cellulose, hemicellulose and lignin, by using different selective media. Their ability to inhibit *F. mediterranea* was also studied. Based on a microcosm experiment, the hypothesis that some bacterial strains inhabiting wood interact with *F. mediterranea* to promote grapevine wood degradation was tested. *Results demonstrated*, for the first time, a synergetic interaction between *F. mediterranea* and the two bacterial strains: *Chryseobacterium* sp. and *Paenibacillus* sp., to degrade the grapevine-wood structures. The whole-genomes of the 2 bacterial strains were sequenced because of their interest in wood degradation. *After wood samples inoculations with F. mediterranea* alone, the bacteria alone, and *F. mediterranea* plus *Paenibacillus* sp., analysis of the wood-degradations that occurred in the cellulose, hemicelluloses, and lignin, were investigated by Solid-State Nuclear magnetic resonance (NMR) method. The contribution of bacteria and fungi alone, or in synergy, in wood degradations will be discussed with regards to GTDs.

The control and control basis of grapevine trunk diseases in China. JIYE YAN, WEI ZHANG, QIKAI XING, JUNBO PENG, MEI LIU, YING ZHOU and XINGHONG LI. *Beijing Key Laboratory for Environmental Friendly Management on Pests of North China Fruits, Beijing Academy of Agriculture and Forestry Sciences, Beijing 100097, China. E-mail: jiyeyan@vip.163.com*

Grapevine trunk diseases (GTDs) are widely spread in almost all grapevine cultivating countries, causing serious economic losses. At present, six species of *Botryosphaeriaceae*, including *Botryosphaeria dothidea*, *Lasiodip-*

lodia theobromae, *Neofusicoccum parvum*, *Diplodia seriata*, *L. pseudotheobromae* and *N. mangiferae*, were proved to be associated with GTDs in China. Recent studies have established a correlation between environmental factors and GTDs occurrence; however, less is known about the factors that can trigger these diseases. Therefore, de novo sequencing of *L. theobromae*, one of the most prevalent species in China, was conducted and resequencing was done for *B. dothidea* and *N. parvum* in this study. Our data showed that gene families associated with cell wall degradation, nutrient uptake, secondary metabolism and membrane transport, which contribute to adaptations for wood degradation were expanded in botryosphaeriaceous genomes. Further, transcriptome analysis was performed and the results revealed that genes involved in carbohydrate catabolism, pectin, starch and sucrose metabolism, and pentose and glucuronate inter-conversion were induced during the infection process of *L. theobromae*. Furthermore, genes involved in carbohydrate-binding modules and the lysine motif domain and glycoyl hydrolase gene families were found that can be induced by high temperature. Among these genes, over-expression of two selected putative lignocellulase genes led to increased virulence in the transformants. These results demonstrate the importance of high temperatures in the opportunistic infections of *Botryosphaeriaceae* species. The current study also presents a set of *Botryosphaeriaceae* specific effectors related to pathogenicity. In conclusion, these findings significantly improve our understanding of the determinants of pathogenicity or virulence in *Botryosphaeriaceae* species and provide new insights for developing new strategies to control them.

***Lasiodiplodia gilanensis* used a model for understanding the pathogenicity of Botryosphaeriaceae.** EDELWEISS AIRAM RANGEL-MONTOYA¹, MARCOS PAOLINELLI^{2,3} and RUFINA HERNANDEZ-MARTINEZ¹. ¹*Centro de Investigación Científica y de Educación Superior de Ensenada (CICESE), Carretera Ensenada-Tijuana, 3918, Zona Playitas, 22860, Ensenada, B.C. México.* ²*Instituto Nacional de Tecnología Agropecuaria (INTA), Estación Experimental Agropecuaria de Mendoza, San Martín 3853 (5507), Luján de Cuyo, Mendoza, Argentina.* ³*Consejo Nacional de Investigaciones Científicas y Técnicas (CONICET), Godoy Cruz 2290 (C1425FQB) CABA, Buenos Aires, Argentina. E-mail: erangel@cicese.edu.mx*

Members of the *Botryosphaeriaceae* are one of the primary fungal pathogens causing trunk diseases on grapevines. Among them, *Lasiodiplodia* spp. are reported as

the most aggressive, causing degenerative diseases, die-back, and plant death. To understand the pathogenicity of the Botryosphaeriaceae we are using *Lasiodiplodia gilanensis* as a model. A transcriptional study suggested that this fungus is capable of using the phenylpropanoid precursors and salicylic acid to avoid the host defense response of the plant. Several genes encoding enzymes involved in different melanin synthesis pathways, 3,4-dihydroxyphenylalanine (DOPA)-melanin, 1,8-dihydroxynaphthalene (DHN)-melanin, and pyromelanin were identified, and their production evaluated, concluding that the fungus use different types of melanin to overcome environmental stress. An *in silico* analysis shows the presence of those genes in all the available genomes of Botryosphaeriaceae in GeneBank, evidencing the importance of the melanin in this family. *Lasiodiplodia gilanensis* also produces siderophores of catechol of hydroxamate-type, as well as naturally esterified fatty acids; those compound might have a role in plant growth regulation. A plethora of hydrolytic enzymes is also produced, including xylanases, ligninases, cellulases, pectinases, cutinases, and hemicelluloses. An organic compound also produced is oxalic acid, reported as a pathogenicity factor in other fungi; its role in *L. gilanensis* is under evaluation. Microscopical observations showed that the fungus uses the starch deposited in the ray cells as carbon source, induces the production of suberin and phenolic compounds, and colonizes the vascular cambium, ray parenchyma, and the vascular bundles. In summary, these studies extend our understanding of the pathogenicity of a widely distributed pathogenic fungus.

Screening of biocontrol agents against black-foot and Petri diseases under field conditions.

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Experimentally, most of the studies on biocontrol agents (BCAs) have been applied so far in vines under con-

trolled conditions and little information is still available about the effectiveness of this strategy under field conditions. In this study, two field experiments were established to evaluate the effect of five BCAs (*Streptomyces* sp. E1+R4, *Pythium oligandrum* Po37, and commercial products containing *Trichoderma atroviride* SC1, *T. koningii* and *Pseudomonas fluorescens*+*Bacillus atrophaeus*) root treatments on black-foot and Petri disease fungal infection in one-year-old dormant grafted plants prior to dispatch. In April 2017, vines were hot-water treated at 53°C for 30 min and roots were immediately soaked in BCAs suspensions for 24 h. Two additional applications of BCAs were applied by drip irrigation in May 2017 and 2018. In each field, 50% of the vines were evaluated in February 2018 and the remaining 50% in February 2019. The fungal incidence and severity in roots and at the base of the rootstock in all vines and the total root mass and shoot weight in 3-year-old vines were determined. The effectiveness of some BCAs in reducing the incidence and severity of both diseases was dependent on the plant zone analysed and the plant age. *Streptomyces* sp. E1+R4, *Pythium oligandrum* Po37 and *Trichoderma atroviride* SC1 were able to reduce significantly fungal incidence and severity in specific scenarios. BCA treatments had no effect on the shoot weight, and root weight was significantly lower in all BCA treatments with respect to the control. This study represents the first approach to evaluate the effectiveness of different antagonistic microorganisms (bacteria, fungi and oomycete) to control black-foot and Petri disease under field conditions. Investigation of BCA able to prevent or at least reduce the development of GTDs should be considered a research priority based on the restriction and difficulties that chemicals are facing in most countries around the world.

Identification and characterization of potential biological control agents for the management of grapevine trunk diseases in British Columbia.

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Species within the *Trichoderma* genus are widely used biocontrol agents (BCA) capable of protecting plants by actively antagonizing plant pathogenic fungi, including grapevine trunk disease (GTD) pathogens, through a wide array of mechanisms. Despite this, no BCA prod-