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ARTICLE

Field Screening for Tomato Spotted Wilt and White Mold (Stem Rot) Resistance among Peanut Genotypes.

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ABSTRACT

White mold (WM), stem rot, and southern blight are common names for the same soilborne peanut (*Arachis hypogaea* L.) disease caused by *Athelia rolfsii* (Curzi) C. C. Tu & Kimbr. = *Sclerotium rolfsii* Sacc. Tomato spotted wilt is a systemic foliar peanut disease caused by *Tomato spotted wilt virus* (TSWV). The objective of this study was to screen several currently available peanut genotypes (cultivars and breeding lines) for combined general field resistance to both of these diseases. Results from these field tests showed significant differences (P≤0.05) among the peanut genotypes evaluated for combined resistance to both WM and TSWV. The overall three-year (2018-20) average found that 'Georgia-12Y' had among the lowest percent incidence of mid-season TSWV, mid-late season TSWV+WM, late-season WM+TSWV, WM after digging, and the highest pod yield compared to other runner-type peanut cultivars. FloRun '331' was found to have comparable WM resistance as Georgia-12Y, however it was also found to be susceptible to TSWV. 'Georgia-14N' was found to have moderate TSWV and WM resistance similar to 'Georgia-07W', and it also has a high-level of root-knot nematode (RKN) resistance.

INTRODUCTION

White mold (WM), stem rot, and southern blight are commonly used names for the same soilborne peanut (*Arachis hypogaea* L.) fungal disease caused by *Athelia rolfsii* (Curzi) C. C. Tu & Kimbr. = *Sclerotium rolfsii* Sacc. Tomato spotted wilt is a systemic foliar peanut disease caused by *Tomato spotted wilt virus* (TSWV). Both of these diseases are major problems in U.S. peanut production, especially in areas with longer growing seasons and hot, wet environmental conditions.

Fungicides have been reliable and effective for control of WM, but are expensive; whereas, TSWV is mainly controlled by cultivar resistance coupled with various cultural practices like planting date, seeding rate, and row patterns (Brown *et al.*, 2005). Therefore, identifying genotypes with high-levels of resistance to both of these peanut pathogens is an ongoing need.

Branch and Csinos (1987) proposed the use of significant (P≤0.05) mean separation into high, medium, and low disease incidence; and high, medium, and low yield performance index to classify peanut genotypes with regard to *A. rolfsii* resistance. Accordingly, 'Sunbelt Runner' (Mixon, 1982) was rated resistant; 'Toalson' (Simpson *et al.*, 1979) and 'Florunner' (Norden *et al.*, 1969) were rated medium; and 'New Mexico Valencia A' (Hsi and Finker, 1972) was rated susceptible.

Genetic variability to (WM) or stem rot resistance was later found among F_6 - F_9 mass-selected peanut populations derived from crosses of Sunbelt Runner x Toalson and Florunner x 'Southern Runner' (Gorbet *et al.*, 1987). Mass-selected populations derived from the Sunbelt Runner x Toalson cross combination had significantly higher yield and higher WM resistance than the mass-selected population derived from the Florunner x Southern Runner cross combination (Branch and Brenneman, 1999). Furthermore, Branch and Brenneman (1993) found that Southern Runner and 'Georgia Browne' (Branch, 1994) each had equally good resistance to WM. Georgia Browne has Southern Runner and Sunbelt Runner as parents in its pedigree and was tested experimentally as GA T-2741.

Branch and Brenneman (2009) also found that the runner-type peanut cultivars, 'Georgia-07W' (Branch and Brenneman, 2008), 'Georgia-03L' (Branch, 2004), and 'AP-3' (Gorbet, 2007) had the best combination of WM and TSWV disease resistance. All of the other Georgia cultivars and advanced Georgia breeding lines performed similar or significantly better than the reportedly resistant check cultivars 'C-99R' (Gorbet and Shokes, 2002) and 'Florida-07' (Gorbet and Tillman, 2009). Most recently, Branch and Brenneman (2015) also found that 'Georgia-12Y' (Branch, 2013) had the best combination of TSWV and WM resistance and highest consistent yield over three years (2011-13) compared to several other genotypes.

Genetic variability among cultivars and breeding lines for these two peanut diseases appears to be additive and quantitatively inherited having a continual gradation ranging from very resistant to very susceptible. However, immunity to these diseases has not been found within the cultivated peanut.

Based on these earlier aforementioned reports, several new cultivars and advanced breeding lines have been developed and released. The objective of this study was to screen current genotypes for combined general field resistance to both tomato spotted wilt and white mold diseases.

MATERIALS AND METHODS

In trials conducted over three years (2018-20), sixteen peanut cultivars and advanced Georgia breeding lines were compared to the resistant check cultivars (Georgia-07W and Georgia-12Y). Each year, the field evaluation tests were conducted on a Tifton loamy sand soil type (fine-loamy, siliceous, thermic, Plinthic Kandiudult) at the Gibbs research farm near the University of Georgia, Coastal Plain Experiment Station, Tifton, GA. This same field site has a long history (>40 yrs) of continuous peanut production and a very high disease incidence of white mold (WM).

Plots consisted of two rows 6.1 m long x 1.8 m wide, and six sound mature seed were planted per 30.5 cm of row. Early April planting dates were used to increase tomato spotted wilt disease pressure (Tillman *et al.*, 2007; Culbreath *et al.*, 2010). Irrigation was applied as needed to provide for host-plant growth development. Cracked corn (*Zea may* L.) kernels were hand-applied over each row at 1000 g rate on 18 June 2019 [71 days after planting (DAP)] to enhance *A. rolfsii* activity. Georgia Cooperative Extension Service recommended production practices were followed throughout each growing season, except no fungicides were used with known white mold control. Individual genotypes were dug and inverted based upon the hull-scrape method for determining maturity from adjacent border plots (Williams and Drexler, 1981). After harvest, peanut pods were dried with forced warm air to approximately 6% seed moisture and cleaned over a screen table before weighing for pod yield.

Incidence of TSWV was first assessed at mid-season (ca. 60 DAP) when TSWV is usually the primary disease present. At mid-to-late season (ca. 100 DAP), the combination of TSWV and WM incidence was also assessed, which generally included predominantly TSWV and some WM. Prior to digging (ca. 140 DAP), the incidence of WM and TSWV combined was again assessed, which generally included a higher proportion of WM than TSWV. Immediately after digging and inverting the incidence of only WM was also assessed among the different genotypes. This assessment is the most definitive WM rating because signs and symptoms of the disease are often found below ground. At each assessment (TSWV and WM), disease incidence was determined by counting the number of 30.5 cm-sections of a row with one or more infected plants and converting to a percentage of total row length for each plot (Rodriguez-Kabana *et al.*, 1975).

A randomized complete block design was used each year with six replications. Data from each test was statistically analyzed by analysis of variance (ANOVA) using PROC GLM procedure in SAS 9.4 version (SAS Institute, Inc., Cary, NC). Waller-Duncan's T-test (k-ratio = 100) was used for mean separation at $P \leq 0.05$.

RESULTS AND DISCUSSION

During the past three years (2018-20), 16 genotypes were evaluated each year (Tables 1-3). Also, there were eight common runner-type cultivars which were combined across these same years (Table 4).

In 2018, there were little or no significant ($P \leq 0.05$) differences among the genotypes for mid-season TSWV and mid-late season TSWV + WM (Table 1). However, significant differences were found among these genotypes for late-season WM+TSWV, WM, and pod yield. The check cultivar, Georgia-12Y, and 'Georgia-18RU' (Branch, 2019) had the lowest percentage of WM + TSWV incidence, and 'Bailey' (Isleib *et al.*, 2011) had the lowest WM incidence after digging. The advanced Georgia breeding line, GA 122706, had the highest pod yield, but it was not significantly different from nine other genotypes.

In 2019, 'Georgia-20VHO' (Branch, 2021) and Georgia-12Y had the lowest mid-season TSWV incidence, but were not significantly different from several other genotypes; whereas, FloRun '331' (Tillman, 2021) had the highest percent TSWV incidence at mid-season (Table 2). However, at mid-late and late-season, GA 132705 had the lowest percentage; whereas, 'ACI 3321' had the highest percentage of TSWV + WM and WM + TSWV. After digging, the check cultivar, Georgia-12Y, had the lowest white mold percentage and highest pod yield; whereas, Georgia-20VHO had the highest percent incidence, but these two cultivars were not significantly different in yield from many other genotypes.

Table 1. Tomato spotted wilt virus (TSWV) and white mold (WM) disease incidence and pod yield among 16 peanut genotypes when planted early in a continuous peanut rotation trial at the Coastal Plain Experiment Station, Tifton, GA, 2018.

Genotype	TSWV†	TSWV + WM	WM + TSWV	WM	Pod Yield
	(%)	(%)	(%)	(%)	(kg/ha)
GA 122706	1.7 a*	3.8 b	20.4 ef	15.0 def	3930 a
Georgia-12Y (ck)	2.1 a	5.8 ab	17.5 f	22.5 b-f	3862 ab
Georgia-07W (ck)	2.5 a	8.3 ab	29.2 cde	17.5 def	3795 abc
Georgia-18RU	2.1 a	5.0 ab	18.3 f	40.4 a	3637 a-d
Georgia-20VHO	2.5 a	5.8 ab	33.8 bcd	27.1 a-e	3542 a-d
FloRun ‘331’	3.8 a	7.5 ab	30.0 cde	13.8 ef	3463 a-d
Georgia-16HO	2.5 a	7.1 ab	44.6 a	27.9 a-e	3365 a-d
TUFRunner ‘297’	2.5 a	7.5 ab	35.0 abc	33.8 ab	3339 a-d
Georgia-13M	3.3 a	8.3 ab	37.5 abc	27.9 a-e	3255 a-d
Georgia-14N	1.7 a	6.2 ab	20.4 ef	17.9 c-f	3187 a-d
Bailey	5.0 a	7.5 ab	24.6 def	12.1 f	3137 bcd
TifNV-High O/L	1.7 a	7.5 ab	35.8 abc	28.8 a-d	3125 bcd
Georgia-06G	2.1 a	7.5 ab	36.7 abc	35.0 ab	3067 cd
Georgia-19HP	2.9 a	7.5 ab	35.4 abc	32.1 abc	2988 d
Georgia Greener	2.1 a	7.5 ab	37.1 abc	22.5 b-f	2970 d
ACI 3321	2.5 a	10.0 a	41.2 ab	16.2 def	2900 d
Mean	2.6	7.1	31.1	24.4	3348
% CV	79.8	43.5	29.1	47.4	16.4

* Means within columns followed by the same letter are not significantly different at P≤0.05.

Disease assessment: TSWV @ ca. 60DAP; TSWV + WM @ ca. 100 DAP; WM + TSWV @ ca. 140 DAP; and WM @ after digging and inverting.

Overall, the average 2019 WM incidence after digging was higher than in 2018 (35.1 vs. 24.4%). This increase might be attributed to the application of cracked corn in 2019. Interestingly in 2020, WM average incidence after digging was still similar to 2019 without another cracked corn application as well as higher than in 2018.

In 2020, Georgia-12Y again had the lowest percent TSWV; whereas, ACI 3321, FloRun ‘331’, and TUFRunner ‘297’ (Tillman, 2018) had the highest percentage of TSWV at midseason (Table 3). At mid-late season TSWV+WM, GA 163120 had the lowest percentage; whereas, ‘Georgia-17SP’ (Branch and Brenneman, 2018) had the lowest percentage at late-season WM + TSWV. However, GA 162722, GA 162724, and GA 162725 had the highest percent incidence of TSWV + WM, WM + TSWV, and WM after-digging. Georgia-12Y again had the lowest percentage of WM incidence after-digging, but it was not significantly different from FloRun ‘331’, ‘Georgia-14N’ (Branch and Brenneman, 2015), Georgia-07W, and Georgia-17SP. Highest pod yield was found with Georgia-12Y, FloRun ‘331’, Georgia-14N, and AU-NPL 17.

Table 2. Tomato spotted wilt virus (TSWV) and white mold (WM) disease incidence and pod yield among 16 peanut genotypes when planted early in a continuous peanut rotation trial at the Coastal Plain Experiment Station, Tifton, GA, 2019.

Genotype	TSWV†	TSWV + WM	WM + TSWV	WM	Pod Yield
	(%)	(%)	(%)	(%)	(kg/ha)
Georgia-12Y (ck)	3.8 ef*	11.7 efg	18.8 fg	19.6 e	4918 a
TUFRunner '297'	11.2 bc	17.5 b-e	35.0 abc	45.0 abc	4677 ab
TifNV-High O/L	12.1 b	21.2 abc	25.4 c-g	26.0 cde	4610 ab
AU-NPL 17	8.3 cd	13.3 d-g	28.8 cde	32.1 b-e	4600 ab
Georgia-20VHO	3.3 f	12.9 d-g	34.2 a-d	54.2 a	4551 ab
Georgia-06G	5.4 def	12.9 d-g	26.7 c-f	33.8 b-e	4534 abc
GA 152545	7.1 de	14.6 d-g	29.6 bcd	34.6 b-e	4516 abc
GA 132705	5.8 def	9.2 g	16.7 g	24.6 de	4514 abc
GA 132712	6.2 def	10.0 fg	19.6 efg	30.4 b-e	4473 abc
FloRun '331'	15.8 a	22.9 ab	38.8 ab	28.3 b-e	4413 abc
Georgia-07W (ck)	7.1 de	11.2 fg	18.8 fg	28.3 b-e	4325 abc
ACI 3321	13.3 ab	24.6 a	40.4 a	46.7 ab	4228 abc
Georgia-21GR	7.1 de	14.2 d-g	31.2 a-d	40.8 a-d	4165 bc
GA 142509	6.7 def	17.9 bcd	29.6 bcd	46.2 ab	4010 bc
Georgia-14N	5.8 def	15.8 c-f	25.0 d-g	29.2 b-e	3954 bc
GA 142510	5.4 def	12.9 d-g	31.2 a-d	42.1 a-d	3789 c
Mean	7.8	15.2	28.1	35.1	4392
% CV	41.9	33.8	29.4	41.0	11.6

* Means within columns followed by the same letter are not significantly different at P≤0.05.

Disease assessment: TSWV @ ca. 60DAP; TSWV + WM @ ca. 100 DAP; WM + TSWV @ ca. 140 DAP; and WM @ after digging and inverting.

Table 3. Tomato spotted wilt virus (TSWV) and white mold (WM) disease incidence and pod yield among 16 peanut genotypes when planted early in a continuous peanut rotation trial at the Coastal Plain Experiment Station, Tifton, GA, 2020.

Genotype	TSWV†	TSWV + WM	WM + TSWV	WM	Pod Yield
	(%)	(%)	(%)	(%)	(kg/ha)
Georgia-12Y (ck)	10.8 e*	18.8 def	34.6 de	10.4 g	4166 a
FloRun '331'	21.2 ab	25.0 cd	36.2 de	10.8 fg	3808 ab
Georgia-14N	16.7 bcd	19.6 def	32.5 de	10.8 fg	3542 abc
AU-NPL 17	15.8 d	20.4 def	40.0 cd	24.6 de	3530 abc
TUFRunner '297'	20.8 abc	24.6 cde	50.8 b	28.8 cde	3449 bcd
Georgia-07W (ck)	13.3 de	17.9 def	33.3 de	17.1 efg	3311 bcd
Georgia-06G	13.3 de	22.9 c-f	50.0 b	41.2 bc	3233 bcd
TifNV-High O/L	15.8 d	19.2 def	38.8 de	24.6 de	3204 bcd
GA 163118	16.2 cd	19.2 def	37.1 de	23.8 ef	3064 cde
Georgia-17SP	13.8 de	16.2 ef	30.4 e	19.2 efg	2896 cde
ACI 3321	24.2 a	30.0 bc	56.2 b	37.1 bcd	2792 de
GA 163119	13.3 de	22.9 c-f	49.2 bc	42.1 bc	2513 e
GA 163120	12.5 de	14.6 f	37.1 de	41.7 bc	2415 ef
GA 162725	12.5 de	39.6 a	77.9 a	67.1 a	1766 fg
GA 162724	14.6 de	37.9 ab	75.4 a	69.2 a	1612 g
GA 162722	14.2 de	38.8 a	72.1 a	67.9 a	1280 g
Mean	15.6	24.2	47.0	33.5	2911
% CV	26.9	31.4	19.1	36.8	21.8

* Means within columns followed by the same letter are not significantly different at P≤0.05.

Disease assessment: TSWV @ ca. 60DAP; TSWV + WM @ ca. 100 DAP; WM + TSWV @ ca. 140 DAP; and WM @ after digging and inverting.

Table 4. Three-year average tomato spotted wilt virus (TSWV) and white mold (WM) disease incidence and pod yield among eight runner-type peanut cultivars when planted early in a continuous peanut rotation trial at the Coastal Plain Experiment Station, Tifton, GA, 2018-20.

Runner Cultivar	TSWV†	TSWV + WM	WM + TSWV	WM	Pod Yield
	(%)	(%)	(%)	(%)	(kg/ha)
Georgia-12Y (ck)	5.6 e*	12.1 d	23.6 d	17.5 d	4316 a
FloRun ‘331’	13.6 a	18.5 ab	35.0 bc	17.6 d	3894 b
TUFRunner ‘297’	11.5 ab	16.5 bc	40.3 ab	35.8 a	3822 b
Georgia-07W (ck)	7.6 cde	12.5 d	27.1 d	21.0 cd	3810 b
TifNV-High O/L	9.9 bc	16.0 bc	33.3 c	26.5 bc	3646 bc
Georgia-06G	6.4 de	14.4 cd	37.8 bc	36.7 a	3618 bc
Georgia-14N	8.1 cd	13.9 cd	26.0 d	19.3 cd	3561 bc
ACI 3321	13.3 a	21.5 a	46.0 a	33.3 ab	3307 c

* Means within the columns followed by the same letter do not differ significantly at $P \leq 0.05$.

Disease assessment: TSWV @ ca. 60DAP; TSWV + WM @ ca. 100 DAP; WM + TSWV @ ca. 140 DAP; and WM @ after digging and inverting.

The overall three-year (2018-20) average found that Georgia-12Y had among the lowest percentages of TSWV, TSWV+WM, WM+TSWV, WM, and the significantly highest pod yield compared to these other seven runner-type peanut cultivars (Table 4). These results agree with previous reports (Branch and Brenneman, 2015; Standish *et al.*, 2019) regarding the WM resistance of Georgia-12Y. FloRun ‘331’ was found to have similar WM resistance as Georgia-12Y, but it was also found to be susceptible to TSWV similar to ACI 3321. Georgia-14N was found to have moderate TSWV and WM resistance similar to Georgia-07W, and it also has a high level of root-knot nematode (RKN) resistance caused by [*Meloidogyne arenaria* (Neal) Chitwood race 1].

CONCLUSIONS

For the past ten years (2011-20), Georgia-12Y has been shown to have a high level of stable combined general field resistance to both TSWV and WM disease and high pod yield performance. Other peanut cultivars seem to have good resistance to only one or the other disease but not both. Long-term resistance to these two diseases would be very desirable, especially when coupled with high pod yield. Such a stable combination has been found in the Georgia-12Y runner-type peanut cultivar.

Additionally, the high susceptibility of the three advanced Georgia breeding lines in 2020 illustrates the continuous need to evaluate for WM disease resistance. It also highlights the progress made so far in peanut breeding for developing WM disease-resistant cultivars.

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