DETECTION, HOST PREFERENCE AND ROLE ON TREE STABILITY OF WOOD DECOY FUNGI IN URBAN ENVIRONMENT. L. Giordano, F. Sillo, P. Gonthier. Department of Agricultural, Forest and Food Sciences (DISAFA), University of Torino, Largo Paolo Braccini 2, 1-10095 Grugliasco (TO), Italy. E-mail: paolo.gonthier@unito.it

Wood decay fungi colonizing stem and root systems can predispose trees to the risk of windthrows or limb failures, thus resulting in significant damages especially in urban environment. Hence, an early detection and identification of hazardous wood decay agents may be pivotal during tree hazard assessment of urban trees. In this paper we report the results of a long lasting research performed in the city of Turin and in other urban contexts, based on the application of conventional diagnostic methods (visual inspection of trees) and molecular biology methods (e.g. multiplex PCRs) for the detection of the most harmful or widespread wood decay agents of both conifers and broadleaves. On average, visual inspection of trees underestimates >90% of infected trees compared with molecular methods. Lower rates of underestimation were observed for Ganoderma spp. and Perenniporia fraxinea; higher rates for Armillaria spp. and Phaeolus schweinitzii. Results of molecular biology methods show that the most frequent fungus in broadleaves was Armillaria spp., followed by Ganoderma resinaceum and P. fraxinea (14%, 5% and 4% of trees, respectively), while in conifers the frequency of Armillaria spp. was higher than that of Fusarium torulosum and P. schweinitzii (13%, 7% and 6% of trees, respectively). Furthermore, analyses show that the frequency of different fungal species greatly varied depending on the host species, suggesting relevant degrees of host preference. Finally, results suggest that wood decay fungi may play a more prominent role as factors of tree instability in the case of broadleaves compared to conifers.

PATHOGENICITY OF ETIOLOGICAL AGENTS OF CROWN ROT DISEASE ON ORGANIC BANANA IN DOMINICAN REPUBLIC. M.A.M. Kamel, P. Cortesi, M. Saracchi. Department of Food, Environmental and Nutritional Sciences (DeFENS), University of Milano, Via Giovanni Celoria 2, 1-20133 Milano, Italy. E-mail: mohamed.kamel@unic.it

Crown rot is a post-harvest disease affecting the fruits quality of banana. Different fungal pathogens are involved in the disease and may vary according to farming area. Fungi associated with crown tissues were isolated from five different organic farming areas in Dominican Republic over a period of two years (2013-2014) with the objective to assess the pathogenicity of the fungi associated to crown rot. We reproduce the conditions of natural infection by inoculating harvested green banana (Musa AAA, Cavendish) at the packinghouse. Experimental inoculations were carried out by spraying asymptomatic trimmed crowns with propagules suspensions of 24 strains of eight identified taxa. In addition, 5 mixed inoculations as well as untreated bananas as a control were included. Following inoculation, the bananas were packed and overseas shipped to Italy. Symptoms assessment was carried out 20 days after inoculation. Disease Incidence (DI) and Disease Severity Index (DSI from 0 to 7) were assessed and fungi were isolated from each treated crown. The results obtained showed that Colletotrichum musae was the most virulent species (100% DI and 7 DSI), followed by Fusarium verticilloides (100% DI and 6 DSI) and Lasiodiplodia theobromae (85% DI and 5 DSI). Fusarium incarnatum, which is considered the main pathogens in many Countries, in Dominican Republic reached a maximum of 50% DI and 4 DSI. Further strains showed low level of pathogenicity but their role could be ancillary in the crown rot development.

RACE TYPING AND MONOCLONAL CHARACTERIZATION OF XANTHOMONAS CAMPESTRIS pv. CAMPESTRIS STRAINS OCCURRING IN ITALY. P. Bella1, C. Moretti2, C.P. Strano1, M. Zaccardelli3, F. Branca4, R. Buanario1, J.G. Vicente1, V. Catara1. 1Department of Agriculture, Food and Environment (D3A), University of Catania, Via Santa Sofia 100, I-95123 Catania, Italy. 2Department of Agricultural, Food and Environmental Sciences (D3A), University of Perugia, Borgo XX Giugno 74, I-06121 Perugia, Italy. 3Agricultural Research Council – Experimental Institute for Horticulture (CRA-ORT), Via Casalleggeri 25, I-84098 Pontecagnano Fatiano (SA), Italy. 4School of Life Sciences, University of Warwick, Wellesbourne Campus, CV35 9EF, United Kingdom. E-mail: patrizia.bella@unic.it

Xanthomonas campestris pv. campestris (Xcc) is the causal agent of black rot, a severe seed-borne systemic vascular disease of vegetable brassica crops. Xcc strains have been grouped into nine physiological races, with races 1 and 4 being the most widespread in Brassica oleracea crops. The characterization of Xcc races is important to identify resistance sources, establish breeding programs and to set up control strategies. To define Xcc race structure and distribution in Italy, a collection of 31 Xcc strains, isolated from six B. oleracea varieties, B. napus var. napobrassica and Crambe maritima in seven Regions, was established from a larger collection according to their geographic and host origin and PCR-based DNA fingerprints. These strains all managed to grow on the semi-selective medium FS, hydrolyzed starch, induced vascular symptoms on B. oleracea and were identified by Xcc specific primers based on the brcC gene. The race of each strain was determined by inoculating eight differential Brassica lines belonging to five species. Xcc strains from international collections and Xcc strain races 1, 4 and 6 were included as reference strains. On the basis of compatible interaction (susceptibility) or incompatible interaction (resistance), Xcc strains isolated in Italy were classified into races 1 (35.5%), 4 (54.8%), and 6 (9.7%). Multilocus sequence analysis (MLSA) based on four housekeeping genes (dnaK, groEL, fyuA and rpoD) showed that Xcc strains in Italy are closely related to strains isolated worldwide. The results are discussed with relation to the strain source.

‘CANDIDATUS PHYTOPlasma PHoeniciUM’ ASSOCIATED WITH ALMOND WITCHES’-BROOM DISEASE: INSIGHTS INTO THE STRAIN POPULATION STRUCTURE AND THE INTERACTIONS WITH HOSTS. P. Quaglini1, M. Kube2, M. Jawhari3, Y. Abou-Jawad4, C. Sweiri2, E. Choueiri5, H. Sobhi3, P. Casati1, R. Tedeschi2, M. Molino Lova4, A. Alma4, P.A. Bianco4. 1Department of Agricultural and Environmental Sciences - Production, Landscape, Agroenergy (DISA), University of Milan, Via Giovanni Celoria 2, 1-20133 Milano, Italy. 2Division Phytopathology, Thaur-Institute, Humboldt-Universität zu Berlin, Lentzeallee 55/57, Berlin, Germany. 3Faculty of Agricultural and Food Sciences, American University of Beirut, P.O. Box 11-0236, Riad El Solh, Beirut 1107 2020, Lebanon. 4Department of Plant Protection, Lebanese Agricultural Research Institute, Tal Amara, Lebanon. 5Department of Agricultural, Forest and Food Sciences (DISAFA), University of Torino, Largo Paolo Braccini 2, I-10095 Grugliasco (TO), Italy. 4AVSI Foundation, Foundieh-Ghadir, Lebanon. E-mail: fabio.quaglini@unic.it

Almond Witches’-Broom (AlmWB), a devastating disease of almond, peach and nectarine in Lebanon, is associated with ‘Candidatus Phytoplasma phoenicium’. In the present study, we generated a draft genome sequence of ‘Ca. P. phoenicium’ strain SA213, representative of phytoplasma strain populations from different host plants, and determined the genetic diversity among phytoplasma strain populations by phylogenetic analyses of 16S rRNA, groEL, tufB and rnpM gene sequences. Sequence-based