confirmed for 24 isolates by sequencing ITS-rDNA region. These isolates were inoculated on pepper, and four on the other plant species. All of the isolates were pathogenic. These results demonstrate simultaneous emergence of *P. capsici* causing soil-borne diseases in different economically important greenhouse crops in Almería.

This research was supported by European Regional Development Fund (ERDF) and European Social Fund (ESF) through the research project PP.AVA.AVA201601.7 and the fellowship granted to M. de Cara by IFAPA.

Assessment of the host status of ornamental rutaceous species to *Xanthomonas citri* pathovars causing citrus bacterial canker. G. LICCIARDELLO[1], O. PROUVOST[2], I. ROUBENE[2], J. CUBERO[3], C. REDONDO[3], A. CARUSO[1], C. LICCIARDELLO[4], P. CARUSO[4], V. CATARA[1]. [1]*Dipartimento di Agricoltura Alimentazione e Ambiente, Università degli Studi di Catania, Via Santa Sofia 100, 95130 Catania, Italy.* [2]*CIRAD, UMR Peuplements Végétaux et Bioagresseurs en Milieu Tropical (PVBMT), 7 chemin de l'irat - 97410 Saint Pierre, La Réunion, France.* [3]*INIA, Departamento de Protección Vegetal, Ctra De La Coruna Km 7.5, 28040 Madrid, Spain.* [4]*Consiglio per la ricerca in agricoltura e l'analisi dell'economia agraria, Centro di Ricerca per l'Agrumicoltura e le Colture Mediterranee, Corso Savoia 190, 95024 Acireale, Italy. E-mail: vcatara@unict.it*

Xanthomonas citri pv. *citri* (*Xcc*) and *X. citri* pv. *aurantifolii* (*Xca*) cause citrus bacterial canker (CBC), a severe disease responsible for defoliation and fruit blemish and drop, requirings costly control measures. *Xcc* and *Xca* are quarantine pathogens for the UE, and are not recorded in the Mediterranean region. The probability of their entry, via import of ornamental rutaceous plants, through the commercial trade and passenger pathways, is rated as likely by EFSA (2014). To provide useful information for pest risk assessment, 25 ornamental rutaceous plants in the genera *Atalantia, Balsamocitrus*, *Clausena*, *Eremocitrus*, *Glycosmis*, *Melicope*, *Microcitrus*, *Murraya* and *Vespris*, not covered by Directive 2000/29EC, as well as *Citrus* and *Fortunella*, were tested for resistance to strains of *Xcc* (pathotypes A, A* and A^w) and *Xca* (pathotypes B and C), in controlled environment detached leaf assays. Nine plant species were presumptively classified as non-hosts, among them *Murraya paniculata.* Only *M. ovatifoliolata* and *Eremocitrus glauca* were susceptible to all pathotypes. The remaining species were susceptible at least to one of the pathotype A strains. Bacterial population densities ranged from 10^3 to 10^6 cfu mL^{-1} in plants showing HR or no response, and 10^7 to 10^9 cfu mL^{-1} in plants showing typical CBC lesions. Crystal violet staining showed aggregation of citrus canker strains on *M. paniculata* leaves similar to that on citrus species but different to that found for a non-citrus *Xanthomonas*. A *de novo* sequencing of the *M. paniculata* genome, already completed, will serve for RNAseq studies on both *Murraya* species.

This research is part of the ORPRAMed (Ornamental Rutaceous Plants Xcc Risk Assessment in Mediterranean) Project funded through the ERA-NET - ARIMNet2 2015 Call (EU FP7 grant no. 618127) by the following funding agencies: MIPAAF, INIA, ANR and GDAR.

Evaluation of the presence of *Gnomoniopsis smithogilvyi* (syn. *castanea*) in chestnuts, rootstocks and grafts of six varieties of chestnut trees. M. CONTI[1], J. CROVADORE[1], B. COCHARD[1], R. CHABLAIS[1], M. JERMINI[2], F. LEFORT[1]. [1]*Plants and Pathogens Group, Institute Land Nature Environment, hepia, University of Applied Sciences and Arts Western Switzerland (HES-SO), 150 route de Presinge, 1254 Jussy, Switzerland.* [2]*Agroscope, Cadenazzo Research Centre, A Ramél 18, 6593 Cadenazzo, Switzerland. E-mail: francois.lefort@hesge.ch.*

Gnomoniopsis smithogilvyi is an endophytic fungus, recently identified in Europe and Switzerland as the main cause of chestnut brown rot and as a cause of chestnut canker. The pathogen causes high plant mortality in chestnut nurseries and orchards. The presence of this fungus and of the chestnut canker agent *Cryphonectria parasitica* was assessed in the propagation material of six chestnut varieties, used by the Ticino Cantonal Nursery to restore fruit orchards. Sixty root samples, 41 shoot samples from germinated chestnuts and 17 chestnut rootstock samples were analysed, along with 112 samples from 56 rootstock/graft pairs, to determine whether the pathogen was transmitted by rootstocks or grafts. DNA extraction was followed by specific amplification primers for *G. smithogilvyi* and *C. parasitica. Gnomoiopsis smithogilvyi* was detected as an endophyte, but *C. parasitica* was never detected. Six of the 60 roots analysed from seed chestnuts were contaminated with *G. smithogil-*

vyi (in varieties *Lüina*, *Torcione Nero*, *Marrone Michelangelo*, *Marrone Lattecaldo* and *Bouche de Bétizac)*, as well as two of 41 shoots from seed chestnuts (*Lüina* and *Bouche de Bétizac*), and two of 17 rootstocks (*Lüina* and *Torcione Nero* varieties). For 112 samples from 56 rootstock/graft pairs, *G. smithogilvyi* was found in 12% of the rootstocks and 60% of the grafts. These results showed low incidence of *G. smithogilvyi* in rootstock propagation material, and high contamination of grafting material in all varieties, and confirm that *G. smithogilvyi* is an endophyte.

This research was supported by the strategic research fund of the University of Applied Sciences and Arts Western Switzerland.

Characterization of *Elsinoë ampelina*, the causal agent of grapevine anthracnose in Brazil. R.F. SANTOS, M. CIAMPI-GUILLARDI, L. AMORIM, N. S. MASSOLA JÚNIOR, M. B SPÓSITO. *Departamento de Fitopatologia e Nematologia, Escola Superior de Agricultura "Luiz de Queiroz", Universidade de São Paulo, 13418-900 Piracicaba, SP, Brazil. E-mail: ricardofeliciano@usp.br*

Anthracnose, caused by *Elsinoë ampelina*, is an important disease in vineyards in South and Southeast Brazil, the main grape-producing regions in the country. This study characterized *E. ampelina* isolates associated with grapevine anthracnose in Brazil through molecular analysis, morphological characterization and pathogenicity tests. Thirty-nine *E. ampelina* isolates were obtained from leaves, stems and berries with anthracnose symptoms collected in the Rio Grande do Sul and São Paulo States. Fungus characterization was carried out using molecular analysis based on ITS, TEF 1-α and HIS3 regions, in combination with cultural and conidial morphology. For pathogenicity tests, ten isolates were inoculated onto *Vitis labrusca* cv. Niagara Rosada. ITS sequences showed only two polymorphic sites within the 602 bp sequenced and TEF 1-α sequences were monomorphic. However, HIS3 was the most informative region showing 55 polymorphic sites. Haplotype network analysis based on multilocus alignment (ITS, TEF 1-α and HIS3) grouped the isolates into seven haplotypes. Colonies of *E. ampelina* isolates showed slow growth (23 to 28 mm diam. at 30 d), variable colouration and wrinkled texture on PDA medium. Conidia were cylindrical to oblong with rounded ends, hyaline, aseptate, 3.6 to 7.0 µm long and 2.0 to 3.4 µm wide. Inoculations on 'Niagara Rosada' confirmed the pathogenicity of all isolates inoculated. These caused reductions of shoot dry weight by up to 80%, and severity of leaf disease reached a maximum of 72%.

This research was supported by São Paulo Research Foundation (FAPESP Projects 2013/24003-9 and 2014/24472-1).

Genetic and phenotypic diversity of *Verticillium dahliae* populations from sunflower in Europe. A. MARTÍN-SANZ[1], A. GARCÍA-CARNEROS[2], S. RUEDA[1], P. MIRANDA-FUENTES[2], L. MOLINERO-RUIZ[2]. *[1]Pioneer Hi-Bred International, Inc., Campus Dupont – Pioneer, Ctra. Sevilla-Cazalla (C-433) km 4.6, 41309 La Rinconada, Spain. [2]Department of Crop Protection, Institute for Sustainable Agriculture (IAS), Spanish National Research Council (CSIC), Alameda del Obispo s/n, 14004 Córdoba, Spain. E-mail: lmolinero@ias.csic.es*

The incidence of *Verticillium dahliae* (*Vd*) affecting sunflower in France, Italy, Spain and countries around Black Sea has greatly increased in the last five years, becoming a major constraint for sunflower production in some regions. Twenty Isolates of *Vd* collected in these countries, and one from Argentina, were characterized under a multidisciplinary study. The isolates were inoculated, by root immersion in suspensions of conidia, to seven sunflower genotypes with different phenotypic responses according to previous experiments. Some of the isolates were also inoculated onto different hosts (artichoke, eggplant, cotton, tomato and lettuce) to determine the host pathogenicity spectrum of *Vd* from sunflower. The vegetative compatibility groups (VCGs) were determined through complementation between nit mutants of the fungal isolates and VCG reference strains. Phenotypic and genetic data indicated that the isolates from Black Sea countries were distinguishable from those from West Europe and Argentina, which could be due to the presence of at least two different races. Artichoke was very susceptible to all the isolates and significant crop × *Vd* isolate interactions were found for disease variables. Ongoing experiments using SSR reference markers for *Vd* will provide extensive information about the molecular structure of populations from sunflower and the re-