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(SIPaV)

*La patologia vegetale tra produttività
e sostenibilità*

BOOK OF ABSTRACTS

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high percentage of identity with several isolates of TSWV (96.0 to 99.5%). Our finding is thought to be the first report of natural occurrence of TSWV in *S. rebaudiana* in Italy. Considering that this virus infects several aromatic and ornamentals crops in this Ligurian area, thrips constitute the main responsible for TSWV spreading as well as increasing of its natural hosts.

56. A REVISED AND EFFECTIVE PIPELINE BASED ON RELATIVE COVERAGE FOR THE GENOME RECONSTRUCTION OF PHYTOPLASMA AND OTHER FASTIDIOUS PROKARYOTES.

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An alternative to the difficult, inefficient and time consuming methods that require purification of the pathogen DNA for its genomic analysis is to sequence a large library of DNA extracted from diseased plants and then select pathogen specific sequences. However, pathogen sequence selection is not trivial and many genome drafts published so far are incomplete. The procedure developed here exploits the differential coverage of sequences originating from pathogen and those from host, due to the size difference between the prokaryote and the plant genomes and the relative abundance of pathogen even in samples with less than 10% pathogen DNA.

In brief, the procedure requires a reference genome for the uninfected plant, and the sequence reads obtained from an Illumina MiSeq. The procedure starts assembling the mixed genome reads and the reference genome reads if necessary. A perl script then calculates the coverages and then groups the contigs accordingly. The following steps are looped to find the optimum cutoff. The reads of the contigs with coverage higher than the cutoff are aligned against the healthy assembly. The non-mapping sequences are assembled with the A5 pipeline, to obtain the non-mapping-on-healthy contigs list. Another perl script queries a database from the reference genome contigs file to check the effectiveness of the cutoff and filtering parameter used.

Using this pipeline we have recently obtained very high quality draft assemblies of the phytoplasma strains associated with Lime Witches' Broom in Brazil, with the Cassava Frogskin Disease, with Chicory Phyllody and of a *Spiroplasma citri* strain.

57. GENETIC DIVERSITY AND VIRULENCE OF STRAINS OF *PSEUDOMONAS SYRINGAE* PV. *ACTINIDIAE* ISOLATED FROM *ACTINIDIA DELICIOSA* IN PIEDMONT. **S. Prencipe¹, A. Garibaldi², D. Spadaro¹.** ¹*Università di Torino, DISAFA, Grugliasco, Italy;* ²*Università di Torino, AGROINNOVA, Grugliasco, Italy. E-mail: angelo.garibaldi@unito.it*

Pseudomonas syringae pv. *actinidiae* (*Psa*), the causal agent of bacterial canker of kiwifruit, is responsible for significant economic losses, both in yield and quality. During the first severe outbreak (2008-2010) and few years afterwards 40 strains of *Psa* were isolated. To analyse the genetic diversity of the pathogen REP, RAPD-PCR, and MLST of six housekeeping and effector genes were performed. RAPD technique, compared to REP-PCR showed an increased level of resolution in evaluating the genetic diversity within the pathovar *actinidiae* of *P. syringae*, with the sets of primers used in this study. The molecular fingerprinting, *Na, Ne, H, I*, polymorphic loci, and AMOVA showed a high level of variability and genetic diversity in the population of *Psa* isolated in 2014 compared to the population of 2010. MLST showed SNPs in two of the effector genes analysed, while no mutation was found in the housekeeping genes. Furthermore, *in vitro* and *in vivo* virulence was evaluated, displaying a higher disease index for the strains isolated in 2014, compared to the older population. This study shows the evolution of genetic diversity and differences in the degree of virulence of *Psa* in the same geographical area, from the first epidemic outbreak to the endemic and established population. The high degree of the intraspecific variability found in *Psa* could be used as a model to study the evolution of bacterial pathogen diversity.

58. NOVEL REGULATORS OF DEFENSE HORMONAL CROSSTALK UNRAVELED BY GENOME-WIDE ASSOCIATION STUDY. **S. Proietti, L. Caarls, S. Coolen, S.C.M. Van Wees, C.M.J. Pieterse.** *Plant-Microbe Interactions, Department of Biology, Padualaan 8, 3584 CH, Utrecht University, the Netherlands. E-mail: s.proietti@uu.nl*

The plant hormones salicylic acid (SA), jasmonic acid (JA) and abscisic acid (ABA) play central roles in biotic and abiotic stress responses. To appropriately respond to specific attackers or to multiple attackers at the same time, their signaling pathways cross-com-

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