Statewide Monitoring and Molecular Characterization of Viral Diseases of Georgia Peanut

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Virus diseases, mainly tomato spotted wilt virus (TSWV), has a great potential economic impact on peanut production in Georgia. Typical symptoms of tomato spotted wilt virus include necrosis (primarily leaves and stems), chlorosis, ring patterns, mosaic, mottling, stunting, and local lesions. To minimize the impact of TSWV and other virus diseases, it is essential to have an up-to-date survey record in Georgia. In this study, we conducted a statewide virus disease survey for monitoring virus isolates present and examine the causes of the increasing virus disease pressure on peanut production in Georgia. In May through August 2019, a total of 380 peanut leaf samples were collected from peanut sites in 19 Georgia counties (20 samples/county) and tested for the presence of the TSWV or other viruses. The collected samples were evaluated for TSWV or other virus presence using ImmunoStrip, ELISA and RT- PCR methods at the Molecular Diagnostic Laboratory in Tifton. In total, 351/380 (92.3%) samples tested positive for TSWV by RT-PCR, with 29/380 (7.6%) negative. To rule out the possibility of the presence of others tospoviruses, we have tested TSWV negative samples with other virus markers. Our results showed negative for groundnut ringspot virus (GRSV) and tomato chlorotic spot virus (TCSV) which were reported in Florida but have not been reported in Georgia. On the basis of these results, we hypothesized that all of these TSWV negative sample symptoms might non-pathogenic (nutrition problems) or infected with untested pathogens. It is well reported that the severity of TSWV epidemics fluctuates significantly from year to year. This variability has not yet been fully explained; however, this may be linked to the introduction of a new, severe strain of TSWV or mutations caused by TSWV strains mixing. To investigate this issue, we have amplified and sequenced a 587 bp region of the N gene (nucleoprotein gene-S RNA) from 10 TSWV positive samples. After comparing among themselves and with one published sequence of TSWV-GA isolate, our results indicated that the sequences among the N gene showed highly identical, ranging from 97%-99% at both nucleotides and amino acid levels. Due to the limited extent of sequence variability within a small number of TSWV isolates, no significant relationships were identified among populations. We also compared the efficiency and the functionality of the three most common detection methods to identify TSWV. Our result showed that RT-PCR was the most sensitive and reliable assay but requires a laboratory setting with a real-time thermocycler. The immunostip method was not only the fastest, but also is portable for field detection. DAS-ELISA was the least sensitive assay in this study and requires lengthy, time consuming work from skilled labor to perform. Based on our survey results, only one virus disease, TSWV, was found in Georgia peanut. The slight variation of the N gene among TSWV isolates in peanut might have a potential role for the fluctuation of severity, but further study would be required to establish the relationship between amino acid changes with disease severity of TSWV in peanut.