



XXII Convegno Nazionale Società Italiana di Patologia Vegetale (SIPaV)

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*La patologia vegetale tra produttività
e sostenibilità*

BOOK OF ABSTRACTS

Edited by: Taglienti A., Tomassoli L., Infantino A.

Roma, 19-20-21-22 Settembre 2016

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of the pathogen have been previously described based on their ability to cause disease on differential lettuce cultivars as well as by molecular tools developed to characterize different races of this pathogen. Only race 1 has been detected in Europe so far. In this study two isolates of *Fusarium oxysporum* obtained from lettuce plants grown in the Netherlands showing symptoms of wilt, were characterized by combining the study of pathogenicity with differential cultivars of lettuce and molecular assays as phylogenetic analysis of elongation factor 1-alpha (EF1- α) gene and intergenic spacer region (IGS region), IGS-RFLP and IRAP-SCAR using primers designed within the LTRs of the *Skippy* element and LTRs of *Han* solo-LTR retrotransposons, to determine whether the isolates were different from the known races of *F. oxysporum* f.sp. *lactucae*. The present study report the presence of *F. oxysporum* f. sp. *lactucae* for the first time in Netherlands. The causal pathogen has been identified using the IRAP-SCAR technique as a new race of *F. oxysporum* f. sp. *lactucae*. The primers FPUF and FPUR have been designed based on a polymorphic band of the IRAP-SCAR specific for this new race of *F. oxysporum* f. sp. *lactucae*.

37. INVESTIGATIONS ON COLLETOTRICHUM SPECIES ON LUPINUS ALBUS IN APULIA REGION. S. Frisullo¹, L. Prudente¹, S.M. Mang², H. Elshafie², I. Camele².

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In Spring 2013 on leaves, pods and stems of white lupin (*Lupinus albus* L.) plants which occupied about 200 ha out of the total cultivated 600 ha located in Lecce Province, typical apthracnose symptoms were observed. Disease incidence ranged from 60% to 80%. The infected organs, leaves and apical stems, initially showed small, circular, brown spots 2-3 mm in diameter that evolved in larger sunken necrotic lesions with central orange conidial masses. In order to isolate the likely pathogen, small pieces of symptomatic plant tissues were previously surface-disinfested with 1% sodium hypochlorite for 1 min, rinsed three times with sterile distilled water and then plated on PDA Petri dishes. Plates were incubated at 25°C and, after ten days, the grown colonies were transferred to PDA to obtain pure cultures. The obtained conidia

were observed under light microscopy. The ITS1-5.8S-ITS2 region of 40 representative isolates was amplified with ITS5/ITS4 primers and sequenced. The obtained sequences were highly similar (99%) to *Colletotrichum acutatum* (AJ749674 and JN543068) or *C. lupini* from lupin (JN943454 and JN943480) present in GenBank. The ITS sequences of two *C. acutatum* (LN877887 and LT160697) and two *C. lupini* (LN877886 and LN877888) isolates were deposited in GenBank. On the basis of colony and conidia morphology and of sequences analyses, the isolates were identified as *C. acutatum* (J.H. Simmonds) or *C. lupini* [(Bondar) Nirenberg, Feiler & Hagedorn]. *Colletotrichum acutatum* was reported for the first time on lupin in Italy.

38. IDENTIFICATION AND CHARACTERIZATION OF GRAPEVINE PINOT GRIS VIRUS IN LAZIO. A. Gentili¹, E. Di Lucca^{1,2}, M. Luigi¹, F. Faggioli¹.

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A new virus, recently discovered and named *Grapevine Pinot Gris Virus* (GPGV), is proving very widespread in Italian north regions causing several damages in grapevine. The symptomatic plants show mottled and deformed leaves, lower growth and lack of production, particularly in white grape cultivars. GPGV has been found also in asymptomatic vines. In order to determine the presence of GPGV also in vineyards of Lazio region, field and molecular investigations were carried out on grapevine samples collected from several symptomatic and asymptomatic plants. Specifically, one hundred and thirty samples, belonging mainly to local but also to national and international varieties, were collected in six different vineyards located in the three principal viticultural areas of Lazio (Castelli romani, Viterbese and Maccarese). Total RNAs extracted from leaves were amplified with specific primers targeting the virus movement protein (MP) gene; several plants of 'Vermentino', 'Sagrantino' and 'Sauvignon' showing either suspected symptoms or no specific symptoms (all from Maccarese area) were found positive in RT-PCR. Molecular characterization, by nucleotide sequence analysis of coat protein (CP), movement protein (MP) and replicase (Rep) genes of three GPGV isolates, was carried