

of *P. spumarius* that tested positive for *Xf* ranged from 25 to 71%. *P. spumarius* transmitted *Xf* to all the recipient plants except grapevine; however, citrus and stone fruit plants were not systemically infected. More than 75% of the insects survived the 7-day IAP on olive, grapevine, GF677 and periwinkle. A lower survival rate was recorded on citrus and on oleander. These data show that field-collected *P. spumarius* in the Salentinian olive groves have high rates of *X. fastidiosa* and are able to transmit the bacterium to different hosts.

### ESTABLISHMENT OF AN EXPERIMENTAL FIELD TO EXPLORE THE DIFFERENTIAL OLIVE CULTIVAR RESPONSE TO *XYLELLA FASTIDIOSA* INFECTION.

M. Saponari<sup>1</sup>, F. Palmisano<sup>2</sup>, C. Dongiovanni<sup>2</sup>, V. Cavalieri<sup>1</sup>, G. Altamura<sup>1</sup>, G. D'Attoma<sup>1,3</sup>, G. Loconsole<sup>3</sup>, M. Morelli<sup>1</sup>, A. Saponari<sup>2</sup>, D. Tavano<sup>1</sup>, S. Zicca<sup>1</sup>, D. Boscia<sup>1</sup>. <sup>1</sup>CNR Istituto per la Protezione Sostenibile delle Piante (IPSP), SS Bari, 70126 Bari, Italy. <sup>2</sup>Centro di Ricerca, Sperimentazione e Formazione in Agricoltura (CRSFA) "Basile Caramia", 70010 Locorotondo (Bari), Italy. <sup>3</sup>Dipartimento di Scienze del Suolo, della Pianta e degli Alimenti (Di.S.S.P.A.) Università degli Studi di Bari Aldo Moro, 70126 Bari. E-mail: maria.saponari@ipsp.cnr.it

While different sources of natural resistance to *Xylella fastidiosa* (*Xf*) have been described in grapevines and citrus, lack of consolidated information exists on the wide panel of cultivars characterizing the vast olive germplasm. Preliminary observations on few cultivars, support the evidence that differential cultivar responses to *Xf* infections may exist. To explore the response of a larger panel of cultivars, in April 2015, an experimental olive plot, located within the *Xf*-heavily affected olive groves, was established in the Apulia Region (Italy). Twenty-four trees for each of the ten different cultivars were planted in randomized blocks. Each tree was caged with 15-20 specimens of *Philaenus spumarius* collected from the neighboring infected olive groves. Upon removing the cages, the trees are then continuously exposed to the natural vector populations occurring in the area. Nine and 12-months after planting, the trees were sampled, tested for *Xf* and inspected for symptoms. The first data confirmed the infectivity of the vector populations occurring in the Apulian contaminated area and the *Xf* susceptibility of the olive cultivars tested. Almost 50% of the trees tested positive, with an infection incidence ranging from 25% (Leccino) to 78% (Koroneiki). Symptoms of shoot dieback started to appear 1-year after planting, limitedly on few repli-

cates of Cellina di Nardò. In April 2016, the number of cultivars has been increased up to 30. Periodical surveys for symptoms and quantitative analyses to monitor the differential bacterial titer and expression of target genes involved in the host response, are underway.

### REPORT OF 'CANDIDATUS LIBERIBACTER SOLANACEARUM' IN COMMERCIAL APIACEAE SEEDS IN ITALY.

V. Ilardi<sup>1</sup>, E. Di Nicola<sup>1</sup>, V. Lumia<sup>1</sup>, M. Tavazza<sup>2</sup>. <sup>1</sup>Consiglio per la ricerca in agricoltura e l'analisi dell'economia agraria, Centro di ricerca per la patologia vegetale (CREA-PAV), via C. G. Bertero, 22 - 00156 Roma, Italy. <sup>2</sup>ENEA, SSPT-BIOAG, Via Anguillarese 301 - 00123- Rome, Italy. E-mail: vincenza.ilardi@crea.gov.it

'*Candidatus Liberibacter solanacearum*' (CaLsol) has been recently shown to be seed-borne in carrot (*Daucus carota*), family Apiaceae. Therefore, exclusion of infected seedlots is necessary to prevent its introduction in new areas, such as Italy. Here, we tested seedlots of five carrot varieties sold in Italy during 2015 for CaLsol by i) real-time PCR assay (rtPCR) of the 16S rRNA locus; ii) PCR assay of the intergenic region between the 16S and 23S rRNA genes (ISR16/23S); and iii) PCR assay of the 50S rpIJ/rpIL ribosomal protein genes (50SrpIJ/L). CaLsol DNA was detected in seedlots of four varieties regardless of the method used. Sequence analysis of PCR-derived 50SrpIJ/L DNA and ISR16/23S DNA amplicons identified two homogeneous groups of CaLsol isolates. The single-nucleotide polymorphism analysis revealed that the first group was closely related to the CaLsol haplotype-E (except for having A at nucleotides 1620 and 1632 of ISR16/23S), while the second to the haplotype-D (except for having A at nucleotide 1648 of ISR16/23S, and T at nucleotides 920 and 1068 of 50SrpIJ/L). The identification of CaLsol in carrot seeds prompted us to investigate its presence in seedlots of another Apiaceae, the parsley (*Petroselinum crispum*). Of note, rtPCR and PCR analyses identified CaLsol in seedlots of all three parsley varieties analyzed. Our data indicate that CaLsol-infected seedlots of different carrot and parsley varieties are commercialized in Italy, a country where the presence of CaLsol has not been reported yet, thus highlighting the requirement of coordinated and harmonized measure to limit its spread.

### COMPARATIVE STUDY AMONG *NEOFABRAEA* SPP. ITALIAN ISOLATES. I. Cameldi, F. Neri, M. Meneghini, I. M. Nanni, M.