12. SURVEY ON SANITARY STATUS OF NATIVE *VITIS VINIFERA* VARIETIES IN GEORGIA. **P. Casati[1], D. Maghradze[2], F. Quaglino[1], A. Ravasio[1], O. Failla[1], P.A. Bianco[1].** *[1]Department of Agricultural and Environmental Sciences - Production, Landscape, Agroenergy (DISAA), University of Milano, Via Giovanni Celoria 2, I-20133 Milano, Italy. [2]Institute of Horticulture, Viticulture and Oenology, Agricultural University of Georgia, David Aghmashenebeli Alley13-th Km, 0159 Tbilisi, Georgia. E-mail: piero.bianco@unimi.it*

In September 2013, a survey was carried out in three collections representing the native Georgian *Vitis vinifera* germplasm, located in Saguramo (Shida Kartli Region), Shumi and Kindzmaraulis (Khaketi Region). Leaf samples were collected from 37 plants of 12 white and 13 red berry varieties showing symptoms of viral diseases, such as leaf rolling and chromatic alterations, with different symptom severity. Total RNAs were extracted from leaves and PCR-based reactions were performed with specific primer pairs to identify *Grapevine rupestris stem pitting-associated virus* (GRSPaV), *Grapevine leaf roll-associated virus 1*, 2, and *3* (GLRaV-1, GLRaV-2 and GLRaV-3), *Grapevine virus A* (GVA), and *Grapevine pinot gris virus* (GPGV). Obtained results revealed the prevalence of GRSPaV (mainly strains of groups 2a and 2b, associated with vein necrosis of 110R, identified in 29 out of 37 plants) and GLRaV-3 (identified in 26 out of 37 plants). Surprisingly, GLRaV-1 and GVA were detected in few plants (three out of 37), always in mixed infection with GLRaV-3. As expected, GLRaV-2 was identified only in two plants. Moreover, GPGV, a *Trichovirus* recently reported in Europe and Korea, was detected in 7 plants of six varieties (Goruli mtsvane, Khikvi, Mtsvane kviteli, Saperavi pachkha, Tavkveri, Korkaula), always in mixed infection with GRSPaV, GLRaV-3 and GVA. Since the response of the Georgian grapevine varieties to the pathogens has not been accurately described, further investigation will be needed to determine the typical symptoms associated with grapevine viruses and to evaluate their potential effects on yield and wine quality.

13. DETECTION AND MOLECULAR CHARACTERIZATION OF A *BADNAVIRUS* IN AN AUTOCHTHONOUS GRAPE FROM APULIA (ITALY). **M. Chiumenti[1], M. Morelli[1], A. Giampetruzzi[1], F. Palmisano[2], V.N. Savino[2,3], P. La Notte[1,2], G.P. Martelli[3], P. Saldarelli[1].** *[1]National Research Council of Italy, Institute for Sustainable Plant Protection (IPSP), Via G. Amendola 122/D, I-70126 Bari, Italy. [2]Centre for Research, Experimentation and Education in Agriculture (CRSFA) "Basile Caramia", Via Cisternino 281, I-70010 Locorotondo (BA), Italy. [3]Department of Soil, Plant and Food Sciences (DiSSPA), University of Bari "Aldo Moro", Via G. Amendola 165/A, I-70126 Bari, Italy. E-mail: michela.chiumenti@ipsp.cnr.it*

Vegetative propagation of grapevines favours the perpetuation and dissemination in nature of intracellular pathogens (over than 70 considering viruses, viroids and phytoplasmas). Once in the field, their presence may affect in various ways the plant's yield and its quality. Preventing infection spreading through a prompt identification, characterization and exclusion approach, is still the most effective action of containment. To this aim, in 2014, registered native grapevine cultivars from Apulia were analyzed to determine their "absolute" sanitary status (virome), i.e. the totality of the infectious agents present in any single accession using a High Throughput Sequencing (HTS) approach. Small RNA libraries were therefore synthesized and analyzed for the presence virus/viroid sequences. Among these, a symptomless accession D205 of cv. "Bombino nero" growing in a foundation block showed the presence of 21 contigs (ranging from 329 to 56 nt in length) identified as *Badnavirus*-like. Using the closest *Badnavirus* found by BLASTX search as a reference sequence, i.e. *Fig Badnavirus 1* (FBV-1, accession No. NC017830), a set of specific primers was designed. Amplification with these primers produced the expected amplicon, which has 91% nucleotide identity with a *Badnavirus* recently discovered in Greece and denoted *Grapevine roditis leaf discoloration-associated virus* (GRLDaV). For a preliminary assessment of the incidence of this virus in the field, a preliminary survey in the same foundation block was conducted. A total of 11 samples from different autochthonous cultivars were checked by PCR but none of them tested positive.

14. CHARACTERIZATION AND PATHOGENICITY OF FUNGAL SPECIES ASSOCIATED WITH EUCALYPT DIEBACK IN SARDINIA (ITALY). **A. Deidda, B.T. Linaldeddu, B. Scanu, A. Franceschini.** *Department of Agriculture, University of Sassari, Viale Italia 39, I-07100 Sassari, Italy. E-mail: adeidda@uniss.it*

Due to their rapid growth and adaptability to different environmental conditions, *Eucalyptus* species have been widely introduced in both hemispheres for pulpwood production. In Sardinia (Italy), eucalypt plantations were established in the 20th Century primarily in areas reclaimed from marshland and subsequently all over the island where they are currently cultivated as ornamental plants, windbreaks and for honey production. In recent years, a severe and unusual disease of unknown aetiology has been observed in several artificially established plantations of *Eucalyptus camaldulensis* throughout the island. The affected plants showed leaf chlorosis, crown thinning, shoot and branch dieback, sunken cankers, epicormic shoots and exudations of Kino. Since there is no information about this unusual disease and given the high ecological and economic relevance of these ecosystems, in 2013 a survey was carried out to establish the causal agents involved in the aetiology of the disease. Isolations from 510 symptomatic woody samples yielded a total of 489 fungal isolates belonging to three distinct families, namely *Botryosphaeriaceae*, *Diaporthaceae* and *Valsaceae*. On the basis of morphological features and DNA sequence data (ITS), seven distinct species: *Diaporthe foeniculina*, *Neofusicoccum australe*, *N. luteum*, *N. mediterraneum*, *N. parvum*, *N. vitifusiforme* and *Valsa fabianae* were identified. In addition, two putative new species of *Cytospora* were obtained. *Neofusicoccum australe* was the only species recovered in all surveyed sites and its isolation frequencies ranged from 51 to 95%. Pathogenicity trials on *E. camaldulensis* trees showed that only the *Neofusicoccum* species, with the exception of *N. vitifusiforme*, are pathogenic on this host.

15. *XANTHOMONAS EUVESICATORIA* IN PEPPER SEEDS: IMPLEMENTATION OF ITS DETECTION AND PRELIMINARY STUDY ON ITS GENETIC FINGERPRINTS. **M. Ferrari[1], B. Xhemali[1,2], D. Giovanardi[1], F. Valentini[2], M. Ignjatov[3], R. Jevtić[3], E. Stefani[1].** *[1]Department of Life Sciences, University of Modena and Reggio Emilia, Via Amendola 2, I-42122 Reggio Emilia, Italy. [2]Centre International de Hautes Etudes Agronomiques Méditerranéennes (CIHEAM-IAMB), Via Ceglie 9, I-70010 Valenzano (BA), Italy. [3]Institute of Field and Vegetable Crops, Maksima Gorkog 30, 21000 Novi Sad, Serbia. E-mail: michele.ferrari@unimore.it*

The bacterial spot of pepper is a destructive disease and its causal agent was formerly known as *Xanthomonas campestris* pv. *vesicatoria*, later reclassified in four different species: *X. vesicatoria*, *X. euvesicatoria*, *X. perforans* and *X. gardneri*. All four species are seed-borne and regulated. *Xanthomonas euvesicatoria* is particularly aggressive on pepper and its detection and identification, particularly in seed lots, is the key for a safe pepper production. We compared a conventional serological detection method (ELISA) with the direct isolation and identification of the pathogen, and with a specific molecular detection (simplex-PCR), but following two