weight loss and preserving vitamin C and carotenoid content during storage.

MICROCANTILEVER RESONATORS FOR OCHRATOXIN A DETECTION IN FOOD SAMPLES. **K. Santoro[1,3], D. Spadaro[1,2], M.L. Gullino[1,2], C. Ricciardi[3].** *[1]Università degli Studi di Torino, DISAFA, Largo Braccini 2, 10095 Grugliasco (TO), Italy. [2]Università degli Studi di Torino, Centro AGROINNOVA, Largo Braccini 2, 10095 Grugliasco (TO), Italy. [3]Politecnico di Torino, DISAT, Corso Duca degli Abruzzi 24, 10129 Torino (TO), Italy. E-mail: davide.spadaro@unito.it*

An innovative and rapid detection method based on microcantilever resonators for ochratoxin A (OTA) detection in food matrix was developed. The harmful effects of OTA on human and animal health lead to develop and optimize highly sensitive, fast and accurate methods for OTA detection. Ochratoxin A can contaminate a wide number of foodstuffs during postharvest representing a serious threat to human health. Microcantilever resonator arrays could effectively identify OTA at low concentrations (less than 6 ng/ml), with relatively low uncertainty (about 10%) and good reproducibility for the same target concentration. Furthermore, the developed immunosensing method showed limited cross-reactivity to different mycotoxins, paving the way to a highly specific technique, able to identify different mycotoxins in the sample. The microcantilever technology was tested in different food matrices, to detect OTA in grape juice, green coffee and red wine with high sensitivity and reproducibility. This work demonstrates the possibility to apply microcantilever technology in food safety field, developing an innovative biosensing platform able to detect OTA with high sensitivity and reproducibility.

IMPROVEMENT OF QUADRUPLEX TAQMAN REAL TIME METHOD TO SCREEN THE PRESENCE OF *XANTHOMONAS VESICATORIA*, *X. EUVESICATORIA*, *X. PERFORANS*, *X. GARDNERI* IN TOMATO SEEDS. **A. L'Aurora, V. Scala, N. Pucci, S. Loreti.** *Council for Agricultural Research and Economics, Research Center for Plant Protection and Certification, Roma, Italy. E-mail: stefania.loreti@crea.gov.it*

Bacterial spot of tomato, a major problem in many tomato production areas, is caused by *Xanthomonas vesicatoria*, *X. euvesicatoria*, *X. perforans* and *X. gardneri*. In the frame of the project ASPROPI financed by the Italian Ministry of Agricolture and Forestry, we investigated the possibility to validate a new protocol for the preliminary screening of *Xanthomonas vesicatoria*, *X. euvesicatoria*, *X. perforans* and *X. gardneri* in tomato seeds. In order to detect the bacterial spot pathogens, the region of *hrpB* operon was evaluated as target for a quadruplex real-time polymerase chain reaction (PCR). The PCR products are highly conserved within each species, with a single-nucleotide polymorphism (SNP) among bacterial spot of tomato agents. Four probes and two primers were employed to detect the four bacterial spot pathogens simultaneously. The optimized quadruplex assay was assessed for analytical specificity and sensitivity showing good performance criteria. The new protocol was validated within a test performance study (TPS) and compared with the already available diagnostic methods. Seven different laboratories of the Plant Protection Services participated to the TPS to verify the reproducibility of the tested method. The obtained results showed that this method holds great potential as a diagnostic tool for the detection of each bacterial spot pathogen from seed tomato matrix, and also for the identification of *Xanthomonas*-like pure cultures.

NEW CLASS OF LIPID COMPOUNDS IN *XYLELLA FASTIDIOSA* STRAIN CoDiRO. **V. Scala[1], N. Pucci[1], S. Lucchesi[1], A. L'Aurora[1], M. Ludovici[2], M. Reverberi[3], S. Loreti[1].** *[1]Council for Agricultural Research and Economics, Research Center for Plant Protection and Certification, Roma, Italy. [2]Laboratory of Cutaneous Physiopathology and Integrated Center of Metabolomics, San Gallicano Dermatologic Institute (IRCCS), Rome, Italy. [3]Department of Environmental biology, Sapienza University of Rome, Italy. E-mail: valeria.scala@crea.gov.it*

Modulating signals involved in plant-pathogen interaction represent a powerful mean to develop innovative and sustainable approaches to control plant pathogens. We investigated some of these signals, *i.e.* oxylipins in *Xylella fastidiosa* CoDiRO strain (variant "sequence type 53"), associated with the olive quick decline syndrome. During plant-pathogen interactions, lipids have different roles, as pathogen perception, signal transduction and downstream defence responses. The composition of the bacterial membrane is not constant but depends on the environmental conditions to which the cells are exposed. Oxidized fatty acids are an important class of signalling molecule especially related to stress responses. Recently, other authors reported that oxylipins have a regulation activity in motility, biofilm formation and virulence of *Pseudomonas aeruginosa*. In the frame of the Xf-actors project we explored the oxylipin signals of *X. fastidiosa* subsp. *pauca* CoDiRO strain CFBP8402 in pure culture and during the interaction with the model plant *Nicotiana tabacum* "Petite Havana SR1". The analyses were performed by LC-MS/MS in dynamic MRM modality allowing quantification of oleic, linoleic and linolenic acid-derived oxylipins. The results showed the presence of oxidized fatty acids in *X. fastidiosa* CoDiRO strain in pure culture and in inoculated tobacco plants.

DEEP SEQUENCING OF TWO *CITRUS TRISTEZA VIRUS* ISOLATES CROSS PROTECTIVE AGAINST HOMOLOGOUS SEEDLING YELLOWS-VT STRAIN. **G. Scuderi[1], M. Russo[1], R. Ferraro[2], M.C. Bazzano[1], O.F. Giarrusso[1], A. Catara[2], G. Licciardello[1].** *[1]Agrobiotech, ZI Blocco Palma I, Via V. Lancia 57, 95121 Catania, Italy. [2]Parco Scientifico e Tecnologico della Sicilia, ZI Blocco Palma I, Via V. Lancia 57, 95121 Catania, Italy. E-mail: glicciardello@agrobiotech.it*

A wide indexing and genotyping of VT-like *Citrus tristeza virus* (CTV) in Sicily has identified some isolates that are potentially cross-protective (CP) on sour orange against the prevalent seedling yellows (SY) isolate SG29, but retain the stem pitting (SP) phenotype on grapefruit. As a result of bioindexing they have a biotype 10 instead of severe SY associated to biotype 4. Deep sequencing of two candidate CP isolates and alignment of their full genomes against the challenger SG29 (KC748392) showed 13 and 14 point mutations, respectively, including 5 and 6 silent mutations. No evidence of recombination and/or additional strains was present. Interestingly, eight changes were shared in the same position and three of them were located within *p33* (positions 11490, 11585, 11756 nt), and one in *p23* (18508 nt). The two isolates differed by nine nucleotides, three within *orf1A* (position 486, 3208, 4780 nt), one in *p33* (positions 11721 nt), three in the intergenic region *p33-p6* (11790, 11791, 11792 nt), one in *p25* (position 16316 nt) and one in *p18* (position 16970). While the precise genomic events that have led to the mutation changes remain to be established, the results show that: (i) the "superinfection exclusion" conditions for cross protection predicted for T36 strains attain also to VT strain; (ii) it may occur "naturally" in the field, eventually from recovered plants and aphid spread; (iii) the genetic determinants of SP phenotype are different from those of SY; (iv) the search for cross protective mutants needs a mandatory genotyping and a phenotype analysis on specific indicators.