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Genetic analysis of yield related traits in landrace × commercial watermelon hybrids

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ABSTRACT

Watermelon [*Citrullus lanatus* var *lanatus* L.] is a major xerophytic crop originating in Africa especially grown in subtropical and tropical parts of the world. However, few adapted varieties are available to promote greater yield and make watermelon a viable commercial crop of choice. Path analysis and combining ability was carried out for yield related traits among three popular local landraces; Landrace 1, Landrace 2 and Landrace 3 collected in Zimbabwe and three commercial watermelon varieties 'Congo', 'Charleston Grey' and 'Crimson Sweet' in plots arranged in an RCBD replicated 3 times. A complete diallel mating design was used to generate 36 F₁ genotypes which together with the parents were evaluated for several quantitative traits. Data on correlations, path analysis, GCA and SCA between fruit yield and other traits were computed using Microsoft Excel and GenStat 17. Individual fruit weight (FIW) and number of fruits per plant (NF) were found to be significantly linked with final fruit yield. Significant positive correlations were also observed on NF and number of female flowers (NFF), number of vines (NV), and FIW and these traits could be recommended as reliable selection indicators for creating high yielding watermelon genotypes. Path analysis showed that FIW and NF were the most important contributors to watermelon yield. GCA and SCA effects were significant and positive for yield which indicates that the traits are controlled by both additive and non-additive genes. 'Crimson Sweet' and 'Landrace 1' were the best pollen sources whereas 'Landrace 1' and 'Landrace 2' were the highest yielders when used as female parents. Overall, results from this study identified usable yield related proxies and need to incorporate local landraces germplasm in watermelon improvement.

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INTRODUCTION

Watermelon [*Citrullus lanatus* var *lanatus* L.], cucurbitaceae family, is a warm season crop (Dube *et al.*, 2021). It has a sweet taste mainly eaten in salads and juice is grown across the globe (Gbotto *et al.*, 2016). Citron watermelon is cooked and can be used as stock feeds, cooked into a thick porridge (*nhopi*) or cooked in a dry maize mixture (*umxhanxa*) (Mujaju *et al.*, 2011). Full commercial potential of the crop in Africa has not been reached due to lack of improved cultivars adapted to local conditions. Furthermore, compared to other crops modern dessert watermelon cultivars have a narrow genetic base which presents challenges when breeders seek to improve other important attributes.

Yield is the primary objective of any breeding programme. The efficiency of yield selection is mostly determined by the direction and is a result interactions of various interconnected traits. For a more practical approach to yield enhancement, selection should be based on yield components. The study of inter-character interactions is crucial because it reveals which qualities can be

addressed simultaneously or concurrently, with those having positive and significant links with each other being improved concurrently (Mulyani & Waluyo, 2020). The most critical challenges in plant breeding programmes are recognising the best combination of two or more parental genotypes. In watermelon, combining potential parents is important since it allows the identification of suitable parents which can help to transmit desirable traits in the commercial hybrids (Nascimento *et al.*, 2019). Therefore the objectives of this study were to determine correlation and path analysis for quantitative traits in watermelon and to estimate the combining ability for yield and yield related traits among selected commercial and landrace watermelon genotypes.

MATERIALS AND METHODS

Experimental Sites

The field study was conducted in the Midlands Province at an altitude of 1065 meters above sea level and between latitude 20°38'S and longitude 29°55'E. The area falls into Natural

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Region IV of Zimbabwe with between 450-600 mm of annual rainfall. Mean annual temperatures are 26°C with soils classified as loamy sands.

Field Layout and Experimental Design

Three popular watermelon landraces were collected from Mberengwa district in Zimbabwe and 3 commercial varieties ‘Charlestone Grey’, ‘Crimson Sweet’ and ‘Congo’ were acquired from agrodealers. A complete diallel mating design was used to generate 36 F_1 genotypes. The plots were arranged in a Randomised Complete Block Design (RCBD) with 3 replicates. Crosses to generate F_1 hybrids were done in the first growing period from 26 July 2020 up to mid- November 2020, the second period was from 27 November up to mid- March 2021. Parents and F_1 seeds were then sown on ridges by hand at a spacing of 0.5 metre between plants and 1.5m between rows during the 07 June to 23 October 2021 period. Manual weeding of experiments was carried out during plant development to prevent weed invasion. Disease and pest control was carried out using a carbamate-based insecticide applied when necessary.

Data Collection and Analysis

Analysis of variance for individual fruit weight (FIW), number of fruits per plant (NF), rind thickness (RT), fruit length (FL), number of female flowers (NFF), number of vines (NV), fruit width (FW) and fruit yield (FY) using the appropriate method for Randomised Complete Block Design in GenStat 17. Data were transformed using the square root transformation prior to analysis of variance where necessary. Correlations between fruit yield and other traits were computed and the partitioning of yield and yield related components into direct and indirect effects on fruit yield using Path coefficient analysis was conducted using Microsoft Excel 2019 as suggested by Shamuyarira *et al.* (2019). A total of 36 F_1 genotypes, parents and their reciprocals using Griffings complete diallel Method I model I (Griffing, 1956) using GenStat 17. The significance of specific and general combining ability (SCA and GCA respectively) was determined using a T-test for yield and related parameters. Baker’s ratio, $2S_{gi}^2 / (2S_{gi}^2 + S_{ij}^2)$ where g_i is the GCA effect of parent i and S_{ij} is the SCA effect of cross $i \times j$ was computed to determine the significance of additive and non-additive gene effects.

RESULTS

Correlation Between Traits

Individual fruit weight (FIW), number of fruits per plant (NF), rind thickness (RT), fruit length (FL), number of female flowers (NFF), number of vines (NV), and fruit width were found to be positively associated to fruit yield (FY) (Table 1). The most highly correlated traits to the final fruit yield were FIW (0.685) and NF (0.580). Positive significant correlations were also found between NF and the following traits NFF (0.665), NV (0.493), FIW (0.327) and RT (0.343). Days to maturity had a significant and negative correlation with the majority of the qualities notably NF and FIW.

Path Coefficient and correlation analysis

Individual fruit weight (0.592) and number of fruits (0.437) had the greatest positive direct contribution to watermelon yield (Table 2). The direct and indirect contribution of other traits towards watermelon yield was minimal. DTF and DTM had a substantial inverse relationship with FY (-0.509 and -0.286 respectively).

Mean Squares of Combined Anova for Yield and its Components in Diallel Cross of 6 Watermelon Genotypes

A combined analysis of variance for the diallel cross of watermelon genotypes for yield components and fruit traits among parents, their F_1 and reciprocals indicated that there were significant differences ($P < 0.05$) for genotypes, SCA, GCA and reciprocals for most of the traits (Table 3). General combining ability (GCA) was found to be significant for all yield components and fruit characters except for the number of fruits. Similarly, the effects of the specific combining ability were also found to be significant for all the measured traits except for the number of fruits. Effects of the reciprocals were found to be significant for days to maturity, number of fruits per plant and fruit yield.

From the GCA effects analyses, ‘Crimson Sweet’ (12.66) and ‘Landrace 1’ (9.43) had the highest positive, significant GCA when used as pollen sources for fruit yield improvement. When used as females, Landraces 1 and 2 had the highest significant GCA effects for fruit yield (14.61 and 11.52 respectively). Furthermore, Landrace 1 when used as a male contributed positively to fruit yield (9.43). Landrace 2 reduced days to maturity with the greatest negative GCA. Of note is that all commercial varieties had a negative GCA effect on yield. All traits had a high Baker’s ratio except for rind thickness and number of fruits per plant which was not significant (Table 3).

GCA and SCA Effects of Watermelon Parental Genotypes for Fruit Yield, Yield Components and Fruit Traits in Watermelon

When used as a seed parent, ‘Landrace 1’ had the highest positive significant GCA for the traits number of fruits, number of vines, number of female flowers and individual fruit weight (Table 4). ‘Crimson Sweet’ was a notable suitable pollen source for the traits individual fruit weight, number of vines, number of female flowers as well as number of fruits. ‘Congo’ and ‘Crimson Sweet’ were found to be suitable pollen sources for increasing the number of female flowers in watermelon as indicated by the high GCA (1.64, 1.31 respectively). Hybridizing landraces with the commercial varieties did not prove beneficial as almost all the cross combinations had negative SCA effects for economically important traits such as number of fruits and fruit yield. The combination of $L1 \times L2$ (7.64) and $L2 \times L3$ (6.63) had the highest SCA effects for fruit yield (Table 5). However, the combination of $L2 \times L3$ (6.03) and $L1 \times L2$ (5.86) had the highest SCA for the number of female flowers (Table 5). Despite negative GCA effects when used as a seed parent, the crosses

Table 1: Genotypic (G) and phenotypic (P) correlation coefficient of 10 selected quantitative characters in watermelon

Traits	DTF	RT	FW	FL	DTM	NFF	NV	FIW	NF
	1								
RT	-0.466**	1							
FW	-0.110 ^{ns}	0.299**	1						
FL	-0.148 ^{ns}	0.200*	0.344**	1					
DTM	0.590**	-0.479**	-0.180 ^{ns}	-0.238*	1				
NFF	-0.061 ^{ns}	0.283**	0.117 ^{ns}	0.253**	-0.456**	1			
NV	-0.347**	0.361**	0.138 ^{ns}	0.268**	-0.431**	0.380**	1		
FIW	-0.397**	0.274**	0.203*	0.219*	-0.521**	0.237*	0.192*	1	
NF	-0.318**	0.343**	0.029 ^{ns}	0.166 ^{ns}	-0.686**	0.665**	0.493**	0.327**	1
FY	-0.286**	0.244*	0.087 ^{ns}	0.194*	-0.509**	0.411**	0.288**	0.685**	0.580**

DTF-day to flowering, RT- rind thickness, FW- fruit width, FL- fruit length, DTM- days to maturity, NFF- number of female flowers per plant, NV- number of vines, FIW- individual fruit weight, NF- number of fruits per plant, FY- fruit yield, * significant at 0.05, ** significant at 0.01, ns-not significant

Table 2: Direct (bold) and indirect effects of various quantitative traits on grain yield per plant

	DTF	RT	FW	FL	DTM	NFF	NV	FIW	NF	FY
DTF	0.031	0.005	0.004	-0.005	0.063	-0.006	-0.003	-0.235	-0.139	-0.286**
RT	-0.014	-0.011	-0.011	0.006	-0.051	0.003	0.004	0.162	0.150	0.244*
FW	-0.003	-0.003	-0.038	0.011	-0.019	0.001	0.001	0.120	0.013	0.087 ^{ns}
FL	-0.005	-0.002	-0.013	0.031	-0.025	0.003	0.003	0.130	0.073	0.194*
DTM	0.018	0.005	0.007	-0.007	0.106	-0.005	-0.004	-0.308	-0.300	-0.509**
NFF	-0.002	-0.003	-0.004	0.008	-0.048	0.011	0.004	0.140	0.291	0.411**
NV	-0.011	-0.004	-0.005	0.008	-0.046	0.004	0.010	0.114	0.215	0.288**
FIW	0.837	-0.003	-0.008	0.007	-0.055	0.003	0.002	0.592	0.143	0.685**
NF	-0.010	-0.004	-0.001	0.005	-0.073	0.007	0.005	0.194	0.437	0.58**

DTF-day to flowering. RT- rind thickness. FW- fruit width. FL- fruit length. DTM - days to maturity. NFF- number of female flowers per plant. NV- number of vines. FIW- individual fruit weight. NF- number of fruits per plant. FY- fruit yield. * significant at 0.05, **0.01, ns-not significant

Table 3: Mean squares of combined ANOVA for yield and its components in diallel cross of 6 watermelon genotypes

Sources of Variation	d.f	DTM	RT	FIW	NFF	NV	NF	FY
Rep	2	9.20 ^{ns}	2.15**	1.04 ^{ns}	0.63 ^{ns}	0.92 ^{ns}	0.55 ^{ns}	17.4 ^{ns}
Genotype	35	113.10 ^{ns}	1.23**	13.31 ^{ns}	4.82**	1.34 ^{ns}	1.82 ^{ns}	46.15 ^{ns}
GCA	5	314.40**	0.20**	5.86**	6.26**	3.84**	4.82 ^{ns}	112.09**
SCA	15	44.22*	0.38**	3.34**	4.37**	3.21**	0.36 ^{ns}	31.21**
Reciprocal	15	58.71**	0.12 ^{ns}	0.22 ^{ns}	12.1 ^{ns}	4.12 ^{ns}	3.68*	42.12**
Error	70	11.7	0.014	2.17	0.26	3.16	0.84	16.2
Baker's Ratio		0.93	0.51	0.79	0.74	0.71	ns	0.87

RT- rind thickness. FW- fruit width. FL- fruit length. DTM- days to maturity. NFF- number of female flowers per plant. NV- number of vines. FIW- individual fruit weight. NF- number of fruits per plant. FY- fruit yield. * Significant at 0.05, **0.01, ns-not significant

Table 4: GCA effects of watermelon parental genotypes for fruit yield, yield components and fruit traits in watermelon

Genotypes	DTM	RT	FIW	NFF	NV	NF	FY
L1 (Male)	-0.28*	0.41**	0.23*	0.14*	0.03**	1.36 ^{ns}	9.43**
(Female)	-2.28 ^{ns}	-0.08*	1.28**	1.47**	0.69*	1.19 ^{ns}	14.61**
L2 (Male)	0.72*	0.27*	-0.36 ^{ns}	-0.69 ^{ns}	0.03 ^{ns}	-0.64 ^{ns}	-4.22*
(Female)	-2.11*	-0.08 ^{ns}	0.93**	0.47*	0.19 ^{ns}	1.19 ^{ns}	11.52**
L3 (Male)	-1.28 ^{ns}	0.14 ^{ns}	-0.22 ^{ns}	-0.86 ^{ns}	-0.14 ^{ns}	0.36 ^{ns}	-0.53 ^{ns}
(Female)	-0.44*	0.11*	-0.14 ^{ns}	0.64**	0.03*	0.53 ^{ns}	1.48*
L4 (Male)	1.72*	-0.68 ^{ns}	-0.67*	-1.53*	-0.47 ^{ns}	-1.14 ^{ns}	-8.81 ^{ns}
(Female)	1.55 ^{ns}	-0.44*	-0.37*	-0.19 ^{ns}	-0.47 ^{ns}	-0.81 ^{ns}	-4.22 ^{ns}
L5 (Male)	0.22 ^{ns}	0.26 ^{ns}	0.13 ^{ns}	1.64**	-0.14*	-0.64 ^{ns}	-8.53 ^{ns}
(Female)	0.22 ^{ns}	0.17 ^{ns}	-0.72*	0.47*	0.19 ^{ns}	0.19 ^{ns}	-4.33 ^{ns}
L6 (Male)	-1.11 ^{ns}	-0.39*	0.89 ^{ns}	1.31**	0.69*	0.69 ^{ns}	12.66*
(Female)	3.06**	0.32**	-0.97 ^{ns}	-2.86 ^{ns}	-0.64 ^{ns}	-2.31 ^{ns}	-19.06 ^{ns}

L1- Landrace 1, L2- Landrace 2, L3- Landrace 3, L4- Charleston Grey, L5- Congo, L6- Crimson Sweet, RT- rind thickness, FW- fruit width, FL- fruit length, DTM- days to maturity, NFF- number of female flowers per plant, NV- number of vines, FIW- individual fruit weight, NF- number of fruits per plant, FY- fruit yield * Significant at 0.05. **0.01, ns-not significant

of 'Charleston Grey' with 'Landrace 2' (9.36) and 'Landrace 3' (11.19) had the highest SCA effects for the number of vines

(Table 5). Number of fruits was not significant for GCA and SCA for all the six parents evaluated.

Table 5: SCA effects of parental watermelon genotypes for fruit yield, yield components and fruit traits in watermelon

Cross/Trait	DTM	RT	FIW	NFF	NV	NF	FY
L1 × L2	-5.56*	0.72*	0.91 ^{ns}	5.86**	1.47*	6.47 ^{ns}	7.64*
L1 × L3	-0.56*	0.58*	0.87 ^{ns}	0.03 ^{ns}	-0.36 ^{ns}	-0.53 ^{ns}	0.83 ^{ns}
L1 × L4	5.44 ^{ns}	0.39*	-2.28*	-0.31*	-0.03 ^{ns}	-1.03 ^{ns}	-3.82**
L1 × L5	0.94 ^{ns}	0.52 ^{ns}	0.32 ^{ns}	-4.47*	-1.36**	-3.53 ^{ns}	-4.17*
L1 × L6	-0.72 ^{ns}	1.11**	0.26 ^{ns}	-1.14*	-1.19*	0.39 ^{ns}	0.73 ^{ns}
L2 × L1	-2.72*	0.01 ^{ns}	0.47*	3.03 ^{ns}	-0.03 ^{ns}	3.47 ^{ns}	4.82*
L2 × L3	-1.72*	0.28*	1.02*	6.03*	1.14*	4.47 ^{ns}	6.63*
L2 × L4	3.28 ^{ns}	0.19 ^{ns}	-0.93 ^{ns}	-4.31**	-1.53 ^{ns}	-4.03 ^{ns}	-5.44**
L2 × L5	0.78 ^{ns}	0.16*	-2.23**	-2.47 ^{ns}	0.14*	0.47 ^{ns}	-4.78 ^{ns}
L2 × L6	-0.89 ^{ns}	1.11 ^{ns}	0.11 ^{ns}	0.86*	-0.69*	-0.86 ^{ns}	-2.07*
L3 × L1	-4.39*	-0.47*	0.74*	2.86*	0.14 ^{ns}	5.14 ^{ns}	5.84*
L3 × L2	3.61*	-0.84 ^{ns}	-0.78 ^{ns}	2.69*	0.14 ^{ns}	-1.86 ^{ns}	-2.77 ^{ns}
L3 × L4	3.61 ^{ns}	-0.29**	-1.46*	-0.47 ^{ns}	-0.36*	-1.36 ^{ns}	-3.14*
L3 × L5	-0.89*	0.48 ^{ns}	0.44 ^{ns}	-2.64**	0.31*	-1.86 ^{ns}	-1.91*
L3 × L6	4.44 ^{ns}	1.03*	1.27*	2.86 ^{ns}	0.47 ^{ns}	4.5 ^{ns}	5.90 ^{ns}
L4 × L1	3.61 ^{ns}	-1.22 ^{ns}	-0.53 ^{ns}	-2.31*	-0.36	-2.53 ^{ns}	-4.03*
L4 × L2	-0.39 ^{ns}	-0.69*	-0.54*	-3.47*	1.36 ^{ns}	-3.17 ^{ns}	-5.69**
L4 × L3	2.61 ^{ns}	-0.36 ^{ns}	-1.38 ^{ns}	-1.31 ^{ns}	1.19*	0.47 ^{ns}	-3.88 ^{ns}
L4 × L5	3.44*	-0.47*	0.43 ^{ns}	2.19*	-1.19**	0.47 ^{ns}	-4.00 ^{ns}
L4 × L6	2.44 ^{ns}	0.48*	-2.99*	-0.47**	-1.03*	-2.86 ^{ns}	-2.11*
L5 × L1	3.61*	0.26 ^{ns}	-0.28 ^{ns}	-0.97 ^{ns}	-0.03 ^{ns}	-1.53 ^{ns}	-2.70*
L5 × L2	-0.39 ^{ns}	-0.41*	-0.59*	-2.14*	-1.03 ^{ns}	0.47 ^{ns}	-4.44*
L5 × L3	2.61 ^{ns}	0.33 ^{ns}	-0.23 ^{ns}	1.03 ^{ns}	0.14**	0.47 ^{ns}	-1.57 ^{ns}
L5 × L4	-10.38*	0.44**	-0.48 ^{ns}	-1.31*	-0.53 ^{ns}	-3.03 ^{ns}	-6.97*
L5 × L6	2.44*	-0.44 ^{ns}	-1.74*	-0.14 ^{ns}	-0.69*	-0.53 ^{ns}	-4.20 ^{ns}
L6 × L1	2.11**	-1.59*	-0.33*	-2.64*	-1.19*	-3.03 ^{ns}	-2.73**
L6 × L2	3.11**	-0.96 ^{ns}	-0.54 ^{ns}	0.19 ^{ns}	-0.19*	0.97 ^{ns}	-7.79*
L6 × L3	1.11*	-1.32 ^{ns}	-0.08 ^{ns}	-1.64**	-1.03 ^{ns}	-1.03 ^{ns}	-7.82 ^{ns}
L6 × L4	-4.89*	-0.20**	-0.73 ^{ns}	1.03 ^{ns}	-0.69 ^{ns}	2.47 ^{ns}	-9.26*
L6 × L5	2.61 ^{ns}	-1.24*	-1.48*	3.86*	-0.03 ^{ns}	-1.03 ^{ns}	-9.61**

L1- Landrace 1, L2- Landrace 2, L3- Landrace 3, L4- Charleston Grey, L5- Congo, L6- Crimson Sweet. RT- rind thickness, FW- fruit width, FL- fruit length, DTM- days to maturity, NFF- number of female flowers per plant, NV- number of vines, FIW- individual fruit weight, NF- number of fruits per plant, FY- fruit yield. * Significant at 0.05, **0.01, ns-not significant

DISCUSSION

Positive significant correlations were found between NF and NFF (0.665), NV (0.493) and FIW (0.327). This may be attributed to the fact that as the number of female flowers increases, the higher the chances of increasing the fruit number and vice versa. Furthermore, the number of vines also influenced the number of fruits, as the number of vines increased, there was a likelihood of getting more fruits. Conversely, days to maturity had a significant and negative correlation with the majority of yield attributes. This was quite interesting given that in most crops a longer period to partition assimilates is required to achieve greater yield.

Several studies investigated the direct and indirect effects of watermelon morphological characteristics on yield using different genotypes. In the present study individual fruit weight (0.592) and number of fruits (0.437) were the key contributors to the watermelon yield in the current study (Table 2). This concurs with other studies which noted that genotypes with numerous and heavier fruits had greater yield (Nisha *et al.*, 2018; Correa *et al.*, 2020). Yield in watermelon is dependent on the weight and number of fruits produced per unit area. This suggests that direct selection based on fruit weight and quantity of fruits will result in a significant increase in yield. Days to flowering and days to maturity had a significant inverse relationship with fruit yield (-0.509 and -0.286 respectively).

Such a negative association between watermelon yield and days to maturity was also found by Nisha *et al.* (2018). The number of female flowers and number of vines (0.291 and 0.215 respectively) had positive significant indirect effects on yield via number of fruits. Therefore, selecting for these traits would indirectly increase the watermelon fruit yield as it gives a higher chance for fruiting.

Estimates of GCA and SCA provide important information for breeding potential of parents for intra-population improvement, utility for inter-population programmes and use of lines in hybrids combinations. Significant positive GCA and SCA for yield indicates that the trait is controlled by both additive and non-additive genes respectively. Population improvement methods such as recurrent selection followed by hybridisation can be used to improve watermelon where both GCA and SCA are significant. The preponderance of additive genes as indicated by a high Baker's ratio (0.87) for yield suggests the high potential for response to selection for this watermelon population. This concurs with observations by Bahari *et al.* (2012) who found GCA significant for most traits in watermelon populations used in hybridisation. 'Crimson Sweet' and 'Landrace 1' (12.66 and 9.33 respectively) were the highest fruit yielders when used as pollen sources in breeding programmes. 'Landrace 1' and 'Landrace 2' were the highest yielders when used as female parents (14.61 and 11.52). This differential contribution depending on whether an individual was a male or female was

evidenced by the significant reciprocals which concurs with other watermelon hybridisation studies (Souza *et al.*, 2004; Bahari *et al.*, 2012). Maternal effects or cytoplasmic inheritance for most of the traits of interest are the main cause of significant reciprocal differences. Accordingly, use of an individual either as a male or female requires careful consideration in watermelon breeding particularly in the traits evaluated in this study.

None of the commercial varieties were found to be suitable female parents as expressed by the negative GCA effects for yield. ‘Crimson Sweet’ was however found to be a good pollen source for fruit yield, number of female flowers, fruit individual weight, number of fruits and number of vines. This variety has the potential to improve the landraces with respect to the mentioned characters. The combinations of the landraces showed promising possibilities to improve watermelon lines in Zimbabwe compared to the crosses with commercial varieties. Furthermore genes for earliness predominated landrace cross combinations which could be an adaptation consequence of the landraces (Table 5). Greater heterosis was exhibited by landrace cross combinations than any other cross. This indicates that there is sufficient genetic variability within the local landraces germplasm to improve watermelon yield. Hence, these landraces may be used in breeding schemes to produce hybrids by utilizing heterosis. The negative GCA and SCA effects of commercial varieties for yield related traits and other traits of importance when crossed with landraces imply the limited value for such cross combinations in watermelon improvement. Overall, results from this study showed the importance of using local landraces in watermelon improvement for yield related traits. It also noted the importance of additive and non-additive gene action in yield and related traits in watermelon.

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