

Genotype × Environment Interaction and Stability Analysis for Watermelon Fruit Yield in the United States

Mahendra Dia, Todd C. Wehner,* Richard Hassell, Daniel S. Price, George E. Boyhan, Stephen Olson, Stephen King, Angela R. Davis, and Gregory E. Tolla

ABSTRACT

One of the major breeding objectives for watermelon (*Citrullus lanatus* [Thumb.] Matsum & Nakai) is improved fruit yield. High yielding genotypes have been identified, so we measured their stability for fruit yield and yield components over diverse environments. The objectives of this study were to (i) evaluate the yield of watermelon genotypes over years and locations, (ii) identify genotypes with high stability for yield, and (iii) measure the correlations among univariate and multivariate stability statistics. A diverse set of 40 genotypes was evaluated over 3 yr (2009, 2010, and 2011) and eight locations across the southern United States in replicated trials. Yield traits were evaluated over multiple harvests, and measured as marketable yield, fruit count, percentage cull fruit, percentage early fruit, and fruit size. There were strong effects of environment as well as genotype × environment interaction (G×E) on watermelon yield traits. Based on multiple stability measures, genotypes were classified as stable or unstable for yield. There was an advantage of hybrids over inbreds for yield components in both performance and responsiveness to favorable environments. Cultivars Big Crimson and Legacy are inbred lines with high yield and stability. A significant ($P < 0.001$) and positive correlation was measured for Shukla's stability variance (σ_i^2), Shukla's squared hat (\hat{S}_i^2), Wricke's ecovalence (W_i), and deviation from regression (S^2_d) for all the traits evaluated in this study.

M. Dia and T.C. Wehner, Dep. of Horticultural Science, North Carolina State Univ., Campus Box 7609, Raleigh, NC 27695-7609; R. Hassell, Clemson University, Coastal Research and Education Center, 2700 Savannah Hwy, Charleston, SC 29414; D.S. Price, Georgia County Extension, SW District, 110 West 13th Ave, Suite C, Cordele, GA 31015; G.E. Boyhan, University of Georgia, Dep. of Hort., 1111 Miller Plant Science Bldg., Athens, GA 30602; S. Olson, North Florida REC, Univ. of Florida, 155 Research Road, Quincy, FL 32351-5677; S. King, Texas A&M University, Dep. of Hort. Sci., 1500 Research Pkwy, Ste A120, College Station, TX 77845; A.R. Davis, USDA-ARS, 911 East Highway 3, Lane, OK 74555; G.E. Tolla, Monsanto/Seminis Veg Seeds, 37437 State Hwy 16, Woodland, CA 95695. Received 12 Oct. 2015. Accepted 2 Feb. 2016. *Corresponding author (tcwehner@gmail.com).

Abbreviations: AEC, average environment coordinate; AMMI, additive main effects and multiplicative interaction; b_i , linear regression coefficient; CI, Clinton, NC; FL, Quincy, FL; GA, Cordele, GA; GGE, genotype main effects plus genotypic × environment interaction effect; GGL, genotype main effects plus genotypic × location interaction effect; G×E, Genotype × environment interaction; G01 or 1, AU-Jubilant; G02 or 2, Allsweet; G03 or 3, Big Crimson; G04 or 4, Black Diamond; G05 or 5, Calhoun Gray; G06 or 6, Calsweet; G07 or 7, Carolina Cross#183; G08 or 8, Charleston Gray; G09 or 9, Congo; G10 or 10, Crimson Sweet; G11 or 11, Desert King; G12 or 12, Early Arizona; G13 or 13, Early Canada; G14 or 14, Fiesta F1; G15 or 15, Georgia Rattlesnake; G16 or 16, Golden Midget; G17 or 17, Graybelle; G18 or 18, Hopi Red Flesh; G19 or 19, Jubilee; G20 or 20, King & Queen; G21 or 21, Legacy; G22 or 22, Mickylee; G23 or 23, Minilee; G24 or 24, Mountain Hoosier; G25 or 25, NC Giant; G26 or 26, Navajo Sweet; G27 or 27, Peacock WR-60; G28 or 28, Quetzali; G29 or 29, Regency F1; G30 or 30, Royal Flush F1; G31 or 31, Sangria F1; G32 or 32, Starbrite F1; G33 or 33, Stars-N-Stripes F1; G34 or 34, Stone Mountain; G35 or 35, Sugar Baby; G36 or 36, Sugarlee; G37 or 37, Sweet Princess; G38 or 38, Tendersweet OF; G39 or 39, Tom Watson; G40 or 40, Yellow Crimson; KN, Kinston, NC; M , trait mean; OK, Lane, OK; PC, principal component; SC, Charleston, SC; SVP, singular value partitioning; TX, College Station, TX; CA, Woodland, CA; σ_i^2 , Shukla's stability variance; \hat{S}_i^2 , Shukla's squared hat; S^2_d , deviation from regression; W_i , Wricke's ecovalence; YS_i , Kang's stability statistic

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ELITE CULTIVARS of watermelon have been developed with high fruit yield, fruit quality, earliness, percentage marketable fruit, excellent shipping characteristics, and disease resistance. A century of breeding has produced uniform hybrids, seedless triploids, tough rind, high sugar content, dark red flesh, 9 kg picnic watermelon, and 3 kg mini watermelon (Gusmini and Wehner, 2008). Since 1960, yield has increased approximately 200% in the United States (USDA, 2010). However, high yield is often associated with decreased yield stability (Calderini and Slafer, 1999; Padi, 2007). Yield stability is important, but limited studies have been done on watermelon (Vasanthkumar et al., 2012).

Genotypes with high yield and stability can be identified using trials in multiple years and locations (Lu'quez et al., 2002). Genotypes respond differently to environmental factors such as soil fertility or the presence of disease pathogens (Kang, 2004). These contribute to genotype \times environment interaction (G \times E), which has been reported in field and vegetable crops (Bednarz et al., 2000; Mekbib, 2003; Riday and Brummer, 2006; Fan et al., 2007; Mulema et al., 2008; Miranda et al., 2009; De Vita et al., 2010; Panthee et al., 2012; Rak et al., 2013).

The presence of G \times E makes it useful to measure both performance and stability for genotypes being evaluated in breeding programs (Magari and Kang, 1993; Ebdon and Gauch, 2002). Genotype \times environment interaction may result in low correlation between phenotypic and genotypic values, thereby reducing progress from selection. This leads to bias in the estimation of heritability and in the prediction of genetic advance (Comstock and Moll, 1963; Alghamdi, 2004). Therefore, the magnitude and nature of G \times E determines the features of a selection and testing program.

Several statistical methods for evaluating stability have been proposed, reflecting different aspects of the G \times E. These statistical methods range include univariate models, such as regression slope, deviation from regression, environmental variance, and Kang's yield-stability, and multivariate models, such as genotype main effect plus genotype \times environment interaction (GGE) biplot, and additive main effects and multiplicative interaction (AMMI) (Finlay and Wilkinson, 1963; Eberhart and Russell, 1966; Yan, 2001; Kang, 1993; Yan and Kang, 2003). However, no single method adequately explains genotype performance across environments. Stability statistics (variation) are best used in combination with trait performance (mean).

Analysis of variance is often used to identify the existence of G \times E in multiple-environment trial data. Analysis of variance measures the components of variance arising from different fixed and random factors (e.g., genotype, location, year, and replication) and their interactions. However, ANOVA has limitations, including the assumption of homogeneity of variance among environments, in its ability to explore the response of genotypes for G \times E (Zobel et al., 1988).

The most widely used approach for stability analysis is based on linear regression: the slope (b) or deviation from regression (S^2_{β}) of genotype performance relative to an environmental index derived from the average performance of all genotypes in each environment (Finlay and Wilkinson, 1963; Eberhart and Russell, 1966; Freeman, 1973; Chakroun et al., 1990). Some researchers have found deficiencies in the regression method for evaluation of G \times E patterns (Zobel et al., 1988; Nachit et al., 1992; Annicchiarico, 1997; Kandung et al., 2010; De Vita et al., 2010). The deficiencies are of four types. First, the estimates of best fitted line have high error when only a few low- and high-yielding locations are included in the study (Crossa et al., 1990). Second, the average of all genotypes evaluated in each environment (environmental index) is not independent of each genotype for that environment (Freeman and Perkins, 1971). Third, the errors associated with the slopes of genotypes are not statistically independent (Kandung et al., 2010). Fourth, there is a required assumption of a linear relationship between interaction and environmental means when the actual responses of the genotypes to the environments are intrinsically multivariate (Crossa et al., 1990).

Shukla (1972) proposed an unbiased estimate of the variance (σ_i^2) of G \times E plus an error term associated with genotype, in which a genotype with low σ_i^2 is regarded as stable. Shukla's stability variance is a linear combination of Wricke's ecovalance (W), which is the proportion of G \times E variance contributed by each genotype. W_i and σ_i^2 are equivalent in ranking genotypes for stability (Kang et al., 1987). Kang's stability statistic (YS_i) is nonparametric, using both trait mean (M) and σ_i^2 , with equal weight on each. Genotypes with YS_i greater than the mean YS_i are stable (Kang, 1993; Mekbib, 2003; Fan et al., 2007).

Multivariate analysis includes the AMMI method, and the GGE method with a graphical display (Casanoves et al., 2005; Dehghani et al., 2006). These models are based on principal component (PC) analysis and have the ability to reveal structure in the data. The AMMI and GGE biplot differ in value for analyzing multi-environment trial data (Gauch, 2006; Yan et al., 2007). The GGE biplot was named by Yan et al. (2000). It is constructed from the first two principal components (PC1 and PC2) that explain maximum variability in the data, derived by singular value decomposition of a two-way (genotype \times environment) data matrix (Yan et al., 2000).

The AMMI model combines the ANOVA (an additive model) to characterize genotype and environment main effects, with PC analysis (a multiplicative model) to characterize interactions (Crossa et al., 1990). Depending on number (n) of PC's used in study the interaction, AMMI models are usually called AMMI1, AMMI2, ... AMMI(n). The AMMI biplot separates genotypes according to their PC scores, making it easy to determine genotype stability (Carbonell et al., 2004).

We measured watermelon yield components including marketable yield (Mg ha^{-1}), fruit count (thousand fruit ha^{-1}), percentage early fruit, percentage cull fruit, and fruit size (kg fruit^{-1}). The objectives of this study were to (i) evaluate the G×E of watermelon genotypes, (ii) identify watermelon genotypes with high stability for yield, and (iii) estimate the correlations among univariate and multivariate stability statistics.

MATERIALS AND METHODS

Germplasm and Location

Forty genotypes of watermelon were evaluated for 3 yr (2009, 2010, and 2011) and in eight locations across the southern United States. Locations were chosen to represent major watermelon production regions in the United States: North Carolina (KN: Kinston, CI: Clinton) and South Carolina (SC: Charleston) in the east to Georgia (GA: Cordele), Florida (FL: Quincy), Oklahoma (OK: Lane), and Texas (TX: College Station) in the South to California (CA: Woodland) in the West. Forty genotypes were chosen to represent new vs. old releases, small vs. large fruit size, round vs. elongate fruit shape, striped vs. solid rind pattern, anthracnose resistance vs. susceptibility, eastern vs. western adapted, and inbred vs. hybrid type (Supplemental Tables S1 and S2). The 40 watermelon genotypes were categorized as inbred or hybrid based on information obtained from seed providers (Gusmini and Wehner, 2005, 2008). Hybrids are identified with F_1 after their name.

Cultural Practices

The experiment design was a randomized complete block with four replications, eight locations and 3 yr. Seeds of each genotype were sown in 72-cell polyethylene flats in the greenhouses at North Carolina State University. The seedlings were transplanted by hand at the two-true-leaf stage. Missing or damaged transplants were replaced 1 wk later.

Plots were planted on raised, shaped beds in rows on 3.1-m centers with plants 1.2 m apart. The beds had drip irrigation tubes covered with black polyethylene mulch. Production practices were according to the North Carolina Extension Service and Southeastern U.S. 2009 Vegetable Crops handbook (Sanders, 2004; Holmes and Kemble; 2009).

Data Collection and Traits

At each location, the 40 watermelon genotypes were evaluated for traits including marketable yield (Mg ha^{-1}), fruit count (thousand fruit ha^{-1}), percentage cull fruit ($100 \times \text{cull fruit yield}/\text{total fruit yield}$), percentage early fruit ($100 \times \text{fruit weight of first harvest}/\text{fruit weight over all harvests}$), and fruit size (kg fruit^{-1}).

Fruit were harvested using the guide of number of days to maturity, as well as the indicators of maturity: a brown and dry tendril at the node bearing the fruit, a dull waxy fruit surface, a light-colored groundspot on the fruit, and a dull sound of the fruit when thumped (Maynard, 2001). Fruit were weighed individually, and yield was calculated as total and marketable fruit weight (Mg ha^{-1}) and number (thousand ha^{-1}) by summing plot yield over harvests. Numbers of cull and marketable fruit were also recorded. Percentage cull fruit was calculated as cull fruit

weight divided by total fruit weight. Culls included crooked, bottle-necked, and other deformed fruit. One to four harvests were made depending on location and year. Most locations had two to three harvests. Harvest data were not collected from Oklahoma in 2009, Georgia in 2010, and Florida in 2011. Data were not collected on percentage cull fruit from South Carolina in 2009, 2010, and 2011; or from Florida in 2009 and 2010. A single harvest was made in California in 2009 and in Georgia in 2011 (no data on percentage early fruit for those environments).

Data Analysis

Data were analyzed for genotype, environment and G×E using the SASGxE program developed by Dia and Wehner (2015) and SAS v9.4 (SAS, 2014). SASGxE computes univariate stability statistics, input files that are ready to use in R packages for multivariate stability statistics, ANOVA, descriptive statistics, and correlation among stability analysis methods (Dia and Wehner, 2015). SASGxE is available at <http://cuke.hort.ncsu.edu/cucurbit/wehner/software.html>. Years, locations, replications, and genotypes were analyzed as random effects. An analysis of variance was used to determine the size and significance (F ratio) of genotype × environment interactions for the traits of interest. If genotype × environment interactions were significant, additional statistics were calculated to determine the stability of each genotype over the 21 environments (location × year combinations).

The univariate stability parameters used were Shukla's stability variance (σ_i^2), Shukla's squared hat (\hat{S}_i^2), Wricke's ecovalence (W_i), regression slope (b_i), deviation from regression (S_d^2) and Kang's yield-stability statistics (YS). Least squared means or adjusted trait means (M) and their LSD for each genotype were computed over the 3 yr and eight locations for the traits of interest. Hereafter, mean will indicate least squared mean or adjusted trait mean. The AMMI and GGE biplots were computed using the AMMI (Agricolae) and GGEbiplot-GUI package, respectively, of R statistical software in RStudio (R Development Core Team, 2007; CRAN, 2014; RStudio, 2014). The AMMI and GGE biplot analysis were used to visually assess the presence of G×E and rank genotype based on stability and mean (Yan et al., 2000; Yan and Kang, 2003). Tests for significance were derived using a t test for each b_i and an F test for each S_d^2 for statistical differences from one and zero, respectively, at 0.05, 0.01, and 0.001 levels of probability. Ranks were assigned to each genotype in increasing order for each stability parameter, except percentage cull fruit (selected for low values). Simple correlation coefficients (using Spearman rank) were calculated for all pairs of stability measures.

RESULTS

The results are presented for the magnitude of G×E, the stability of genotypes, and the correlations among stability measures.

Genotype × Environment Interaction Analysis of Variance

The combined ANOVA indicated highly significant environment, genotype, and G×E effects for marketable yield, fruit count, percentage cull fruit, percentage early fruit, and fruit size (Table 1). Except for fruit size, all yield traits

Table 1. Significance values and variance (mean squares) for marketable yield (Mg ha⁻¹), fruit count, percentage cull fruit, percentage early fruit, and fruit size (kg fruit⁻¹) of 40 watermelon genotypes tested in 3 yr and eight locations in the United States.

Source	df†	Marketable yield	Fruit count	Percentage cull fruit	Percentage early fruit	Fruit size
Environment (E)	20	106825**	1554**	10327**	40143**	226**
Location (L)	7	231712**	3036**	17835 NS‡	63207**	346 NS
Year (Y)	2	3240 NS	108 NS	10925 NS	11356**	21 NS
L × Y	11	40726**	752**	5801**	4880**	180**
Replication within E	63	2366**	30**	360**	1301**	10**
Genotype (G)	39	9227**	456**	1792**	3499**	413**
G × E	780	1023**	24**	234**	649**	5**
G × L	273	1323**	34**	306**	743**	6**
G × Y	78	870 NS	21 NS	293**	783**	9**
G × L × Y	429	850**	18**	186**	542**	4**

** Significant at the 0.01 level of probability.

† Note: degrees of freedom (df) were lower for percentage cull fruit and percentage early fruit due to missing data.

‡ NS = nonsignificant.

had large variances due to environment (ranged from 26–48%), with large differences among environments for genotype means causing most of the variation in genotype performance (Table 1). Marketable yield, percentage cull, and percentage early had large genotype × environment effect (18, 23, and 21% of total sum of squares, respectively) and small genotype effect (8, 10, and 7% of total variance, respectively) (Table 1). For fruit count, the environment effect, genotype effect, and genotype × environment effect had similar contribution to total variation. In contrast, fruit size had large genotype effect (52% of total variance), small environment effect (15% of total variance) and genotype × environment effect (13% of total variance) (Table 1).

Polygon View of GGE Biplot

The polygon (which–won–where) view of the GGE biplot divides the biplot into sector via perpendicular lines (rays) passing from the polygon sides (Fig. 1). The polygon is drawn by joining extreme genotypes of the biplot. If environments fall into different sectors, then different genotypes won in different sectors, and a crossover G×E pattern exists. The winning genotype for an environment or set of environments in a sector is the vertex genotype. Conversely, if all environments fall into a single sector, a single genotype had the highest yield in all environments. The vertex genotype in a sector where no environment is present is considered to be a poor performer in all test environments. Genotypes within the polygon were less responsive to location than the vertex genotypes. A polygon view of the GGE biplot explained 79, 81, 84, 68, and 96% of the genotype and genotype × environment variation for the marketable yield, fruit count, percentage cull fruit, percentage early fruit, and fruit size, respectively (Fig. 1: Panel A, B, C, D, and E). Other than fruit count and fruit size, yield traits had environments in two sectors with different winning genotypes (vertex genotype) in each (Fig.

1: Panel A, B, C, D, and E). This confirms the existence of G×E for marketable yield, percentage cull fruit and percentage early fruit (Fig. 1: Panel A, C, and D). Genotype main effects plus genotype × location interaction effect (GGL) biplots for individual year were constructed and showed that location grouping did not vary across years. Results of GGL biplots are not presented here.

Additive Main Effects and Multiplicative Interaction 2

In AMMI2, the biplot abscissa and ordinate used the first and second principal component terms (PC1 and PC2), respectively. The AMMI2 biplot explained 68, 68, 72, 61, and 71% of the genotype and genotype × environment variation for marketable yield, fruit count, percentage cull fruit, percentage early fruit, and fruit size, respectively (Fig. 2: Panel A, B, C, D, and E). Horizontal and vertical lines passing from the origin (0, 0) of the biplot divide it into four sectors. Like GGE biplot, the genotypes at the vertex of the polygon are the winners for the environments included in that sector. A location close to the biplot origin is a less interactive location and is considered to be good for the selection of genotypes with average adaptation (Murphy et al., 2009). The angle between genotype and environment vectors determined the nature of G×E: it is positive for acute angles, negligible for right angles, and negative for obtuse angles. Also, the distance of genotype and environment vectors from the biplot origin indicates the magnitude of G×E exhibited by genotypes over environment or environments over genotype. For marketable yield, fruit count and fruit size, environments fell into all four sectors, and different winning genotypes (vertex genotypes) were observed in each sector (Fig. 2: Panel A, B, and E). Similarly, percentage cull and percentage early had environments falling into three sectors (Fig. 2: Panel C and D). Thus, AMMI2 biplot validated the existence of interaction of 40 watermelon genotypes with 21 environments for

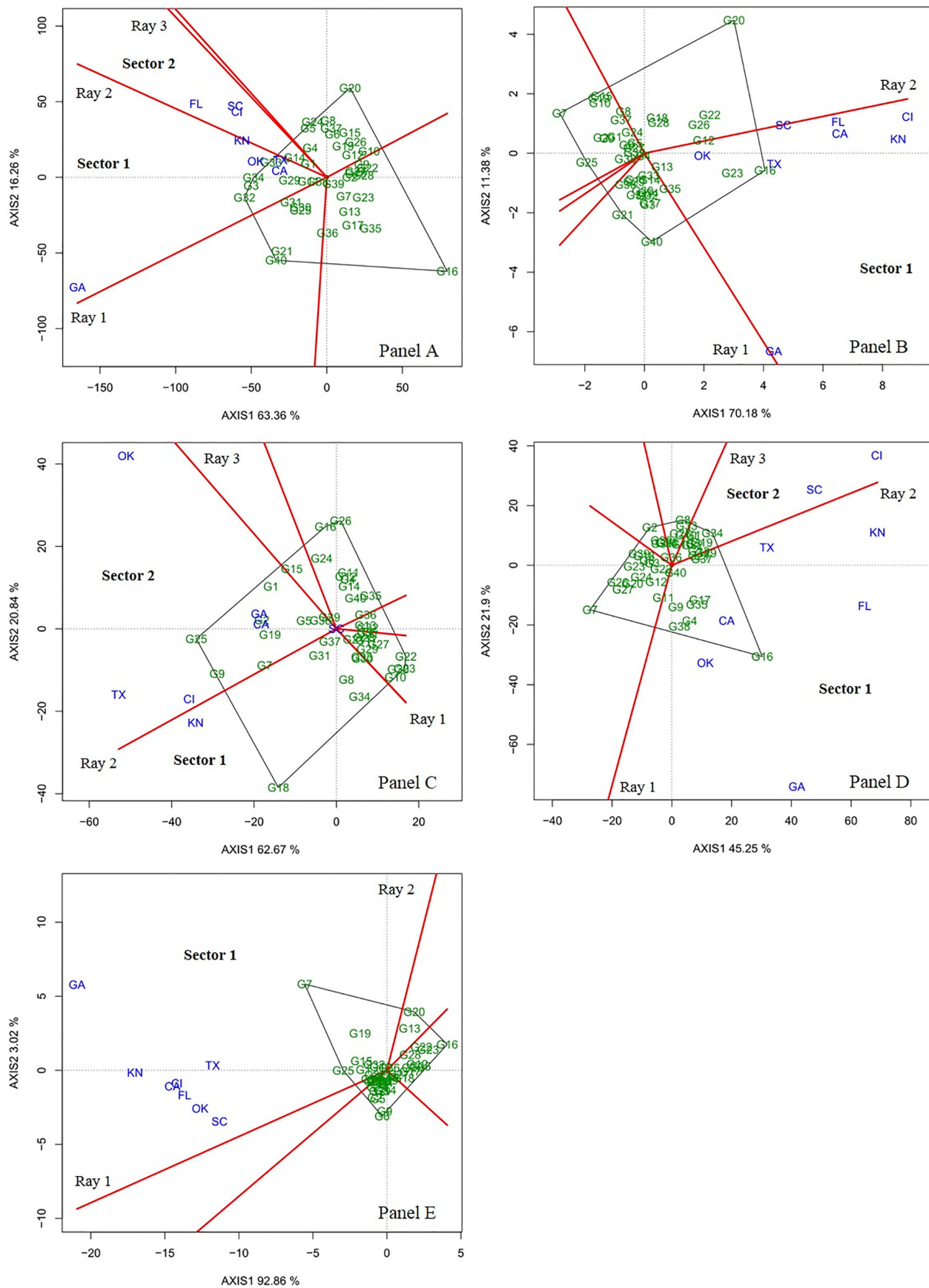


Fig. 1. The polygon (which–won–where) view of genotype main effects plus genotypic × environment interaction effect (GGE) biplot of 40 watermelon genotypes tested in 3 yr and eight locations for (Panel A) marketable yield, (Panel B) fruit count, (Panel C) percentage cull fruit, (Panel D) percentage early fruit, and (Panel E) fruit size. The biplots were based on Scaling = 0, Centering = 0, and SVP = 2.

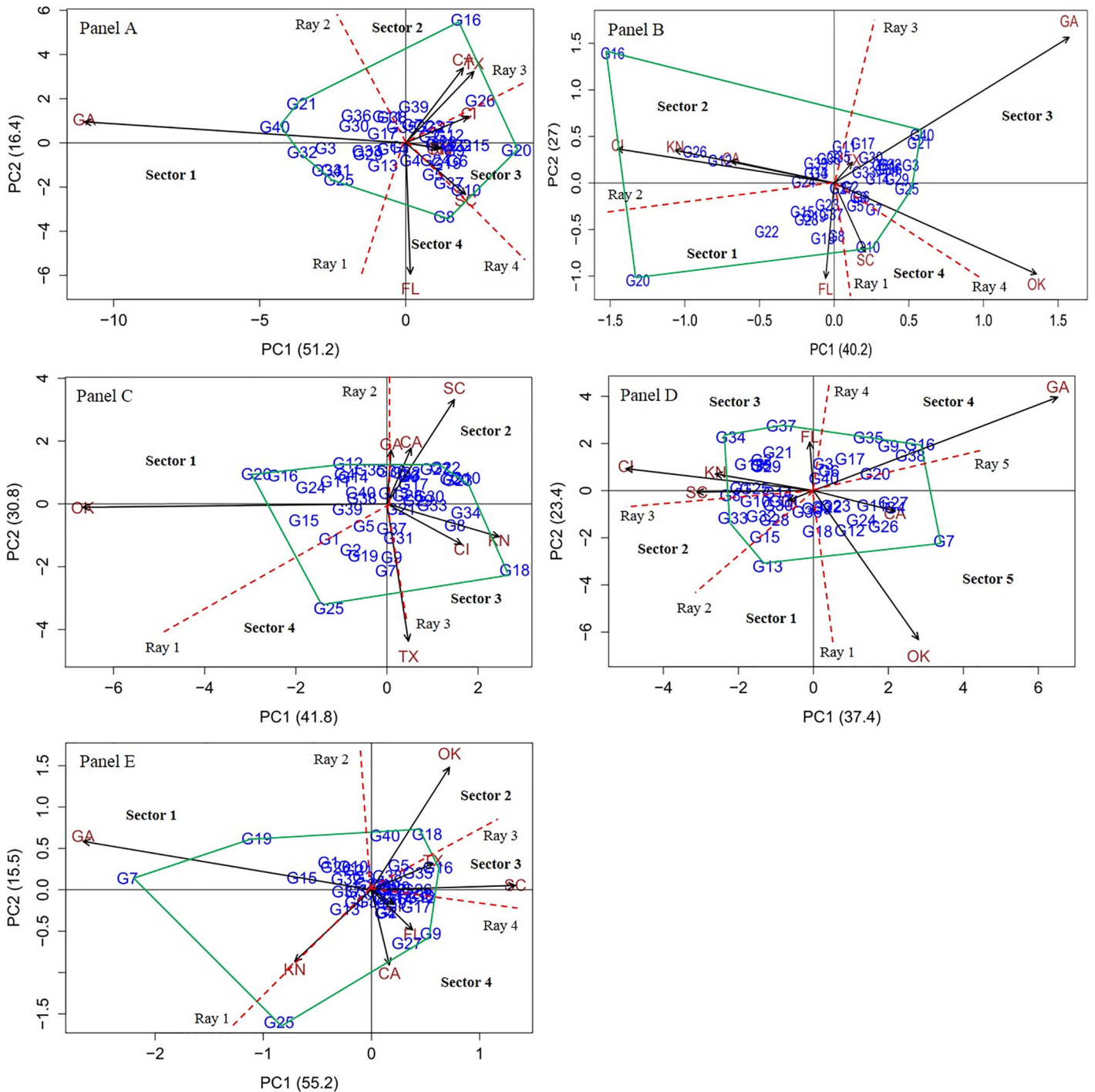


Fig. 2. Additive main effects and multiplicative interaction 2 (AMMI2) biplot of the first two principal component (PC1 and PC2) showing the genotype \times environment interaction (G \times E) for (Panel A) marketable yield, (Panel B) fruit count, (Panel C) percentage cull fruit, (Panel D) percentage early fruit, and (Panel E) fruit size of 40 watermelon genotypes tested in 3 yr and eight locations.

all the traits evaluated. However, AMMI2 exhibited a different crossover pattern than the GGE biplot (Fig. 1 and 2: Panel A, B, C, D, and E). Also, AMMI2 for individual year was analyzed for all traits, and some inconsistencies were observed, since locations fell into different sectors. However, the general pattern of location grouping did not vary across years. Results of AMMI2 are not presented here.

Genotype Evaluation

The significant G \times E justified our evaluation of watermelon genotypes for yield stability over environments.

Genotype Means

Marketable yield ranged from a high of 80.44 to a low of 27.43 Mg ha⁻¹. Highest marketable yield was recorded for genotypes Big Crimson, Stone Mountain, Stars-N-Stripes F1, and Starbrite F1 (Table 2). Other high yielding genotypes

were Fiesta F1, Regency F1, Calhoun Gray, Legacy, and Mountain Hoosier. Genotype Golden Midget had marketable yield significantly lower than the other genotypes (Table 2). Fruit count ranged from 1.61 to 6.31 thousand fruit ha⁻¹ (Table 2). Highest fruit count was for Golden Midget, followed by genotype Minilee and King & Queen (Table 2). Lowest fruit count was for genotype Carolina Cross #183, significantly lower than the other genotypes (Table 2).

Large fruit size was correlated with high percentage cull fruit (Table 2). Genotype NC Giant and Congo had large fruit and the highest percentage cull fruit (23.42 and 20.55%, respectively, Table 2). Lowest percentage cull fruit were for Minilee, which was similar to high yielding genotypes Starbrite F1 and Regency F1 (Table 2). Genotypes Carolina Cross#183, NC Giant, Georgia Rattlesnake, AU-Jubilant, and Jubilee had the largest fruit size; genotypes Golden Midget, Minilee, and Mickylee had the smallest fruit size (Table 2). Genotypes Golden Midget, Early Canada, Stone Mountain, and Regency F1 had the highest percentage early fruit (Table 2). Genotypes Navajo Sweet, Peacock WR-60, King & Queen, Minilee, and Tom Watson produced the lowest percentage early fruit (Table 2).

Regression Coefficient or Slope

According to Eberhart and Russell (1966), a regression coefficient (b_i) approximating unity along with S^2_d near zero indicate stability. For marketable yield, the b_i value for many genotypes was close ($P > 0.01$) to unity, except for genotypes Big Crimson, Carolina Cross#183, Charleston Gray, Congo, Early Canada, Golden Midget, Graybelle, King & Queen, Royal Flush F1, Starbrite F1, and Tom Watson (Tables 3 and 4). Similarly, b_i for fruit count was close to unity for genotypes Sugar Baby, Stars-N-Stripes F1, Tendersweet OF, Crimson Sweet, Fiesta F1, Desert King, Mountain Hoosier, Legacy, and Peacock WR-60 (Table 3). Genotypes Black Diamond, Congo, and Starbrite F1 had b_i significantly different from unity (Table 3). Black Diamond and Congo had b_i of zero.

For percentage cull fruit, b_i ranged from -1.35 to 2.79 (data not shown). Genotypes such as Congo and Hopi Red Flesh with high percentage cull fruit had high b_i . Conversely, genotypes such as Stars-N-Stripes F1, Fiesta F1, Peacock WR 60, and Yellow Crimson with low percentage cull fruit were resistant to environmental effects. Genotypes Minilee, Navajo Sweet, and Calsweet had low percentage cull fruit and negative b_i value. The b_i value for percentage early fruit for all the genotypes was positive and close to 1.0, except genotype Georgia Rattlesnake (Table 3).

Deviation from Regression and Shukla's Stability Variance

The genotypes with the highest marketable yield in this study were Starbrite F1, Stars-N-Stripes F1, Fiesta F1, Regency F1, Big Crimson, Stone Mountain, Calhoun Gray, and Legacy.

Table 2. Means (corrected by least squares) (M) for marketable yield (Mg ha⁻¹), fruit count (thousand fruit ha⁻¹), percentage cull fruit, percentage early fruit and fruit size (kg fruit⁻¹) of 40 watermelon genotypes tested in 3 yr and eight locations (in order by marketable yield).

Genotype	Marketable yield†	Fruit count	Percentage cull fruit	Percentage early fruit	Fruit size
Big Crimson	80.44	3.73	06.5	23.2	08.60
Starbrite F1	80.40	3.69	05.8	37.4	08.54
Stone Mountain	79.10	3.67	07.1	39.7	08.52
Stars-N-Stripes F1	77.25	3.72	06.3	35.2	08.30
Fiesta F1	71.25	3.76	06.9	29.8	07.62
Regency F1	70.13	3.39	05.3	39.1	08.09
Calhoun Gray	69.36	3.37	11.3	35.6	08.31
Legacy	68.28	3.09	06.3	35.8	08.81
Mountain Hoosier	68.19	3.23	09.6	23.1	08.34
Yellow Crimson	67.31	3.74	05.8	30.2	07.31
Desert King	67.06	3.34	06.4	27.5	07.98
AU-Jubilant	67.01	2.84	13.6	36.1	09.55
Black Diamond	66.92	3.46	06.5	36.2	07.59
Sangria F1	66.62	3.35	09.6	28.5	07.93
Royal Flush F1	66.44	3.53	06.2	28.6	07.55
Calsweet	63.59	3.21	05.3	24.4	07.94
Tendersweet OF	63.23	3.06	10.5	29.7	08.09
NC Giant	63.11	4.74	24.9	31.4	11.37
King & Queen	62.65	5.57	02.9	18.9	04.72
Sweet Princess	62.23	2.99	08.6	36.8	08.47
Charleston Gray	61.29	3.00	09.4	35.3	08.39
Tom Watson	59.71	3.23	07.7	21.4	07.42
Georgia Rattlesnake	59.56	2.51	11.4	34.6	09.64
Navajo Sweet	59.14	2.21	05.8	17.4	05.03
Jubilee	58.10	2.45	15.2	38.3	09.54
Sugarlee	56.86	3.15	05.6	30.5	07.15
Early Arizona	55.76	4.82	07.8	26.7	04.59
Carolina Cross#183	55.72	1.61	15.9	10.1	14.56
Allsweet	55.23	2.53	16.0	23.8	08.65
Peacock WR-60	54.03	3.33	05.5	17.7	06.47
Hopi Red Flesh	53.90	3.87	16.3	24.0	05.90
Congo	52.74	2.67	21.4	29.2	07.79
Quetzali	51.58	3.86	05.6	31.4	05.25
Mickylee	51.18	5.08	01.7	29.7	04.10
Crimson Sweet	50.31	2.64	03.6	36.0	08.10
Minilee	50.05	5.67	01.8	21.0	03.51
Early Canada	49.67	3.86	05.0	40.7	05.08
Graybelle	49.43	3.65	05.5	36.8	05.27
Sugar Baby	45.00	4.11	04.6	36.3	04.25
Golden Midget	27.43	6.31	08.2	49.9	01.72

† LSD of marketable yield, fruit count, percentage cull fruit, percentage early fruit and fruit size is 6.20, 0.35, 3.67, 5.37, and 0.45, respectively.

Among these high yielding genotypes, two inbreds (Big Crimson and Legacy) and a hybrid (Starbrite F1) had significant S^2_d and high σ_i^2 for marketable yield (Table 3). Similarly, two high yielding inbreds (Big Crimson and Legacy) had significant S^2_d and high σ_i^2 for yield components, including fruit count and percentage early fruit (Table 3). For percentage early fruit, except two hybrids (Fiesta F1 and Starbrite F1), all high yielding genotypes had nonsignificant S^2_d and

Table 3. Significance value of regression coefficient (b_i), deviation from regression (S^2_d), Shukla's stability variance (σ_i^2), and Kang stability statistic (YS_i) for marketable yield (Mg ha⁻¹), Fruit Count (thousand fruit ha⁻¹), percentage cull fruit, percentage Early Fruit and Fruit Size (kg fruit⁻¹) of 40 watermelon genotypes tested in 3 yr and eight locations.

Genotype	Marketable yield				Fruit count				Percentage cull fruit				Percentage early fruit				Fruit size			
	b_i	S^2_d	σ_i^2	YS_i	b_i	S^2_d	σ_i^2	YS_i	b_i	S^2_d	σ_i^2	YS_i	b_i	S^2_d	σ_i^2	YS_i	b_i	S^2_d	σ_i^2	YS_i
AU-Jubilant	.	.	*	√‡	√	.	.	.	√
Allsweet	*	**	√
Big Crimson	*	**	**	√	.	**	.	√	.	***	*	√	.	*	√
Black Diamond	.	*	**	√	**	**	.	√	*	**	√	.	.	.	√	
Calhoun Gray	.	.	.	√	.	.	.	√	*	*	.	.	.	**	**	√	.	**	.	√
Calsweet	.	**	**	√	**†	.	.	√	.	*	**	.	.	***	.	√
Carolina Cross#183	**	*	*	.	.	**	**	.	.	**	**	.	***	***	**	√
Charleston Gray	*	***	**	.	.	***	√	.	*	.	√
Congo	*	.	.	.	**†	.	.	.	*	.	**	√
Crimson Sweet	.	***	**	.	.	***	√	.	.	**	√	**†	*	*	.
Desert King	.	.	**	√	.	.	.	√	.	.	.	√	.	**	**
Early Arizona	**	.	√	**	.	.	*	.	.
Early Canada	*	**	√	.	.	.	√	.	.	**	√	.	***	.	.
Fiesta F1	.	.	*	√	.	**	.	√	*	*	√	.	.	.	√
Georgia Rattlesnake	*	**	.	*	.	.	√	.	.	.	√
Golden Midget	**	***	**	.	.	***	**	√	.	***	**	√	.	***	**	√	***	.	.	.
Graybelle	*	√	***†	**	.	√	.	.	.	√	*	.	.	.
Hopi Red Flesh	.	*	*	.	.	***	.	√	*	***	**	***	.	.
Jubilee	*	**	.	.	.	**	√	*	.	.	√
King & Queen	**†	**	**	.	.	***	**	√	***	***	.	√	*	***	.	.
Legacy	.	***	**	√	.	***	.	.	**†	.	.	√	.	***	**	√	.	.	.	√
Mickylee	.	***	*	.	.	**	.	√	***†	***	.	√	.	**	**	.	***	**	.	.
Minilee	*	*	√	***	**	.	√	.	**	**	.	*	*	.	.
Mountain Hoosier	.	***	**	√	.	***	.	.	.	*	√
NC Giant	.	***	**	.	.	***	.	√	.	**	**	√	.	.	*	.	.	**	**	.
Navajo Sweet	.	***	**	.	.	***	.	.	**†	***	.	.	.	*	*	√	*	.	.	√
Peacock WR-60	*	.	.	*	.	.	√	*	.	.
Quetzali	√	***†	.	.	√	.	**	**	.	.	***	.	.
Regency F1	.	.	.	√	.	.	.	√	.	.	.	√	.	*	*	√	.	.	.	√
Royal Flush F1	**	*	.	√	.	.	.	√	**	*	.	√	.	*
Sangria F1	.	.	.	√	.	.	.	√	**	**	*	√
Starbrite F1	**	**	**	√	*	.	.	√	*	.	.	√	.	.	.	√	.	.	.	√
Stars-N-Stripes F1	.	.	.	√	.	.	.	√	.	.	.	√	.	***	**	√	.	.	.	√
Stone Mountain	.	.	**	√	.	.	.	√	**	**	.	.	.	**	**	√	.	.	.	√
Sugar Baby	.	**	.	.	.	*	.	√	**	**	.	√	.	.	**	√	**	***	.	.
Sugarlee	√	.	.	.	√	.	*	.	.
Sweet Princess	.	***	**	*	√	.	.	.	√
Tendersweet OF	.	*	*	√	*	.	*	.	.	.	**	√
Tom Watson	*	.	**	.	.	*	.	.	.	*	.	.	.	*	**	.	.	**	.	.
Yellow Crimson	.	***	**	√	.	***	.	.	**	**	.	√	.	.	.	√

* Significantly different from unity for the regression coefficients or slope (b_i) and from zero for the deviation from regression (S^2_d) at 0.05 level of probability.

** Significantly different from unity for the regression coefficients or slope (b_i) and from zero for the deviation from regression (S^2_d) at 0.01 level of probability.

*** Significantly different from unity for the regression coefficients or slope (b_i) and from zero for the deviation from regression (S^2_d) at 0.001 level of probability.

† Indicates negative slope.

‡ √ indicate stable according to Kang stability statistic (YS_i).

low σ_i^2 (Table 3). In contrast, for fruit size all high yielding genotypes had nonsignificant S^2_d and low σ_i^2 , except inbred Calhoun Gray (Table 3).

Hybrids with high marketable yield consistently had nonsignificant S^2_d and low σ_i^2 for fruit count and percentage early fruit (Table 3). The top three yielding hybrids

(Starbrite F1, Regency F1, and Stars-N-Stripes F1) had nonsignificant S^2_d and low σ_i^2 for fruit count and percentage cull fruit (Table 3). On the other hand, high yielding inbreds had significant S^2_d and high σ_i^2 for both fruit count and percentage cull fruit (Table 3).

Table 4. Means (corrected by least squares) (M), regression coefficient (b_i), deviation from regression (S^2_d), Shukla's stability variance (σ_i^2), and Kang stability statistic (YS_i) for marketable yield of 40 watermelon genotypes tested in 3 yr and eight locations.

Genotype	Marketable yield				
	M †	b_i	S^2_d	σ_i^2	YS_i
			Mg ha ⁻¹		
AU-Jubilant	67.01	0.51	729.93	627.02	26
Allsweet	55.23	1.20	529.91	461.84	11
Big Crimson	80.44	1.81*	1221.68**	1147.63	35
Black Diamond	66.92	0.47	975.78*	827.32	21
Calhoun Gray	69.36	1.06	357.14	328.05	36
Calsweet	63.59	0.50	826.28**	760.13	18
Carolina Cross #183	55.72	2.05**	958.57*	713.76	05
Charleston Gray	61.29	0.42*	2969.41***	2738.22	13
Congo	52.74	0.25*	489.92	390.70	07
Crimson Sweet	50.31	0.59	3441.21***	3328.37	-04
Desert King	67.06	1.11	780.30	717.13	23
Early Arizona	55.76	0.94	578.07*	525.57	12
Early Canada	49.67	0.44*	539.23**	445.37	02
Fiesta F1	71.25	1.33	656.44	616.62	34
Georgia Rattlesnake	59.56	1.43	674.45	557.60	15
Golden Midget	27.43	0.47**	944.24***	1079.91	-10
Graybelle	49.43	0.41*	509.83	433.72	01
Hopi Red Flesh	53.90	1.29	757.71*	690.31	00
Jubilee	58.10	1.18	535.55	782.96	07
King & Queen	62.65	-0.48**	1869.72**	1375.31	15
Legacy	68.28	1.09	1406.18***	1351.33	27
Mickylee	51.18	0.84	623.40***	572.04	03
Minilee	50.05	0.48*	461.80*	435.90	03
Mountain Hoosier	68.19	1.03	1195.74***	1126.19	26
NC Giant	63.11	1.24	1749.65***	1682.30	08
Navajo Sweet	59.14	1.12	1155.01***	1091.29	16
Peacock WR-60	54.03	0.72	584.19	528.58	07
Quetzali	51.58	1.07	312.54	273.09	06
Regency F1	70.13	0.56	614.90	566.88	35
Royal Flush F1	66.44	1.91**	713.50*	539.54	25
Sangria F1	66.62	1.32	461.87	442.03	28
Starbrite F1	80.40	2.21**	1365.50**	1221.86	34
Stars-N-Stripes F1	77.25	1.13	432.06	416.09	40
Stone Mountain	79.10	1.57	497.48	523.36	41
Sugar Baby	45.00	0.75	335.32**	322.94	-01
Sugarlee	56.86	1.23	524.47	478.75	14
Sweet Princess	62.23	1.02	956.33***	882.04	14
Tendersweet OF	63.23	0.84	600.27*	564.54	23
Tom Watson	59.71	1.94*	1023.61	922.92	10
Yellow Crimson	67.31	1.00	1798.93***	1736.10	24

* Significantly different from unity for the regression coefficients or slope (b_i) and from zero for the deviation from regression (S^2_d) at 0.05 level of probability.

** Significantly different from unity for the regression coefficients or slope (b_i) and from zero for the deviation from regression (S^2_d) at 0.01 level of probability.

*** Significantly different from unity for the regression coefficients or slope (b_i) and from zero for the deviation from regression (S^2_d) at 0.001 level of probability.

† LSD of marketable yield is 6.20.

Kang's Stability Statistics

According to Kang's stability statistics (YS_i), genotypes with YS_i higher than the mean YS_i are stable. For a trait where lower value is desired (e.g., percentage cull fruit) YS_i lower than the mean YS_i are stable. The mean YS_i for marketable yield, fruit count, percentage cull fruit, percentage early fruit, and fruit size was 16.3, 16.5, 18.6, 16.9, and 17.3, respectively. According to YS_i , the top five genotypes with highest marketable yield and stable across all the evaluated traits were Stone Mountain, Stars-N-Stripes F1, Calhoun Gray, Big Crimson, and Regency (Table 3).

Mean vs. Stability and Genotype Comparison with Ideal Genotype Views of GGE Biplot

The average environment coordinate (AEC) view based on genotype-focused singular value partitioning (SVP = 1) can be referred as the "mean vs. stability" view of GGE biplot (Yan et al., 2007). That view facilitates genotype comparisons based on mean performance and stability across environments within a mega-environment. The mean vs. stability view of GGE biplot explained 80, 82, 83, 67, and 96% of genotypic and genotype \times environment variation for the marketable yield, fruit count, percentage cull fruit, percentage early fruit, and fruit size, respectively (Fig. 3: Panel A, B, C, D, and E). The arrow shown on the AEC abscissa points in the direction of higher trait performance of genotypes and ranks the genotypes with respect to trait performance. Thus, genotype Starbrite F1 (G32) had the highest marketable yield and Golden Midget (G16) had the lowest (Fig. 3: Panel A). Similarly, genotypes Golden Midget (G16), NC Giant (G25), Golden Midget (G16), and Carolina Cross #183 (G7) had the highest fruit count, percentage cull, percentage early and fruit size, respectively. Genotype Mickylee (G22) had the lowest percentage cull, genotype Carolina Cross #183 (G7) had the lowest fruit count and percentage early and Golden Midget (G16) had the lowest fruit weight (Fig. 3: Panel B, C, D, and E). The stability of each genotype was explored by its projection onto the AEC vertical axis. The most stable genotype was located almost on the AEC abscissa (horizontal axis) and had a near-zero projection onto the AEC (vertical axis). Thus, genotypes Fiesta F1 (G14), AU-Jubilant (G1), Tom Watson (G39), and Carolina Cross #183 (G7) were the most stable and Yellow Crimson (G40), and King & Queen (G20) were the least stable for marketable yield (Fig. 3: Panel A).

According to Yan and Tinker (2006), stability is meaningful only when associated with high trait mean. Therefore, an ideal genotype has both high trait mean and stable performance. An ideal genotype is represented by a circle on the head of arrow on the AEC abscissa (horizontal axis) (Fig. 3: Panel A, B, C, D, and E). For marketable yield, genotypes Fiesta F1 (G14), Stars-N-Stripes F1 (G33), Regency F1 (G29), Black Diamond (G4), and AU-Jubilant

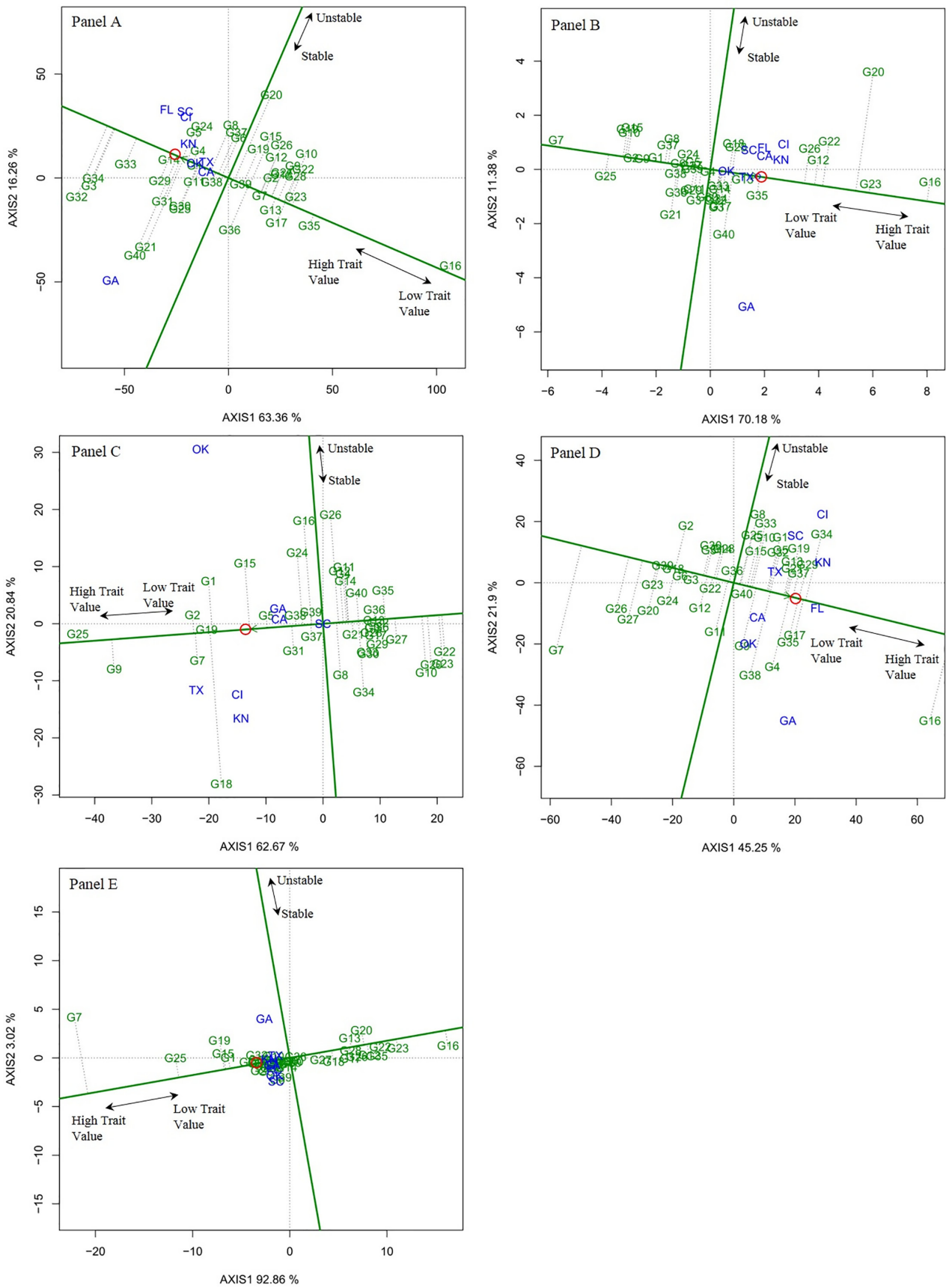


Fig. 3. The mean vs. stability view of genotype main effects plus genotypic × environment interaction effect (GGE) biplot of 40 watermelon genotypes tested in 3 yr and eight locations for (Panel A) marketable yield, (Panel B) fruit count, (Panel C) percentage cull fruit, (Panel D) percentage early fruit, and (Panel E) fruit size. The biplots were based on Scaling = 0, Centering = 2, and SVP = 1. The ideal genotype is represented by a circle on average environment coordinate (AEC)-abscissa which passed through biplot origin.

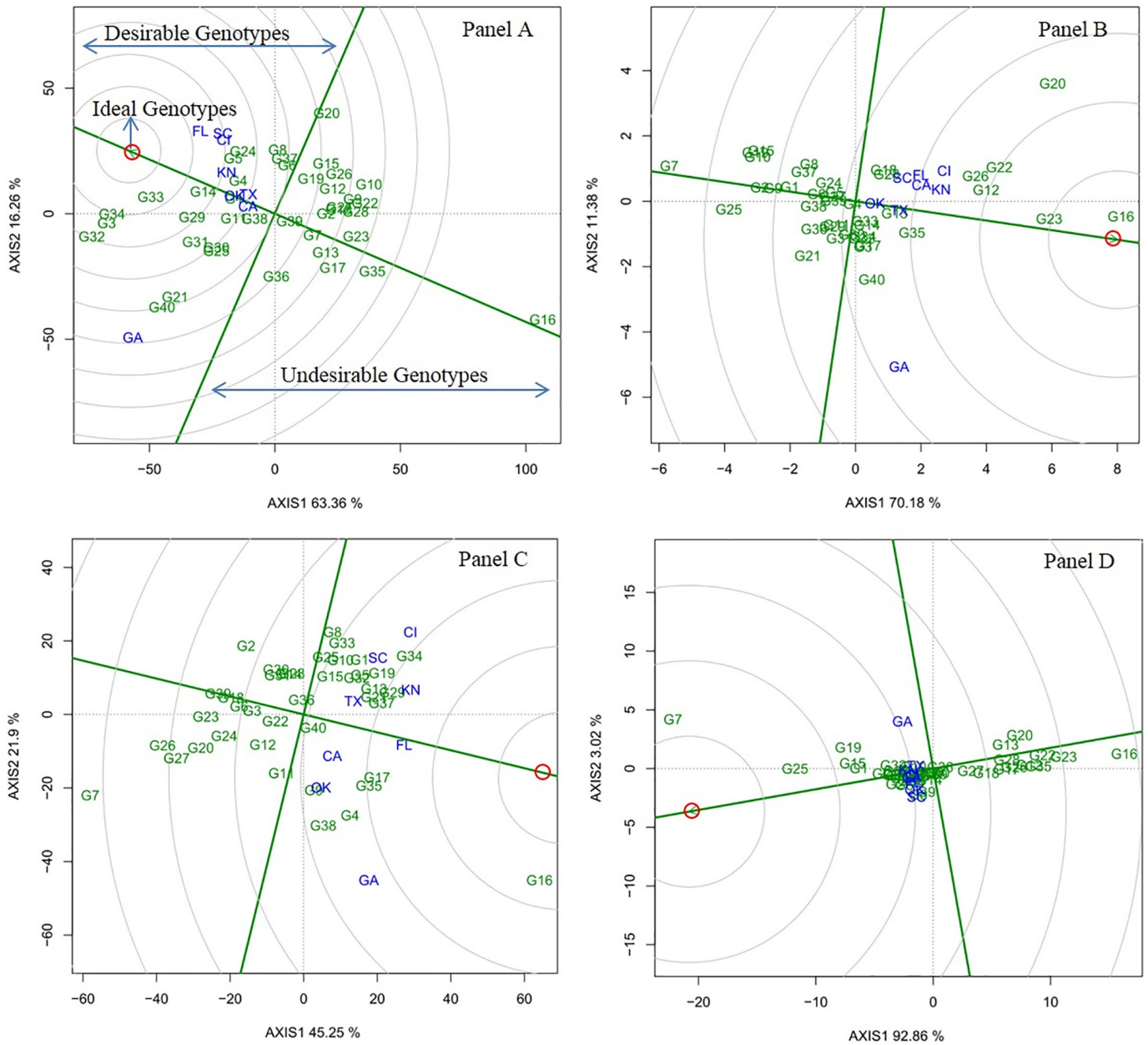


Fig. 4. The genotypes comparison with ideal genotype view of genotype main effects plus genotypic \times environment interaction effect (GGE) biplot of 40 watermelon genotypes tested in 3 yr and eight locations for (Panel A) marketable yield, (Panel B) fruit count, (Panel C) percentage early fruit, and (Panel D) fruit size. The biplots were based on Scaling = 0, Centering = 2, and SVP = 1. An ideal genotype is represented by circle within innermost concentric circles on average environment coordinate (AEC)-abscissa which passed through biplot origin.

(G1) could be regarded as the best genotypes (Fig. 3: Panel A). Similarly, for fruit count genotypes Minilee (G23), Golden Midget (G16), Early Arizona (G12), and Sugar Baby (G35) were best (Fig. 3: Panel B). For percentage cull genotypes Early Canada (G13), Starbrite F1 (G32), Big Crimson (G3), and Calsweet (G6) were best (Fig. 3: Panel C). For percentage early genotypes Sweet Princess (G37) and Legacy (G21) were best (Fig. 3: Panel D). For fruit weight genotypes AU-Jubilant (G1), NC Giant (G25), and Georgia Rattlesnake (G15) were best (Fig. 3: Panel E).

The “comparison with ideal genotype” view of GGE biplot has concentric circles with the ideal genotype in the inner circle and the head of the arrow is the center of the

circle (the arrow is highlighted) (Fig. 4: Panel A, B, C, and D). The genotypes grouped in the inner circle (ideal genotypes) are more desirable than the others. Thus, Golden Midget (G16) and Minilee (G23) were the most desirable genotypes for fruit count (Fig. 4: Panel B). However, for marketable yield, percentage early and fruit size, no genotypes were in the inner circle (Fig. 4: Panel A, C, and D). Therefore, genotypes next to the ideal circle were desirable. Genotypes Stars-N-Stripes F1 (G33); Golden Midget (G16); and NC Giant (G25) with Carolina Cross #183 (G7) were desirable genotypes for marketable yield, percentage early and fruit size, respectively (Fig. 4: Panel A, C, and D).

Additive Main Effects and Multiplicative Interaction 1

In AMMI1, the biplot abscissa and ordinate show the trait main effect and first principal component (PC1) term, respectively. The genotypes with PC1 scores close to zero indicate general adaptation across environments, whereas larger PC1 scores indicate specific adaptation of genotypes to the environment having the same PC1 score and sign (Murphy et al., 2009). Thus, genotypes Regency F1 (29), Tendersweet OF (38), Stars-N-Stripes F1 (33), Starbrite F1 (32), Stone Mountain (34), Big Crimson (3), AU-Jubilant (1), and Calsweet (6) were stable across environments for marketable yield (Fig. 5: Panel A). Plant breeders are interested in genotypes having high and stable yield: those with a PC1 score close to zero and a high trait mean. Thus, for marketable yield genotypes Peacock WR-60 (27), Mickylee (22), Calsweet (6), Minilee (23), and Quetzali (28) were best (Fig. 5: Panel B). For other traits, the best genotypes were Golden Midget (16), Georgia Rattlesnake (15) and Regency F1 (29) for fruit count; Georgia Rattlesnake (15), Golden Midget (16), Early Canada (13), Allsweet (2), and Regency F1 (29) for percentage cull; Carolina Cross #183 (7), Peacock WR-60 (27), Black Diamond (4) and Tendersweet OF (38) for percentage early; and Hopi Red Flesh (18), AU-Jubilant (1), Carolina Cross #183 (7), Desert King (11) and Tendersweet OF (38) for fruit size (Fig. 5: Panel B, C, D, and E).

Rank Correlations for Stability Measures Spearman's Rank Correlation

Spearman rank correlations were computed between the genotype ranks of all evaluated trait means and stability measures. Stability measures include σ_i^2 , Shukla's squared hat (\hat{S}_{ii}^2), W_i , b_i , deviation from regression (S_d^2), GGE (mean vs. stability view) and AMMI (mean vs. stability view). In mean vs. stability view of GGE and AMMI biplot for fruit size, the majority of the genotypes were clustered near the biplot origin (0, 0). Therefore, correlation for fruit size could not be computed between GGE and AMMI and the other stability measures.

Trait mean was significantly ($P < 0.001$) and positively correlated (Spearman) with GGE and YS_i for all traits evaluated in this study (Table 5). Results for YS_i are not presented in Table 5. Similarly, significant correlations were measured between σ_i^2 with \hat{S}_{ii}^2 , W_i and S_d^2 for all the traits evaluated in this study; and among all stability measures (except, AMMI) for percentage cull fruit (Table 5). However, nonsignificant correlation was measured between some of the stability statistics (b_i , S_d^2 , σ_i^2 , GGE, and AMMI) with trait mean for marketable yield, fruit count, percentage early and fruit size (Table 5). Thus, stability statistics provide information that cannot be obtained from trait mean (Mekbib, 2003).

DISCUSSION

For all the yield traits evaluated in this study, environment explained most of the variation, and genotype and $G \times E$ were small (Table 1). The partitioning of variance components for environment showed that both predictable (location) and unpredictable (year and location \times year) components were important. For marketable yield, fruit count and percentage early, location effects were significant, suggesting that plant breeders can either develop specialist genotypes for selected environments or generalist genotypes adapted to a wide range of environments. Since location \times year was significant for all traits evaluated, plant breeders should develop stable genotypes that perform well over environments. The ideal genotype should have high mean and high stability.

When the 40 genotypes were grouped into high (top 10), mid-high (11–20), mid-low (21–30) and low (bottom 10), the high yielding hybrids Starbrite F1, Stars-N-Stripes F1, Fiesta F1, and Regency F1 had mid-high fruit count, low to mid-low percentage cull, mid-high to mid-low percentage early and high to mid-high fruit size (Table 2). The high yielding inbreds Big Crimson, Stone Mountain, Calhoun Gray, and Legacy had mid-high to mid-low fruit count, high to low percentage cull and percentage early, and high to mid-low fruit size (Table 2). Genotypes with the lowest marketable yield had high fruit count; high to low percentage cull and percentage early; and mid-low to low fruit size.

The stability rank correlation of GGE with mean marketable yield, fruit count and percentage cull was positive and significant, suggesting that PC1 of the GGE biplot captured a large part of the variation due to genotype. Unlike AMMI analysis, which removed genotype as a main effect, GGE biplot did not remove genotype as a main effect. Thus, GGE biplot captured more variation for all watermelon yield traits evaluated in this study. A similar observation was reported by Ding et al. (2008), Karimizadeh et al. (2013), and Yan et al. (2007). Other advantages of GGE biplot were interactive graphics for genotype evaluation and identification of mega-environments and test locations. Thus, GGE biplot was preferred over AMMI analysis when applying stability-selection criteria. However, GGE biplot has certain limitations including its ability to explore only a small portion of total genotype effect and $G \times E$ effect. That occurs when the genotype effect is smaller than the $G \times E$ effect, and the $G \times E$ pattern is not constant over years (Ding et al., 2008). However, GGE biplot analysis captured a large part of genotype and $G \times E$ variation for all yield traits evaluated in this study.

Similarly, for YS_i , the F test value for σ_i^2 was nonsignificant for all the traits evaluated. Thus, it captured a large portion of the trait mean, causing the rank for M and YS_i remain unchanged. Significant correlations for σ_i^2 with \hat{S}_{ii}^2 , W_i , and S_d^2 for all the traits evaluated in this study

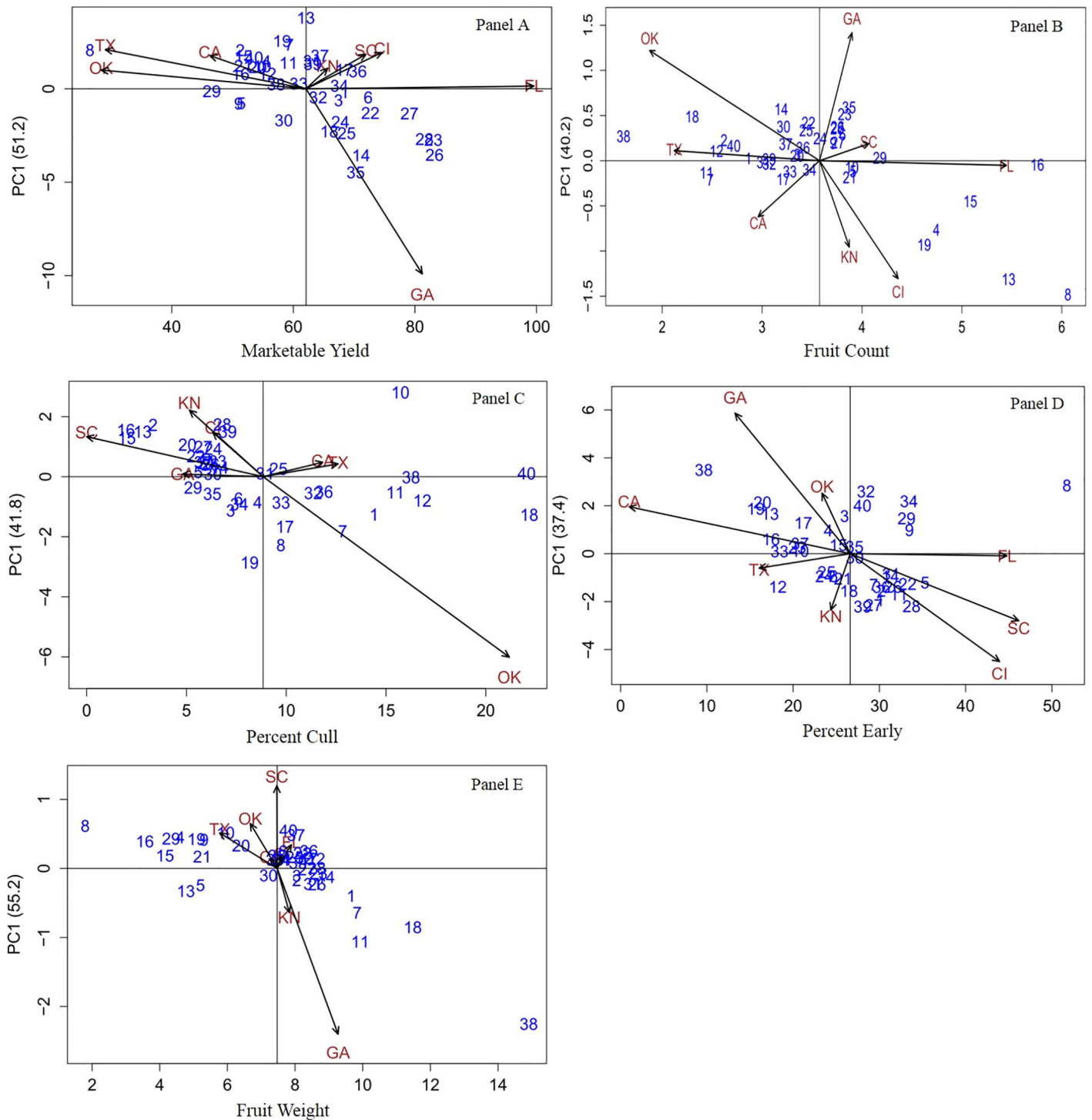


Fig. 5. Additive main effects and multiplicative interaction 1 (AMMI1) biplot showing the main and first principal components (PC1) effects of both genotypes and environments on (Panel A) marketable yield, (Panel B) fruit count, (Panel C) percentage cull fruit, (Panel D) percentage early fruit, and (Panel E) fruit size of 40 watermelon genotypes tested in 3 yr and eight locations.

suggested that these statistics were measuring the same thing (Wachira et al., 2002), and that they could be used interchangeably to select stable genotypes. Conversely, nonsignificant correlation was found for some of the stability statistics (b_i , S^2_d , σ_i^2 , GGE, and AMMI) and trait mean for marketable yield, fruit count, percentage early and fruit size (Table 5). Thus, stability statistics provide information that cannot be obtained from trait mean (Mekbib, 2003).

Similarly, the weak correlation of stability statistics (σ_i^2 , S^2_d , W_i , b_i , S^2_d , GGE, and AMMI) with trait mean indicated the need to use these statistics simultaneously (Kang and Pham, 1991; Kang and Gauch, 1996; Mekbib, 2003). The negative and nonsignificant correlation of σ_i^2 and S^2_d with mean for marketable yield indicated that high yielding genotypes were often stable (low σ_i^2 and S^2_d).

Table 5. Spearman rank correlations among trait mean (M) and stability parameters (regression coefficient [b_i], deviation from regression [S^2_d], Shukla's stability variance [σ_i^2], GGE, and AMMI for watermelon based on 40 genotypes tested in 24 environments.

	M	σ_i^2	\hat{s}_i^2	W_i	b_i	S^2_d	GGE	AMMI
Marketable yield								
M	1							
σ_i^2	-0.27	1						
\hat{s}_i^2	-0.28	0.95***	1					
W_i	-0.27	1***	0.95***	1				
b_i	0.28	0.03	-0.02	0.03	1			
S^2_d	-0.25	0.91***	0.97***	0.91***	0.05	1		
GGE	0.94***	-0.16	-0.15	-0.16	0.23	-0.12	1	
AMMI	-0.07	0.18	0.19	0.18	0.07	0.22	-0.06	1
Fruit count								
M	1							
σ_i^2	-0.38	1						
\hat{s}_i^2	-0.50***	0.92***	1					
W_i	-0.38**	1	0.92***	1				
b_i	0.14	0.05	-0.10	0.05	1			
S^2_d	-0.53***	0.90***	0.98***	0.90***	-0.08	1		
GGE	0.73***	-0.22	-0.31*	-0.23	0.12	-0.34*	1	
AMMI	-0.10	-0.11	-0.12	-0.11	-0.17	-0.08	-0.04	1
Percentage cull fruit								
M	1							
σ_i^2	0.67***	1						
\hat{s}_i^2	0.86***	0.83***	1					
W_i	0.67***	1	0.83***	1				
b_i	0.77***	0.62***	0.64***	0.62***	1			
S^2_d	0.74***	0.76***	0.94***	0.76***	0.55***	1		
GGE	0.82***	0.61***	0.71***	0.61***	0.60***	0.69***	1	
AMMI	0.06	-0.01	-0.02	-0.01	0.06	-0.02	0.12	1
Percentage early fruit								
M	1							
σ_i^2	-0.35*	1						
\hat{s}_i^2	-0.44**	0.95***	1	1				
W_i	-0.44**	0.95***	1	1				
b_i	0.04	-0.03	-0.03	-0.03	1			
S^2_d	-0.41**	0.88***	0.92***	0.92***	0.06	1		
GGE	0.87***	-0.28	-0.35*	-0.35*	-0.05	-0.37*	1	
AMMI	-0.36*	0.08	0.13	0.13	-0.01	0.14	-0.34*	1
Fruit size								
M	1							
σ_i^2	-0.27	1						
\hat{s}_i^2	-0.48***	0.89***	1					
W_i	-0.27	1	0.89***	1				
b_i	0.61***	-0.01	-0.21	-0.01	1			
S^2_d	-0.43**	0.78***	0.92***	0.78***	-0.16	1		
GGE	-	-	-	-	-	-	1	
AMMI	-	-	-	-	-	-	-	1

* Significance level at 0.05 level of probability.

** Significance level at 0.01 level of probability.

*** Significance level at 0.001 level of probability.

Based on multiple stability measures (σ_i^2 , b_i , S^2_d , YS_i , and GGE), watermelon genotypes were classified into three categories. Category 1 was genotypes having high marketable yield and high stability. These genotypes are widely adapted across diverse environmental conditions. Those were genotypes Stars-N-Stripes F1 (G33), Fiesta F1 (G14),

Stone Mountain (G34), and Calhoun Gray (G5). These genotypes had high marketable yield and low σ_i^2 ; b_i equal to unity; nonsignificant S^2_d ; close to ideal genotype and near-zero projections onto the AEC (vertical axis) on mean vs. stability view of GGE biplot and YS_i higher than the mean YS_i . Genotypes Stars-N-Stripes F1 (G33), Fiesta F1 (G14),

Stone Mountain (G34), and Calhoun Gray (G5) exhibited consistent high marketable yield in varied environmental conditions. Hybrids Stars-N-Stripes F1 (G33) and Fiesta F1 (G14) had average high fruit count, percentage early, and fruit size; and low percentage cull. In contrast, inbreds Stone Mountain (G34) and Calhoun Gray (G5) had low performance for yield components. Category 1 genotypes had long or round fruit shape, medium size fruit (7–8 kg fruit⁻¹), medium rind thickness, and red flesh color.

Category 2 genotypes exhibited high marketable yield but low stability, so these genotypes are suited for specific environments. This category includes genotypes Big Crimson (G3), Starbrite F1 (G32), Legacy (G21) and Mountain Hoosier (G24). Genotypes Big Crimson (G3) and Starbrite F1 (G32) had high marketable yield and were significantly higher than Legacy (G21) and Mountain Hoosier (G24). For marketable yield, category 2 genotypes had b_i greater than unity, significant S^2_d , high σ_i^2 , and high projections onto the AEC (vertical axis) on the mean vs. stability view of GGE biplot. These findings suggest that Big Crimson (G3), Starbrite F1 (G32), Legacy (G21) and Mountain Hoosier (G24) were sensitive to environmental change (below average stability) and had greater specificity of adaptability to high yielding environments. However, according to YS_i , category 2 genotypes were better than average and should be considered stable. Unlike category 1 genotypes that had mid-low to low percentage early and fruit size, category 2 genotypes had high % early and fruit size. For fruit count and percentage cull, category 2 genotypes had high to mid-low. Overall, for marketable yield, percentage cull, percentage early and fruit size, category 2 genotypes were slightly better in performance than category 1 genotypes. Plant breeders can use Big Crimson (G3), Starbrite F1 (G32), Legacy (G21) and Mountain Hoosier (G24) to develop high performers for specific locations.

Category 3 genotypes had low marketable yield and stability. These genotypes are suitable for breeding for traits other than yield, for example, disease resistance or fruit quality. Category 3 genotypes include Golden Midget (G16), Sugar Baby (G35), and Early Canada (G13). These genotypes had marketable yield significantly lower than the other genotypes. For other yield components, category 3 genotypes recorded high fruit count, and low percentage early and small fruit size. The phenotype of category 3 genotypes included small fruit (1.5–2.5 kg/fruit), green or yellow fruit skin, thin rind, and red flesh color.

CONCLUSIONS

Several watermelon genotypes had significant G×E for yield and yield components, and there was evidence for the advantage of hybrids over inbreds for yield and responsiveness to favorable environments. We classified watermelon genotypes into three categories based on yield and stability. Category 1 genotypes had high marketable

yield and stability, and are widely adapted across diverse environmental conditions: Stars-N-Stripes F1, Fiesta F1, Stone Mountain, and Calhoun Gray. Category 2 genotypes exhibited high marketable yield but low stability and were suited to specific locations: Big Crimson, Starbrite F1, Legacy, and Mountain Hoosier. Category 3 genotypes had low marketable yield and stability: Golden Midget, Sugar Baby, and Early Canada.

The highest performing inbred and hybrid genotypes for watermelon fruit yield and yield components (Big Crimson and Starbrite F1) were not the highest for yield stability. Not all genotypes from the three categories were stable for all yield components. Therefore, there is room for improvement. Category 1 hybrids Fiesta F1 and Stars-N-Stripes F1 were more stable for yield components evaluated in this study than inbreds Stone Mountain and Calhoun Gray. Inbreds Stone Mountain and Calhoun Gray from category 1 had lower quality than inbreds Legacy and Big Crimson of category 2. Although, Legacy and Big Crimson were unstable for marketable yield, they were stable in performance for some yield components, which were lacking in Stone Mountain and Calhoun Gray.

The strong positive correlation ($P < 0.001$) of σ_i^2 with \hat{S}_i^2 , W_i , and S^2_d (for all the traits) suggested these statistics measure the same aspect of stability (Wachira et al., 2002). Therefore, these stability statistics could be used interchangeably to select stable genotypes. The GGE biplot captured more variation than AMMI biplots for all the watermelon yield traits evaluated in this study. Additionally, GGE biplot generated more interactive visuals for genotype evaluation. G×E plays a significant role in breeding watermelons for high yield, wide or specific adaptation, and stability.

Supplemental Materials Available

Supplemental material is available with the online version of this article.

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Supplemental Material Description

The supplemental tables provide a listing of pedigree and phenotype of all genotypes used in the study.

Table S1. The 40 watermelon genotypes tested with pedigree information.

ID	Genotype	Year of release	Pedigree
G01	AU-Jubilant	1985	Jubilee x PI 271778
G02	Allsweet	1972	[(Miles x Peacock) x Charleston Gray]
G03	Big Crimson	NA†	NA
G04	Black Diamond	1949	Segregation within Cannonball or Black Diamond
G05	Calhoun Gray	1965	Calhoun Sweet x Charleston Gray
G06	Calsweet	NA	[(Miles x Peacock) x Charleston Gray]
G07	Carolina Cross #183	NA	NA
G08	Charleston Gray	1954	[{(Africa 8 x Iowa Belle) x Garrison} x Garrison] x [(Hawkesbury x Leesburg) x Garrison]
G09	Congo	1949	(African x Iowa Belle) x Garrison
G10	Crimson Sweet	1963	(Miles x Peacock) x Charleston Gray
G11	Desert King	NA	NA
G12	Early Arizona	NA	NA
G13	Early Canada	NA	NA
G14	Fiesta F1	1991	Unknown (Plant Variety Protection)
G15	Georgia Rattlesnake	1870	
G16	Golden Midget	1959	New Hampshire Midget x Pumpkin Rind
G17	Graybelle	1963	Sugar Baby x Charleston Gray sister line
G18	Hopi Red Flesh	NA	NA
G19	Jubilee	1963	Africa 8, Iowa Belle, Garrison, Hawkesbury, and Leesburg
G20	King & Queen	NA	NA
G21	Legacy	1997	(Early Gray x Little Jubilee 4) x Verona
G22	Mickylee	1986	Texas W5, Fairfax, Summit, and Graybelle
G23	Minilee	1986	Texas W5, Fairfax, Summit, and Graybelle
G24	Mountain Hoosier	NA	NA
G25	NC Giant	NA	NA
G26	Navajo Sweet	NA	NA
G27	Peacock WR-60	1955	Klondike R7 x Peacock
G28	Quetzali	1965	NA
G29	Regency F1		Unknown (Plant Variety Protection)
G30	Royal Flush F1	1995	Unknown (Plant Variety Protection)
G31	Sangria F1	NA	Unknown (Plant Variety Protection)
G32	Starbrite F1	NA	Unknown (Plant Variety Protection)
G33	Stars-N-Stripes F1	NA	Unknown (Plant Variety Protection)
G34	Stone Mountain	1924	NA
G35	Sugar Baby	1955	Tough Sweets selection, inbred 13 yr
G36	Sugarlee	1981	Texas W5, Summit, Charleston Gray, Fairfax, Crimson Sweet, and Graybelle
G37	Sweet Princess	1967	small-seeded Congo type x Charleston Gray
G38	Tendersweet OF	NA	NA
G39	Tom Watson	1906	NA
G40	Yellow Crimson	NA	NA

† Not available.

Table S2: Fruit and seed traits for the 40 watermelon genotypes evaluated.

ID	Genotype	Fruit			Rind		Seed		Flesh color ^{¶¶}
		Shape [†]	Size [‡]	Color [§]	Thickness ^{¶¶}	Pattern [#]	Size ^{††}	Color ^{‡‡}	
1	AU-Jubilant	L	M	LG	S	M	L	R	R
2	Allsweet	L	M	LG	N	W	S	R	S
3	Big Crimson	R	M	MG	M	W	M	R	R
4	Black Diamond	R	S	DB	M	S	L	R	R
5	Calhoun Gray	L	M	G	M	S	M	R	R
6	Calsweet	L	M	LG	T	W	S	B	S
7	Carolina Cross #183	E	G	LG	T	N	L	W	R
8	Charleston Gray	L	L	G	T	R	M	R	R
9	Congo	L	M	DG	M	R	L	T	R
10	Crimson Sweet	R	M	LG	M	M	S	B	R
11	Desert King	O	S	SG	S	S	M	R	O
12	Early Arizona	O	S	SG	N	S	L	R	R
13	Early Canada	R	S	G	N	R	S	R	R
14	Fiesta F1	L	M	LG	M	W	S	B	R
15	Georgia Rattlesnake	L	G	LG	M	N	L	R	R
16	Golden Midget	O	C	Y	N	S	L	R	R
17	Graybelle	G	S	G	N	S	S	R	R
18	Hopi Red Flesh	O	M	SG	M	S	L	B	R
19	Jubilee	L	L	LG	T	N	L	R	R
20	King & Queen	O	M	LG	N	N	M	B	R
21	Legacy	L	M	LG	N	N	M	R	R
22	Mickylee	R	N	LG	N	R	M	R	S
23	Minilee	R	S	G	N	R	S	R	S
24	Mountain Hoosier	O	M	SG	T	S	L	W	R
25	NC Giant	L	G	LG	T	R	L	R	R
26	Navajo Sweet	R	S	LG	M	N	M	R	R
27	Peacock WR-60	L	S	SG	M	S	S	R	R
28	Quetzali	R	S	LG	N	S	M	R	R
29	Regency F1	O	S	MG	M	M	S	T	R
30	Royal Flush F1	L	M	MG	M	W	S	B	S
31	Sangria F1	O	M	MG	M	S	S	B	S
32	Starbrite F1	O	M	LG	L	S	S	R	R
33	Stars-N-Stripes F1	O	M	DG	T	W	L	B	S
34	Stone Mountain	O	M	SG	T	S	L	T	R
35	Sugar Baby	R	M	MB	S	S	S	R	S
36	Sugarlee	R	S	LG	M	N	M	R	R
37	Sweet Princess	O	M	G	M	R	T	R	R
38	Tendersweet OF	E	M	DG	M	W	L	W	O
39	Tom Watson	E	M	MG	T	S	L	T	R
40	Yellow Crimson	L	L	LG	N	S	L	B	C

† Fruit Shape: elongate (E), oval (O), round (R)

‡ Fruit Size: micro (< 3 lb.) (C), mini (3–8 lb.) (N), icebox (9–13 lb.) (B), small (S), sometimes called pee-wee (14–18 lb.), medium (19–24 lb.) (M), large (25–32 lb.) (L), and giant (> 32 lb.) (G).

§ Rind thickness: thick (> 10mm) (T), medium (5–10mm) (M), thin (< 5mm) (N).

¶ Rind Color: light green (LG), medium green (MG), dark green (DG), solid light black (LB), solid medium black (MB), solid dark black (DB) golden (G), solid green (SG), gray (R), Yellow (Y), mottled (M).

Rind Pattern: wide stripe (W), medium stripe (M), narrow stripe (N), gray (G), solid (S), Rattle Snake (R) [Dark green is dominant, stripe is decided by dark green].

†† Seed Size: tomato size (T), small (S), medium (M), large (L).

‡‡ Seed Color: black (B), brown (R), tan (T), dotted (D), white (W).

§§ Flesh Color: scarlet red (S), coral red (R), orange (O), salmon yellow (Y), canary yellow (C), or white (W).