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sp. by 43.7% and 50.3% respectively, but showed no inhibition on *Alternaria* sp. The phytochemical analysis of these plant extracts revealed that EE of *S. cayennensis* was the richest in polyphenols and flavonoids. EE from *O. barrelieri* was particularly rich in alkaloids. The inhibitory effects on the phytopathogenic fungi were possibly related to the amount of polyphenols and alkaloids obtained through the extraction. Field experiments are being conducted on tomato to confirm the action of such extracts *in vivo*. These findings may contribute to develop new biofungicides to protect tomato from some fungal pathogens.

EVALUATION OF AN ENDOPHYTIC SYMBIONT AS A PUTATIVE BIOCONTROL AGENT OF THE CoDiRO STRAIN OF *XYLELLA FASTIDIOSA*. **M. Morelli[1], G. D'Attoma[1,2], M. Saponari[1], P. Saldarelli[1].** *[1]CNR-Istituto per la Protezione Sostenibile delle Piante (IPSP), 70126 Bari, Italy. [2]Università degli Studi di Bari Aldo Moro, Dipartimento di Scienze del Suolo, della Pianta e degli Alimenti, 70126 Bari, Italy. E-mail: massimiliano.morelli@ipsp.cnr.it*

The quarantine bacterium *Xylella fastidiosa* (*Xf*) is responsible for diseases of a wide range of cultivated and wild plants. Few efforts have been made to investigate the potential use of endophytic symbionts on the disease phenotype of *Xf*-infected plants. The aim of our study was to evaluate if *Paraburkholderia phytofirmans* PsJN strain, a plant growth-promoting rhizobacterium, whose beneficial effects in the reduction of symptom severity caused by *Xf* in grapevine affected by Pierce's Disease have recently been proven, may play a role as biocontrol agent against *Xf* CoDiRO strain, the agent of a severe disease of olives in Apulia (southern Italy). Greenhouse trials are being conducted to test the ability of *P. phytofirmans* to colonise xylem vessels of olive, *Nicotiana benthamiana* and oleander, following inoculation of bacterial suspensions by needle puncture and root dipping. A conventional PCR assay for detection of *P. phytofirmans* movement in plants has been developed to be used in combination with plate isolation and a qPCR specific assay. Preliminary results showed that needle-inoculated bacterial cells were detectable in the leaf petioles of the three hosts, away from the inoculation site. Root dipping proved successful in infecting *in vitro*-cultured olive plantlets. Double-infection assays, currently underway, will prove if *P. phytofirmans* PsJN shows a beneficial interaction with *Xf* CoDiRO.

DRAFT GENOME OF A HIGH VIRULENT ITALIAN STRAIN OF *PSEUDOMONAS SYRINGAE* pv. *SYRINGAE* ISOLATED FROM EGGPLANT. **C. Moretti[1], P. Rallo[1], E. Caballo-Ponce[2], A. Pintado[2], C. Ramos[2], G. Carannante[3], V. Stravato[3], R. Buonaurio[1].** *[1]Università degli Studi di Perugia, Dipartimento di Scienze Agrarie, Alimentari e Ambientali, Borgo XX Giugno 74, 06121 Perugia (PG), Italy. [2]Área de Genética, Facultad de Ciencias, Universidad de Málaga, Instituto de Hortofruticultura Subtropical y Mediterránea "La Mayora" (IHSM-UMA-CSIC), Málaga, Spain. [3]GENISTA s.r.l., via San Vincenzo 13, 04022 Fondi (LT), Italy. E-mail: chiaraluce.moretti@unipg.it*

Two identical strains of *Pseudomonas syringae* pv. *syringae* (*Psy*) were isolated from the stem of eggplants (*Solanum melongena* L.) showing severe wilting symptoms. Since both strains showed a high virulence when inoculated in eggplant seedlings, several molecular and phenotypic analyses were carried out for a better characterization. A phylogenetic analysis of one of these isolates, *Psy* DAPP-PG 773, in comparison with 22 other *Psy* strains was carried out based on three housekeeping genes (*gapA*, *rpoA* and *recA*). The results revealed that *Psy* DAPP-PG 773 clustered with other *Psy* strains infecting herbaceous plants. To better understand the molecular basis of the virulence of *Psy* DAPP-PG773, its genome was sequenced on an Illumina MiSeq platform using indexed paired-end 250-nucleotide v2 chemistry. A total of 7.907.342 pairs of reads were obtained, representing approximately 182-fold coverage of the genome and comprising 320 contigs. The assumed genome size was 5.95 Mb and the G/C content was 59.4%. Annotation of the *Psy* DAPP-PG 773 draft genome sequence assigned a total of 4872 candidate protein coding genes. Furthermore, several phenotypic traits relevant for the epiphytic and pathogenic lifestyle of *Psy* were investigated, *i.e.* biofilm formation, indol-3-acetic acid and exopolysaccharides production, motility and production of quorum sensing signal molecules. In order to verify the colonization of this bacterium in the host plant, *Psy* DAPP-PG773 was transformed with the green fluorescent protein and inoculated in eggplants. Observations are in progress to monitor the distribution of the bacterium in the host.

IDENTIFICATION AND CHARACTERIZATION OF A NEGATIVE STRAND RNA VIRUS CLOSELY ASSOCIATED WITH CITRUS CONCAVE GUM DISEASE. **B. Navarro[1], M. Minutolo[2], A. De Stradis[1], F. Palmisano[3], D. Alioto[2], F. Di Serio[1].** *[1]Istituto per la Protezione Sostenibile delle Piante, Consiglio Nazionale delle Ricerche, Bari, Italy. [2]Dipartimento di Agraria, Università degli Studi di Napoli Federico II, Portici (NA), Italy. [3]Centro di Ricerca, Sperimentazione e Formazione in Agricoltura Basile Caramia, Locorotondo (BA), Italy. E-mail: beatriz.navarro@ipsp.cnr.it*

Concave gum (CG) is a virus-like disease of citrus first described in the early 1930s, whose aetiology has remained elusive. Here we report a novel negative strand RNA (nsRNA) virus identified in CG-affected citrus trees. A field survey confirmed the close association between the disease and the novel virus denoted Citrus concave gum-associated virus (CCGaV). CCGaV has a bipartipe genome composed of a negative-sense RNA-1, coding for the RNA-dependent RNA polymerase (RdRp), and an ambisense RNA-2 encoding the nucleocapside (N) and a putative movement protein (MP). RNA-2 contains an intergenic region involved in the regulation of the transcription of CCGaV mRNAs in both polarity strands. Electron microscopy coupled with immunolabelling of the viral CP showed that CCGaV has flexuous not enveloped particles. The need of creating a new genus for classifying this bipartite negative-stranded RNA virus will be discussed. Interestingly, phylogenetic links were detected between CCGaV and members of the genus *Phlebovirus*, which are arthropod-transmitted viruses infecting mammals, and some phlebo-like viruses exclusively infecting arthropods. Phylogenetic reconstructions also showed that, as for other nsRNA viruses, the candidate ancestor of CCGaV was an invertebrate-restricted virus, although the adaptation of the CCGaV ancestor to plant hosts may have taken place independently of that of the other known plant-infecting nsRNA viruses. The impact of specific detection methods developed in the course of this study on sanitation and certification programs of citrus will also be discussed.

ISSR MARKERS DETECT LOW GENETIC VARIATION AMONG *FUSARIUM CULMORUM* ISOLATES FROM TUNISIA. **S. Oufensou[1,2], V. Balmas[1], B. Scherm[1], D. Rau[1], M. Ben Attia[2], S. Gargouri[3], M. Pasquali[4], Q. Migheli[1].** *[1]Dipartimento di Agraria, Università degli Studi di Sassari, Via E. De Nicola 9, I - 07100 Sassari, Italy. [2]Laboratoire de Bio-surveillance de l'environnement, Faculté des Sciences de Bizerte, Route de Tunis, 7021 Zarzouna, Université de Carthage, Tunisia. [3]Laboratoire de Protection des Végétaux, Institut National de Recherche Agronomique de Tunis, Rue Hédi Karray, 2049 Ariana Tunisia. [4]DeFENS-Department of Food*