**DISEASE NOTE**

**FIRST REPORT OF TWO DISTINCT STRAINS OF PEPINO MOSAIC VIRUS INFECTING TOMATOES IN GREENHOUSES IN LITHUANIA**

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During 2010 and 2011, one hundred thirty one symptomatic samples of tomato leaves and fruits were collected from commercial greenhouses in Lithuania and analyzed for the presence of *Pepino mosaic virus* (PepMV). Two isolates of this virus (NV and KK) were found in two different greenhouses on a tomato plant exhibiting mild yellow leaf spotting and on tomato fruits with marble symptoms, respectively. The presence of the virus was confirmed by RT-PCR and DAS-ELISA, using commercial antibodies (DSMZ, Germany). Filamentous virus particles were observed by electron microscopy. The coat protein (CP) gene of the two viral isolates was amplified using a two-step RT-PCR with the PepTGB-F/PepUTR-R primer pair (Mumford and Metcalfe, 2001). A specific 845 bp PCR product was obtained, purified and sequenced. The nucleotide sequence of the CP gene of PepMV-NV and -KK was submitted to GenBank under the accession numbers JQ979169 and JQ979170, respectively. Nucleotide sequence analysis showed that the two Lithuanian PepMV isolates differ from each other and belong to two distinct PepMV genotypes. PepMV-NV belongs to the EU genotype while PepMV-KK was assigned to the CH2 genotype. These results are consistent with an expansion of the distribution of PepMV in many European countries, including Poland (Pospieszny et al., 2008). They also show that both PepMV EU and CH2 genotypes are becoming common in Europe.


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**FIRST REPORT OF GIBBERELLA AVENACEA CAUSED WET APPLE CORE ROT IN ITALY**

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*Gibberella avenacea* R.J. Cook, [syn. *Fusarium avenaceum* (Fr.) Sacc.] is a widely distributed plant pathogen and the causal agent of wet apple core rot (wACR), a disease that develops inside the fruits and remains undetected until they are eaten (Sørensen et al., 2009). In 2012, wACR symptoms were observed in apples cv. Golden Delicious from a southern Italian orchard. Diseased carrot tissues were colonized by a white mycelium, whereas the surrounding mesocarp tissues showed a light-brown wet rot. Single spore cultures were grown on PDA slants and carnation leaf agar (CLA) plates. On PDA slants, after 14 days at alternating day/night temperatures of 25/20°C and a 12 h photoperiod, the fungus formed abundant floccose white mycelium with pale orange sporodochia and released a greyish-rose pigment in the agar. Macroconidia formed on CLA were 40-80×3.5-4 µm, slightly falcate, thin-walled, usually 5 septate, with a tapering apical cell. Microconidia and chlamydospores were absent. Based on these morphological characters the fungus was identified as *G. avenacea*. For molecular confirmation, DNA was extracted from the fungal mycelium (Sanzani et al., 2012), its internal transcribed spacer regions ITS1 and ITS2, including the 5.8S gene, were amplified using the universal primers ITS5/ITS4 (White et al., 1990) and sequenced (GenBank KC342826). BLAST analysis of the 424 bp amplicon showed 100% identity with other *G. avenacea*/*F. avenaceum* ITS sequences from database. This is the first report of *G. avenacea* as causal agent of wACR in Italy. *G. avenacea* infections constitute an economical problem for growers and a safety issue due to the potential production of mycotoxins such as moniliformin and enniatins (Sørensen et al., 2009).


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