Disease Note

Diseases Caused by Viruses

First Report of the Detection of Soybean Vein Necrosis Virus (SVNV) in Peanut in the United States

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During the screening of peanuts (*Arachis hypogaea* L.) for tomato spotted wilt virus (TSWV) in 2024, 36 plant samples expressing symptoms of tomato spotted wilt were collected from three locations in Alabama: Brewton Agricultural Research Unit (BARU), Brewton, AL; Wiregrass Research and Extension Center (WGREC), Headland, AL; and Gulf Coast Research and Extension Center (GCREC), Fairhope, AL. Foliar necrosis symptoms, not typically associated with TSWV, were also observed in all samples. Symptoms varied from moderate light brown to severe dark necrosis along the midveins and lateral veins. Samples were tested for four orthotospoviruses: TSWV, groundnut ringspot virus (GRSV), tomato chlorotic spot virus (TCSV), and soybean vein necrosis virus (SVNV) using ELISA (Agdia Inc., Elkhart, IN). All samples were positive for TSWV and negative for both GRSV and TCSV; however, one sample tested positive for SVNV (BARU 4). SVNV was previously reported not to infect peanuts (Zhou and Tzanetakis 2013). The 36 samples were subjected to RT-PCR using specific primers for the nucleocapsid (N) protein of SVNV (Shehata et al. 2024). Twenty-four of 36 samples were positive for SVNV (12 from BARU, two from WGREC, and 10 from GCREC). The amplified bands showed lower intensity than the positive control, possibly indicating a low titer of SVNV, which may explain the negative ELISAs. Following the manufacturer's instructions, these bands were cloned using the CloneJET PCR Cloning Kit (Thermo Fisher Scientific) and sent for Sanger sequencing. The resulting SVNV-N sequences were submitted to GenBank under accessions PQ821900 to PQ821905. The sequences demonstrated 98.19% nucleotide and 96.75% amino acid identities with SVNV from Tennessee (GCF_004789395.1). Nine conserved amino acid mutations were identified compared with the Tennessee strain, resembling those found in soybeans (Shehata et al. 2024). Additionally, RT-PCR was also used for TSWV-N detection (Martin et al. 2025), and 26 samples tested positive (12 from BARU, three from WGREC, and 11 from GCREC), which confirmed the presence of both SVNV and TSWV in positive samples. Further research is necessary to investigate co-infection between SVNV and TSWV, potential genome reassortment, and its mechanisms to understand the interactions between these viruses. These interactions could adversely impact legume production in Alabama, valued at $315 million in 2023 (soybean and peanut, USDA 2023). Since both TSWV and SVNV are transmitted by tobacco thrips (*Frankliniella fusca*) (Hameed et al. 2022; Keough et al. 2016), this is likely how SVNV was introduced to peanuts. This constitutes the first report on the detection of SVNV in peanuts in the United States, suggesting that SVNV has been adapting to new hosts since its discovery (Tzanetakis et al. 2009; Zhou et al. 2018).

References:

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