1360 Combining Ability and Utility of Interspecific Gossypium Matings

S.S. Hague[1], C.W. Smith[1], D.M. Stelly[1], C. Souder[1], and P. Thaxton[2]

[1] Texas A&M University, Texas Agricultural Experiment Station, College Station, TX.
[2] Mississippi State University, Delta Experiment Station, Stoneville, MS.

Abstract

Infusion of new alleles into the Upland cotton, *Gossypium hirsutum* L., gene pool is needed for increased genetic variation and subsequent improvement of qualitative and quantitative traits. An excellent source of unique alleles is from other *Gossypium* species such as *G. barbadense* L., *G. tomentosum* Nutt, and *G. mustelinum,* Miers. In recent years, researchers at Texas A&M University in College Station have made several interspecific cross-pollinations with Upland genotypes. Individual plants and progeny rows were evaluated for fiber yield and qualities as well as agronomic adaptation in $F_{1:4}$ generations. Several lines were competitive in terms of yield and most had superior fiber characteristics such as fiber length and length uniformity in comparison to commercial cultivars. The most promising genotypes were derived from *G. barbadense.* Interspecific matings among *G. tomentosum* and *G.* mustelinum with G. *hirsutum* parents generated progeny that were reasonably productive and may also contain important alleles for other cotton breeding objectives.

Introduction

The 2006 U.S. cotton crop had an average fiber length of 28 mm, micronaire of 4.4, and strength of 286 Kn m Kg^{-1} (USDA, 2007). This same crop had a larger percentage of bales falling into the upper echelon of quality than in previous years. The US cotton crop is trending to greater quality fiber largely in response to market demand and a large component of this improvement has been the adoption of cotton cultivars with a potential for better fiber qualities. Commercial breeding programs are now releasing cultivars with higher fiber quality standards in response to grower and textile mills demands at much more rapid rate than twenty years ago. Any new germplasm developed needs to meet minimum fiber parameters.

Genetic variability in *Gossypium hirsutum* is limited particularly among elite germplasm and even more so among commercial cultivars (Bowman, 2000; Gutierrez, et al., 2002; Van Esbroeck, et al. 1998). Many valuable alleles probably exist in the wild but are rarely used in *Gossypium* spp. cultivar development. The difficulty in using wide crosses as sources of improvement is the vast amount of negative alleles that are brought along with hybridization (Tanksley and Nelson, 1996). Therefore, germplasm resulting from wide-crosses for improvements would require breaking several negative linkages. In the absence of a dense QTL marker map, traditional cotton breeding programs must use a stepwise progression in development of elite germplasm from interspecific hybrids (ISH). The first step is developing ISH plants that are non-photoperiodic, can mature within a temperate growing season, and have reasonable fecundity. The second step is to improve ISH populations to the point where yield components and fiber traits meet minimum standards. The final stage is to improve interspecific populations to the point where elite traits (e.g. fiber properties, stress tolerance, pest resistance, etc) can be coupled with acceptable yield, which enables creation of useful germplasm for commercial cultivar development.

Because *G. hirsutum* is a functional tetraploid, it can be hybridized with tetraploids with important traits such as *G. barbadense, G. tomentosum,* and *G. mustelinum*. *G. tomentosum* originated from the Hawaiian Islands. The nectariless trait which provides some insect pest resistance was introgressed from *G. tomentosum* into elite *G. hirsutum* (Meredith and Bridge, 1977). *G. mustelinum* originated from northeast Brazil (Wendel et al. 1994). This species has been identified as having great amounts of terpenoid aldehydes, which confers insect resistance (Khan et al. 1999). *G. barbadense* originated from northwestern South America and is well regarded for its long and strong fiber properties. This species has been domesticated with 'Pima', 'Egyptian' and 'Sea Island' cultivars.

The objective of this study was to examine the fiber properties and yield performance of ISH plants and lines of *G. hirsutum* and 'Sea Island' (*G. barbadense), G. tomentosum,* and *G. mustelinum*.

Methods and Materials

Line development

G. tomentosum and *G. mustelinum* were backcrossed with TM-1, which is a highly inbred derivative of 'Deltapine 14', with TM-1 serving as the recurrent parent. This strategy was employed to mitigate photoperiodism and improve productivity. Resulting lines were mated with several *G. hirsutum* parents in a series of complex crosses and backcrosses (Table 1). Two Sea Island, *G. barbadense*, breeding lines, 'NMSI-1331' and 'SI-Barbados' were also hybridized with several Upland breeding lines.

Early generation progeny were planted in nurseries in College Station, TX, in 2000-2006. During this period, individual plants were selected based on agronomic adaptation, fiber qualities, and yield components, especially lint fraction. Elite plants were replanted each year in a plant-to-row configuration. In 2005, several ISH Sea Island lines were entered into a preliminary yield performance trial in College Station, TX.

Statistical analysis

Common commercial checks were included in ISH nurseries. These checks were included at regular intervals within the field to measure intra-field variation. They served as an estimate of environmental variance in the estimation of broad-sense heritability (H^2). Measured traits included lint fraction, micronaire, fiber length, length uniformity index, strength, and elongation. Means of these traits for each pedigree within and across *Gossypium* spp. were calculated as well as the co-efficient of variation (C.V.) for each trait. The C.V. was calculated with the variance calculated as that of the entire population and not a sample. The replicated performance trial was analyzed with SAS using the PROC GLM command (SAS, 2002).

Results and Discussion

Combination of *G. mustelinum*, *G. tomentosum* and *G. barbadense* resulted in great variability among individual plants and within specific pedigrees. Many ISH plants, especially in early generations, were very non-productive. A high selection pressure was applied to quickly improve the population mean. Progeny lines resulting from the hybridization of *G. hirsutum* and *G. barbadense* resulted in the greatest amount of variance for lint fraction, fiber length, length uniformity index, strength, and elongation (Table 2). Overall, the least amount of variance was garnered from the *G. hirsutum* by *G. tomentosum* IHS progeny.

On average, the lint fractions of ISHs were acceptable with a mean of 36.7 in the 2004 nursery. Not surprisingly, ISH from Sea Island parents had the greatest fiber length, length uniformity, and strength. What was unexpected was the relative high quality of fiber traits from *G. mustelinum* and *G. tomentosum* ISH progeny. In consideration of the wild nature of these species, improvement of ISH was rapid. Further improvement looks possible based on CV estimations.

Because ISH populations had several cycles of selection pressures from breeders, distribution of values was typically not normal for the Sea Island ISHs (Table 3). *G. mustelinum* and *G. tomentosum* ISH generally had more normal distribution of values than Sea Island ISH. This is likely the result of less selection pressure placed on lint fraction and fiber properties, and more emphasis placed on adaptability traits for these derivatives of wild germplasm. In addition, most of the Sea Island ISH plants were one to three generations more advanced than the other ISH populations in 2004. Transgressive segregants with favorable traits were more common in Sea Island ISHs, whereas transgressive segregants for unfavorable traits were more common with *G. mustelinum* and *G. tomentosum* ISH populations.

Broad-sense heritability estimates were in-line with those of other research findings (May and Bridges, 1995; Percy et al. 2006; Ulloa 2006). Means, variance, and estimates of heritability of lint fraction, micronaire, fiber length, length uniformity, strength, and elongation were analyzed across four generations in three Sea Island ISH pedigrees (Table 4). Variance and subsequently H^2 fell precipitously each generation as the dominance variance was reduced by half and more alleles became fixed. Nevertheless there was still substantial genetic variation at the F_5 generation, which suggests additional inbreeding and reselection is warranted for population improvement.

In the *G. mustelinum* and *G. tomentosum* ISH, H^2 was not consistent across pedigrees nor measured traits (Tables 5 and 6). Much of this inconsistency is attributable to small population sizes and very early generations in which dominant genetic variation is great. In F_1 generation analyses, fewer H^2 estimates were possible, but with the F_2 generation some H^2 estimates were possible with the manifestation of additive genetic variance (i.e. fixation of alleles).

Several elite lines were pulled from the Sea Island ISH nurseries and placed in a performance trial in 2005. Many of these lines had competitive yield and superior fiber parameters in comparison to the commercial check cultivars (Table 7). Overall, the pedigree of (TAMCOT 94L-25 * NMSI 1331) produced the most high yielding lines. Several Sea Island ISH lines are promising germplasm lines.

Conclusions

Sea Island progeny appear to be the most likely wide crosses to be competitive enough to compete against *G. hirsutum* x *G. hirsutum* elite lines without further screening or inter-mating with elite lines. *G. tomentosum* and *G. mustelinum* are more problematic. They generally are non-adapted agronomically, specifically for stress tolerance, maturity and other important yield-related qualities. Further work with these ISH populations would necessitate screening for specific traits, e.g. drought tolerance, pest resistance, and/or inter-mating with elite lines to further reduce the amount of negative alleles.

References

Bowman, D.T. 2000. Attributes of public and private cotton breeding programs. J. Cotton Sci. 4:130-136.

Gutierrez, O.A., S. Basu, S. Saha, J.N. Jenkins, D.B. Shoemaker, C.L. Cheatham, and J.C. McCarthy, Jr. 2002. Crop Sci. 42:1841-1847.

Khan, M.A., J. McD. Stewart and J.B. Murphy. 1999. Evaluation of the *Gossypium* gene pool for foliar terpenoid aldehydes. Crop Sci. 39:253-258.

May, O.L. and B.C. Bridges, Jr. 1995. Breeding cottons for conventional and late-planted production systems. Crop Sci. 35:132-136.

Meredith, W.R., Jr., and R.R. Bridge. 1977. Registration of nine germplasm lines of nectariless cotton. Crop Sci. 17:189.

Percy, R.G., R.G. Cantrell and J. Zhang. 2006. Genetic variation for agronomic and fiber properties in an introgressed recombinant inbred population of cotton. Crop Sci. 46:1311-1317.

SAS. 2002. SAS Institute Inc., Cary, NC, USA.

Tanksley, S.D. and J.C. Nelson. 1996. Advanced backcross QTL analysis: a method for the simultaneous discovery and transfer of valuable QTLs from unadapted germplasm into elite breeding lines. Theor. and Appl. Gene. 92(2): 191-203.

Ulloa, M. 2006. Heritability and correlations of agronomic and fiber traits in an okra-leaf Upland cotton population. Crop Sci. 46:1508-1514.

USDA. 2007. Cotton quality crop of 2006. Annual Report. USDA-AMS, Memphis, TN. Vol. 80 (9).

Van Esbroeck, G.A., D.T. Bowman, D.S. Calhoun, and O.L. May. 1998. Changes in the genetic diversity of cotton in the USA from 1970 to 1995. Crop Sci. 38:33-37.

Wendel, J.F., R. Rowley, and J.M. Stewart. 1994. Genetic diversity in and phylogenetic-relationships of the Brazilian endemic cotton, *Gossypium mustelinum* (Malvaceae). Plant Syst. Evol. 192:49-59.

Tables

Table 1. Pedigrees of interspecific hybrids in the Texas A&M University cotton breeding program, College Station, TX, 1999-2007.

Interspecific parents	TM-1 * *G. mustelinum* / BC1	TM-1 * *G. tomentosum* / BC1	NMSI 1331 (*G. barbadense*); SI- Barbados (*G. Barbadense*)
***G. hirsutum* parents**	TAMCOT Pyramid TAMCOT 94L-25 TAMCOT 96WD-18 (TAM 94L-25 * SI-Barbados) CA 3250 Acala 1517-99	TAMCOT Pyramid TAMCOT 94L-25 TAMCOT 96WD-18 (TAM 94L-25 * SI-Barbados) CA 3250 Acala 1517-99 DPL 491	TAMCOT 97M-16 TAMCOT 96WD-18 TAMCOT Sphinx CA 3250 Acala 1517-99

Table 2. Variance and mean values of lint fraction, length, length uniformity index, strength, and elongation of all pedigrees of interspecific hybrid progeny of *G. mustelinum, G. tomentosum*, and *G. barbadense*.

No. Lines	Pedigree	Lint Fraction %		Fiber Length (UHM) mm		Fiber Length Uniformity Index		Strength kN m Kg^{-1}		Elongation %	
		mean	C.V., %	mean	C.V., %	mean	C.V., %	mean	C.V., %	mean	C.V., %
154	All *G. mustelinum* ISH	35.7	10.4	31.5	5.3	85.1	1.7	329	10.4	5.1	21.1
159	All *G. tomentosum* ISH	37.5	9.2	30.5	5.5	84.9	1.6	314	7.8	5.5	18.4
455	All *G. barbadense* ISH	36.6	11.0	32.5	4.3	85.7	1.8	341	10.4	5.1	24.1
768	All ISH	36.7	10.6	31.8	6.8	85.5	1.8	334	10.1	5.2	22.6

Table 3. Distribution of individual ISH plants divided into quartiles as defined by the highest and lowest individual value from plants selected in 2004, College Station, TX.

	G. mustelinum		*G. tomentosum*		*G. barbadense*	
	Quartile Range	Single Plants	Quartile Range	Single Plants	Quartile Range	Single Plants
Lint fraction						
0-25%	20.4 – 26.6	3	29.3 – 33.2	20	20.7 – 27.3	6
25-50%	26.7 – 32.9	20	33.3 – 37.2	52	27.3 – 33.8	85
50-75%	33.0 – 39.2	103	37.3 – 41.2	63	33.8 – 40.4	300
75-100%	39.3 – 45.6	28	41.3 – 45.3	24	40.4 – 46.9	65
Fiber length (mm)						
0-25%	26.2 – 28.6	11	25.9 – 28.5	23	24.6 – 27.8	5
25-50%	28.7 – 31.1	50	28.6 – 31.2	98	27.9 – 31.1	110
50-75%	31.2 – 33.5	60	31.3 – 34.0	35	31.2 – 34.4	256
75-100%	33.6 – 36.1	27	34.1 – 36.8	3	34.5 – 37.8	84
Fiber length UI (%)						
0-25%	81.7 – 83.5	15	79.9 – 81.9	5	80.6 – 82.7	22
25-50%	83.6 – 85.4	53	82.0 – 84.0	33	82.8 – 84.9	115
50-75%	85.5 – 87.2	63	84.1 – 86.2	96	85.0 – 87.1	244
75-100%	87.3 – 89.2	23	86.3 – 88.3	25	87.2 – 89.4	74
Strength (kN m Kg^{-1})						
0-25%	248 – 289	9	261 – 293	33	263 – 320	118
25-50%	290 – 331	66	294 – 325	77	321 – 377	275
50-75%	332 – 372	68	326 – 358	44	378 – 435	61
75-100%	373 – 415	11	359 – 391	5	436 – 494	1
Elongation (%)						
0-25%	1.7 – 3.3	6	2.6 – 3.9	7	1.8 – 3.6	49
25-50%	3.4 – 5.0	70	4.0 – 5.3	66	3.7 – 5.4	237
50-75%	5.1 – 6.7	68	5.4 – 6.7	66	5.5 – 7.3	156
75-100%	6.8 – 8.5	10	6.8 – 8.2	20	7.4 – 9.3	13

Table 4. Means, variance, and estimates of heritability of three pedigrees of Sea Island interspecific hybrids through four generations in College Station, TX, 2001-2004.

Trait	(94L-25 * SI-Barbados)			(94L-25 * NMSI 1331)			(NMSI 1331 * 97M-16)		
Lint %	Mean	Variance	H^2	Mean	Variance	H^2	Mean	Variance	H^2
Generation									
F_2	-	-	-	-	-	-	-	-	-
F_3	31.9	24.14	83.4	35.9	48.16	92.2	32.0	26.06	85.5
F_4	34.2	12.02	72.3	35.4	13.24	74.9	35.4	28.92	88.5
F_5	28.0	4.13	6.5	32.7	13.97	72.3	34.3	16.72	76.9
Micronaire									
F_2	4.7	-	-	4.3	-	-	3.7	-	-
F_3	3.9	0.47	78.0	3.8	0.55	81.4	3.8	0.43	76.2
F_4	3.9	0.27	57.7	3.9	0.29	61.2	4.0	0.27	57.6
F_5	3.6	0.12	11.3	3.7	0.25	58.8	3.8	0.37	71.5
Fiber length (mm)									
F_2	34.5	-	-	33.8	-	-	34.0	-	-
F_3	32.8	3.16	84.4	31.3	3.34	85.0	31.6	6.06	91.7
F_4	32.6	1.97	53.5	32.4	2.53	63.8	31.9	2.35	61.0
F_5	35.0	1.20	27.7	33.6	1.22	28.8	32.6	2.82	69.2
Length UI (%)									
F_2	81.5	-	-	83.0	-	-	83.9	-	-
F_3	83.7	3.99	82.7	84.0	4.82	85.4	85.5	2.31	69.6
F_4	83.2	3.51	61.1	83.8	2.58	47.8	84.6	1.72	21.9
F_5	83.8	2.83	39.9	84.4	2.48	31.3	84.8	2.61	34.7
Strength (kN m Kg^{-1})									
F_2	312	-	-	313	-	-	339	-	-
F_3	351	1456	79.1	359	2550	88.3	359	1626	81.7
F_4	335	865	64.9	352	945	67.8	360	654	53.4
F_5	319	852	42.6	326	505	3.2	320	712	31.4
Elongation (%)									
F_2	4.0	-	-	4.0	-	-	4.7	-	-
F_3	3.7	1.10	64.0	3.9	1.17	65.4	5.1	1.99	79.7
F_4	5.4	0.94	58.3	4.8	1.07	63.4	6.0	1.26	68.9
F_5	4.3	0.54	10.8	4.2	0.50	2.4	5.0	1.60	69.7

Table 5. Means, variance (V), and estimates of heritability (H^2) of four pedigrees of *G. mustelinum* interspecific hybrids through four generations in College Station, TX, 2001-2004.

Trait	(TM-1**G. mus.*)/BC_1) * (94L-25 * SI-Barbados)			(TAM 96WD-18 * ((TM-1 **G. mus.*)/BC1)))			(TAM Pyramid * ((TM-1 * *G. mus*)/BC1)))			(TM-1**G. mus.*)/BC1		
Lint%	**Mean**	**V**	**H^2**	**Mean**	**V**	**H^2**	**Mean**	**V**	**H^2**	**Mean**	**V**	**H^2**
Gen												
F_1	28.3	3.13	53.8	34.8	15.34	90.6	35.8	7.83	81.5			
F_2	33.5	16.25	85.7	35.0	5.97	61.0	36.8	4.78	51.3	32.8	9.49	84.8
F_3										38.0	10.16	77.1
BC_1F_2				35.2	0.46	0	39.2	21.7	89.3			
Micronaire												
F_1	3.0	0.01	0	4.3	0.03	0	4.2	0.02	0			
F_2	3.9	0.40	79.8	4.2	0.11	25.8	4.0	0.16	49.8	4.0	0.08	59.1
F_3										4.5	0.23	65.3
BC_1F_2				3.9	0.01	0	4.3	0.33	76.1			
Length (mm)												
F_1	32.6	0.02	0	30.3	1.62	45.0	29.8	0.27	0			
F_2	32.9	3.39	62.2	31.7	2.10	39.1	32.6	2.54	49.6	29.0	1.18	24.2
F_3										30.5	2.94	56.4
BC_1F_2				33.4	0.14	0	29.1	2.60	50.8			
UI (%)												
F_1	84.7	0.04	0	84.6	1.20	65.8	83.9	0.98	57.9			
F_2	85.8	1.46	3.13	86.1	1.61	37.7	87.1	2.25	55.5	82.6	1.10	62.7
F_3										84.9	1.33	24.7
BC_1F_2				86.4	0.36	0	84.3	1.14	12.6			
Strength (kN m Kg^{-1})												
F_1	376	351	54.0	346	295	45.2	319	1034	84.4			
F_2	348	633	55.5	337	656	57.1	334	934	69.8	314	616	73.8
F_3										312	513	45.1
BC_1F_2				338	108	0	305	299	5.9			
Elongation (%)												
F_1	4.6	0.24	0	6.1	0.05	0	6.5	1.62	60.2			
F_2	4.7	1.15	45.8	5.3	0.88	28.7	5.5	0.91	31.4	5.9	0.72	10.2
F_3										5.4	1.34	53.2
BC_1F_2				5.8	0.17	0	4.9	0.44	0			

Table 6. Means, variance (V), and estimates of heritability (H^2) of four pedigrees of *G.* tomentosum interspecific hybrids through three generations in College Station, TX, 2001-2004.

Trait	TAM 96WD-18 * ((TM-1 * *G. tom.*)/BC1)			Acala 1517-99 * ((TM-1 * *G. tom.*)/BC1)			CA3250 * ((TM-1 * *G. tom.*)/BC1)			Pyramid * ((TM-1 * *G. tom.*)/BC1)		
Lint%	**Mean**	**V**	**H^2**	**Mean**	**V**	**H^2**	**Mean**	**V**	**H^2**	**Mean**	**V**	**H^2**
Gen												
F_1	33.5	0.29	0	34.8	0.31	0	38.3	0.29	0	39.1	0.97	0
F_2	35.4	3.50	33.5	38.0	9.32	75.0	39.2	5.84	60.2	39.0	10.59	78.0
BC_1F_2	38.1	10.15	77.1	41.2	8.51	72.7	39.0	3.58	34.9	38.9	13.02	82.1
Micronaire												
F_1	4.2	0.20	84.0	4.4	0.02	0	4.1	0.03	3.4	5.0	0.13	75.1
F_2	4.2	0.20	60.4	4.5	0.32	74.7	4.3	0.17	53.0	4.7	0.26	69.3
BC_1F_2	4.6	0.13	37.9	4.3	0.30	72.9	4.3	0.74	89.1	4.7	0.14	41.3
Length (mm)												
F_1	28.2	0.00	0	31.5	3.31	73.1	28.5	0.04	0	27.8	1.33	33.0
F_2	30.1	0.89	0	31.6	4.99	74.4	30.2	1.92	33.2	30.5	3.07	58.4
BC_1F_2	29.4	1.32	3.2	30.2	1.33	4.1	31.1	0.44	0	28.9	4.18	69.4
UI (%)												
F_1	83.6	0.81	49.3	81.0	1.30	68.4	83.6	0.13	0	80.9	1.29	68.1
F_2	85.2	0.35	0	85.3	1.38	27.4	85.0	1.49	32.9	85.1	2.37	57.8
BC_1F_2	84.9	0.92	0	84.4	0.04	0	85.2	0.42	0	83.5	4.10	75.6
Strength (kN m Kg^{-1})												
F_1	317	87	0	352	441	63.4	328	334	51.6	306	1.00	0
F_2	319	285	1.2	330	773	63.6	323	636	55.7	309	547	48.5
BC_1F_2	308	477	41.0	328	1753	83.9	292	94	0	298	505	44.2
Elongation (%)												
F_1	7.3	0.02	0	5.5	0.35	0	6.6	0.29	0	6.0	0.08	0
F_2	5.9	0.62	0	5.0	1.34	53.3	5.9	0.73	14.0	5.1	0.96	35.1
BC_1F_2	6.3	1.08	41.9	5.6	2.36	73.5	5.9	0.92	31.7	5.5	0.92	31.8

Table 7. Performance trial of interspecific hybrids (Sea Island x *G. hirsutum*) in College Station, TX, 2006.

Name	Pedigree	Lint kg ha^{-1}	Lint %	Mic	Length mm	Strength kN m Kg^{-1}	UI %	Elong %
DPL 491		1397.8	42.6	4.5	29.7	303	84	5.1
FM 966LL		1342.9	38.8	4.9	28.7	326	84	4.6
TAM 96 WD-18		1302.6	35.8	4.5	31.0	314	85	6.9
03ISH E-61	(TAM 94L-25*NMSI 1331)	1293.6	37.3	4.7	31.0	301	84	4.4
03ISH E-58	(TAM 94L-25*NMSI 1331)	1227.5	32.5	4.1	32.0	337	85	5.4
03ISH E-122	(TAM 94L-25*NMSI 1331)	1213.0	37.3	4.6	30.5	330	85	4.7
PSC 355		1211.8	40.2	5.4	27.7	284	84	7.6
03ISH E-63	(TAM 94L-25*NMSI 1331)	1190.6	34.3	4.4	31.8	319	85	5.4
FM 832		1165.9	34.3	4.7	30.5	314	84	5.5
03ISH E-106	(TAM 94L-25*NMSI 1331)	1148.0	35.8	4.6	31.2	331	84	4.4
03ISH E-162	(TAM 94L-25*NMSI 1331)	1140.2	37.3	4.4	32.3	343	86	4.5
03ISH E-148	(TAM 94L-25*NMSI 1331)	1109.9	36.0	4.5	32.5	339	87	4.4
03ISH E-179	(TAM 94L-25*NMSI 1331)	1088.6	37.0	5.0	30.7	331	85	4.5
03ISH E-177	(TAM 94L-25*NMSI 1331)	1083.0	35.5	4.7	31.2	336	85	4.5
03ISH E-197	(TAM 94L-25*NMSI 1331)	1073.0	35.8	4.5	31.2	328	84	4.4
03ISH E-67	(TAM 94L-25*NMSI 1331)	1064.0	35.6	4.5	31.5	305	83	5.6
03ISH E-83	(TAM 94L-25*NMSI 1331)	1041.6	36.6	4.8	31.0	312	84	4.0
03ISH E-55	(TAM 94L-25*NMSI 1331)	1030.4	36.0	4.7	30.5	333	85	4.4
03ISH E-133	(TAM 94L-25*NMSI 1331)	967.7	36.3	4.5	30.7	319	83	4.1
03ISH E-118	(TAM 94L-25*NMSI 1331)	964.3	33.1	4.5	32.0	324	86	4.7
03ISH D-21	(TAM 94L-25*SI-Barbados)	955.4	36.2	4.4	30.2	327	82	6.0
03ISH F-32	(TAM 97M-16*NMSI 1331)	955.4	34.8	4.9	29.7	300	85	5.4
03ISH D-155	(TAM 94L-25*SI-Barbados)	952.0	35.4	4.3	30.2	316	82	4.6
03ISH E-247	(TAM 97M-16*NMSI 1331)	933.0	34.1	4.3	31.0	321	85	8.2
03ISH E-103	(TAM 94L-25*NMSI 1331)	926.2	36.1	4.8	31.0	332	85	4.3
03ISH E-154	(TAM 94L-25*NMSI 1331)	925.1	35.0	4.4	31.0	322	84	3.9
03ISH D-218	(TAM 94L-25*SI-Barbados)	911.7	36.5	4.6	30.0	321	84	6.9
TAM 94 L-25		869.1	34.3	4.5	29.5	292	83	5.3
03ISH F-175	(TAM 97M-16*NMSI 1331)	857.9	34.3	4.2	31.0	312	84	7.1
03ISH E-136	(TAM 94L-25*NMSI 1331)	816.5	36.8	4.7	30.5	304	83	5.6
03ISH E-45	(TAM 94L-25*NMSI 1331)	816.5	36.7	4.6	30.2	318	84	6.3
03ISH E-142	(TAM 94L-25*NMSI 1331)	813.1	32.6	4.1	29.7	316	83	5.6
03ISH D-83	(TAM 94L-25*SI-Barbados)	806.4	34.7	4.6	29.0	288	82	6.8
03ISH F-227	(TAM 97M-16*NMSI 1331)	791.8	34.5	4.5	30.5	301	83	7.7
03ISH E-54	(TAM 94L-25*NMSI 1331)	768.3	35.0	4.5	31.0	322	84	5.0
03ISH D-27	(TAM 94L-25*SI-Barbados)	674.2	35.8	5.0	30.2	322	83	6.1
03ISH E-48	(TAM 94L-25*NMSI 1331)	653.0	31.1	4.0	33.0	304	85	7.1
03ISH F-98	(TAM 97M-16*NMSI 1331)	636.2	31.6	4.3	31.8	380	86	6.2
03ISH E-172	(TAM 94L-25*NMSI 1331)	622.7	33.6	4.1	30.7	313	85	6.3
03ISH D-74	(TAM 94L-25*SI-Barbados)	599.2	32.1	3.9	29.0	307	82	6.3
03ISH D-196	(TAM 94L-25*SI-Barbados)	594.7	33.4	4.2	31.2	330	83	6.3
03ISH D-67	(TAM 94L-25*SI-Barbados)	590.2	34.8	4.1	29.2	318	82	6.1
03ISH D-81	(TAM 94L-25*SI-Barbados)	342.7	33.2	3.9	31.0	289	82	5.5
LSD $_{(0.05)}$		180.3	2.6	0.3	1.8	29	2.6	0.6
%,C.V.		14.5	3.7	3.2	2.6	4.2	1.3	6.2
Mean		948.6	35.4	4.5	30.5	318	84.0	5.5