

while HTS provided a comprehensive overview of viral and viroid diversity at the genomic level. The findings of this study contribute to a better understanding of viral infections affecting grapevine production in Algeria. The application of advanced diagnostic tools supports the development of improved disease surveillance and management strategies, ultimately aiding in the protection of vineyards and the sustainability of grapevine cultivation in the region.

V4

DETECTION AND IDENTIFICATION OF TOMATO BROWN RUGOSE FRUIT VIRUS IN COMMERCIAL TOMATO VARIETIES IN PALESTINE, AND ASSESSMENT OF THEIR TOLERANCE USING NEXT GENERATION SEQUENCING (NGS) TECHNOLOGY. Osama Alabdallah^{1*}, Raed Alkownie² and Ibrahim Abbassi³. (1) National Agricultural Research Center (NARC) MoA, Palestine; (2) Biology and Biotechnology Department, Faculty of Science, An-Najah National University, Nablus, Palestine; (3) Microbiology department, Al-Quds University, Palestine. *Email: oalabdallah@gmail.com

Tomato, a high-value cash crop, is susceptible to infection with several viruses that cause significant yield losses. Recently, an unusual viral disease syndrome commonly associated with tomato mosaic virus was observed in northern Palestine. A study aimed at revealing the identity of the causal disease agent, identified the presence of a previously unreported tobamovirus in Palestine. The virus genome was entirely sequenced and shown to be composed of 6391 nucleotides. Sequence analysis indicated that this virus was an isolate of tomato brown rugose fruit virus (TBRFV). This is the first report of TBRFV on tomatoes in Palestine, and the name tomato brown rugose fruit virus-Palestinian isolate (TBRFV-Ps) was suggested. Molecular tools were developed for specific detection of the virus. Moreover, 15 different commercial tomato varieties commonly used by farmers were assessed for their tolerance to TBRFV infection using NGS technology. The tomato plants were inoculated with TBRFV and the typical viral symptoms were produced on different varieties. The plant samples were collected at different times of the growing period to assess and quantify the viral infection. The NGS sequence data was transformed into actual viral load for each individually analysed sample. The results revealed that eight varieties exhibited tolerance to TBRFV infection. Based on our findings, NGS technology proves to be a highly sensitive and comprehensive approach for the diagnosis and quantification of plant viral infections.

V5

FIRST REPORT OF MULBERRY BADNAVIRUS-1 (MaBadV-1) AND MULBERRY CRYPTIC VIRUS 1 (MaCrV-1) INFECTING MULBERRY, MORUS ALBA IN SAUDI ARABIA. Mahmoud Ahmed Amer, Muhammad Amir, Ibrahim M Al-Shahwan, Muhammad Ali Al-Saleh*, Plant Protection Department, College of Food and Agriculture Sciences, King Saud University, P.O. Box 2460, Riyadh, 11451, Saudi Arabia. *Email: malsaleh@yahoo.com

The mulberry, *Morus alba*, is a deciduous tree that has been cultivated for thousands of years in China. It is a member of the genus *Morus* within the Moraceae family. Viral infections have the potential to significantly reduce the mulberry yield and quality, which would be extremely detrimental to the sericulture sector. In a field survey conducted in 2022, twenty plant samples that showed symptoms suggestive of virus infection such as mosaic, interveinal yellowing and cupping of leaves were collected from Bisha, Saudi Arabia. Furthermore, these samples were analyzed by PCR and RT-PCR. Amplification was carried out against two viruses, Mulberry badnavirus-1 (MaBadV-1), (family *Geminiviridae*) and Mulberry cryptic virus-1 (MaCrV-1), (family *Partitiviridae*) with two specific pair of primers MuBadV1-F:5'-gcagttgccatcagctcagaa-3', MuBadV1-R:5'-tactgagactgcgacgtagtc-3' and MaCrV-CP-F:5'-atggataacctgaacaagacg-3', MaCrV-CP-R: 5'-ttaatcacggtagctcgagct-3, respectively. The results obtained showed that MaBadV-1 was detected in 10 samples (50%) and the amplified fragment was at the expected size of 920 bp. However, MaCrV-1 was detected in 3 samples (15%) and the amplified fragment was as expected (1254 bp). After sequence analysis of the two Saudi Arabian isolates MaBadV-1 and MaCrV-1, the following sequences were submitted to the NCBI, GenBank database under the following accession numbers: PP259111 (MaBadV-1), PP259112 (MaBadV-1), PP259113 (MaCrV-1) and PP259114 (MaCrV-1). The collective phylogenetic tree of the two isolates of each MaBadV-1 and MaCrV-1 exhibited two separated clades. Whereas nucleotide identity of two MaBadV-1 Saudi Arabian isolates showed 99.1% identity among themselves, and 95.9-96.5% with an Italian isolate of MaBadV-1 and 95.6%-96.2% with a Lebanese isolate of MaBadV-1. In case of the two MaCrV-1-Saudi Arabian isolates, both showed 100% identity among themselves, whereas the similarity observed with a USA and United Kingdom isolates were 81.9% and 82.7%, respectively. Thus, to our knowledge, this is the first report of MaBadV-1 and MaCrV-1 in Saudi Arabia.

V6

ASSESSMENT OF THE SANITARY STATUS OF CITRUS IN PALESTINE. Raed Alkowni^{1*}, Osama Alabdallah², Nuha Shalabi¹, Mohammad Abo Eid², Samer Jarrar³ and Raied Abou Kubaa⁴. (1) Department of Biology and Biotechnology, An-Najah National University, Nablus, Palestine; (2) National Agricultural Research Center (NARC), Jenin, Palestine; (3) Nablus University for Vocational and Technical Education, Nablus, Palestine; (4) Department of Plant Pathology, University of California, Davis, CA 95616, USA. *Email: ralkowni@najah.edu

Citrus hosts several viruses and viroids. This study aimed to assess the phytosanitary status of citrus trees in the northern part of the West Bank in Palestine in terms of infection with viruses such as Citrus tristeza virus (CTV), Citrus psorosis virus (CPsV), Citrus leaf blotch virus (CLBV), and Citrus variegation virus (CVV). A total of 1,000 samples were collected and tested for CTV using Direct Tissue Blot Immunoassay (DTBIA), while a representative subset (10–25%) of these samples was processed for CPsV, CVV and CLBV using DAS-ELISA

and RT-PCR. Additionally, Mexican lime and citron were used as indicator plants in bioassays on 10% of the samples to detect the presence of any graft-transmissible virus. As a result, these indicator plants exhibited vein corking, leaf discoloration, and vein clearing, which are characteristic symptoms of CTV infection. CTV was the only virus detected in the tested samples, in all districts surveyed. The incidence of infection varied by district; for instance, CTV infection reached 23.5% in the Qalqiliya region, followed by the Nablus districts (12%), while Tulkarm exhibited a lower incidence (6%). Overall, the CTV incidence reached 10.9%, with the highest infections observed on Pomelo, Clementine, and Valencia orange cultivars; meanwhile, no infections were detected in grapefruits and Fransawi oranges. Interestingly, the infection rate in nurseries was recorded as high as 4%. The variation in incidence may be attributed to differences in citrus varieties and agricultural practices followed. According to the findings of this study, CTV continues to pose a threat to the citrus production in Palestine. This study further reinforces the effectiveness of the DTBIA for CTV surveillance in large-scale monitoring programs, emphasizing its practical application in routine nursery testing. This method proved effective and practical for large-scale detection, supporting its strong recommendation for nurseries monitoring programs. The dissemination and distribution of healthy propagating materials to farmers and the sanitary selection of suitable rootstock are crucial steps in significantly improving citrus health, and therefore highly recommended. Future research should focus on the genetic diversity of CTV strains in Palestine and the potential implementation of certified virus-free planting programs.

V7

SANITARY ASSESSMENT OF SOLANACEOUS CROPS IN LEBANON AND SYRIA. Elia Choueiri^{1*},

Fouad Jreijiri¹, Khaled Heinoun² and Raied Abou Kubaa³. (1) Department of Plant Protection, Lebanese Agricultural Research Institute, Tal Amara, P.O. Box 287, Zahlé, Lebanon; (2) Ministry of Agriculture and Agrarian Reform, Department of Plant Protection, Damascus, Syria; (3) Department of Plant Pathology, University of California, Davis, USA. *Email: echoueiri@lari.gov.lb

Potatoes, eggplants and peppers are among the most widely grown solanaceous crops in Lebanon and Syria and are considered an important crop, representing a significant source of income for growers. However, plant viruses are among the major pathogens affecting solanaceous crops, resulting in considerable losses in yield and fruit quality and consequently negatively impacting farmers' income. In Lebanon and Syria, during the last twenty years, field surveys were undertaken, and many viruses were recorded on these vegetable crops. The main potato viruses in both countries were PVY, PLRV, PVX, PVS and PVM. Accordingly, field observations and laboratory tests indicated that PVY was the major virus problem. PVA was found in Lebanon, while AMV, CMV, PAMV and PYDV were encountered in Syria. Mild and severe mosaic, rugosity and crinkling of leaves were the most common symptoms observed on plants infected with PVY, in addition to PTNRD caused by PVY^{NTN} recorded in certain varieties in Lebanon.

The viral infections causing severe disease in eggplant plants collected from Lebanon showed that PVY was the most prevalent virus detected by ELISA, followed by EMDV and CMV, while PVX was found highly present in the tested plants by PCR. Disease symptoms on eggplant plants consisted of leaf mottling and plant dwarfing mainly due to infection with EMDV, mosaic due to infection with PVY, chlorotic spots and mosaic due to infection with CMV and ring spots due to infection with PVX. Concerning pepper cultivation, CMV was the most widespread virus in Syria, in addition to AMV, TSWV, PVY and TMV. However, in Lebanon, TSWV was the most common. Recently, ToBRFV characterized by chlorosis, mosaic and fruit deformation and pepper plants showing symptoms suggestive of virus infection were found infected by BPEV and occurred in Syria and Lebanon. These findings highlight the widespread occurrence and diversity of viruses affecting solanaceous crops in Lebanon and Syria.

V8

SOUTHERN BEAN MOSAIC VIRUS: THE ECONOMIC SIGNIFICANCE FOR RUSSIAN FEDERATION AND NEW DIAGNOSTIC METHODS.

Bondarenko Galina Nikolaevna^{1,2*}, Magomedova Kalimat Nurudinovna¹ and Shilkina Natalia Konstantinovna^{1,2}. (1) Institution All-Russian Plant Quarantine Center, P.O. Box 140150, Moscow, Russia; (2) Russian University of Friendship by Patrice Lumumba, Russia, Moscow. *Email: bondarenko.galina@vniikr.ru

Southern bean mosaic virus (SBMV), the type species of the genus *Sobemovirus*, is a pathogen affecting key leguminous crops, including soybean, *Glycine max* (L.) Merr., common bean, *Phaseolus vulgaris* L., and cowpea, *Vigna unguiculata* (L.) Walp. SBMV induces chlorosis, mosaic leaf pattern, leaf deformation (curling), and reduced productivity in host plants. Its spread poses a significant threat to Russia's agro-industrial sector, where legume cultivation occupied 1.7 million hectares and soybean cultivation 4.3 million hectares in 2024. Soybean production has intensified in the Central Black Earth region (Kursk, Belgorod Oblasts), the Far East (Amur Oblast - 22% of national soybean acreage), and Siberia. Over the past two decades, global soybean cultivation areas have increased by 2.5 times (to 58 million hectares), and seed production has quadrupled (reaching around 100 million tons), indicating the crop's economic importance. This study analyzed the molecular-genetic features of SBMV and phylogenetically related *Sobemovirus* species. Building on previous research, detection methods were upgraded to include PCR with electrophoretic detection. Genome sequencing of an SBMV isolate enabled the development of specific oligonucleotide primers and a fluorescent probe for real-time PCR, resulting in a patent (No. 2025109585). These advancements improved diagnostic accuracy, mitigate phytosanitary restrictions from importers (e.g., China, the EU), and ensure stable legume exports, which totaled 1.4–1.5 million tons in 2023. Future research will focus on studying virus vectors and developing improved plant protection strategies.