

DISEASE NOTE

FIRST REPORT OF WHITE MOULD CAUSED BY *SCLEROTINIA SCLEROTIUM* ON ROSEMARY IN ITALY

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In the winter of 2017, in a commercial farm located in Albenga (northern Italy), about 300 6-month-old potted plants of *Rosmarinus officinalis* growing in a potting mix made up of peat and fertilizer (ca. pH 6 and E.C. 600 µS) showed symptoms of white mould. Affected leaves and stems became pale brown, withered and were covered by a whitish mycelium that produced dark sclerotia. Finally, affected plants rotted and died. Little pieces of mycelium were taken from affected tissues and white colonies developed on potato dextrose agar producing sclerotia similar to those previously observed. Symptoms and signs as well as morphological characteristics observed *in vitro* permitted to identify the causal agent of the disease as *Sclerotinia sclerotiorum*. The Internal Transcribed Spacer (ITS) region of rDNA belonging to the isolate DB17GEN01 was amplified using the primers ITS1/ITS4 and sequenced (GenBank Accession No. KY947523). BLAST analysis (Altschul *et al.*, 1997) of the 518 bp amplified sequence showed 100% homology with the sequence of *S. sclerotiorum* KX184720. Five plants of *R. officinalis* were inoculated by placing at the collar wheat kernels (3 g/l) colonized by mycelium and sclerotia (Bohár and Kiss, 1999). Five control plants were treated with sterilised kernels without inoculum. All plants were maintained in a humid chamber (average temperature 22.2-23.0°C; RH 76.4-89.5%). Four days post inoculation, browning appeared on leaves and stems of inoculated plants that were colonised by a whitish mycelium and withered. *S. sclerotiorum* was constantly reisolated from affected plants, whereas controls remained symptomless. *S. sclerotiorum* was reported on *R. officinalis* in India and in the United States (Putnam, 2004). To our knowledge, this is the first report of *S. sclerotiorum* on *R. officinalis* in Italy and in Europe. This disease could cause economic losses due to the widespread cultivation of rosemary in Italy.

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DISEASE NOTE

FIRST REPORT OF GRAPEVINE VIRUS E AND GRAPEVINE VIRUS F IN TUNISIAN GRAPEVINES

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Grapevine virus E (GVE) and *Grapevine virus F* (GVF), two members of the genus *Vitivirus* in the family *Betaflexiviridae*, have a genome organization similar to that of other grapevine vitiviruses associated with rugose wood disease (Al Rawhni *et al.*, 2014). This disease is very common in Tunisian vineyards and associated with viruses such as grapevine virus A, grapevine virus B, grapevine virus D and grapevine Rupestris stem pitting-associated virus (Mahfoudhi *et al.*, 2014). No information is available on the presence of GVE and GVF in Tunisian grapevines. To address the occurrence of GVE and GVF in Tunisian grapevine-growing areas, a survey was conducted and dormant canes from 403 plants were collected. All samples were tested by RT-PCR for the presence of GVE and GVF using specific primers for the amplification of 327 bp and 217 bp fragments for GVE and GVF, respectively (Alabi *et al.*, 2013; Jooste *et al.*, 2015). Results showed that 7% and 22% of the tested samples were infected by GVE and GVF, respectively. To confirm the identity of these viruses, two isolates of GVE and one isolate of GVF were sequenced and sequences were compared with those available in GenBank. The nucleotide sequences of two GVE Tunisian isolates CR08125 (LT860201) and GN12194 (LT860202) showed identities of 97-99% with GVE isolates SA94 (GU903012) and TvAQ7 (AB432910), respectively. For GVF, Tunisian isolate Tun63 (LT860203) shared 93% nucleotide identity with the isolate AUD46129 (JX105428). To our knowledge this is the first report of GVE and GVF in Tunisian grapevines.

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