

**NEW TAXA OF *PHYTOPHTHORA* INVADING ITALIAN FORESTS AND PLANTATIONS.** B. Ginetti, A. Ragazzi and S. Moricca. *Dipartimento di Biotecnologie Agrarie, Sezione di Protezione delle Piante, Università degli Studi, Piazzale delle Cascine 28, 50144 Firenze, Italy. E-mail: beatrice.ginetti@unifi.it*

A number of *Phytophthora* species were recovered from host tissue, soil and pond water during surveys in forests, plantations and nurseries in north and central Italy. Fungal isolates were recovered on the selective V8-PARPNH agar medium following apple fruit baiting. V8 Juice agar and frozen pea (FPM) media were used to induce formation of reproductive structures. Morpho-physiological characters such as colony phenotypes, morphology and size of sporangia, type and size of oogonia, and growth rates at a range of temperatures were employed for a first screening of the isolates, all of which were then analysed molecularly. The ITS1 and ITS2 regions including the internal 5.8S gene of the rRNA operon, and the mitochondrial *cox1* gene were amplified by PCR. The ITS region was then subjected to digestion with *MspI* and *AluI* restriction enzymes, whereas the *cox1* gene was digested with *RsaI*. Amplicons of ITS region and *cox1* gene of isolates from different hosts, matrices and geographical origin, or displaying different morphological characters and restriction endonuclease cleavage data, were also sequenced for making phylogenetic inferences. Species previously only partially described but not formally named, taxa new to Italy, species hybrids, and a new species were discovered.

**GIS-BASED ANALYSIS INDICATES THAT THE EXOTIC PINE-ASSOCIATED FOREST PATHOGEN *HETEROBASIDION IRREGULARE* MAY COLONIZE BROADLEAF STANDS IN ITALY.** P. Gonthier<sup>1</sup>, G. Lione<sup>1</sup>, L. Giordano<sup>1</sup> and M. Garbelotto<sup>2</sup>. <sup>1</sup>*Dipartimento di Valorizzazione e Protezione delle Risorse Agroforestali, Università degli Studi di Torino, Via L. da Vinci 44, 10095 Grugliasco, Italy.* <sup>2</sup>*Department of Environmental Science, Policy and Management, University of California, 137 Mulford Hall, Berkeley, 94720 CA, USA. E-mail: paolo.gonthier@unito.it*

The North American forest pathogen *Heterobasidion irregulare* was introduced in Italy and is currently widespread in coastal pine stands of Latium (central Italy) often in association with significant mortality of *Pinus pinea* trees. The forest of Sabaudia in the Circeo National Park is characterized by five different vegetation types, and was known to harbour both *H. irregulare* and the closely relative native species *H. annosum*, both thought to be able to become established only in the presence of conifers. In this work, we compared the distribution of infectious spores of *H. irregulare* and *H. annosum* in the forest of Sabaudia. Geostatistical and statistical analyses were employed to test for association between either species and the five Mediterranean vegetation types. Results show that, as expected, *H. annosum* is positively associated with pines and negatively associated with deciduous oaks. The probability to find its spores decreases to almost 0 at distances over 500 m from pines, and this species is virtually absent in pure oak forests. Spores of *H. irregulare* are present irrespective of vegetation type. The exotic pathogen can be found not only where pines are present, but also in pure oak forests, and this is supported by spore samplings in additional forest stands. This knowledge implies that spread of *H. irregulare* is not limited by the fragmented distribution of pine woodlands in central Italy.

*Research supported by MIUR within a PRIN project.*

**INFLUENCE OF MAIZE KERNEL COMPONENTS ON FUMONISIN B-, A-, C- PRODUCTION IN *FUSARIUM VERTICILLIOIDES*.** I. Lazzaro<sup>1</sup>, C. Falavigna<sup>2</sup>, C. Dall'Asta<sup>2</sup>, G. Galaverna<sup>2</sup> and P. Battilani<sup>1</sup>. <sup>1</sup>*Istituto di Entomologia e Patologia Vegetale, Università Cattolica del Sacro Cuore, Via Emilia Parmense 84, 29122 Piacenza, Italy.* <sup>2</sup>*Dipartimento di Chimica Organica e Industriale, Università degli Studi, Viale Uberti 17/A, 43124 Parma, Italy. E-mail: paola.battilani@unicatt.it*

*Fusarium verticillioides* is one of the main maize pathogen worldwide, causing pink ear rot and producing fumonisins, highly toxic metabolites both for human and animal health. Fumonisin B (FB) are the most commonly recovered in nature, but the fungus can also produce fumonisin A (FA), C (FC) and P (FP), and masked fumonisin have been recovered in maize and its derivatives. This study aimed at studying the dynamic of FB, FA, FC and FP production in *F. verticillioides* cultures grown on maize-based media. We used 3 high-FB producers, the *F. verticillioides* strains ITEM10026, ITEM10027, ITEM1744, cultured on cornmeal- and maize starch-based media specifically developed in our laboratory for this study and incubated for 7, 14, 21, 30 and 45 days at 25°C in the dark. At the end of each incubation period, Fumonisin B, A and C were extracted and determined through LC-MS/MS. Whereas starch allowed only the production of FB-series fumonisins in small amounts and with no significant differences between incubation periods, on cornmeal the highest FB production was detected, showing also a typical trend of production for each *F. verticillioides* strain here studied. Moreover, also FA and FC were detected in addition to FB and their production pattern was compared with that of the main analogues in order to obtain new information on the biosynthetic pathway of such compounds.

**NEXT GENERATION SEQUENCING AND METAGENOMIC ANALYSIS ADVANCES PLANT VIRUS DIAGNOSIS AND DISCOVERY.** G. Loconsole<sup>1</sup>, A. Giampetruzzi<sup>1</sup>, R. Roberto<sup>1,2</sup>, M. Saponari<sup>2</sup>, F. Palmisano<sup>2</sup>, M. Chiumenti<sup>1</sup>, M. Morelli<sup>2</sup>, A. Minafra<sup>2</sup>, V. Savino<sup>1,2</sup> and P. Saldarelli<sup>2</sup>. <sup>1</sup>*Dipartimento di Scienze del Suolo, della Pianta e degli Alimenti, Università degli Studi, Via Amendola 165/A, 70126 Bari, Italy.* <sup>2</sup>*Istituto di Virologia Vegetale del CNR, UOS Bari, Via Amendola 165/A, 70126 Bari, Italy. E-mail: p.saldarelli@ba.ivv.cnr.it*

The advent of next generation sequencing (NGS) technologies has dramatically advanced our ability to comprehensively investigate diseases of unknown aetiology and expedited the entire process of virus discovery, identification, viral genome sequencing and, subsequently, the development of routine assays for new viral pathogens. Unlike traditional techniques, these novel approaches require no preliminary knowledge of the suspected virus(es). Currently, the RNA-Seq approach is widely used to identify new viruses in infected plants, by analyzing virus-derived small interfering RNA populations, or single- and double-stranded RNA (dsRNA) molecules extracted from infected plants. The method generates sequence in an unbiased fashion, thus allowing the detection of all viruses that are present in a sample. We applied the Illumina NGS, coupled with metagenomic analysis, to generate large sequence dataset in different woody crops affected by diseases of unknown origin or infected with uncharacterized viruses or new virus strains. This approach has allowed the identification of five novel viral species and the sequencing of the whole genome of several viruses and viroids infecting *Citrus* spp., *Prunus* spp., grapevines, fig, hazelnut, olive, persimmon and mulberry. Combined analysis of the datasets generated by using either siRNA fractions or dsRNA templates, favoured the charac-