

allergens detection, was used to trace *Penicillium* spp. in musts and wines. The method consists of two sets of primers specifically designed to target β -tubulin gene, with the aim of lowering the limit of detection of the conventional real-time PCR. The assay was able to detect up to 1 fg of *Penicillium* DNA. Related wine/must samples were almost all contaminated by patulin. Although further large-scale trials are needed, these results support the suitability of newly developed methods for the detection of *Penicillium* DNA in processed grapes.

101. COMPARATIVE GENOMICS OF CITRUS TRISTEZA VIRUS IN A NON-ERADICATIVE AREA OF EASTERN SICILY REVEAL WIDE GENETIC DISTANCES AND PHENOTYPE REACTIONS OF THE ISOLATES. G. Scuderi^{1,2}, R. Ferraro², M. Russo^{1,2}, M.C. Bazzano¹, A. Catara², G. Licciardello^{1,2}. ¹Agrobiotech Z.I. Blocco Palma I, Str.le V. Lancia 57- 95121 Catania, Italy. ²Parco Scientifico e Tecnologico della Sicilia ZI. Blocco Palma I, Str.le V. Lancia 57- 95121 Catania, Italy. E-mail: glicciardello@agrobiotech.it

Citrus tristeza virus (CTV) is a phenotypically complex virus causing serious economic losses to citrus industry worldwide, depending on the isolate and the variety/rootstock combination. Therefore, molecular-based strategies to control the disease, require an insight on the genetic assessment of the local virus population structure, supported by phenotype/genotype analysis. As result of an intensive biological and immunological testing of isolates collected in a non-eradicated area of eastern Sicily, selected isolates were analyzed by a new lab-on-chip (LoC) device running on an In-Check platform, enabling a multiplex RT-PCR with six pairs of primers and microarray hybridization of the amplicons with a set of 44 probes representative of the CTV strains in GenBank, which revealed three strains (VT, T30 and T36) with many isolates. Six of them were deep-sequenced and the genetic distance of their genomes analyzed in comparison with 42 genomes present in GenBank. Four isolates belong to the VT genotype and are largely divergent from the genome of SY568 isolate. Two show 98% homology sequence with T318A, and induce seedling yellow on sour orange, but not on lemon, whereas the remaining two have a mild cross protective phenotype. The T30-like and T36-like isolates fit 97-98% with the genomes of the respective strains. As expected, the former has a mild phenotype whereas the latter affects sour orange. The divergent results of phenotype/genotype analysis show that a multiple approach is required to assess the best management strategy of tristeza disease for each specific circumstance.

102. EFFECTS OF CERTIFIED MATERIAL ON RECONVERSION OF SICILIAN CITRUS ORCHARDS. G. Sorrentino, S. Di Silvestro, M.C. Strano, M. Guardo. Consiglio per la ricerca in agricoltura e l'analisi dell'economia agraria - Centro di Ricerca per l'Agromicoltura e le Colture Mediterranee (CREA-ACM), Corso Savoia 190, 95024, Acireale (CT), Italy. E-mail: guido.sorrentino@crea.gov.it

In 2007 CREA-ACM started a monitoring of citrus tristeza virus (CTV) and viroids in field-grown plants, collecting results on citrus grafted first on Sour Orange and subsequently (2014-2015) on Citrange Carrizo and Troyer. The spread of CTV in 2013 led to a reconversion of citrus orchards. Sour Orange was the most distributed rootstock in Sicily and for its high sensitivity to CTV it was replaced with Citrange Carrizo and Troyer, both susceptible to viroids infections. In 2007 62.5% of samples, grafted on sour orange, collected in commercial citrus orchards, were infected by viroids. In particular 59.4% of infected samples showed ISA1-CT-I mild strain of citrus exocortis viroid (CEVd)

in combination with either citrus viroid III (CVd-III), citrus viroid IV (CVd-IV) or hop stunt viroid (HSVd) and 40.6% in single infection. In 2014 in Catania province, new citrus crops, originated from certified material, showed that 12% of samples were infected by CEVd ISA1-CT-I alone, 1% in combination with CVdIII and 2.4% with HSVd. In particular CEVd in combination with CVdIII shows symptoms like plants decaying and cracking or peeling of the bark. In 2015 in others citrus orchards viroids infections were caused by CEVd (1%), HSVd (8%) and CVdIII (28%). In greenhouses young plants were infected with CEVd (24%) and HSVd (37%). By using the certification system, viroid infection decreased in orchards, however it was still detectable in young plants grown in greenhouses. That is dangerous for the risks of field infection that the symptomatic contemporary presence of CEVd with CVdIII induces.

103. PLANT HEALTH AND SOCIOECONOMIC DIAGNOSIS OF FRUIT IN THE DA MATA RONDONIA AREA. G. Souza Gudin, D. Gomes da Silva, G. Lima Duarte. Universidade Federal Rondônia, Rolim de Moura (RO), Brazil. E-mail: geovanes805@gmail.com

The survey was conducted in the municipalities of Rondonia Territory forest area. With a questionnaire seeking to understand the economy of 20 farmers, photographic records were made of the main symptoms of diseases of fruit, a check post in the literature. Economic issues were treated as the producer monthly income and other sources of income. The fruits are sold in agricultural business and free markets. There is the use of pesticides on crops in 15 properties. There are symptoms of *Moliniophthora pernicious* in cupuaçu crops, *Didymella bryoniae* in melon, *Mycosphaerella fijiensis* and *M. musae* in banana, *Cladosporium herbarum* in passion fruit, in guava *Meloidogyne enterolobii*, *Alternaria* spp., *Citrus Leprosis* virus, *Phytophthora nicotianae* var. *parasitica* and *Phytophthora citrophthora*, *Guignardia citricarpa*, *Elsinoë fawcetti* in Citrus. Two producers said they do not use personal protective equipment (PPE). Use much monoculture, seeds / seedlings are proper, conferences and labor market influence the advancement of fruit production in the region, but low prices are the problems faced by farmers in marketing. Therefore, the fruit still has a long way to go, additional technical assistance is required and monitoring, as well as new technologies to increase production.

104. EVALUATION OF A SAMPLING METHOD FOR XYLELLA FASTIDIOSA DETECTION IN OLIVE TREES. L. Susca¹, O. Potere¹, V. Roseti¹, F. Civita¹, G. Loconsole¹, D. Boscia², V.N. Savino^{1,2}. ¹Dipartimento di Scienze del Suolo, della Pianta e degli Alimenti, Università degli Studi di Bari Aldo Moro, Via Amendola 165/A - 70126 Bari, Italy. ²Istituto per la Protezione Sostenibile delle Piante, CNR, SS di Bari, Via Amendola 165/A - 70126 Bari, Italy. E-mail: leonardo.susca@uniba.it

To assess the presence of the xylem-limited bacterium *Xylella fastidiosa* subsp. *pauca* strain CoDiRO in olive trees, a specific sampling method was evaluated. Symptomatic and symptomless plants were randomly selected in four olive orchards located in the province of Lecce (Southern Italy). The crown of each plant was subdivided into a lower and an upper portion; four samples were collected from each layer in the main four cardinal directions. A total of eight samples per plant, composed of one- or two-year-old asymptomatic twigs, were collected next to branches showing leaf-scorch symptoms. In this preliminary study, the null hypothesis was tested. i.e. there is no difference between the lower and the upper portions of the tree canopy and across the four cardinal directions.