

according to winter rain patterns. In Panquehue location, spore release was observed during spring, while in fall-winter release was null or very low. The Botryosphaeriaceae species identified were *Diplodia seriata*, *Dothiorella* sp. and *Neofusicoccum* sp.

Genetic analysis of *Neofusicoccum parvum* and *N. luteum* isolates from nurseries and vineyards indicates different infection sources. R. BILLONES-BAAIJENS^{1,2,*}, J. BASKARATHEVAN^{1,3}, M.V. JASPERS¹, E.E. JONES¹, R.H. CRUICKSHANK¹ and H.J. RIDGWAY¹. ¹Faculty of Agriculture and Life Sciences, Lincoln University, Lincoln, New Zealand, 7647. ²National Wine and Grape Industry Centre (NWGIC), Charles Sturt University, Mckeown Drive, Wagga Wagga, NSW 2678 Australia. ³Plant Health and Environment Laboratory, Ministry for Primary Industries, PO Box 2095, Auckland 1140, New Zealand. *E-mail: rbaaijens@csu.edu.au

Surveys in 2007–08 showed that *Neofusicoccum parvum* and *N. luteum* are the two most prevalent and virulent species found in New Zealand vineyards and nurseries. However, *N. parvum* is more common in vineyards while *N. luteum* dominates in nurseries. Pathogenicity studies also showed that *N. parvum* was more aggressive and produced more severe, darker external lesions on canes than *N. luteum*. This study used genetic data to elucidate population origins of *N. parvum* and *N. luteum* from vineyards and nurseries. Vineyard and nursery isolates of *N. parvum* (n=79) and *N. luteum* (n=64) were genotyped using five universally-primed polymerase chain reaction (UP-PCR) primers. The five primers were able to amplify a total of 51 loci for *N. parvum* (66% polymorphic) and 54 loci for *N. luteum* (44% polymorphic). Phylogenetic analysis using parsimony (PAUP) showed that 92% and 78% of the *N. parvum* and *N. luteum* populations, respectively, were of unique genotypes. The neighbour joining trees showed that *N. parvum* from nurseries clustered separately from the vineyard isolates indicating the two populations were genetically distinct. This supported the initial hypothesis that the nursery infections by this aggressive species were intercepted during the grading process and, therefore, there was less movement of this species to the vineyards. In contrast, the *N. luteum* nursery and vineyard populations showed high genetic similarities. This indicated that the less distinct symptoms caused by this species are not graded out and, therefore, these infections can easily migrate from the nurseries to the vineyards.

Spore release patterns of Petri disease fungi in South African vineyards and rootstock mother blocks. M.A. BALOYI¹, L. MOSTERI² and F. HALLEEN^{1,2,*}. ¹Plant

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Phaeoconiella chlamydospora and *Phaeoacremonium* species have been associated with Petri disease in grape growing regions around the world. Spores of these pathogens are aerially dispersed and infect vines through susceptible wounds. However, no information is available about the time when these spores are released in South African vineyards. A study was undertaken in six vineyards and two rootstock mother blocks within the Western Cape Province, over two seasons, from May–November 2012 and March–November 2013. Microscope slides coated with petroleum jelly were affixed to five vines (or rootstock mother plants) in each vineyard. The slides were changed weekly, washed in 5ml sterile water and passed through 5- and 0.45-µm filters. The filters were backwashed and the suspensions plated onto PDA. Colonies resembling Petri disease pathogens were recorded, sub-cultured and identified on the basis of cultural characteristics (*Pa. chlamydospora*), and with species-specific primers or sequencing of the partial betatubulin and actin genes (*Phaeoacremonium* species). Spores of various species were detected within each of the vineyards and inoculum was available whenever pruning or sucker wounds were made in winter and spring. Over the two seasons 13 *Phaeoacremonium* species were detected, namely *Pm. aleophilum*, *Pm. alvesii*, *Pm. australiense*, *Pm. viticola*, *Pm. parasiticum*, *Pm. scolyti*, *Pm. sicilianum*, *Pm. subulatum*, *Pm. iranianum*, *Pm. inflatipes*, *Pm. venezuelense*, *Pm. prunicola* and *Pm. griseo-olivacea*, the latter two for the first time in South African vineyards. *Pa. chlamydospora* and *Pm. aleophilum* were the only species detected in all the vineyards. This study confirms the need for effective wound protection strategies.

Studying and modelling the summer development of esca foliar symptoms. P. LECOMTE¹, E. BRUEZ^{1,4}, J. GERBORE^{1,2}, P. PIERI³, L. GUERIN-DUBRANA^{1,4}, D. BARKA¹, Y. MEZIANI¹, C. BENETREAU¹, M. FERMAUD¹ and P. REY^{1,4}. ¹INRA, Université de Bordeaux, ISVV, UMR1065 SAVE, CS 20032, F-33882, Villenave d'Ornon cedex, France. ²BIOVITIS, F-15400 Saint Etienne de Chomeil. ³INRA, Université de Bordeaux, ISVV, UMR1287 EGFV, F-33140 Villenave d'Ornon, France. ⁴Université de Bordeaux, Bordeaux Sciences Agro, ISVV, UMR1065 SAVE, CS20032, F-33882, Villenave d'Ornon cedex, France. *E-mail: lecomte@bordeaux.inra.fr

A survey carried out in Aquitaine vineyards (France) from 2004 to 2006 showed that the occurrence of esca foliar symptoms had a similar progressive pattern in all the plots surveyed. This pattern corresponded to a