# Preference of *Gossypium* Genotypes to *Bemisia argentifolii* (Homoptera: Aleyrodidae)

ROBERT. L. MEAGHER, JR.,[1] C. WAYNE SMITH, AND WENDY J. SMITH

Department of Soil and Crop Sciences, Texas A&M University, College Station, TX 77843-2474

J. Econ. Entomol. 90(4): 1046–1052 (1997)

**ABSTRACT** Several *Gossypium* species and genotypes were evaluated in field and greenhouse tests in the Lower Rio Grande Valley, Texas, for preference to the whitefly, *Bemisia argentifolii* Bellows & Perring. Genotypes within *G. hirsutum, G. barbadense, G. herbaceum,* and *G. arboreum* were examined, including commercial and obsolete cultivars (cultivars that are no longer commercially produced), and modern and diploid genotypes. These genotypes possessed different leaf shapes, pubescence, and foliage color. Field results showed that the highest whitefly populations were on 'Stoneville 453' and the modern genotype 89F46h. The lowest populations were on the obsolete 'Lone Star' and genotypes 88G104 and 'MACAOS'. Greenhouse choice bioassays indicated that several genotypes from *G. hirsutum* had lower egg or nymph numbers than 'Deltapine 50', including Lone Star, MACAOS, 88G104, and 89E62. Greenhouse bioassays appeared to provide information comparable to field testing, at least for whitefly oviposition. Therefore, in preliminary screening tests where cotton seed is in short supply or certain genotypes cannot be incorporated into field testing, greenhouse bioassays can offer a complementary method.

**KEY WORDS** *Bemisia argentifolii, Gossypium hirsutum, Gossypium barbadense, Gossypium herbaceum, Gossypium arboreum,* plant resistance

COTTON (*GOSSYPIUM* spp.) occupies ≈ 2.5% of cultivated land worldwide, and is a major cash crop in many countries (Matthews 1989). Presently, U.S. cotton production requires high insecticide use, averaging 0.6 applications per hectare for the bollworm/budworm, *Heliothis/Helicoverpa,* complex, 0.3 for boll weevil, *Anthonomus grandis grandis,* 0.4 for aphids, *Aphis gossypii* Glover, and 0.2 for plant bugs, *Lygus* spp. (Head 1992).

A cotton pest of recent concern is the whitefly *Bemisia argentifolii* Bellows & Perring [previously the b-strain sweetpotato whitefly, *B. tabaci* Gennadius (Bellows et al. 1994)]. Since the late 1980s, *B. argentifolii* has been a serious pest from Florida to California, infesting cole crops (*Brassica* spp.), cucurbits (Cucurbitaceae), tomato (*Lycopersicon esculentum* Miller), lettuce (*Lactuca sativa* L.), ornamental plants, and cotton (USDA 1992, Riley and Wolfenbarger 1993).

Plant resistance has potential as a management strategy in an integrated approach for control of whiteflies in field and vegetable crops. Several plant characters have been suggested as possible factors conferring resistance. Cotton leaves possessing fewer trichomes have been shown in field and greenhouse tests to support lower populations of adult (Butler and Henneberry 1984; Butler and Wilson 1984; Butler et al. 1986, 1991) or immature (Ozgur and Sekeroglu 1986, Flint and Parks 1990) *B. tabaci* or *Trialeurodes abutilonea* (Haldeman). Other physical plant characters, such as okra leaf shape and an open crop canopy, have conferred resistance to whitefly in some instances (Ozgur and Sekeroglu 1986, Butler et al. 1988, Flint and Parks 1990). Biochemical characters, such as pH level and the concentration of various tannins and phenols, also have been shown to influence whitefly populations (Husain et al. 1936, Berlinger et al. 1983, Butter et al. 1992).

The objective of this study was to evaluate various *Gossypium* species and genotypes within these species in terms of *B. argentifolii* response in field and greenhouse tests. Field testing of cotton genotypes is expensive in terms of labor and land space, and whitefly populations may be extremely variable because of abiotic factors. Therefore, greenhouse testing may provide a better initial evaluation technique to separate genotypes that show high levels of resistance (Lambert et al. 1982).

## Materials and Methods

**Cotton Genotypes.** Genotypes within *G. hirsutum, G. barbadense, G. herbaceum,* and *G. arboreum* were used in field and greenhouse tests (Table 1). Leaf shape, pubescence, and foliage color varied among genotypes. 'Deltapine 50' and 'Stoneville 453' are resistant and susceptible, re-

[1]Current address: USDA–ARS CMAVE, 1700 S.W. 23rd Drive, Gainesville, FL 32604.

**Table 1. Morphological characteristics of cotton genotypes tested against *B. argentifolii* in greenhouse and field evaluations, 1992–1993, Weslaco, TX**

| Species/genotype | Status | Leaf shape[a] | Visible leaf pubescence | Foliage color |
|---|---|---|---|---|
| *G. hirsutum* | | | | |
| Deltapine 50 | CC | Normal | Smooth | Green |
| Stoneville 453 | CC | Normal | Hairy | Green |
| Lone Star | OC | Normal | Smooth | Green |
| Tamcot CAB-CS | CC | Normal | Smooth | Green |
| Victoria | CC | Normal | Smooth | Green |
| MACAOS | MG | Okra | Moderate | Red |
| LA 213 RL | MG | Normal | Hairy | Red |
| LA 213 RS | MG | Normal | Hairy | Green with red stems and petioles |
| LA 213 RM | MG | Normal | Hairy | Green with red leaf margins |
| LA 213 RV | MG | Normal | Hairy | Green with red veins |
| 86E-20 HT | MG | Normal | Glabrous | Green |
| 86L29 | MG | Normal | Moderate | Green |
| 86L$^2$14L | MG | Okra | Smooth | Green |
| 88G104 | MG | Normal | Smooth | Green |
| 89E51 | MG | Normal | Hairy | Green |
| 89E62 | MG | Normal | Smooth | Green |
| 89F46h | MG | Normal | Hairy | Green |
| 89F46s | MG | Normal | Smooth | Green |
| 90C19h | MG | Normal | Hairy | Green |
| 90C19s | MG | Normal | Smooth | Green |
| 91PSO19 | MG | Normal | Smooth | Green |
| *G. barbadense* | | | | |
| Pima S-6 | CC | Normal | Hairy | Green |
| *G. arboreum* | | | | |
| A2-90 | DG | Normal | Hairy | Green |
| *G. herbaceum* | | | | |
| A1-37 | DG | Normal | Hairy | Green |

CC, current cultivar; OC, obsolete cultivar; MG, modern genotype; DG, diploid genotype. Hairy, trichomes obvious and prevalent on abaxial leaf surfaces; smooth, very few to no trichomes obvious; glabrous, no trichomes except on off-type plants. HT, high tannin; RL, red leaf; RS, red stem; RM, red margin; RV, red vein.

[a] Normal for species or okra leaf shape.

spectively, in field trials (C.W.S. and J. Norman, unpublished data). Other *G. hirsutum* genotypes evaluated were 'Lone Star', an obsolete cultivar (no longer commercially produced) released in Texas in 1906; 'Tamcot CAB-CS', a modern smooth-leaf cultivar released by the Texas Agricultural Experiment Station's Multiple Adversity Resistance Program (MAR) in 1985; 'Victoria', a smooth-leaf cultivar released in Spain about 1990. 'MACAOS', LA 213 RL, LA 213 RS, LA 213 RM, and LA 213 RV were included because they contain varying amounts of anthocyanin as indicated by varying degrees of red foliage color. The remaining *G. hirsutum* entries were genotypes developed by the Texas Agricultural Experiment Station Cotton Improvement Laboratory (CIL) and included smooth-leaf genotypes (88G104, 89E62, 91PSO19), 1 genotype having elevated levels of condensed tannins (86E-20HT), okra leaf shape (86L$^2$14L), and 2 sets of near isogenic lines for leaf pubescence (89F46h and 89F46s, and 90C19h and 90C19s). 'Pima S-6', a commercial cultivar grown in Texas, represented *G. barbadense*. Two diploid genotypes from *G. arboreum* and *G. herbaceum* were included in greenhouse trials.

**Field Choice Test.** Fifteen genotypes were grown in the field at the Texas A&M Research and Extension Center, Weslaco, in 1992. Each plot consisted of 2 rows (12 by 1.02 m) with 4 replicates. Cotton seeds were planted 13 March and cultural practices were standard for the area. Because natural *B. argentifolii* populations (identified as in Tan et al. 1996) were initially low, plots were treated with insecticides (oxamyl, Vydate C-LV, DuPont, Wilmington, DE, 64 ml/ha, 7 applications; cyfluthrin, Baythroid 2 (emulsifiable), Miles, Kansas City, MO, 38 ml/ha, 4 applications) to remove natural enemies. Arbitrarily selected upper and lower leaves from 2 selected plants per plot were sampled for whitefly eggs and nymphs by removing a leaf disk with a cork borer (1 cm diameter) and counting under a stereomicroscope. Upper leaves were located on the upper 3rd of the plant, lower leaves were located on the lower 3rd of the plant. Sample dates were 7, 14, 21, 28 July, and 4 August.

Egg and nymph densities were averaged across dates for analysis of variance (ANOVA) (PROC GLM, SAS Institute 1995). The ANOVA model contained replication (4), genotype (16), plant sampled (2), leaf location (2), and interactions. Genotypic means were compared with Stoneville 453 (susceptible) and Deltapine 50 (resistant) using a

set of orthogonal comparisons (PROC GLM, CONTRAST statement, SAS Institute 1995).

**Greenhouse Choice Tests.** *Plant Growth Conditions.* Cotton genotypes were grown in 11.3-liter pots containing Metro Mix 200 (Grace-Sierra, Milpitas, CA) commercial potting media, fertilized with Nutrileaf 20:20:20 ($N:P_2O:K_2O$) or Peters Professional (W. R. Grace, Fogelsville, PA), and watered as needed. The fall 1992 test was conducted with plants grown from seed; tests for summer 1992 and fall 1993 used ratoon plants (seed-grown plants pruned and allowed to regrow).

*Individual Tests.* The summer 1992 test had 17 genotypes in a randomized complete block experiment with 8 replications. This test compared the same genotypes as the field test, except that 2 near isogenic lines of the modern genotype 90C19, smooth and hairy, were used in place of an earlier selection of 90C19. Plants were placed in large cages (1.8 by 1.8 by 2.4 m) within a greenhouse (fan and cooling pad design, clear plastic covering, no shadecloth). The cages had contiguous wooden frames and were covered with white organdy cloth. Seams and joints of the cages were sealed with caulk to prevent arthropod escape. Plants at the R-1 growth stage (Elsner et al. 1979) were infested by interspersing *B. argentifolii*-infested *Hibiscus rosa-sinensis* L. plants within each cage. The fall 1992 test included 15 of the same genotypes replicated 5 times; near isogenic lines 89F46h and 89F46s were not included. The fall 1993 test used 9 genotypes with 3 replicates. This test included a choice evaluation of near isogenic lines for degree of red foliage color in a 'Stoneville 213' background. The greenhouse choice tests were designed primarily to evaluate selected current and obsolete cultivars and advanced genotypes for an upland cotton breeding program at the Texas Agricultural Experiment Station.

*Whitefly Sampling—Greenhouse.* Whitefly population density samples were estimated using the method of Meagher and Estrada (1994). Whitefly eggs and nymphs were sampled from each genotype by cutting 3 disks (7 mm diameter, total sampled area = 1.15 $cm^2$) from an arbitrarily selected upper plant leaf using a paper punch. The number of eggs and 1st through 4th instar nymphs on the underside of each leaf disk were counted using a stereomicroscope and numbers for each disk were combined to give a mean per plant (replicate). Samples were taken weekly 4 times during the test period.

*Statistical Analysis—Greenhouse.* Because weekly samples were taken from the same plants, a repeated measures ANOVA was conducted (PROC GLM, repeated, SAS Institute 1995). If the sample date by genotype interaction was not significant, then further analysis was conducted on egg and nymph means across dates. This second ANOVA compared genotypic means to Stoneville 453 (susceptible) and Deltapine 50 (resistant) using a set of orthogonal comparisons (PROC GLM, CONTRAST statement, SAS Institute 1995).

**Leaf Trichome Density.** Trichome densities on interveinal, underside leaf surface tissue were determined on field-grown plants at College Station, TX, in 1992 and on greenhouse grown plants in fall 1993. For field samples, 10 fully expanded upper-plant leaves (4–6th leaf from terminal node) from 10 plants of each genotype were collected and transported to the laboratory. Trichomes (not individual hairs) were measured by imprinting a circle 16 mm diameter with a cork borer from the area next to the midvein and counting under a stereomicroscope (10×). For greenhouse samples, trichomes were counted using 3 leaves on 3 plants per genotype. Each leaf was carefully dusted with talc powder (Johnson's Baby Powder, Johnson & Johnson, Skillman, NJ) before observation under a stereomicroscope (50×) (Kishaba et al. 1992, Meagher and Estrada 1994). Trichome densities were compared across genotypes (PROC GLM, CONTRAST statement, SAS Institute 1995), and correlation analysis was used to identify a possible relationship between whitefly egg or nymph density and number of trichomes (PROC CORR, SAS Institute 1995).

## Results

**Field Choice Test.** ANOVA for numbers of eggs and nymphs indicated a significant difference among genotypes and leaf location ($P < 0.0001$), and no difference between plants sampled ($P > 0.10$). Whitefly densities increased from the 1st to last samples indicating a seasonal increase in the population. Cotton leaf sampled had a significant impact on whitefly densities, as more eggs and nymphs were collected on lower leaves than upper leaves (eggs, lower 15.0 ± 1.5, upper 8.9 ± 0.9; $F = 17.8$; df = 1, 189; $P < 0.0001$; nymphs, lower 9.0 ± 0.9, upper 3.3 ± 0.4; $F = 52.0$; df = 1, 189; $P < 0.0001$). There was a significant interaction between genotype and leaf location for both eggs and nymphs (eggs, $F = 2.5$; df = 15, 189; $P = 0.0026$; nymphs, $F = 2.1$; df = 15, 189; $P = 0.0098$), which advocated separate ANOVAs for upper and lower leaves.

Seasonal means of whitefly egg numbers were highest on Stoneville 453 and 89F46h, and lowest on Lone Star, 88G104, and MACAOS (Table 2). Except for the 2 isogenic lines of 89F46, upper leaf samples showed that all genotypes contained significantly fewer eggs than Stoneville 453. Lower leaf samples from Stoneville 453 contained more eggs than all except 86L29 and Pima S-6. Comparisons with Deltapine 50 showed that 88G104 and Lone Star had fewer eggs oviposited on upper leaves. Lower leaf samples showed that 89F46h contained more eggs and Lone Star and MACAOS had fewer eggs than Deltapine 50 (Table 2).

Both upper and lower leaf samples showed that most genotypes contained fewer nymphs than

**Table 2. Whitefly eggs and nymphs per square centimeter (means ± SE), and trichome density per square centimeter across different *Gossypium* genotypes in a field test, summer 1992, Weslaco, TX**

| Species/genotype | Eggs | | Nymphs | | Trichomes |
|---|---|---|---|---|---|
| | Upper leaves | Lower leaves | Upper leaves | Lower leaves | |
| *G. hirsutum* | | | | | |
| Deltapine 50 | 11.1 ± 5.7[a] | 16.6 ± 4.9[a] | 4.0 ± 1.3 | 12.5 ± 5.7 | 7.8 ± 1.5[b] |
| Stoneville 453 | 21.0 ± 4.3[c] | 31.6 ± 10.3[c] | 5.8 ± 1.0 | 16.7 ± 3.0 | 119.2 ± 7.5[f] |
| Lone Star | 2.2 ± 0.6[a,c] | 3.2 ± 0.4[a,c] | 1.0 ± 0.2[d] | 2.9 ± 0.3[d,e] | 3.0 ± 0.5[b] |
| MACAOS | 9.9 ± 6.8[a] | 3.3 ± 0.3[a,c] | 3.7 ± 2.7 | 2.5 ± 0.4[d,e] | 14.4 ± 1.7[b] |
| Tamcot CAB-CS | 4.5 ± 1.0[a] | 9.0 ± 2.3[a] | 2.5 ± 1.2[d] | 6.7 ± 1.4[d] | 12.6 ± 2.8[b] |
| 86E-20 HT | 7.6 ± 1.8[a] | 6.8 ± 2.1[a] | 1.3 ± 0.4[d] | 4.5 ± 0.8[d,e] | 3.2 ± 3.2[b] |
| 86L$^2$9 | 11.2 ± 2.6[a] | 18.7 ± 5.4 | 4.6 ± 1.1 | 13.7 ± 1.8 | 15.0 ± 1.6[b] |
| 86L$^2$14L | 10.6 ± 3.0[a] | 11.5 ± 1.3[a] | 1.4 ± 0.3[d] | 6.1 ± 1.2[d] | 1.8 ± 0.4[b] |
| 88G104 | 1.6 ± 0.5[a,c] | 5.0 ± 0.9[a] | 1.1 ± 0.2[d] | 3.8 ± 0.9[d,e] | 9.2 ± 1.3[b] |
| 89E51 | 4.2 ± 1.2[a] | 15.8 ± 4.9[a] | 2.1 ± 0.9[d] | 7.4 ± 0.8[d] | 119.0 ± 5.4[f] |
| 89E62 | 3.2 ± 1.0[a] | 9.9 ± 2.4[a] | 1.1 ± 0.3[d] | 7.2 ± 1.3[d] | 6.4 ± 1.2[b] |
| 89F46h | 13.0 ± 2.3 | 47.2 ± 11.4[a,c] | 8.2 ± 2.0[e] | 25.6 ± 8.7[d,e] | 41.7 ± 2.6[b,f] |
| 89F46s | 16.7 ± 4.7 | 18.0 ± 4.7[a] | 7.0 ± 2.3 | 7.4 ± 1.2[d] | 14.1 ± 2.9[b] |
| 90C19 | 10.4 ± 1.9[a] | 10.6 ± 1.5[a] | 5.3 ± 1.1 | 9.0 ± 1.9 | 30.2 ± 5.1[b,f] |
| 91PSO19 | 5.0 ± 1.0[a] | 8.4 ± 1.4[a] | 2.2 ± 0.5[d] | 5.8 ± 0.8[d] | 5.6 ± 1.2[b] |
| *G. barbadense* | | | | | |
| Pima S-6 | 9.6 ± 1.9[a] | 24.8 ± 5.5 | 2.3 ± 0.6[d] | 12.2 ± 2.3 | 108.2 ± 4.5[b,f] |

ANOVA for eggs on upper leaves: $F = 3.1$; df = 15, 93; $P = 0.0004$; lower leaves, $F = 5.6$; df = 15, 93; $P < 0.0001$; for nymphs on upper leaves, $F = 3.5$; df = 15, 93; $P < 0.0001$; lower leaves, $F = 4.4$; df = 15, 93; $P < 0.0001$; for trichomes, $F = 163.0$; df = 15, 135; $P < 0.0001$.

[a] Eggs: means within columns are siguificantly different than Stoneville 453 ($P < 0.05$).
[b] Trichomes: means within columns are significantly different than Stoneville 453 ($P < 0.05$).
[c] Eggs: means within columns are significantly different than Deltapiue 50 ($P < 0.05$).
[d] Nymphs: means within columns are significantly different than Stoneville 453 ($P < 0.05$).
[e] Nymphs: means within columns are significantly different than Deltapine 50 ($P < 0.05$).
[f] Trichomes: means within columns are significantly different than Deltapine 50 ($P < 0.05$).

**Table 3. Whitefly eggs and nymphs per square centimeter (means ± SE) across different *Gossypium* genotypes in greenhouse test, summer 1992, Weslaco, TX**

| Species/genotype | Eggs | Nymphs |
|---|---|---|
| *G. hirsutum* | | |
| Deltapine 50 | 19.4 ± 3.3[a] | 8.5 ± 1.9[b] |
| Stoneville 453 | 74.9 ± 19.7[c] | 29.4 ± 9.4[d] |
| Lone Star | 27.5 ± 5.1[a] | 12.3 ± 3.0[b] |
| MACAOS | 12.3 ± 3.2[a] | 5.4 ± 1.3[b] |
| Tamcot CAB-CS | 29.9 ± 8.8[a] | 15.2 ± 5.7[b] |
| 86E-20 HT | 29.2 ± 10.7[a] | 11.3 ± 5.5 |
| 86L$^2$9 | 48.9 ± 9.8[a,c] | 19.6 ± 5.3 |
| 86L$^2$14L | 31.7 ± 8.2[a] | 14.4 ± 4.9 |
| 88G104 | 34.7 ± 6.0[a] | 12.6 ± 2.6[b] |
| 89E51 | 64.5 ± 15.4[a,c] | 26.3 ± 5.7[d] |
| 89E62 | 17.5 ± 3.1[a] | 8.6 ± 2.6[b] |
| 89F46h | 40.8 ± 7.5 | 16.2 ± 5.2 |
| 89F46s | 38.0 ± 15.0[a] | 14.0 ± 7.0 |
| 90C19h | 84.2 ± 29.2[c] | 34.4 ± 18.8[d] |
| 90C19s | 48.0 ± 11.5[c] | 22.0 ± 6.8 |
| 91PS019 | 56.8 ± 13.9[c] | 30.1 ± 8.8[d] |
| *G. barbadense* | | |
| Pima S-6 | 58.9 ± 8.2[c] | 21.5 ± 4.2 |

ANOVA for eggs, $F = 4.0$; df = 16, 90; $P < 0.0001$; for nymphs, $F = 2.0$; df = 16, 90; $P = 0.0205$.

[a] Eggs: means within columns are significantly different than Stoneville 453 ($P < 0.05$).
[b] Nymphs: means within columns are significantly different than Stoneville 453 ($P < 0.05$).
[c] Eggs: means within columns are significantly different than Deltapine 50 ($P < 0.05$).
[d] Nymphs: means within columns are significantly different than Deltapine 50 ($P < 0.05$).

Stoneville 453, although 89F46h contained significantly more nymphs on lower leaves. MACAOS, Lone Star, 88G104, and 86E-20 HT contained fewer numbers of nymphs than Deltapine 50 in lower leaf samples (Table 2).

Stoneville 453, 89E51, and Pima S6 contained leaves with >100 trichomes per square centimeter, and along with 89F46h and 90C19, had significantly more trichomes than Deltapine 50 (Table 2). 86L$^2$14L, Lone Star, and 86E-20HT contained <4 trichomes per square centimeter. Seasonal means of egg and nymph numbers on upper and lower leaves were compared to leaf trichome density. Trichome number was not correlated with egg or nymph density ($P > 0.05$).

**Greenhouse Choice Tests.** *Summer 1992.* In the repeated measures ANOVA, the interaction between sample date and genotype was not significant for egg or nymph density sample data ($P > 0.18$). Therefore, mean numbers of eggs and nymphs across sample dates were used. Large numbers of eggs and nymphs were found on 90C19h, 90C19s, 89E51, 91PSO19, Stoneville 453, and Pima S-6 (Table 3). No genotype contained significantly fewer eggs or nymphs than Deltapine 50, although MACAOS and 89E62 also contained low whitefly densities.

*Fall 1992.* Repeated measures ANOVA suggested that the date-by-genotype interaction was sig-

**Table 4. Whitefly eggs and nymphs per square centimeter (means ± SE) across different *Gossypium* genotypes in greenhouse test, fall 1992, Weslaco, TX**

| Species/genotype | Eggs | | | Nymphs |
|---|---|---|---|---|
| | 28 Oct. | 4 Nov. | 11 Nov. | |
| *G. hirsutum* | | | | |
| Deltapine 50 | 66.6 ± 24.6 | 152.2 ± 34.7 | 144.3 ± 59.7[a] | 21.7 ± 9.8 |
| Stoneville 453 | 59.8 ± 15.8 | 279.0 ± 87.8 | 315.5 ± 109.7 | 38.5 ± 9.9 |
| Lone Star | 12.5 ± 5.0[a,b] | 84.0 ± 41.4[a] | 140.9 ± 55.3[a] | 16.1 ± 6.4[c] |
| MACAOS | 8.0 ± 2.1[a,b] | 30.8 ± 13.4[a] | 41.7 ± 9.0[a] | 5.3 ± 0.7[c] |
| Tamcot CAB-CS | 43.8 ± 15.6 | 124.3 ± 45.2 | 88.2 ± 25.3[a] | 12.9 ± 5.5[c] |
| 86E-20 HT | 28.2 ± 15.2 | 82.3 ± 29.0[a] | 116.5 ± 60.6[a] | 7.1 ± 2.1[c] |
| 86L29 | 51.3 ± 23.3 | 178.6 ± 58.0 | 122.8 ± 44.4[a] | 32.6 ± 10.7 |
| 86L214L | 19.1 ± 5.0[a,b] | 184.9 ± 48.9 | 64.7 ± 19.9[a] | 23.2 ± 7.5 |
| 88G104 | 25.9 ± 7.1[b] | 141.4 ± 39.8 | 228.5 ± 59.6 | 31.5 ± 7.0 |
| 89E51 | 31.5 ± 7.1 | 151.7 ± 53.9 | 126.6 ± 39.7[a] | 32.7 ± 9.8 |
| 89E62 | 12.7 ± 7.7[a,b] | 59.8 ± 21.0[a] | 101.0 ± 44.5[a] | 23.6 ± 13.3 |
| 90C19h | 56.9 ± 20.9 | 195.8 ± 45.8 | 131.8 ± 51.6[a] | 18.0 ± 5.8 |
| 90C19s | 59.7 ± 27.9 | 243.3 ± 89.4 | 172.7 ± 52.4[a] | 40.2 ± 11.8 |
| 91PSO19 | 62.4 ± 29.5 | 185.2 ± 58.2 | 217.0 ± 75.7 | 37.4 ± 10.3 |
| *G. barbadense* | | | | |
| Pima S-6 | 22.4 ± 14.8[b] | 319.5 ± 140.2[b] | 159.7 ± 62.3[a] | 13.3 ± 4.4[c] |

ANOVA for eggs, 28 October, $F = 2.1$; df = 14, 56; $P = 0.0248$; 4 November, $F = 1.9$; df = 14, 56; $P = 0.0406$; 11 November, $F = 2.3$; df = 14, 56; $P = 0.0126$; for nymphs, $F = 2.3$; df = 14, 56; $P = 0.0164$.

[a] Eggs: means within columns are significantly different than Stoneville 453 ($P < 0.05$).

[b] Eggs: means within columns are significantly different than Deltapine 50 ($P < 0.05$).

[c] Nymphs: means within columns are significantly different than Stoneville 453 ($P < 0.05$).

nificant for egg density sample data (Wilks lambda: $F = 1.5$; df = 56, 208.3; $P = 0.0182$), but not for nymph density data ($P > 0.57$). Individual analyses by date showed the 3 middle sampling dates contained differences in egg density among genotypes ($P < 0.05$), whereas there were no differences in egg density in the 1st and last sampling dates ($P > 0.18$). Lone Star, MACAOS, and 89E62 contained significantly lower numbers of eggs than Stoneville 453 on all 3 dates (Table 4). MACAOS, 86E-20 HT, Tamcot CAB-CS, Pima S-6, and Lone Star contained lower numbers of nymphs than Stoneville 453.

*Fall 1993.* This test compared genotypes within *hirsutum, arboreum, barbadense,* and *herbaceum* species against Deltapine 50. ANOVA for egg and nymph densities did not indicate a significant difference among genotypes (Table 5). However, results suggested a trend for *G. herbaceum* A1-37 to contain large number of eggs and Victoria to support low numbers of eggs and nymphs. Leaf trichome density was highest on *G. arboreum* A2-90, and except for Tamcot CAB-CS and Victoria, all genotypes contained significantly more trichomes than Deltapine 50 (Table 5). Trichome density was not related to number of whitefly eggs or nymphs in this test ($P > 0.05$).

## Discussion

Two recent reports from Arizona and California evaluated cotton genotypes against *B. argentifolii*

**Table 5. Whitefly eggs and nymphs and trichome density per square centimeter (means ± SE) across different *Gossypium* genotypes in greenhouse test, fall, 1993, Weslaco, TX**

| Species/genotype | Eggs | Nymphs | Trichomes |
|---|---|---|---|
| *G. hirsutum* | | | |
| Deltapine 50 | 90.6 ± 35.3 | 34.6 ± 11.2 | 19.0 ± 3.0 |
| LA 213 RV | 122.3 ± 28.8 | 33.9 ± 11.5 | 70.3 ± 3.5[a] |
| Tamcot CAB-CS | 174.6 ± 103.9 | 118.5 ± 60.2 | 29.6 ± 2.7 |
| LA 213 RM | 156.3 ± 64.9 | 38.6 ± 23.5 | 76.7 ± 5.9[a] |
| LA 213 RL | 113.4 ± 58.6 | 31.0 ± 18.0 | 73.6 ± 5.9[a] |
| LA 213 RS | 113.8 ± 57.9 | 30.4 ± 10.5 | 86.0 ± 6.6[a] |
| Victoria | 49.8 ± 21.3 | 12.1 ± 8.7 | 31.2 ± 9.8 |
| *G. arboreum* | | | |
| A2-90 | 62.1 ± 4.3 | 27.8 ± 5.7 | 232.6 ± 16.1[a] |
| *G. herbaceum* | | | |
| A1-37 | 239.1 ± 66.4 | 95.2 ± 37.9 | 108.8 ± 7.0[a] |

ANOVA for eggs, $F = 1.2$; df = 8, 16; $P = 0.3839$; for nymphs, $F = 2.2$; df = 8, 16; $P = 0.0885$; for trichomes, $F = 76.6$; df = 8, 272; $P < 0.0001$.

[a] Trichomes: means are significantly larger than Deltapine 50 ($P < 0.05$).

in field tests. Because of our desire to compare genotypes that are productive in south Texas, most genotypes that we tested were not included in those reports. Two exceptions were Deltapine 50 and Pima S-6. Results from the Arizona tests showed that only a selection of *G. thurberi* Todaro (D1) supported significantly lower eggs and nymphs levels than Deltapine 50 (Wilson et al. 1993). Pima cottons in the earlier reports and in our tests supported high whitefly populations compared with upland genotypes (Wilson et al. 1993, Natwick et al. 1995).

Number, length, type, and spatial arrangement of leaf trichomes appear to influence the population density of whiteflies on different crops (Bilderback and Mattson 1977, Kishaba et al. 1992, Heinz and Zalom 1995). It has been suggested that the preferential behavior of whiteflies to oviposit near trichomes is because of selection pressure exerted by natural enemies (Heinz and Zalom 1995) or improved microhabitat caused by hirsute leaves (Chu et al. 1995). Our inability to correlate trichome numbers with whitefly density was related to 2 factors. First, several genotypes had either high trichome densities and low whitefly numbers or low trichome densities and high whitefly numbers. 89E51 was nearly the most pubescent genotype tested, but it supported relatively low numbers of eggs and nymphs. In the fall 1993 greenhouse test, *G. arboreum* A2-90 was the most pubescent genotype but contained relatively low egg and nymph numbers. Contrarily, 89F46s had relatively high numbers of eggs and nymphs and relatively low densities of trichomes. Second, trichome densities in our study formed two loci, either $< 40$ or $> 100/cm^2$. This factor made statistical testing unreliable. However, even our pubescent genotypes had much lower trichome densities than genotypes tested in other studies. One study compared *B. tabaci* numbers against *G. hirsutum* and *barbadense* genotypes that had a range of 1.5–847 trichomes per square centimeter (Butler et al. 1991).

One objective of our research was to associate ranking results between field and greenhouse tests. Greenhouse bioassay results indicating the order of genotypes from more to less preferred, generally agreed with those from the field. For instance, in all 3 tests where comparisons were made with Stoneville 453 (1 field, 2 greenhouse), Lone Star, MACAOS, and 89E62 had lower egg numbers and Lone Star and Tamcot CAB-CS had lower nymph numbers. Whitefly densities on Deltapine 50 were compared with those found on other genotypes in 4 tests (1 field, 3 greenhouse), and Lone Star, MACAOS, and 88G104 had lower numbers of eggs in 2 tests (1 field, 1 greenhouse). Therefore, in preliminary screening tests where cotton seed is in short supply or certain genotypes cannot be incorporated into field testing, greenhouse bioassays appear to offer a complementary method (Lambert et al. 1982). Successful use of plant resistance as an integrated management strategy requires that future research efforts investigate the specific mechanisms of resistance (Wilson et al. 1993, Natwick et al. 1995), and through traditional breeding or biotechnology, incorporate appropriate genes into modern genotypes.

## Acknowledgments

Special thanks are given to R. Bredthauer (Cotton Improvement Laboratory, College Station), J. Norman (Texas Agricultural Extension Service-Weslaco), R. Saldaña (Texas Agricultural Experiment Station-Weslaco), and staff at the Cotton Improvement Laboratory for their valuable assistance in the field and laboratory. M. Gallo-Meagher (University of Florida), J. Norman (Texas Agricultural Extension Service), and D. Riley (University of Georgia-Coastal Plain Experiment Station) kindly reviewed an early version of the manuscript.

## References Cited

**Bellows, Jr., T. S., T. M. Perring, R. J. Gill, and D. H. Headrick. 1994.** Description of a species of *Bemisia* (Homoptera: Aleyrodidae). Ann. Entomol. Soc. Am. 87: 195–206.

**Berlinger, M. J., Z. Magal, and A. Benzioni. 1983.** The importance of pH in food selection by the tobacco whitefly, *Bemisia tabaci*. Phytoparasitica 11: 151–160.

**Bilderback, T. E., and R. H. Mattson. 1977.** Whitefly host preference associated with selected biochemical and phenotypic characteristics of poinsettias. J. Am. Soc. Hortic. Sci. 102: 327–331.

**Butler, Jr., G. D., and T. J. Henneberry. 1984.** *Bemisia tabaci*: effect of cotton leaf pubescence on abundance. Southwest. Entomol. 9: 91–94.

**Butler, Jr., G. D., and F. D. Wilson. 1984.** Activity of adult whiteflies (Homoptera: Aleyrodidae) within plantings of different cotton strains and cultivars as determined by sticky-trap catches. J. Econ. Entomol. 77: 1137–1140.

**Butler, Jr., G. D., T. J. Henneberry, and F. D. Wilson. 1986.** *Bemisia tabaci* (Homoptera: Aleyrodidae) on cotton: adult activity and cultivar oviposition preference. J. Econ. Entomol. 79: 350–354.

**Butler, Jr., G. D., D. Rimon, and T. J. Henneberry. 1988.** *Bemisia tabaci* (Homoptera: Aleyrodidae): populations on different cotton varieties and cotton stickiness in Israel. Crop Prot. 7: 43–47.

**Butler, Jr., G. D., F. D. Wilson, and G. Fishler. 1991.** Cotton leaf trichomes and populations of *Empoasca lybica* and *Bemisia tabaci*. Crop Prot. 10: 461–464.

**Butter, N. S., B. K. Vir, G. Kaur, T. H. Singh, and R. K. Raheja. 1992.** Biochemical basis of resistance to whitefly *Bemisia tabaci* Genn. (Aleyrodidae: Hemiptera) in cotton. Trop. Agric. (Trinidad) 69: 119–122.

**Chu, C.-C., T. J. Henneberry, and A. C. Cohen. 1995.** *Bemesia argentifolii* (Homoptera: Aleyrodidae): host preference and factors affecting oviposition and feeding site preference. Environ. Entomol. 24: 354–360.

**Elsner, J. E., C. W. Smith, and D. F. Owen. 1979.** Uniform stage descriptions in upland cotton. Crop Sci. 19: 361–363.

**Flint, H. M., and N. J. Parks. 1990.** Infestation of germplasm lines and cultivars of cotton in Arizona by whitefly nymphs (Homoptera: Aleyrodidae). J. Entomol. Sci. 25: 223–229.

**Head, R. B. 1992.** Cotton insect losses 1991, pp. 621–625. *In* D. J. Herber and D. A. Richter [eds.], Proceedings, Beltwide Cotton Conference of the National Cotton Council of America, Memphis, TN.

**Heinz, K. M., and F. G. Zalom. 1995.** Variation in trichome-based resistance to *Bemisia argentifolii* (Homoptera: Aleyrodidae) oviposition on tomato. J. Econ. Entomol. 88: 1494–1502.

**Husain, M. A., A. N. Puri, and K. N. Trehan. 1936.** Cell sap acidity and the incidence of white-fly (*Bemisia gossypiperda*) on cottons. Current Sci. 4: 486–487.

**Kishaba, A. N., S. Castle, J. D. McCreight, and P. R. Desjardins. 1992.** Resistance of white-flowered gourd to sweetpotato whitefly. HortScience 27: 1217–1221.

**Lambert, L., J. N. Jenkins, W. L. Parrott, and J. C. McCarty. 1982.** Greenhouse technique for evaluating resistance to the bandedwinged whitefly (Homoptera: Aleyrodidae) nsed to evaluate thirty-five foreign cotton cultivars. J. Econ. Entomol. 75: 1166–1168.

**Matthews, G. A. 1989.** Cotton insects and their management. Wiley, New York.

**Meagher, Jr., R. L., and J. A. Estrada. 1994.** Hibiscus resistance to sweetpotato whitefly. Subtrop. Plant Sci. 46: 69–71.

**Natwick, E. T., C. C. Chu, H. H. Perkins, T. J. Henneberry, and A. C. Cohen. 1995.** Pima and upland cotton susceptibility to *Bemisia argentifolii* under desert conditions. Southwest. Entomol. 20: 429–438.

**Ozgur, A. F., and E. Sekeroglu. 1986.** Population development of *Bemisia tabaci* (Homoptera: Aleurodidae) on various cotton cultivars in Cukurova, Turkey. Agric. Ecosyst. Environ. 17: 83–88.

**Riley, D., and D. Wolfenbarger. 1993.** Cultivated hosts and population dynamics of sweetpotato whitefly in the lower Rio Grande Valley of Texas, pp. 667–670. *In* D. J. Herber and D. A. Richter [eds.], Proceedings, Beltwide Cotton Conference National Cotton Council of America, Memphis, TN.

**SAS Institute. 1995.** SAS user's guide: statistics, release 6.11. SAS Institute, Cary, NC.

**Tan, W.-J., D. G. Riley, and D. A. Wolfenbarger. 1996.** Quantification and genetic analysis of bifenthrin resistance in the silverleaf whitefly. Southwest. Entomol. 21: 265–275.

**U.S. Department of Agriculture. 1992.** Conference report and 5-year national research and action plan for development of management and control methodologies for the sweetpotato whitefly. USDA–ARS-107. USDA, Washington, DC.

**Wilson, F. D., H. M. Flint, B. R. Stapp, and N. J. Parks. 1993.** Evaluation of cultivars, germplasm lines, and species of *Gossypium* for resistance to biotype "B" of sweetpotato whitefly (Homoptera: Aleyrodidae). J. Econ. Entomol. 86: 1857–1862.

*Received for publication 10 September 1996; accepted 4 March 1997.*