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In Tunisia, citrus faces salinity problems especially in coastal areas where several aquifers are reported to be affected by seawater intrusion. Citrus orchards are endangered by citrus tristeza virus (CTV) and consequently Tunisian growers are now replacing sour orange, the commonly used rootstock sensitive to this disease, by tolerant rootstocks. This work aims to study the response to saline water irrigation of two old years trees of *Citrus clementina* var. *Hernandina* and *Citrus sinensis* var. *Washington Navel* grafted on five CTV tolerant rootstocks (Citrange C35, Citrange Carrizo, Citrumelo Swingle 4475, Volkamer Lemon and Cleopatra Mandarin) and on sour orange as control, through symptomatic observations and morphological analysis. The experiment was performed under field conditions in a sandy loamy non saline soil at the experimental station of the INRGREF situated at the Cap Bon peninsula in Tunisia. Trees were irrigated twice a week according to citrus water requirements based on Penman Monteith equation and the electrical conductivity of irrigation water was about 4 dS/m. For the two citrus species, the intensity and frequency of chlorosis symptoms appeared after 6 months of saline water irrigation to assess the sensitivity of combinations grafted on different tolerant rootstocks were measured. The tree canopy volume estimated with hemispherical photography treated with CANY-EYE software showed that the greatest canopy was with Volkamer Lemon, followed by Cleopatra mandarin and Sour orange. The same trend was observed in relation to growth rate diameter, plant height and pruning wood biomass. Moreover, Washington navel orange showed more tolerance to chlorosis than *Hernadina clementina*. Differences between citrus combinations were more pronounced with *Hernadina* than with *Washington Navel*.

V32

MOLECULAR INSIGHTS INTO CITRUS TRISTEZA VIRUS (CTV) GENOTYPES RECOVERED FROM SYRIA. Raied Abou Kubaa¹, Insaf Akel², Elia Choueiri³, Rehab Hamdan², Ali El-Khatib², Imad Ismail⁴ and Maria Saponari¹. (1) CNR, Institute for Sustainable Plant Protection, via Amendola 122/D, 70126 Bari, Italy, Email: raied.aboukubaa@ipsp.cnr.it; (2) General Commission for Scientific Agricultural Research, Lattakia, Syria; (3) Department of Plant Protection, Lebanese Agricultural Research Institute, Tal Amara, PO Box 287, Zahlé, Lebanon; (4) Plant Protection Department, Faculty of Agriculture, Tishreen University, Lattakia, Syria.

Citrus tristeza virus (CTV) (genus *Closterovirus*, family *Closteroviridae*) is one of the most economically important citrus viruses threatening citrus industry, characterized by a large biological and molecular diversity, i.e. viral strains categorized from mild to severe according to the type and severity of symptoms. After the first finding of CTV in Syria in 2006, several subsequent studies have been carried out to identify the genotype(s) associated with the

viral infections occurring in the infected areas, either through molecular tests based on (1) reverse-transcription polymerase chain reaction (RT-PCR) with multiple molecular markers (MMM), (2) single-strand conformation polymorphism (SSCP) analysis of the coat protein (CP) gene, or (3) by biological indexing on indicator woody plants. In the present study, CTV isolates recovered from Lattakia, Jableh and Tartous (the Syrian coastal region) during 2017 were graft inoculated onto different indicator plants (*Citrus aurantifolia*, *C. aurantium* cv *Madam vinous* and *C. paradise* cv *Duncan*). Each isolate was grafted in three replications and the new shoots inspected for foliar symptoms and growth alterations, including stem pitting. The presence of CTV was confirmed by a TaqMan-based quantitative real-time RT-PCR (qPCR) for broad spectrum detection. Furthermore, to differentiate CTV genotypes, a one-step multiplex real-time RT-PCR assay was carried out using TaqMan probes and primers that can distinguish T3 and VT (virulent genotype) from T30 (mild genotype). Results showed different symptoms on indicator plants, particularly on leaves such as leaf cupping, yellowing and stunting. However, even up to one year, no severe stem pitting symptoms were observed. Molecular tests confirmed the occurrence of VT-like genotypes associated with several field infections. The VT-genotypes are generally associated with severe field symptoms in other citrus growing areas, as also confirmed by the development of severe stunting and yellowing detected in our bioassay on *Madame Vinous* and *Duncan* grapefruit. It is therefore important to monitor and prevent the further spread of the isolates harboring the VT-genotypes, which under different management conditions and in presence of different scion/rootstock combinations may cause severe damage to the citrus crops.

V33

CHARACTERIZATION OF FAB A BEAN AND CHICKPEA VIRUSES CAUSING YELLOWING AND STUNTING SYMPTOMS IN TUNISIA. Samia Mghandef^{1,2}, Safaa G. Kumari² and Asma Najjar³. (1) Faculté des Sciences de Bizerte, Bizerte, Tunisia, Email: mghandefsamia91@gmail.com; (2) International Center for Agricultural Research in the Dry Areas (ICARDA), Terbol Station, Beka's Valley, Zahle, Lebanon; (3) National Agricultural Research Institute of Tunisia (INRAT), Ariana, Tunisia.

In Tunisia, faba bean (*Vicia faba*) and chickpea (*Cicer arietinum*) are considered as strategic crops because of their economic and social relevance and significant direct contribution towards the national food balance. However, production levels of these crops remain quite low which is often attributed to abiotic and biotic stresses that are prevailing in the major growing areas. Viruses causing yellowing and stunting symptoms represent one of the major constraints that reduce the genetic potential of most cultivated species and varieties. To characterize these viruses in Tunisia, field surveys were conducted in five main regions (Béja, Bizerte, Cap-Bon, Jendouba and Kef) during 2018 and 2019 growing seasons. A total of 389 faba bean and 182 chickpea samples with yellowing and stunting symptoms were collected and tested by tissue blot immunoassay

(TBIA) using specific monoclonal antibodies (MAbs). Laboratory results showed that Chickpea chlorotic stunt virus (CpCSV) was the most common virus detected in 47.6% of faba bean and 18.7% of chickpea tested samples, followed by Beet western yellows virus (BWYV) (28% in faba bean and 4.4% in chickpea). Whereas, only 8.8% of faba bean samples were infected with Faba bean necrotic yellows virus (FBNYV), and Bean leafroll virus (BLRV) in faba bean (6.7%) and chickpea (9%) samples. To confirm the presence of yellowing viruses in Tunisia, total RNA was extracted from 5 faba bean and 27 chickpea samples that showed positive reaction to BLRV MAb (8 samples: 2 faba bean, 6 chickpea), BWYV MAb (7 samples: 2 faba bean, 5 chickpea) and CpCSV MAb (17 samples: 1 faba bean, 16 chickpea). Reverse transcription-polymerase chain reaction (RT-PCR) was performed using specific luteovirus primer pairs. RT-PCR amplicons of the expected size of each primer were obtained from 32 samples and were sequenced in both directions. Molecular results showed that BWYV and CpCSV (both belong to genus *Polerovirus*, family *Solemoviridae*) and BLRV (belong to genus *Luteovirus*, family *Tombusviridae*) were identified in Tunisia, and the coat protein nucleotide sequence analysis of the Tunisian isolates showed 99% homology to Moroccan isolate (CpCSV), 97% homology to the French isolate (BWYV), and 98% homology to Argentina isolate (BLRV).

V34

OCCURRENCE OF STONE FRUIT VIRUSES IN TUNISIAN GERmplasm COLLECTIONS. Ilhem Selmi and Naima Mahfoudhi, Laboratory of Plant Protection, National Institute of Agronomic Research of Tunisia (INRAT), El Menzah, Tunis, Tunisia, Email: ilhemselmi@hotmail.com

Stone fruit trees are traditionally grown in Tunisia, with a total cultivated area of 266,250 ha. However, stone fruits are affected by several viruses which cause damage whether in terms of yield or fruit quality. Among them *Ilarvirus* and *Foveavirus* occupy an important position due to their worldwide distribution. To assess the sanitary status of Tunisian stone fruit species, surveys were conducted in the stone fruit germplasm collections, which represent a rich patrimony and the budwood source for mother blocks for orchards and nurseries in Tunisia, thus indicated their potential role in spread of virus diseases into new plantings. A total of 268 samples collected from almond (62), peach (70), apricot (72), and plum (64), were tested for the presence of Prunus necrotic ring spot virus (PNRSV) (*Ilarvirus*), Prune dwarf virus (PDV) (*Ilarvirus*) and Apricot latent virus (ApLV) (*Foveavirus*), by RT-PCR using primers specific for each virus. Molecular analysis showed that 46.6% of tested samples were infected with at least one virus. Among infected samples, 42.9% were single infections and 3.7% were mixed infections. PNRSV was the most frequently encountered virus with an infection rate reaching 37.7%, followed by PDV (9.3%) and ApLV (4.5%). With an infection rate of 68.6%, peach was the most infected species, followed by apricot (51.4%) and almond (38.7%). Whereas plum was the least infected, with an infection rate of 28.1%.

V35

BARLEY YELLOW DWARF VIRUS IN MAIZE IN TUNISIA: DETECTION AND MOLECULAR CHARACTERIZATION. Imen Hamdi¹, Asma Najjar¹, Hajer Ben Ghanem², Arvind Varsani³ and Ahmed Jemali¹. (1) Laboratoire de Protection des Végétaux, Institut National de la Recherche Agronomique de Tunisie, El Menzah, Tunisie, Email: imenhamdi@yahoo.fr; (2) Laboratoire de Grandes Cultures, Institut National de la Recherche Agronomique de Tunisie, El Menzah, Tunisie; (3) The Biodesign Center for Fundamental and Applied Microbiomics, Center for Evolution and Medicine, School of Life sciences, Arizona State University, Tempe, USA.

Barley yellow dwarf virus (BYDV) complex causes one of the economically most important viral diseases of cereals worldwide, with significant yield losses in major cereal crops such as wheat, barley, rice, maize and oat. BYDV has been identified on barley and wheat in Tunisia since 2000. As summer crop, maize (*Zea mays*) could be an important reservoir of BYDV and may serve as a potential source of early virus infection to small grains. In this regard, a field survey was conducted during spring of 2018 in the northeastern region (El Alia, governorate of Bizerte) of Tunisia. A total of 140 samples were randomly collected from five maize fields and were tested by tissue-blot immunoassay (TBIA) using polyclonal antibodies provided by ICARDA's virology laboratory. Fifty-two maize samples (37%) were found positive for BYDV. In parallel, 38 out of 52 (73%) maize samples tested by DAS-ELISA using a polyclonal antibody raised against BYDV-PAV were positive, suggesting a prevalence of BYDV-PAV in maize in Tunisia. The occurrence of BYDV-PAV was further confirmed by RT-PCR using Total RNA and specific BYDV-PAV primer pairs. An amplicon of the expected size was obtained for all ELISA-positive samples. Then, four amplicons were randomly selected and used for Sanger sequencing. The four BYDV-PAV sequences (GenBank accession No#MK224487-MK224489 and MK224491) share >96% identity amongst them and with sequences of BYDV-PAV isolates from barley in Tunisia (KJ467220-23 and KJ410741) and Iowa-USA (KY593457), and from wheat in Kansas-USA (KU170668).

V36

STUDY OF FIG MOSAIC DISEASE IN TUNISIA: RELATION BETWEEN VIRUSES AND SYMPTOMS EXPRESSION. Manel Elair¹, Ikhlas Skhiri² and Naima Mahfoudhi¹. (1) Laboratoire de Protection des Végétaux, Institut National de la Recherche Agronomique de Tunisie, Université Tunis-Carthage, El Menzah, Tunis, Tunisia, Email: manel_elair@hotmail.com; (2) École Supérieure d'Agriculture du Kef, Université Jendouba, Tunisia.

Fig (*Ficus carica*L.) tree is a typical Mediterranean fruit crop of Middle eastern origin that is characterized by large adaptation to various ecological areas. In Tunisia fig tree has been cultivated traditionally since many decades and covers all areas throughout the country. Fig mosaic disease (FMD) is the most serious pathological constraint of fig production that affect figs worldwide. Affected trees show extremely variable mosaic symptoms on leaves and fruits, and can exhibit defoliation and premature fruit drop. To date,