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13 APRIL 2019 SATURDAY

07:30 DEPARTURE FROM HOTELS TO CONGRESS CENTER

08:00 DEPARTURE FROM HOTELS TO CONGRESS CENTER

08:30-10:30 PLANT PATHOLOGY/MYCOLOGY
SESSION 23 *Hall 1*
Moderator: Yasemin Bektaş- Sibel Derviş

08:30-09:00 Fulya Baysal-Gurel
O105. Track and Trace: Plant Pathogen Detection
09:00-09:15 Mahdi Arzanlou
O106. Pathogenic, phenotypic and molecular characterization of fungal species involved in trunk disease of pomegranate in Iran
09:15-09:30 Davut Soner Akgül
O107. Phylogenetic discrimination and pathogenicity of fungi causing *Botryosphaeria* dieback disease on grapevine in Southern Turkey
09:30-09:45 Nuray Körükmez
O108. Fruit rot caused by *Botryosphaeria dothidea* on olive in Turkey
09:45-10:00 Hela Chikh-Rouhou
O109. Marker-assisted selection of *Fusarium* wilt and Aphid resistance in Tunisian melon genotypes
10:00-10:15 Houda Boureghda
O110. Molecular identification and characterization of some isolates of the genus *Trichoderma* with high potential antagonist against phytopathogenic fungi
10:15-10:30 Wassila Dendouga
O111. Cell wall degrading enzymes (CWDE) of *Trichoderma* strains as key factors on biocontrol of wheat Fusarium

08:30-10:30 PLANT PATHOLOGY/VIROLOGY
SESSION 24 *Hall 2*
Moderator: Ozgur Batuman-Bayram Çevik

08:30-09:00 Francisco Ochoa Corona
O112. Detection of host selected pathogens sets by E-probe Diagnostic Nucleic acid Analysis (EDNA)
09:00-09:15 Kadriye Çağlayan
O113. Application of next generation sequencing for detection of a novel virus in raspberries
09:15-09:30 Snezhana Milusheva
O114. Experiments on Plum pox virus elimination from micropropagated plum plants through non-thermal plasma treatment
09:30-09:45 Serap Açıkgöz
O115. Virus disease of the fig and their management
09:45-10:00 Behçet Kemal Çağlar
O116. Genetic characterization and group analysis of *Spiroplasma citri* from citrus trees in Adana and Mersin Provinces of Turkey
10:00-10:15 Sevgi Coşkan
O117. The assessment of tomato genetic sources resistance to tomato spotted wilt tospovirus (TSWV) and its distribution and genetic diversity in Turkey
10:15-10:30 Eminur Elçi
O118. Molecular Screening of new emerging viral diseases of tomato in Mersin and Niğde Provinces of Turkey

10:30-11:00 COFFEE BREAK

11:00-12:30 PLANT PATHOLOGY/MYCOLOGY
SESSION 25 *Hall 1*
Moderator: Yusuf Yanar

11:00-11:30 Mahmut Tör
O119. SIGS and HIGS: investigation into silencing genes in the obligate downy mildew pathogen.
11:30-11:45 Mesut Keser
O120. Allelic variation for disease and pest resistance genes in a breeding program and implication of it on developing resistant germplasm
11:45-12:00 Pierre Van Cutsem
O121. The COS-OGA elicitor induces systemic acquired resistance in plants
12:00-12:15 Sabrina Sarrocco
O122. Competition between *Trichoderma gamsii* and *Fusarium graminearum* in the biocontrol of *Fusarium* Head Blight
12:15-12:30 Nasir Ahmed Rajput
O123. PSCRN70 effector enhances susceptibility to *Phytophthora parasitica* and confers resistance to salinity and drought in *Nicotiana benthamiana*

11:00-12:45 PLANT PATHOLOGY/BACTERIOLOGY
SESSION 26 *Hall 2*
Moderator: David Guttman- Yeşim Aysan

11:00-11:30 Robert Jackson
O124. A genomic island carrying a type III effector undergoes chromosomal excision and supercoiling to stealthily exist at low levels in a pathogen population infecting a resistant plant
11:30-12:00 Fikrettin Şahin
O125. Development of a novel seed coating formulation used for management of seedborn plant pathogens
12:00-12:15 Mine Saraçoğlu
O126. Investigation of *Xylella fastidiosa* and its potential vector species in Central Anatolian Region
12:15-12:30 Ümit Özyılmaz
O127. Specificity of conventional and Real-time PCR assays for the detection of *Clavibacter michiganensis* subsp. *michiganensis* in Turkey
12:30-12:45 Nurşen Ustun
O128. *Xylella fastidiosa* threat in Turkey: Risks and survey results in the Aegean Region

12:45-13:30 QUICK LUNCH

: Keynote speech **STU : Student speech**

13 APRIL 2019 SATURDAY

08:30-10:30 PLANT PATHOLOGY/MYCOLOGY SESSION 23 *Hall 1*

Moderator: Yasemin Bektaş- Sibel Derviş

O105. 08:30-09:00 Track and trace: Plant pathogen detection KEY

Fulya Baysal-Gurel

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There are a number of potential critical control points in plant production systems where plant pathogens are at a high risk of introduction and spread. Contamination of irrigation water by plant pathogens can occur directly at the water source or at points along the distribution path that may come in contact with infested plant. Early and accurate detection of plant pathogens in the production is critical as these pathogens are quickly transported to healthy plants though the irrigation system. Diagnostic tests including molecular tests are available for plant pathogen detection, however there are no protocols adapted to detect these plant pathogens in large volumes of irrigation water. A side-by-side comparison of the plant pathogen diagnostic tests was conducted for screening of irrigation water for the presence of plant pathogens. Reliable and sensitive detection of plant pathogens in source and production water will be critical for making timely production management decisions by growers and will also help researchers and regulatory agencies to determine the distribution of plant pathogens.

Key words: Plant pathogen, diagnostic, irrigation water

O106. 09:00-09:15 Pathogenic, phenotypic and molecular characterization of fungal species involved in trunk disease of pomegranate in Iran

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Trunk diseases are considered as major threats for production and longevity of fruits trees worldwide, including the pomegranate (*Punica granatum* L.). Iran is one of the leading courtiers in pomegranate production; however, several biotic and abiotic factors adversely affect production and longevity of pomegranate in Iran. The present study was initiated to chateraise fungal agents involved in pomegranate trunk and canker diseases in Iran. Towards this aim, wood samples were collected from symptomatic pomegranate trees in northern and northwest zone of Iran. A total number of 161 fungal isolates, were recovered from symptomtic tissues using routine plant pathology techniques and pure cultures were established. Based on a combination of morphological data and phylogenetic analysis of ITS-rDNA region, the identity of the fungal isolates were determined as *Cytospora punicae*, *Biscogniauxia mediterranea*, *Neofusicoccum parvum* and *Asordaria sibutii*. A PCR assay, based on species-specific primer set was used to detect *B. mediterranea* isolates. *Cytospora punicae* was the predominant fungal species (with frequency of 73 %), associated with trunk and canker diseases of pomegranate in sampled areas. An excised shoot method was employed to fulfill Koch's postulates. The results of pathogenicity assay revealed all of the fungal species being pathogenic on pomegranate shoots, except *A. sibutii*. *Biscogniauxia mediterranea*, which is a major pathogen of Oak trees (*Quercus* spp.) in Iran, represents a new trunk pathogen on pomegranate worldwide.

Key words: Canker, *Biscogniauxia mediterranea*, ITS-rDNA, *Punica granatum*, species- specific primer

O107. 09:15-09:30 Phylogenetic discrimination and pathogenicity of fungi causing *Botryosphaeria* dieback disease on grapevine in Southern Turkey

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Grapevine trunk diseases associated with Botryosphaeriaceae fungi are common and important diseases in Turkey vineyards. The members of Botryosphaeriaceae family cause Botryosphaeria Dieback and the disease are described by symptoms such as wedge-shaped dark brown cankers, xylem necrosis, and lack of spring growth. Up to date 24 species of this family have been reported to cause these symptoms all over the World. These species can easily be isolated from a symptomatic vine in a laboratory but species discrimination doing based on morphological and microscopic examinations is very complicated and time consuming. Moreover, misidentification can change achievement of disease control due to different species have a different susceptibility to various control methods (hot-water treatments, protective fungicide applications etc.). For a long time, molecular tools have been using to confirm classical identification of Botryosphaeriaceae fungi and to get fast and accurate results in all studies. In this study, symptomatic vines (showing Botryosphaeria Dieback) were received to the laboratory (by extension service) from Adana, Mersin and Kahramanmaraş vineyards (18) for disease diagnosis and 21 Botryosphaeriaceous isolates were obtained in 2015-2018 years. Their identification and phylogenetic discrimination were done by molecular and phylogenetic analysis. DNA of the isolates was extracted using CTAB protocol and DNA samples were used in PCR reactions as template. ITS and translation elongation factor 1-alpha (TEF1-α) gene regions were amplified with PCR using primers ITS4/ITS5, EF728F/EF976R and EF688F/EF1251R. PCR products were subsequently sequenced and the sequences were compared with those deposited in the NCBI GenBank database using the BLASTn program. Two sets of sequences were aligned using MEGA7 software and a combined (ITS and TEF1-α) phylogenetic tree was made. After BLASTn and phylogenetic analysis 7 Botryosphaeriaceous fungi (*Botryosphaeria dothidea, Diplodia seriata, Lasiodiplodia theobromae, L. pseudotheobromae, Neofusicoccum parvum, N. vitifusiforme, Neoscytalidium novaehollandiae*) were identified and pathogenicity tests were performed on one-year old grapevine plants in greenhouse conditions (for two months). According to lesion occurrence, their pathogenicity was proven (measuring lesion lengths) and variance analysis was performed for statistical separation of the isolates' virulence. This study is important for the new studies aiming at determination of Botryosphaeriaceae diversity in Turkey viticulture.

Key words: Botryosphaeria dieback, grapevine, phylogenetic analysis, identification