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and pathogen. This COST Action has duration of 4 years (March 2017-March 2021) and will generate a platform that gathers experts from different disciplines, such as molecular diagnostics, molecular host-microbe interactions, plant resistance breeding, etc. The network includes 43 working groups from 21 different countries. Joining their efforts will help to develop and implement effective plant protection schemes, be it via resistant crop cultivars or via other control mechanisms. This goal will be achieved by mobilizing and training scientists from major European institutions, regulatory bodies and commercial companies working on the various aspects of this complex of problems.

NEXT GENERATION ECOFRIENDLY CONTROL OF GRAM NEGATIVE PLANT PATHOGENIC BACTERIA: VIRULENCE INHIBITING PEPTIDES AND POLYPHENOLS FROM NO-FOOD PLANT BIOMASS. S. Tegli, M. Cerboneschi, C. Biancalani, S. Calamai, L. Bini. *Dipartimento di Scienze Produzioni Agroalimentari e dell'Ambiente (DISPAA), Laboratorio di Patologia Vegetale Molecolare, Università degli Studi di Firenze, Via della Lastruccia 10, 50019 Sesto Fiorentino (Firenze), Italy. E-mail: stefania.tegli @unifi.it*

Plant diseases caused by bacteria may be highly destructive under adverse environmental conditions or in the case of quarantine pathogens. Bacterial diseases of plants still remain a challenging issue, basically relying on the use of copper and antibiotics, the latter not allowed in EU for plant protection. Given the negative ecotoxicological profile of copper, alternatives to its use are urgently needed, to meet the demands concerning agro-industry productivity and environmental protection. Here we propose an innovative strategy, based on the use of newly designed peptides and of plant polyphenols extracted from no-food biomass by a "green chemistry" process, targeting bacterial pathogenicity and virulence mechanisms, but not viability, thus avoiding the risk to develop any resistance. Both virulence inhibiting peptides (VIPs) and plant polyphenol extracts affect the TTSS and QS functionality, both *in vitro* and *in planta*, at concentrations of 30-60 µM, using *Pseudomonas savastanoi*, *P. syringae* pv. *tabaci* and *P. syringae* pv. *actinidiae* as model systems. Their effectiveness was demonstrated by pathogenicity trials and by bacterial gene expression studies, through real time PCR and several promoter-reporter systems. VIPs effectiveness was also demonstrated in *Nicotiana tabacum* and *Actinidia chinensis* stably transformed for VIPs expression, when challenged by *P. syringae* pv. *tabaci* and pv. *actinidiae*, respectively. No negative side-effects and no toxicity have been found on soil microflora, on model organisms and microorganisms, on biomimetic cellular membranes, as well as on Ca-ATPase pumps.

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SURVEYS ON SWEET PEPPER (*CAPSICUM* spp.) IN SICILY (ITALY). A. Tiberini[1], A. Fontana[1], G. Leo[1], L. Tomassoli[2], S. Davino[3]. *[1]Università degli Studi "Mediterranea" di Reggio Calabria, Feo di Vito, 89122 Reggio Calabria (RC), Italy. [2]Consiglio per la ricerca in agricoltura e l'analisi dell'economia agraria - Centro di ricerca difesa e certificazione, Via C.G. Bertero 22, 00156 Roma (RM), Italy. [3]Università degli Studi di Palermo, Dipartimento Scienze Agrarie e Forestali, Viale delle Scienze ED. 5, 90128 Palermo, Italy. E-mail: antonio.tiberini@unirc.it*

Surveys to determine the incidence, diversity and distribution of viruses infecting sweet pepper (*Capsicum annuum*) in controlled conditions were conducted in several farms located in the two main production districts (Mazzara del Vallo and Ragusa) in Sicily, in 2017. Symptomatic plants were collected showing mosaic, mottling, puckering, reduction in leaf size, vein yellowing, interveinal yellowing, fruit deformation and stunting. Preliminary, symptomatic leaf samples were examined by ELISA for the most common viruses reported on pepper as: Potato virus Y (PVY), Pepper mild mottle virus (PMMoV), Tobacco mosaic virus (TMV), Cucumber mosaic virus (CMV), Tomato mosaic virus (ToMV), Tomato spotted wilt virus (TSWV), Alfalfa mosaic virus (AMV). Further, after nucleic acid extraction (Real Kit, Durviz), RT-PCR assays were performed using species-specific and genus-specific primer sets to investigate the presence of Tomato chlorosis virus (ToCV), Tomato infectious chlorosis virus (TICV), Pepper yellow leaf curl virus (PYLCV) and Pepper vein yellows virus (PeVYV). Results showed that the highest viral incidence in both surveyed areas is related to TSWV and poleroviruses (PYLCV and PeVYV), thereof few representative isolates were included in a phylogenetic analysis to better investigate the evolutionary status. Data confirmed how the *Polerovirus* genus can be regarded as a new phytosanitary threat in Sicily, especially in view of their high recombination capability.

SOURCES OF RESISTANCE TO THE DOWNY MILDEW AGENT IN THE EUROPEAN GRAPEVINE GERMPLASM. S.L. Toffolatti[1]*, G. De Lorenzis[1]*, G. Maddalena[1], A. Costa[2], C. Bonza[2], P. Casati[1], G. Venturini[1], M. Pindo[3], A. Cestaro[3], O. Failla[1], P.A. Bianco[1], F. Quaglino[1]. *[1]Università degli Studi di Milano, Dipartimento di Scienze Agrarie e Ambientali - Produzione, Territorio, Agroenergia (DISAA), via Celoria 2, 20133 Milano, Italy. [2]Università degli Studi di Milano, Dipartimento di Bioscienze, via Celoria 26, 20133 Milano, Italy. [3]Fondazione E. Mach, Centro Ricerca e Innovazione, Via E. Mach 1, 38010 San Michele all'Adige (TN). E-mail: silvia.toffolatti@unimi.it*

Exploiting the natural defense mechanism of a plant is one of the most specific, environmentally safe and innovative ways to protect agricultural crops from pathogen infections. Grapevine is affected by *Plasmopara viticola* (Berk. *et* Curt.) Berl. and De Toni, a pathogen of North American origin that causes downy mildew. Since the most common cultivars of *Vitis vinifera* L., the European grapevine, are highly susceptible to *P. viticola*, sources of resistance have been traditionally searched in the American germplasm that co-evolved with the pathogen. The availability of a huge collection of less common *V. vinifera* germplasm coming from Eastern Europe, recently led to the discovery of a cultivar, 'Mgaloblishvili N', showing low susceptibility to *P. viticola*. The interaction between the pathogen and 'Mgaloblishvili N' was characterized by analyzing phenotypic traits and genes differentially expressed in inoculated and non-inoculated leaves, to identify putative pathways of the plant response to the pathogen. The same analysis was carried out on two reference cultivars: 'Pinot noir N', susceptible to the pathogen, and 'Bianca B', a *Vitis* interspecific cross holding resistance traits. The results showed a significantly reduced disease severity and sporulation in 'Mgaloblishvili N', compared to 'Pinot noir N', associated with alterations of the pathogen structures, and significant differences in the expression levels of genes encoding defense proteins. 'Mgaloblishvili N' transcriptome proved to be different from that of the reference cultivars, highlighting specific molecular mechanisms of plant-pathogen interaction that should be more deeply investigated to exploit the resistant traits in *V. vinifera* breeding programs.

**These authors contributed equally to the work*

MOLECULAR IDENTIFICATION OF *VENTURIA ASPERATA* FROM ATYPICAL SCAB-LIKE SYMPTOMS ON APPLES IN ITALY. C. Turan[1], M. Menghini[1], G. Ceredi[2], M. Mari[1],