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Evaluation of Genotypes and Association of Traits in Watermelon Across Two Southern Texas Locations

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Abstract: Watermelon is the most important horticultural crop in Texas and is grown across the state under diverse environments. Our study was conducted in the southern region of Texas to understand genotype-by-environment interactions and the contribution of yield components to yield. To accomplish this, twenty genotypes were evaluated for important traits and characteristics at two locations, Uvalde and Weslaco TX, for two years, 2018 and 2019. The genotypes were evaluated for total yield, total fruit count, total soluble solids, rind thickness, fruit length, diameter and weight. Genotype-by-environment (G x E) interaction was not significant, possibly due to similarity in climatic conditions and nutrient management practices. In the grouped analysis, cultivars Crimson Diamond, Sunshade and the breeding line TAM 2 had a higher total yield. Path analysis showed a high direct effect for total fruit count and fruit diameter of 0.89 and 0.85, respectively. However, total fruit count had a high indirect effect of −0.44. Fruit weight was the only trait that showed a significant ($p < 0.01$) correlation towards total yield at r = 0.58. Neither of the high direct effects, total fruit count and fruit diameter, had a significant correlation. The study inferred that breeding resources could be optimized by reducing the testing location to only one representative location for measured traits in southern Texas. The indirect selection of total fruit or fruit diameter could result in better yield. The study suggested selecting for optimum total fruit and fruit diameter for higher yield.

Keywords: genotype-by-environment interaction; path coefficient; stability

1. Introduction

Watermelon (*Citrullus lanatus* (Thunb.) Matsum and Nakai), considered a refreshing summertime fruit, is grown throughout the country with major production in the southern United States and California. In 2018, the top producing states within the U.S. included Florida (411,499 t), Texas (397,272 t), and California (324,456 t). Although production in these states was high, their average yields were 45.2, 42.7 and 67.8 t ha^{-1}, respectively. This suggests high environmental effects on watermelon yield. Dia et al. [1] evaluated 40 genotypes at eight locations in the U.S and found a significant genotype-by-environment interaction for marketable yield and other yield component parameters, indicating that watermelon genotypes perform differently for yield parameters across different growing regions. Therefore, watermelon breeding requires evaluation at multiple locations to perform significant advances in selection for high total yield (TY), total fruit count (TF), fruit weight (FW), shape index and total soluble solids (TSS).

Yield component traits include TF, early fruit number, cull fruit number and fruit weight (FW) [1]. Broad and narrow-sense heritability for TY, TF and FW are low to moderate [2], indicating that

selection based on these traits would not be effective and the need exists to test genotypes in multiple environments. Selection for yield and its components is ineffective via single-plant hills due to environmental effects and low heritability. It is more effective to select at later generations when genotypes can be tested at multiple locations and in replications [2,3]. In Dia et al. [1], genotype by environmental interaction was identified for yield and its components. The study included a location in Texas (College Station, TX, USA). These conclusions point to variability in yield, requiring evaluations to identify stable or suitable genotypes for a region.

Watermelon fruit can be grouped either by weight or size. There are six distinct weight categories: mini (1.5 to 4.0 kg), icebox (4.0 to 5.5 kg), small (5.0 to 8.0 kg), medium (8.0 to 11 kg), large (11.0 to 14 kg) and giant (>14 kg). Commercially, fruits are grouped by the number that fits into 24" bins, such as 36-count (7.7 to 10 kg per fruit), 45-count (6.4 to 7.7 kg per fruit) and 60-count (4.5 to 6.4 kg per fruit) [4]. Mini size watermelons are packaged into cartons of four to six fruits per carton. Currently, consumers prefer mini to medium watermelon fruits and have been moving away from the large and giant fruits since the early 2000s [5,6]. FW can be shifted within a few years of high selection intensity, but due to a small number of effective factors regulating weight, the trait may be fixed within a few generations of selection. Instead, it would be easier to introgress specific traits into individuals with a FW of interest via pedigree or backcross breeding. Although yield and its components are important for producers, fruit quality traits such as TSS, fruit shape, rind pattern, flesh color and nutritional factors are also of importance for retailers and consumers.

For consumers, one of the most important traits in watermelons is sweetness or TSS, which is measured as degree Brix (°Brix). According to the U.S. Standards for Grades of Watermelons, any watermelon with ≥ 8 °Brix at the center of the flesh is sufficiently ripe and considered good internal quality by the USDA, and that 10 °Brix is very good internal quality [7]. Total soluble solid content can be divided into three sugars: fructose, glucose and sucrose. Watermelons at maturity have a higher level of either fructose or sucrose, which can vary across varieties [8–10]. The broad-sense heritability for °brix, fructose, glucose and sucrose was calculated using an recombinant inbred line (RIL) mapping population Klondike Black Seeded x New Hampshire Midget (Elite x Elite), which resulted in low heritabilities of 0.30, 0.41, 0.51 and 0.70 [11], respectively. Unfortunately, °Brix can vary with the year and location, but Dia et al. [12] were able to identify genotypes that showed a level of stability for °Brix in an experiment with 40 genotypes in three years, and at eight locations within the United States. A majority of commercial varieties produce fruits with ≥ 8 °Brix, satisfying the minimum requirement for USDA standards, with most having more than 10 °Brix.

One of the major goals in breeding programs is to develop varieties that perform similarly across locations, years and environments for wider adaptability and longevity. Therefore, before the release of a new variety, it is evaluated in trials to assess G x E interaction [13]. These trials are done across different locations and for several years to ensure consistent performance of the variety, or stability. Various types of analyses can be performed to evaluate stability across environments, and one of the first analyses performed was based-on linear regression, such as slope or deviation regression [14–16]. However, there are several associated problems using linear regression. For example, Crossa et al. [17], identified high standard error when only a few low and high-yielding locations were analyzed, and an assumption that a linear relationship between the interaction and environment means was required. Consequently, alternative methods of analyses were developed, such as Shukla's stability variance, which is an unbiased estimate of variance that uses a linear combination of Wricke's ecovalence [18], and Kang's stability statistic, a nonparametric method that includes both mean and variance [19–21]. Recently, more graphical methods have been developed that include additive main effect and multiplicative Interaction (AMMI) and genotype, genotype x environment (GGE) biplots, which are multivariate analyses based on principal components, and account for previous issues [17,22,23].

Path analysis allows one to identify the influence of independent factors on dependent factors by the simple correlation of the independent factors and regressing all independent factors on each dependent factor separately [24–26]. This has been used in various fields such as life sciences, transportation and

marketing [27–29]. It has allowed for the explanation of interrelationship effects between dependent and independent traits; for example, in plant breeding the effect of yield components on yield has been investigated [30,31]. Diverse populations are best used to identify how much an independent trait influences a dependent trait for a certain crop [32]. The direct and indirect effects of various traits towards yield have been evaluated in both agronomic [32,33] and horticultural crops [34,35]. The direct and indirect effects of watermelon phenotypic traits on yield have been previously evaluated by Choudhary et al. [36], who identified high direct effects from FW and TF.

The current research aimed to evaluate a set of genotypes across two main producing locations in Texas, Weslaco (WES) at the Rio Grande Valley and Uvalde (UVD) at the Texas Wintergarden, for yield, its components and various quality traits, for two years. Furthermore, we aimed to identify G x E interactions across Texas locations and between traits to improve breeding selection.

2. Results and Discussion

2.1. Analysis of Variance

Analysis of variance indicated a significant ($p < 0.05$) effect of Genotype for TF, FW, FD (fruit diameter) and TSS (Table 1). The statistical differences between the genotypes for those traits are indicative of having germplasm that shows a degree of diversity. TY was a dependent variable that did not show a statistically significant effect on Genotype. Dia et al. [1] observed a low genotype variance from marketable yield, which was 8% of the total variance. Ultimately, a majority of the traits showed no significant genotype-by-environment effect (Table 1). This indicated that there was not a significant difference in yield between WES and UVD over the years and genotypes evaluated. This suggests that improved progeny can be developed and tested in one location only, and these progenies should rank similarly in the other location, which is a large watermelon producing region in Texas. Contrasting our results, a previous study identified significantly ($p < 0.01$) genotype-by-environment effects for various yield and quality parameters across eight locations: Kinston NC, Clinton NC, Charleston SC, Cordele GA, Quincy FL, Lane OK, College Station TX, and Woodland CA [1]. The similar environmental conditions during plant growth between WES and UVD, as well as field management, could potentially indicate why no significant genotype by environment interaction was observed. As for the study conducted by Dia et al. [1], it encompassed 40 genotypes, three years and eight different locations throughout the United States. The locations covered diverse and distinct environments across the United States, which could account for the genotype-by-environment interaction for the traits evaluated. The method of fertilization was not mentioned by Dia et al. [1], and there is the possibility that sufficient and direct fertigation to the roots may have led to no genotype by environment interaction in our study.

Table 1. Analysis of variance with mean square of twenty watermelon genotypes evaluated at Uvalde and Weslaco TX in 2018 and 2019.

Source	DF [y]	TY	TF	FW	FL	FD	TSS	RT
G [z]	19	336.57	31.97 *	21.98 *	316.03	41.82 ***	13.68 *	0.51
LC	1	0.02	103.55 *	1.46	17.17	75.74	9.87	1.18
YR	1	6554.94	51.48	148.25	326.27	73.18	1.97	7.58
G × LC	19	202.03	11.19	1.30	6.77	2.12	0.23	0.19
G × YR	19	57.14	3.87	3.95	5.83	3.56	0.79	0.12
LC × YR	1	7802.81 ***	4.23	182.61 **	225.24 *	499.08 **	73.35 **	5.09 **
RP (LC × YR)	4	80.12	1.31	5.05	12.82	7.31 *	0.53	0.14
G × LC × YR	19	157.62	5.36	2.85	10.52	1.83	0.65	0.11

[z] G = genotype, LC = location, YR = year, RP = replication. [y] DF = degree of freedom, TY = total yield, TF = total fruit, FW = fruit weight, FL = fruit length, FD = fruit diameter, TSS = total soluble solids, RT = rind thickness, *, **, *** Significant at $p \leq 0.05$, 0.01 or 0.001, respectively.

Although genotypes were not statistically different, Crimson Diamond had a TY of 45.4 t ha^{-1}, while Sugar Baby had a TY of 23.0 t ha^{-1} (Table 2). Sugar Baby had previously shown low yields across studies [1,37,38]. Sunshade and TAM 2 had a TY of 44.6 and 43.7 t ha^{-1}, respectively. The performance

of commercial checks evaluated at UVD was provided (Supplementary Materials Table S1). Crimson Diamond and Sunshade were released through the Plant Varietal Protection Act (PVP). In our evaluation, these genotypes performed better than their predecessors, such as Crimson Sweet and Charleston Gray, which were ranked 9th and 15th, respectively. Sunshade is a germline derived from Charleston Gray, where Sunshade is a mutant identified from Charleston Gray that has broad leaves instead of lobed leaves, while Crimson Diamond is derived from a cross between Black Diamond and Crimson Sweet (Supplementary Materials Table S2).

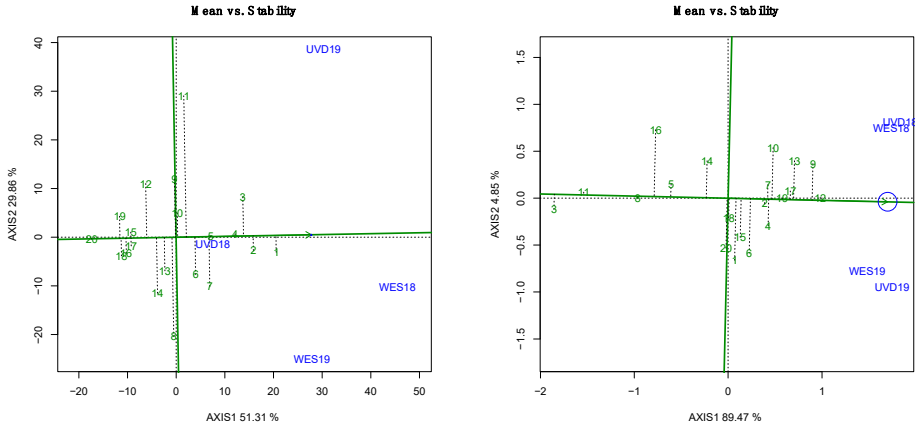
Table 2. Mean for yield parameters and fruit appearance characteristics on twenty genotypes evaluated at Uvalde and Weslaco TX in 2018 and 2019.

#	Genotype [z]	TY [y]	TF	FW	FL	FD	TSS	RT	Flesh Colorx	Rind Pattern	Fruit Shape
1	Crimson Diamond (PI 600950)	45.4	4.8	9.0	27.6	25.3	9.4	1.7	Coral Red	Wide Striped	Round
2	Sunshade (PI 635726)	44.6	7.0	8.1	41.5	18.7	9.9	1.2	Coral Red	Gray	Elong
3	TAM 2	43.7	10.8	6.1	24.1	22.1	6.1	1.3	Pale Yellow	Narrow Striped	Round
4	Verona (PI 635712)	40.9	5.2	8.8	26.2	24.4	10.0	1.4	Coral Red	Dark Green	Round
5	Muchas shandia (PI 543210)	39.6	11.0	4.2	24.9	17.2	8.2	1.6	Pink	Medium Striped	Blocky
6	Chubby Gray (PI 600951)	38.3	5.4	8.4	32.8	21.8	9.6	1.6	Coral Red	Gray	Blocky
7	TAM 22	37.8	7.1	6.4	24.1	22.8	10.0	1.6	Orange	Gray	Oval
8	TAM 14	36.0	9.5	5.0	20.9	21.2	7.6	1.5	White	Wide Striped	Blocky
9	Crimson Sweet	35.1	6.3	6.3	24.0	21.9	10.8	1.4	Coral Red	Medium Striped	Oval
10	Calhoun Gray	34.7	6.2	8.0	39.5	19.6	10.0	1.6	Coral Red	Gray	Elong
11	TAM 9	33.8	6.6	5.8	30.4	19.4	6.6	2.1	Orange	Gray	Oval
12	TAM 6	33.4	8.2	5.4	23.1	21.2	11.0	1.1	Coral Red	Gray	Round
13	ZWRM50	31.7	6.7	7.8	24.8	23.0	10.5	1.8	Coral Red	Narrow Striped	Round
14	Strain II	31.2	6.8	5.7	22.8	21.9	8.9	1.1	Yellow	Light Green	Round
15	Charleston Gray	31.1	4.9	7.4	38.7	18.7	9.5	1.5	Coral Red	Gray	Elong
16	Klondike Black seeded	29.6	10.4	4.2	27.5	16.5	7.9	1.4	Scarlet Red	Green	Blocky
17	TAM 4	28.6	9.8	4.1	25.1	17.4	10.4	1.6	Scarlet Red	Green	Blocky
18	V-CI-9 (PI 512375)	26.4	7.7	4.6	20.7	20.2	9.3	1.0	Scarlet Red	Dark Green	Round
19	Tastigold (PI 547106)	25.6	5.1	5.8	22.5	21.7	10.2	1.6	Orange	Gray	Round
20	Sugar Baby	23.0	6.0	4.6	21.2	20.2	9.2	1.2	Scarlet Red	Dark Green	Round
	Grand Mean	34.5	7.3	6.3	27.1	20.8	9.3	1.5			
	LSD [w]	10.4	2.6	1.5	2.7	1.5	0.8	0.3			

[z] Genotypes evaluated, Individuals with TAM were developed by the program. [y] TY = total yield (Mg ha^{-1}), SE = standard error, TF = total fruit (thousand fruit ha^{-1}), FW = fruit weight (kg), FL = fruit length (cm), FD = fruit diameter (cm), TSS = total soluble solids (°Brix), RT = rind thickness (cm). [x] Fruit characteristics as described in the literature. [w] LSD = least significant difference.

The three genotypes with a low TY in the combined analysis were Sugar Baby, Tastigold and V-CI-9. Their TY ranged from 23.0 to 26.4 t ha^{-1} and all of them had an FW below the grouped average. Overall, there was a lower TY compared to other studies that have evaluated watermelon germplasm in a single harvest [1,37]. Genotypes in common with previous germplasm evaluations showed lower TF and FW averages, two traits that are important in determining TY. In watermelon production, there are usually two or three harvests, but up to five harvests are possible. The lower FW observed could be attributed to year, location or management.

Chubby Gray, Tastigold and Sugar Baby are genotypes that performed similarly to a study conducted by Gusmini and Wehner [37] in relation to TY, where there were seven common genotypes evaluated between the studies. Both Tastigold and Sugar Baby were poor performing genotypes in both studies, 54th and 75th out of 80, respectively [37]. In a large-scale multienvironment genotype evaluation conducted by Dia et al. [1] Sugar Baby showed similarities to our results and those of Gusmini and Wehner [37]. These genotypes and Calhoun Gray were found to be stable varieties according to various stability parameters such as regression coefficient, deviation from regression and Shukla's stability variance [1]. In our study, the mean vs stability biplot for TY (Figure 1A) showed Verona (4), Muchas Shandia (5) and Sugar Baby (20) to be the most stable, while TAM 14 (8) favored the UVD19 environment and TAM 9 (11) favored the WES19 environment. Chubby Gray (6) and Tastigold (19), which had similar performance to the previous study, showed moderate stability but were not the most stable genotypes.



(**a**) (**b**)

Figure 1. Mean vs. stability biplot (**a**) for TY and (**b**) for total soluble solids (TSS) evaluated in Weslaco and Uvalde in 2018 and 2019. Locations were showed with three letters abbreviation and years were shown with 2-digits (in blue color; UVD = Uvalde TX; WES = Weslaco TX; 18 = summer 2018; 19 = summer 2019). The numbers (green colored) on the biplots correspond to the corresponding numbers for genotypes found in Table 2.

Although yield is an important trait, TSS are of higher importance since they dictate if the variety will be sold and consumed. The top three sweetest genotypes were TAM 6, Crimson Sweet and ZWRM 50, with a TSS ranging from 11.0 to 10.5 °Brix. TAM 6, the sweetest genotype, showed stability across the environments (Figure 1B). Two of the three sweetest genotypes, TAM 6 and ZWRM 50, had TYs below the average. Dia et al. [12] found Crimson Sweet to be the sweetest genotype, with a 12.1 °Brix, in a study evaluating the fruit quality of 40 genotypes across multiple environments. They also identified that the sweetest genotypes usually had poor yields. In our study, the five genotypes with the lowest TSS were TAM 2, TAM 9, TAM 14, Klondike Black Seeded and Muchas Shandia with °Brix ranging from 6.1 to 8.2, which are lower than the standards set by the USDA [7]. TAM lines can be found at both the highest and lowest sweetness groups, with TAM 9 showing 6.6 °Brix and resistance to downy mildew, with slight lesions on multiple leaves.

2.2. Correlation and Path Analysis

Examining correlations, direct effects and indirect effects allow breeding programs to gain a better understanding of the relationship between traits. The correlations between traits show the degree of a linear relationship between two traits, which can be positive or negative. There was a positive significant ($p < 0.01$) correlation coefficient of TY to FW of 0.58 (Table 3). Several studies have indicated a correlation between yield and FW in watermelon and other crops, such as tomato, cantaloupe and

pepper: these studies evaluated improved varieties [3,39]. FW, a yield component trait, also had a significant ($p < 0.01$) positive correlation to fruit length (FL) and FD, with a negative correlation to TF (Table 3). A potential explanation for the negative correlation between FW and TF could be the source-sink relationship that exists in plants, which has been found to be complex in cucurbit fruits [40]. The amount of carbohydrates is limiting (source), so the increase in the number of fruits (sinks) leads to the partition of nutrients to all developing fruits. Ultimately for high yielding genotypes, a balance between the TF and FW would be required.

Table 3. Pearson's correlation between yield parameters on twenty genotypes evaluated at Uvalde and Weslaco, TX in 2018 and 2019.

Traits	TY [z]	TF	FW	FD	FL	TSS	RT
TY [z]		0.34	0.58 **	0.52 *	0.15	−0.10	0.17
TF			−0.52 *	−0.21	−0.43	−0.38	−0.19
FS				0.59 **	0.57 **	0.24	0.34
FD					−0.30	0.15	0.26
FL						0.11	0.14
TSS							−0.21

[z] TY = total yield, TF = total fruit, FW = fruit weight, FL = fruit length, FD = fruit diameter, TSS = total soluble solids, RT = rind thickness. *,**,*** Significant at $p \leq 0.05$, 0.01 or 0.001, respectively.

Path analysis takes a standardized partial regression of traits to identify the direct and indirect effects between traits. A positive direct effect of TF and FD on TY (0.89 and 0.85, respectively), (Table 4) shows that one could select for these traits and indirectly increase TY. Sidhu and Brar [41] evaluated F1 hybrids and found a negative direct effect of the number fruits per plant, TSS and an average FW, on yield. They concluded that to indirectly select for yield it would be best to select for increased FW and the number of nodes of the first female flower. Although TF has a high direct effect towards TY, it has negative indirect effects on all other traits. Important traits such as FW, FL and FD all have negative indirect effects toward TF (−0.22, −0.22 and −0.44, respectively, Table 4), causing the total correlation to be low. If early generation selection from this set of germplasm was solely based on TF, the population would shift towards smaller fruits. This can be observed from all the negative indirect effects from TF on the rest of the traits measured. The early generation selection of watermelon germplasm for improved productivity would require the consideration of both the FW and TF, as well as TSS. In this set of germplasm there was a negligible direct effect of TSS and rind thickness (RT) on TY. The correlation was also low at −0.19 between TSS and TY. This indicates that for this set of genotypes there may be a slight decrease in TSS as the TY increase, which could be an issue. This case is seen with TAM 2 which has a high TY, but the lowest TSS. Since °Brix and the various sugars have low heritability, improving the sugar content would be difficult, unless crossed to high TSS cultivars and making selections. The correlation and path analysis obtain from our study pertains to the set of genotypes that we evaluated and may differ from other studies that used a different set of genotypes. In general, there were some similarities to previous studies [41–43].

Sidhu and Brar [41] suggested that progeny selection should be based on those traits that showed a positive direct effect on yield to develop improved watermelon progeny. To develop progeny with improved TY, it is possible to indirectly select progeny with higher FW and TF early on in progeny development. However, it is necessary to find a balance between selecting for higher FW and TF because the indirect effect between each lowers their direct effects on TY. During selection, we should also consider TSS, due to its importance as a fruit quality parameter and has a set requirement by the USDA.

Table 4. Path analysis with path coefficient of traits onto TY on twenty watermelon genotypes evaluated at Uvalde and Weslaco TX in 2018 and 2019.

Traits	TF [z]	FW	FD	FL	TSS	RT	Total Corr TY
TF [z]	0.88 [y]	−0.20 [x]	−0.13	−0.22	0.01	0.01	−0.34
FW	−0.46	0.39	0.38	0.29	0.00	−0.01	0.58
FD	−0.18	0.23	0.64	−0.15	0.00	−0.01	0.52
FL	−0.38	0.22	−0.19	0.50	0.00	0.00	0.15
TSS	−0.33	0.09	0.10	0.06	−0.02	0.01	−0.10
RT	−0.17	0.13	0.17	0.07	0.00	−0.04	0.17

[z] TF = total fruit, FW = fruit weight, FL = fruit length, FD = fruit diameter, TSS = total soluble solids, RT = rind thickness, Total Corr TY = Total correlation towards total yield. [y] direct effects on TY (diagonal). [x] indirect effects towards respective traits (off-diagonal).

From the path analysis and correlation, we were able to find that FW and FD influenced TY. Developing populations with parents that have high FW and FD should lead to progeny with the potential to have good yield. At the same time, it is important to select progeny that have a moderate to a high level of TSS to ensure consumer acceptance. The selection of medium fruits (8 to 11 kg) would be adequate for consumer preference. TF showed a negative correlation to several fruit shape parameters, such as FL (fruit length) and FD, as well as FW. The identification and selection of progeny with moderate FW and high TF would be optimal.

Although these traits showed a potential influence on TY, additional vegetative parameters should be evaluated that could predict or assess the potential yield of genotypes, such as vegetative growth or leaf type and weight. Interestingly, Sunshade, one of the top total yielding genotypes, had broad leaves instead of lobed leaves. There is the potential that additional photo assimilates could be obtained from broad leaves, which could allow for an increase in the TF and higher TSS, although with broad leaves there may be increased disease and insect incidence. During the 2019 season, Sunshade transplants showed a higher incidence of cucumber beetle damage compared to the other varieties.

There are fruit quality parameters that could potentially be evaluated, such as fruit firmness, lycopene content, beta carotene and citrulline, which add nutritional value to the genotype. There has been variation identified in these fruit quality traits in previous studies [42–44]. For seedless triploid watermelon development, seed size would be a trait of interest. Triploid watermelons are not truly seedless, the fruit flesh contains the seed coat of the aborted seeds, so the smaller seeds are less distinguishable. These additional quality traits, such as nutritional fruit quality, are more difficult to obtain and should be evaluated at later generations.

3. Materials and Methods

3.1. Location and Plant Material

Trials were performed during the spring of 2018 and 2019 at UVD (29.2097° N, 99.7862° W) and WES (26.1595° N, 97.9908° W). UVD has heavy soils with silty clay loam soil (sand = 28%, clay = 47%, silt = 25%, pH = 8.2), while WES has lighter soils with sandy clay loam soil (sand = 63%, clay = 25%, silt = 12%, pH = 7.9). Evaluated germplasm (Table 2) included lines developed by the Texas A&M watermelon breeding program. Tested genotypes also included historic cultivars kindly donated by Dr. C. McGregor at the University of Georgia, and publicly available germplasm from the USDA-ARS National Germplasm System.

3.2. Plant Growth

Seeds were sown into 128 square cell polystyrene trays (34 cm × 67 cm; (Hortiblock, Beaver Plastics Ltd., Edmonton, AB, Canada) that contained Sungro Metro-Mix (Agawam, MA, USA). Seedlings were placed in the greenhouse at 35 °C day/22 °C night. Four-week-old seedlings were transplanted into the field on April 1st in WES 2018, while the plants in UVD 2018 were direct seeded on April 14th. In 2019,

seedlings in WES were transplanted on March 14th, while in UVD they were transplanted on April 5th. The management and growing practices for the plants were according to the recommendation of Matocha et al. [45] and Southeastern Vegetable Extension Workers [46]. Plastic mulch rows were 3 m center-to-center and plots were 7.3 m long with 0.91 m of an alley between plots. Within the plots, the plants were 0.91 m from each other, with a total of eight plants per plot. Plots were in a randomized complete block design with two replications at each location. Seedlings were irrigated and fertilized via drip tape.

3.3. Harvest and Data Collection

Harvests were conducted for the two locations and years at approximately 105 days after sowing. Maturity was assessed by a dried tendril, yellow ground spot, and hollow sound when fruits were tapped. The number of plants at the end of the season were counted before harvest to assess yield on a plant basis. All the fruits from the plot were harvested and weighted for TW per plot, which was used to calculate the TY (t ha^{-1}). The TF (thousand ha^{-1}) was assessed at the same time as the TY. There were three marketable fruits set aside that represented the overall plot. These chosen fruits were mature fruits that represented the FW, shape and rind pattern of the whole plot.

The fruits were assessed for FW (kg), FL (cm), FD (cm), RT (cm) and TSS (°Brix). Fruit appearance was recorded during the 2018 and 2019 growing season, such as flesh color, rind pattern and fruit shape, according to the literature and personal observations [47]. FL was measured from the blossom end to the stem end, while FD was measured across the fruit between the blossom end and stem end. TSS and RT were measured with a refractometer (Sper Scientific Direct, Scottsdale, AZ, USA), and caliper (Electron Microscopy Sciences, Hatfield, PA, USA), respectively. Two measurements of TSS were taken from flesh located at the center of the fruit. RT was measured from the flesh to the outer rind of the fruit and taken at the midway point between the blossom end and stem end, on each side.

3.4. Statistical Analysis

Analysis of variance was conducted on the twenty genotypes evaluated according to the SAS (SAS Institute, Cary, NC, USA) code developed by Dia et al. [48]. Grouped means were used to identify direct and indirect effects of all the traits on TY via path analysis. R software (R Core Team, 2014; v. 1.1.383) was used to construct the GGE biplots via the 'GGEBiplotGUI' package [49]. The 'Agricolae' package [50,51] was used to run the path analysis and Pearson's correlation.

4. Conclusions

Twenty genotypes were evaluated during the growing season of 2018 and 2019 at two locations, WES and UVD, for yield, yield components and quality traits. From these trials there was no genotype-by-environment interaction identified, possibly due to their geographical proximity and similar weather conditions, suggesting that improved progeny may be developed and tested in one location only, and these progenies could perform similarly in each environment. Hence, resources could be optimized by evaluating and selecting early breeding populations at one location. The study also showed that to increase TY one can either choose TF or FD, since increasing TF decreased FD and vice-versa. The results could be valuable to develop a watermelon breeding program strategy based on breeding for mini or standard watermelon. As mini watermelon is popular in the U.S. market, breeding should focus on selecting for TF to increase yield. However, a program focused on breeding for standard watermelon would require the consideration of both the FW and TF for higher productivity.

Supplementary Materials: The following are available online at http://www.mdpi.com/2311-7524/6/4/67/s1&s2, Table S1: Mean results and fruit appearance characteristics for varietal checks evaluated at Uvalde, TX. Table S2: List of germplasm with its pedigree.

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