First report of *Neofusicoccum australe* associated with grapevine cordon dieback in Italy

BENEDETTO T. LINALDEDDU, BRUNO SCANU, ANGELA SCHIAFFINO and SALVATORICA SERRA

Dipartimento di Protezione delle Piante – sezione di Patologia vegetale, Università degli Studi di Sassari, Via E. De Nicola 9, 07100 Sassari, Italy

Summary. This is the first report of *Neofusicoccum australe* associated with grapevine dieback in Italy. Fungal isolates obtained from symptomatic tissues were identified on the basis of morphological and cultural characteristics as well as ITS sequence data. Pathogenicity was verified by inoculation of excised green grapevine shoots from cv. Cannonau under controlled laboratory conditions.

Key words: Botryosphaeriaceae, grapevine diseases, Sardinia.

Grapevine trunk diseases are a serious economic problem in Sardinian vineyards (Serra et al., 2008; Serra et al., 2010). These diseases are usually linked to infections by Eutypa lata and other fungal pathogens belonging to the genera Fomitiporia, Phaeomoniella and Phaeoacremonium (Mugnai et al., 1999, Mostert et al., 2006, Sosnowski et al., 2007). Moreover, several species of Botryosphaeriaceae have recently been recognized as important pathogens of grapevines worldwide (Phillips, 2002, Van Niekerk et al., 2006; Úrbez-Torres and Gubler, 2009, Pitt et al., 2010). Since only limited information about the occurrence and identity of the Botryosphaeriaceae associated with dieback and trunk diseases of grapevines in Sardinia is available, a field survey has been in progress since 2009.

Grapevines showing poor growth, defoliation, cankers and dieback (Figure 1a), were collected

Corresponding author: B.T. Linaldeddu

Fax: +39 079 229316 E-mail: ben@uniss.it from six vineyards (local varieties Cannonau and Vermentino) in northern Sardinia. Common internal wood symptoms were wedge-shaped necrotic sectors and/or brown streaks below the bark running from cordon to rootstock, 2-3 cm wide and a few millimetres thick (Figure 1b, c). Fragments measuring approximately 5 mm² were aseptically cut from the margin of infected tissues and cultured in Petri dishes containing malt extract agar (MEA, Oxoid Ltd, Basingstoke, UK). After incubation at room temperature for 5 days, fungal colonies resembling Botryosphaeriaceae were sub-cultured onto both potato dextrose agar (PDA, Oxoid Ltd) and malt extract yeast agar (MEYA, 2% malt extract, 0.2% yeast extract, 1.5% agar) and incubated at room temperature until differentiation of the reproductive structures. To induce sporulation, the fungal isolates were sub-cultured on PDA with sterile pine needles. Microscope slides of conidia and ascospores were prepared in lactophenol for morphological examination. Spore dimensions were recorded using an Optika™ Vision Pro version 2.7 digital camera connected to a Leitz Diaplan (Ernest Leitz, Wetzlar, Germany) microscope. The colony appearance of cultures growing







Figure 1. Grapevine disease symptoms associated with *Neofusicoccum australe*: cordon dieback (a); cordon wedge-shaped necrotic sector (b); trunk brown stripes under the bark (c).

on PDA at $25^{\circ}\mathrm{C}$ in the dark for 1 week was also recorded.

Fungal genomic DNA was extracted from 20 mg of mycelium following the CTAB method of Doyle and Doyle (1987). The entire Internal Transcribed Spacer region (ITS) of the rDNA, including the 5.8S gene, was amplified by polymerase chain reaction (PCR) using the primers ITS1 and ITS4 (White *et al.*, 1990). The amplifications were performed using a Hybaid PCR Express and the following protocol: 95°C for 3 min initial denaturation; 35 cycles of 95°C for 15 s, 55°C for 20 s, 72°C for 1 min; and 72°C for 5 min final extension. The PCR products were purified using the Eurogold

extraction kit (EuroClone S.p.A., Milano, Italy) following the manufacturer's instructions. Both strands were sequenced by the BMR Genomics DNA sequencing service (www.bmr-genomics.it). The nucleotide sequences were read and edited with FinchTV 1.4.0 (Geospiza, Inc.; http://www.geospiza.com/finchtv), aligned using ClustalW (www.ebi.ac.uk/clustalw/) and compared with sequences deposited in GenBank using the BLAST software (http://blast.ncbi.nlm.nih.gov).

A total of 113 Botryosphaeriaceous isolates were obtained from 15 of the plants sampled. Some isolates (44%) sporulated within one or two months. The conidial morphology and cultural fe-

atures of six isolates from one vineyard (cv. Cannonau) were in close agreement with the morphological description of both Neofusicoccum australe and N. luteum (Phillips et al., 2002, Slippers et al., 2004). On PDA at 25°C, these isolates developed a moderately dense mycelium, with a yellow pigment diffusing into the medium that became dark grey after 4 to 5 days. The conidia were hyaline, aseptate, fusiform with a truncate base and measured 18.7±2×6.8±0.9 µm, with a length/width ratio of 2.8±0.4 (mean±SD, n=100). Average conidial size was less than the 24.7×5.1 µm previously reported for N. australe by Slippers et al. (2004), but similar to the size reported for *N. australe* by Lazzizera et al. (2008). Conidial size was also similar to the size reported for *N. luteum* by Phillips *et al.* (2002). Only one isolate produced ascomata and conidiomata in the same Petri dish on PDA within 2 months. Ascospores were hyaline, aseptate, fusoid to ovoid, and measured $20.2\pm1.2\times8.5\pm0.7 \mu m$, with a length/width ratio of 2.4±0.2 (mean±SD, n=50).

The identity of this *Botryosphaeriaceae* species was defined by analysis of the ITS sequence of a representative isolate. BLAST searches in GenBank revealed that the sequence of this isolate differed by only 1 bp from the sequence of the ex-type iso-

late of *N. australe* (AY339262) and other isolates (e.g. EU856059, FJ157192). However, it had 100% similarity to sequences of other isolates identified as *N. australe* including isolates from olives in southern Italy (EF638770–EF638778) and pistachio in Spain (EU375516). Furthermore, the sequence of our isolate differed by three bp from the ex-type isolate (AY259091) and other isolates of *N. luteum*. Thus we consider that the isolate from Sardinian grapevines is *N. australe*.

The representative sequence of N. australe strain BOT48 obtained in this study was deposited in GenBank (accession number HQ011406). The strain BOT48 was stored in the culture collection of the Department of Plant Protection at the University of Sassari. Its pathogenicity was verified by inoculating it on five excised green grapevine shoots (30 cm in length) from cv. Cannonau. A mycelial plug (3 to 4 mm²) taken from the margin of an actively growing colony on PDA was placed in a shallow wound (~3 mm) made by a scalpel on the middle of each shoot. The inoculation point was covered with cotton wool soaked in sterile water and wrapped with Parafilm®. The inoculated shoots were placed in a beaker containing 200 mL of sterile distilled water and maintained in an



Figure 2. Grapevine shoot showing dark-brown lesion 12 days after inoculation with *Neofusicoccum australe* (top). Asymptomatic control shoot (bottom).

enclosed transparent plastic bag at room temperature (18–30°C). Twelve days after inoculation, the shoots displayed dark-brown to black discoloration, measuring 7.3±3.5 cm (mean±SD) of the bark and vascular tissues (Figure 2). The pathogen was successfully reisolated from the margin of symptomatic tissues, thus fulfilling Koch's postulates. Five control shoots inoculated with sterile PDA plugs remained symptomless.

The plurivorous pathogen N. australe was originally thought to be native to the southern hemisphere (Slippers et al. 2004; Burgess et al., 2006). However, it has recently been reported on a variety of hosts, including grapevine, worldwide (Armengol et al., 2008, Amponsah et al., 2009, Espinoza et al., 2009). Until now, in Italy N. australe was only found associated with drupe rot of olives (Lazzizera et al., 2008). Interestingly, our isolates conform morphologically and phylogenetically more closely to the isolates of Lazzizera et al. (2008) than to typical isolates of N. australe. To our knowledge, this is the first report of N. australe on grapevine in Italy. Further investigations are currently underway to study the spread of this pathogen in Sardinian vineyards and its role in grapevine dieback.

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