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COMBINING ABILITY ANALYSIS FOR YIELD RELATED TRAITS DIRECTING SPECIFIC COMBINERS TOWARDS HETEROSIS IN TOMATO (*SOLANUM LYCOPERSICUM* L.)

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Abstract

Combining ability and heterosis analysis are applied tools to identify the potential parents and best performing hybrids for yield and yield contributing traits in tomato. Four lines, viz., LA-2711, BL-1174, PB-LO-017904, Pioneer-2761 and four testers 01786, Yaqui, CLN-2413, and BA-1079 were crossed in line × tester crossing fashion to develop 16 F_1 hybrids. Analysis of variance showed significant differences for genotypes for all agronomic traits including yield and its associated traits. In case of parents all the traits showed significant differences except, days to 50% flowering, clusters per plant, fruit weight and yield per plant. All traits showed significant differences in crosses except days to first flowering and days to 50% flowering. Comparison between parents and crosses were significant for days to first flowering, days to 50% flowering, fruits per cluster, fruit setting percentage, clusters per plant, plant height and fruit length. Differences among lines were significant for days to first flowering, days to 50% flowering, flowers per cluster, days to first harvest, clusters per plant, plant height and fruit length, days to 50% flowering. For testers, flowers per cluster, fruits per cluster, fruit setting percentage, plant height, fruit length and fruit per plant and fruit width showed significant differences. Interaction between lines and testers showed significant results for flowers per cluster, cluster per fruit weight and fruit length. Most of the traits were controlled by non-additive gene action. The genotype CLN-2413 was good general combiners for most of the characters, i.e. for flowers per cluster, branches per plant, plant height and fruits per plant. While BA-1079 for plant height, fruit weight, fruit length, fruit width and yield per plant and must be exploited in further breeding programs in future. Among crosses, good specific combiners were BL-1174 × BA-1079 for days to first flowering, BL-1174 × Yaqui for flowers per clusters and clusters per plant and Pioneer-2711 × 01786 for clusters per plant, LA-2711 × 01786 for plant height, PB-LO-017904 × 01786 for fruit weight and fruit length and may have the potential of commercial exploitation after further evaluation. On the basis of mid parent heterosis and better parent heterosis, the crosses i.e., BL-1174 × CLN-2413, BL-1174 × BA-1079, BL-1174 × Yaqui, Pioneer-2711 × 01786 , LA-2711 × 01786 and PB-LO-017904 × 01786 were marked to be the best indigenous experimental hybrids for most of the traits and the best combiners may also be useful in transferring the genes into other adapted genotypes, for exploiting heterosis on commercial scale after further evaluation.

Key words: Combining ability; Heterosis; Hybrids; Line × Tester analysis; Analysis of variance

Introduction

Agriculture sector in Pakistan is contributing about 24 percent in its GDP by accommodating 37.4 percent share in employment. An overall increase in growth of about 6.25 percent was well documented during 2023-24. Notably, there has been a remarkable growth of 11.03 percent, pointing towards significant improvement compared to last year. This sector is providing source of livelihood to around 70% of population directly or indirectly which finally leads towards alleviating the country's poverty (Anon., 2023-24b).

Tomato (*Solanum lycopersicum*) is an important horticulture crop; globally grown in the world after potato. It is grown all over the world for fresh consumption and in the processed form as ketchup, juice, soup, paste, powder and puree and has nutritive value, i.e.; lycopene, antioxidants carotenoids, phenolics, vitamin C and E (Dhaliwal *et al.*, 2000; Sekhar *et al.*, 2010). China is the top tomato producing country in the world with its share of 31% percent in the world tomato production (Anik, 2017) whereas; Pakistan is ranked on the 33rd position in the world (Nawab *et al.*, 2024) contributing only 0.42% of the world production thereby, occupying about 67 thousand hectares of area with the production of 797 thousand tonnes and yield of 11.83 tonnes hectares^{-1} (Anon., 2023-24a). Tomato is grown in the field as well as off-season crop. The off-season/indeterminate tomato tunnel technology is a very profitable business being adopted by the farmers spread (Nawab *et al.*, 2024).

Unfortunately, the farmers are bound to rely upon the expensive imported seed of open pollinated varieties and hybrids because of the absence of indigenous seed development/breeding system in tomato. The farmers are therefore, relied upon the expensive imported hybrid tomato seed in order to retain the yield response. Only a few number of open pollinated varieties and hybrids of tomato have been developed by the public sector which are either limited in

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quantity or not productively well suited to the various ecologies. There is a need to up bring productive and stable genotypes of tomato to bridge up the low tomato yield which has to be followed up by the improvement in the genetics through selection and breeding.

On the basis of above mentioned facts, there is an urgent need to substitute current varieties with new and improved hybrids and varieties with high yielding potential along with better quality traits. Before starting breeding programmes for the development of high yielding cultivars, information regarding the combining ability analysis of various characters is a prerequisite. The prospects of development of hybrids/varieties especially in tomato are very brilliant. The best performing cross combinations may be treated as hybrids while the others may flow into the segregation studies following hybridization to identify the elite plant material after rapid cycles of selections leading to homozygosity. The case study comprised of 8 indeterminate tomato parents along with 16 cross combinations was conducted to assess the combining ability of parents towards breeding of hybrids and varieties.

Material and Methods

Plant material: Eight diverse genotypes including LA-2711, BL-1174, PB-LO-017904, Pioneer-2761, 01786, Yaqui, CLN-2413 and BA-1079 (Table 1) were used for the estimation of combining ability in tomato for yield related traits. Out of these 8 genotypes 4 were used as lines viz., LA-2711, BL-1174, PB-LO-017904 and Pioneer-2761 and 4 were used as testers viz., 01786, Yaqui, CLN-2413 and BA-1079 for developing crosses in a line × tester mating design.

Field evaluation of single cross F_1 hybrids: Sixteen F_1 hybrids were developed and evaluated along with 8 parents in randomized complete block design in three replications. The experimental work was carried out in the research area of the Department of Plant Breeding and Genetics, University of Agriculture Faisalabad. Planting geometry was maintained as 30 cm and 60 cm for plant to plant and row to row distances respectively. Standard agronomics and plant protection measures were taken into account to ensure healthy crop growth.

Data analysis: At maturity, data was recorded for days to first flowering, days to 50% flowering, flowers per cluster, fruits per clusters, fruit setting percentage, number of branches per plant, days to first harvest, clusters per plant, fruit weight(g), fruit length(cm), fruit width(cm), plant height(cm), fruits per plant and fruits yield per plant (kg).

Statistical analysis: Analysis of variance was applied on the data collected by using the method outlined by Steel *et al*., (1997). Line × Testers analysis described by Kempthorne (1957) for assessing the general and specific combining ability and their effects was utilized. The percent heterosis (mid/better parent) was calculated by using formula as proposed by Falconer & Mackay (1996). ANOVA, Line × Testers, combining abilities and heterosis analyses were subjected to SPSS (Version 17.0).

Results

Analysis of variances was applied on 14 traits and their mean squares were presented in Table 2. For genotypic assessment, significant and highly significant differences were noticed for all of the traits like flowers per cluster, fruits per cluster, fruit setting percentage, clusters per plant, days to first harvest, plant height, fruit weight, fruit length, fruits per plant, fruit yield per days to first flowering, days to 50% flowering, number of branches per plant and fruit width. In case of parents, all traits showed significant differences except, days to 50% flowering, clusters per plant, fruit weight and yield per plant. All traits showed significant differences in crosses excepting for, days to first flowering and days to 50% flowering. Comparison between parents and crosses was significant for days to first flowering, days to 50% flowering, fruits per cluster, fruit setting percentage, clusters per plant, plant height and fruit length. Variations among lines were highly significant for days to first flowering, days to 50% flowering, flowers per clusters, days to first harvest, clusters per plant, plant height and fruit length and significant for days to 50% flowering. For testers, flowers per cluster, fruits per cluster, fruit setting percentage, plant height, fruit length and fruit per plant showed highly significant differences and fruit width showed significant differences. Highly significant differences for interaction between lines and testers were seen for flowers per cluster and cluster per plant while significant differences were observed for fruit weight and fruit length.

General combining ability effects of parents: The GCA effects are meant to identify good general combiners of yield and yield attributing traits as shown in Table 3. It is obvious from the results that the testers: CLN-2413 proved good as general combiner for flowers per cluster, branches per plant, plant height and fruits per plant while the tester BA-1079 proved to be efficiently good as general combiner for plant height, fruit weight, fruit length, fruit width and yield per plant. Among lines, LA-2711 for fruits per clusters and plant height, 01786 for fruits per cluster, fruit setting percentage and fruit width, BL-1174 for fruit setting percentage, PB-LO-17904 for fruit length. Thus, from the obtained results it was concluded that following two parents were practically proven good general combiners for most of the characters i.e. CLN-2413 for flowers per cluster, branches per plant, plant height and fruits per plant and BA-1079 for plant height, fruit weight, fruit length, fruit width and yield per plant and may be utilized for future breeding programs. **Specific combining ability effects of hybrids:** For number of days to first flowering, cross between BL-1174 × BA-1079 was proved as good specific combiner (Table 4). Parents of BL-1174 × BA-1079 were of poor × poor GCA effects. Cross between BL-1174 × Yaqui was proved as good specific combiner for flowers per cluster. Parents of BL-1174 × Yaqui were of poor × poor GCA effect. For clusters per plant, cross between Pioneer-2761 × 01786 was turned out to be good specific combiner and were of poor × poor GCA effects. LA-2711 × 01786 was proved as good specific combiner for plant height and were of good × poor GCA effects. For fruit weight, cross between PB-LO-017904 × 01786 was proved to be a good specific combiner. For fruit length, cross between PB-LO-017904 × 01786 turned out to be good specific combiner and were of good × poor GCA effects. Among the crosses the following crosses showed good results and were good specific combiners: BL-1174 × BA-1079 for days to first flowering, BL-1174 × Yaqui for flowers per clusters, LA-1174 × Yaqui and Pioneer-2711 × 01786 for clusters per plant, PB-LO-017904 × 01786 for fruit weight and fruit length.

Table 1. Source of parental lines and their role in breeding.

S. No.	Parental lines	Role in breeding	Source
1.	LA-2711	Line	Department of Plant Breeding & Genetics, University of Agriculture, Faisalabad. Pakistan
2.	BL-1174	Line	
3.	PB-LO-017904	Line	
4.	Pioneer-2761	Line	Procured from market
5.	01786	Tester	Plant Genetic Resource Institute, NARC, Islamabad. Pakistan
6.	Yaqui	Tester	
7.	CLN-2413	Tester	Vegetable Research Institute, AARI, Faisalabad. Pakistan
8.	BA-1079	Tester	

Table 2. Mean squares for agronomic traits in tomato.

SOV	DF	D50FLR	FLRC	FRTC	F.SET%	NBP	CP	DH	PH	FW	FL	FWD	FRTP	YP
Replication	328.90ns	373.29ns	6.47**	0.50ns	369.65*	6.88**	94.52 ns	8.42ns	562.50ns	154.47ns	35.33*	43.47ns	1109.44*	0.78ns
Genotypes	226.54*	295.61*	0.81**	4.01**	559.44**	2.63*	172.30**	80.69**	5782.92**	162.22**	57.86**	32.58*	562.10**	1.48**
Parents	305.40*	309.42ns	1.42**	6.14**	606.26**	3.53*	126.16ns	123.55**	5340.01**	66.47ns	48.68**	34.97*	646.18*	0.91ns
Crosses	157.83ns	249.87ns	0.57**	1.9**	309.38**	2.33*	164.20**	66.02*	5657.56**	204.39**	62.42**	33.50*	556.83*	1.73**
Parent vs. Crosses	705.25*	885.06*	0.02ns	20.74**	3982.66**	0.86ns	616.69**	0.68ns	10764.75**	199.75ns	53.77*	2.05ns	52.56ns	1.67ns
Lines	528.50**	534.88*	1.02**	0.20ns	105.02ns	1.57ns	205.90**	181.24**	8871.67**	21.43ns	51.81**	7.79ns	244.57ns	0.78ns
Testers	81.39ns	89.11ns	1.62**	11.18**	1054.43**	1.91ns	60.35ns	15.48ns	3276.60**	112.28ns	52.46**	48.72*	1135.18**	1.13ns
Lines × testers	217.17ns	319.40ns	0.74**	1.00ns	57.25ns	1.07ns	231.21**	40.34ns	723.27ns	165.43*	29.79*	22.09ns	274.31ns	0.87ns
Error	107.69	155.81	0.22	0.53	78.79	1.21	48.04	30.67	353.09	59.87	11.99	15.52	230.57	0.58
Total	10822.36	14717.87	41.81	117.73	17230.95	130.10	6362.27	3284.04	150375	6794.33	1953.54	1550.38	25753.50	62.46

DF= Days to first flowering, D50FLR= Days to 50% flowering, FLRC=Flowers per cluster, FRTC=Fruits per clusters, F.SET%= Fruit setting percentage, NBP= Number of branches per plant, DH= Days to 1st harvest, CP=Clusters per plant, FW= Fruit weight(g), FL= Fruit length(cm), FWD= Fruit width(cm), PH= Plant height(cm), FRTP= Fruits per plant, YP= Fruits yield per plant (kg)

Table 3. Estimates of general combining ability for lines and testers for various agronomic traits in tomato.

Genotypes	DF	50%F	FLRC	FRTC	F.SET%	NBP	CP	DH	PH	FW	FL	FWD	FRTP	YP
LA-2711	-3.36	-4.90	0.06	0.46	4.87	0.20	-1.96	1.70	25.36	2.63	1.71	1.18	-2.77	-0.18
BL-1174	0.44	0.77	-0.20	0.32	6.30	-0.21	3.54	0.22	1.18	-1.98	0.70	-2.05	7.52	-0.04
PB-LO-017904	3.86	4.44	0.03	-0.90	-11.83	-0.09	-2.63	3.12	-18.58	1.96	2.45	1.28	-1.56	0.49
PIONEER-2761	0.94	-0.31	0.12	0.12	0.65	0.50	1.04	-5.03	-7.96	-2.61	-3.45	-0.40	-3.19	-0.27
01786	-0.39	0.19	-0.08	0.58	8.85	-0.80	-0.42	-1.67	-20.45	-3.01	0.35	1.94	3.85	0.28
YAQUI	-0.95	-2.56	-0.08	-0.06	0.76	-0.45	-0.25	-2.09	-50.32	-2.72	1.38	-1.44	-15.02	0.75
CLN-2413	2.28	4.27	0.28	-0.36	-7.83	0.91	2.21	1.83	32.01	-3.34	-4.50	0.09	13.02	0.49
BA-1079	-0.94	-1.90	-0.12	-0.17	0.27	0.33	-1.54	1.94	38.76	9.07	3.47	3.47	-1.85	0.54

DF= Days to first flowering, D50FLR= Days to 50% flowering, FLRC=Flowers per cluster, FRTC=Fruits per clusters, F.SET%= Fruit setting percentage, NBP= Number of branches per plant, DH= Days to 1st harvest, CP=Clusters per plant, FW= Fruit weight(g), FL= Fruit length(cm), FWD= Fruit width(cm), PH= Plant height(cm), FRTP= Fruits per plant, YP= Fruits yield per plant (kg).

Table 4. Specific combining ability effects of various cross combinations for agronomic traits in tomato.

Cross combinations	DF	D50%	FLRC	FRTC	F.SET%	NBP	CP	DH	PH	FW	FL	FWD	FRTP	YP
LA-2711 × 01786	-6.94	-9.02	-0.43	-0.42	-0.00	0.41	-2.0	1.34	24.52	3.20	2.19	0.93	3.65	0.26
LA-2711 × YAQUI	7.16	8.06	-0.13	-0.33	-1.07	0.28	0.67	1.09	-6.06	2.64	1.69	1.59	-4.15	0.08
LA-2711 × CLN-2413	0.61	2.23	0.14	0.24	-1.39	-0.30	3.38	-0.16	-10.15	-3.30	-1.76	0.60	-7.02	-0.51
LA-2711 × BA-1079	-0.83	1.27	0.43	0.51	2.45	-0.38	-2.04	-2.27	-8.30	-2.55	-2.12	-1.92	7.52	0.17
BL-1174 × 01786	3.58	2.31	0.38	-0.05	-4.43	-0.58	-9.50	0.38	0.04	-11.39	-5.13	-4.57	6.69	-0.51
BL-1174 × YAQUI	-14.53	16.27	0.56	0.65	2.42	0.24	10.33	-5.76	9.85	-2.78	0.00	-1.21	2.23	-0.30
BL-1174 × CLN-2413	-1.08	1.56	-0.47	-0.22	1.41	0.71	5.04	3.83	-19.10	8.78	3.59	2.40	2.85	0.93
BL-1174 × BA-1079	12.03	12.40	-0.47	-0.38	0.60	-0.37	-5.88	1.55	9.21	5.39	1.54	3.38	-11.77	-0.12
PB-LO-017904 × 01786	-1.17	-1.69	0.42	0.52	1.39	-0.20	-1.17	-4.24	-7.05	11.64	4.48	3.63	-0.73	0.27
PB-LO-017904 × YAQUI	9.17	13.40	-0.69	-0.84	-5.12	-0.72	-8.83	5.17	-2.71	-2.58	-1.48	0.68	-11.02	-0.47
PB-LO-017904 × CLN-2413	-1.83	-5.77	0.19	-0.11	-0.94	0.09	1.21	-0.58	12.45	-3.36	-2.40	-1.03	8.77	0.01
PB-LO-017904 × BA-1079	-6.17	-5.94	0.08	0.43	4.67	0.84	8.79	-0.35	-2.69	-5.71	-0.61	-1.92	2.98	0.19
PIONEER-2761 × 01786	4.53	8.40	-0.37	-0.05	3.04	0.38	12.67	2.52	-17.51	-3.46	-1.54	0.02	-9.60	-0.02
PIONEER-2761 × YAQUI	-1.81	-5.19	0.26	0.52	3.76	0.20	-2.17	-0.51	-1.08	2.72	0.22	0.30	12.94	0.68
PIONEER-2761 × CLN-2413	2.30	1.98	0.14	0.09	0.92	-0.50	-9.63	-3.09	16.81	-2.12	0.57	-0.78	-4.60	-0.43
PIONEER-2761 × BA-1079	5.03	-5.19	0.03	-0.56	-7.73	-0.08	-0.88	1.08	1.78	2.86	1.19	0.46	1.27	-0.24

DF= Days to first flowering, D50FLR= Days to 50% flowering, FLRC=Flowers per cluster, FRTC=Fruits per clusters, F.SET%= Fruit setting percentage, NBP= Number of branches per plant, DH= Days to 1st harvest, CP=Clusters per plant, FW= Fruit weight(g), FL= Fruit length(cm), FWD= Fruit width(cm), PH= Plant height(cm), FRTP= Fruits per plant, YP= Fruits yield per plant (kg)

Table 5. Mid parent heterosis estimates for various agronomic traits in tomato.

Crossing combinations	DF	D50%	FLRC	FRTC	F.SET%	NBP	CP	DH	PH	FW	FL	FWD	FRTP	YP
LA-2711 × 01786	-7.33	-11.23	-11.72	2.41	17.8	-4.3	3.23	2.1	28.4	26.30	14.71	11.11	0.47	5.54
LA-2711 × YAQUI	8.07	4.71	1.40	31.26	34.65	7.25	14.2	0.7	-6.9	23.84	14.45	6.26	-26.0	-3.28
LA-2711 × CLN-2413	-0.39	0.33	9.08	38.47	26.87	4.0	18.5	2.0	19.8	4.89	2.66	5.73	-11.2	-4.62
LA-2711 × BA-1079	-5.59	-9.27	8.19	44.48	39.12	6.06	10.4	0.7	30.	21.73	10.54	4.35	14.55	27.80
BL-1174 × 01786	-4.56	-5.95	-8.89	7.18	18.08	-19	8.06	-1.0	-6.4	-28.2	-12.2	-15.92	44.86	-16.31
BL-1174 × YAQUI	-20.94	-24.81	2.45	51.35	48.56	9.68	71.0	-5.4	-13.8	-7.85	1.99	-12.37	48.86	-10.43
BL-1174 × CLN-2413	-9.38	-6.47	-7.00	28.49	39.69	23.3	49.4	1.4	-0.5	16.18	8.21	0.80	40.23	59.26
BL-1174 × BA-1079	-1.04	-2.35	-11.63	26.19	44.49	9.37	28.2	0.09	25.3	22.21	11.21	4.97	12.47	27.76
PB-LO-017904 × 01786	-8.28	-8.08	-2.16	0.69	3.72	-22.0	-10.2	-2.1	13.03	36.23	12.89	14.59	-11.5	15.20
PB-LO-017904 × YAQUI	1.56	3.93	-7.03	-0.58	8.35	-19.4	-24.9	1.5	-2.7	1.25	0.12	-2.23	-46.8	-13.79
PB-LO-017904 × CLN-2413	-9.38	-11.40	8.76	10.14	6.89	1.20	-2.8	0.5	49.5	-3.92	-5.82	1.58	10.81	21.43
PB-LO-017904 × BA-1079	-16.36	-16.88	2.50	23.13	23.57	16.2	19.0	0.4	51.0	6.43	7.27	1.48	-0.85	34.48
PIONEER-2761 × 01786	-0.38	4.53	-6.16	5.94	12.30	5.71	55.5	1.54	11.30	-7.55	-3.98	0.02	-22.3	-1.83
PIONEER-2761 × YAQUI	-5.98	-10.46	12.97	47.81	29.52	16.92	20.0	-1.3	9.79	7.55	1.04	-4.78	26.27	33.94
PIONEER-2761 × CLN-2413	-3.27	-1.71	15.50	34.10	18.10	10.5	-2.1	-0.7	59.8	-7.89	-0.64	-2.81	-4.69	1.89
PIONEER-2761 × BA-1079	-13.59	-14.15	8.03	21.14	11.85	22.3	28.3	1.3	62.0	19.15	10.52	2.19	4.23	17.24

DF= Days to first flowering, D50FLR= Days to 50% flowering, FLRC=Flowers per cluster, FRTC=Fruits per clusters, F.SET%= Fruit setting percentage, NBP= Number of branches per plant, DH= Days to 1st harvest, CP=Clusters per plant, FW= Fruit weight(g), FL= Fruit length(cm), FWD= Fruit width(cm), PH= Plant height(cm), FRTP= Fruits per plant, YP= Fruits yield per plant (kg)

Table 6. Heterobeltiosis estimates for various agronomic traits in tomato.

CROSSES	DF	D50%	FLRC	FRTC	F.SET%	NBP	CP	DH	PH	FW	FL	FWD	FRTP	YP
LA-2711 × 01786	-16.5	-19.69	-14.52	-6.94	8.02	-13.16	0.84	0.78	9.26	19.67	14.22	2.70	-12.02	-1.76
LA-2711 × YAQUI	-1.70	-4.46	-4.90	4.86	15.40	-9.68	7.98	-1.56	-26.96	19.02	11.67	5.56	-41.09	-13.87
LA-2711 × CLN-2413	-12.7	-12.17	3.09	9.35	5.56	2.63	16.13	-0.34	19.74	2.87	-6.47	3.52	-27.21	-18.31
LA-2711 × BA-1079	-17.6	-20.58	1.65	16.76	20.73	-7.89	-2.10	-1.86	25.06	10.66	8.20	0.08	13.09	13.64
BL-1174 × 01786	-5.96	-8.06	-9.84	-3.98	4.69	-25.00	0.44	-1.60	20.77	-35.6	-14.51	-25.06	9.84	-25.79
BL-1174 × YAQUI	-22.9	-27.16	-7.64	22.38	31.46	-5.56	64.15	-5.81	-32.65	-16.1	1.70	-16.30	38.62	-16.26
BL-1174 × CLN-2413	-10.9	-7.83	-15.54	2.68	19.86	21.62	33.47	0.93	-1.03	7.72	-3.34	-5.06	0.93	30.59
BL-1174 × BA-1079	-3.19	-3.77	-20.19	3.24	29.55	-2.78	24.62	0.68	19.75	17.37	11.17	4.73	-4.10	8.52
PB-LO-017904 × 01786	-11.8	-11.78	-4.75	-12.5	-8.95	-34.78	-22.2	-2.82	-8.67	21.49	4.30	3.00	-17.21	7.65
PB-LO-017904 × YAQUI	-3.45	-1.15	-13.25	-17.3	-3.17	-36.96	-36.7	1.24	-14.55	-8.50	-4.95	-5.77	-59.87	-31.69
PB-LO-017904 × CLN-2413	-10.1	-11.78	2.26	-9.58	-7.41	-8.70	-12.5	0.17	6.98	-11.5	-19.81	-3.46	-3.49	18.52
PB-LO-017904 × BA-1079	-16.7	-17.24	-4.18	3.59	11.91	-6.52	-5.16	-0.17	10.95	2.95	1.53	0.30	-8.78	31.91
PIONEER-2761 × 01786	-3.54	0.94	-13.10	-6.63	6.71	-5.13	52.42	-2.11	-8.54	-14.3	-7.69	-10.79	-34.43	-15.72
PIONEER-2761 × YAQUI	-7.98	-12.74	10.87	21.26	7.56	-2.56	18.35	-5.81	-1.68	0.78	-5.51	-8.99	3.97	29.82
PIONEER-2761 × CLN-2413	-9.17	-8.41	14.27	8.69	-4.65	7.69	-8.06	-5.26	15.94	-11.9	-5.68	-8.39	-24.42	-18.83
PIONEER-2761 × BA-1079	-19.2	-20.00	6.23	0.58	-5.99	5.13	18.35	-3.58	20.76	11.0	3.67	1.88	1.12	-3.41

DF= Days to first flowering, D50FLR= Days to 50% flowering, FLRC=Flowers per cluster, FRTC=Fruits per clusters, F.SET%= Fruit setting percentage, NBP= Number of branches per plant, DH= Days to 1st harvest, CP=Clusters per plant, FW= Fruit weight(g), FL= Fruit length(cm), FWD= Fruit width(cm), PH= Plant height(cm), FRTP= Fruits per plant, YP= Fruits yield per plant (kg)

Heterosis: Estimates of heterosis over mid/better parent are shown in Tables 5 & 6. For flowers per cluster; the cross Pioneer-2761 × CLN-2413 showed highest heterosis (15.50) and (14.27) over mid/ better parents respectively. Parents of Pioneer-2761 × CLN-2413 were of poor × good GCA effect. Cross between Pioneer-2761 and Yaqui (10.87) showed highest better parent heterosis. Parents of Pioneer-2761 × Yaqui were of poor × poor GCA effects. SCA effects were higher than GCA effects that highlighted its governance by non-additive gene action. For the trait; fruits per cluster the cross BL-1174 × Yaqui showed highest mid parent heterosis (51.35) and better parent heterosis (22.28). Parents of BL-1174 × Yaqui were of poor × poor GCA effects. Pioneer 2761 × Yaqui showed highest better parent heterosis (21.26) and were of poor × poor GCA effects. Higher values of variance were due to SCA effect (0.18) than that of the corresponding GCA effect (0.03) which suggested that fruits per cluster were controlled by non-additive gene actions. Among crosses, cross BL-1174 × Yaqui showed highest heterosis (48.56) and (31.46) over mid and better parents respectively and were of good × poor GCA effects. Higher value of GCA than SCA value suggested that fruit setting percentage was genetically under the control of additive gene action. For clusters per plant, the cross BL-1174 × Yaqui (71.01) showed the highest mid parent heterosis (71.01) and better parent heterosis (64.15) which was due to poor × poor GCA effects. Higher values of SCA effects for this trait indicated the involvement of non-additive gene action. The cross between Pioneer-2761 and BA-1079 showed highest mid parent heterosis (62.09) for plant height which was due to poor × good GCA effects. However, for better parent heterosis, the cross between LA-2711 × BA-1079 (25.06) showed highest better parent heterosis which was mainly due to good × good GCA effects. Higher GCA values marked that plant height was controlled by additive gene action. For fruit weight, cross between PB-LO-017904 × 01786 showed highest mid parent heterosis (36.23). Parents of PB-LO-107904 × 01786 were of poor × poor GCA effects. Higher values of SCA indicated that fruit weight was governed by non-additive gene action. For mid parent heterosis, the cross between LA-2711 and 01786 (14.71) showed the highest mid parent heterosis for fruit length and were due to poor × poor GCA effects. Higher value of SCA indicated that this character was controlled by non-additive gene action. For fruit width, the cross between PB-LO-017904 and 01786 (14.59) showed highest mid parent heterosis and were due to poor × good GCA effects. The SCA values again indicated the presence of non-additive gene action for this trait as that of fruit length. By considering, fruit yield per plant; the cross between BL-1174 × CLN-2413 showed highest mid parent heterosis (59.26) which was of poor × poor GCA effects.

The testers contributed more in the total variance than the lines and the interaction of line × tester for six traits i.e. number of branches per plant, plant height, fruit length, fruit width, fruits per plant and fruit yield per plant. Share of lines was more for three traits, i.e. fruits per cluster, fruit setting percentage and days to first harvest. Share of the interaction of line × tester was found more than that of the lines and testers separately for rest of the traits, i.e. days to first flowering, days to 50% flowering, flowers per clusters, fruit weight and clusters per plant. Among the crosses, the following crosses showed good results and were good specific combiners: BL-1174 × BA-1079 for days to first flowering, BL-1174 × Yaqui for flowers per clusters, LA-1174 × Yaqui and Pioneer-2711 × 01786 for clusters per plant, LA-2711 × 01786 for plant height, PB-LO-017904 × 01786 for fruit weight and fruit length and are considered to be top outlined hybrids and may serve to exploit heterosis after further evaluation.

Discussion

Plant characters can be changed or replaced for improvement either through genetic change or by external changes, changes due to environmental factors cannot be permanent and can be changed according to time or place to place. In these situations, the only solution was genetic change. For genetic change there should be genetic differences among the genotypes which can be exploited. Selection of genetically different genotypes may help in genetic improvement programs and diversity can be exploited (Kumar *et al.,* 2013, Nawab *et al*; 2023). In case of tomato, yield is very important character in Pakistan as well as in different part of the world. To increase yield of tomato, a breeder should focus on those traits which are linked to the total yield of tomato plants (Saleem *et al.*, 2013).

Biometrical analysis was used to exploit genetic variability of diverse parents. Selected parents were crossed in line × tester design. Variation among single crosses and parents was divided into three components i.e. variation among male/female parents and their interaction. Crosses were made by selecting four lines and four testers (Akram *et al*., 2019), all testers were crossed with one line to get four crosses, and a total of sixteen crosses were obtained from four lines in 2018. GCA and SCA effects outlined the performances of parents in crosses and of crosses respectively. GCA variance estimated the additive genetic variance while dominant variance was estimated through SCA variance (Nadarajan *et al.,* 2005; Sukrutha *et al.*, 2023).

Both of the additive genetic variance and dominance genetic variance for any trait gives evidence about the pattern of inheritance. Ratio between these two also provide information about the pattern of inheritance. Greater magnitude of variance for additive gene action in comparison to the dominant gene action propose the governance of additive genes. In contrary, if the magnitude of variance of dominant gene action is found greater than the additive gene action, then the trait has a non-additive gene action. The same inferences can be deduced from the variances of GCA and SCA and their ratio (Nadarajan *et al.*, 2005; Iqbal *et al.*, 2024).

For number of days to first flowering, cross between BL-1174 × BA-1079 (12.03) was proved as good specific combiners. Parents of BL-1174 × BA-1079 were of poor × poor GCA effects. Thus, it was influenced by non-additive gene action. Similar results were found by Kumari and Sharma (2012), Zengin *et al*., (2015) and Sunny *et al*., (2022).

All testers and lines for GCA effects showed non-significant results for number of days to 50% flowering. All crosses exposed non-significant for SCA effects. For mid parent heterosis, only two crosses showed negative significant effects. Number of days to 50% flowering showed higher value of SCA effect and suggested to be influenced by non-additive gene action. Similar type of conclusions came through the studies by Kapur & Chadha (2013), Raj *et al*., (2017) and Sunny *et al*., (2022).

Tester CLN-2413 (0.28) turned out to be good general combiner for flowers per clusters. Cross between BL-1174 × Yaqui (0.56) was proved as good specific combiner for flowers per cluster. Parents of BL-1174 × Yaqui were of poor × poor GCA effect. Crosse between Pioneer-2761 × CLN-2413 showed maximum heterosis (15.50) and (14.27) over the mid and better parent respectively. Parents of Pioneer-2761 × CLN-2413 were of poor × Good GCA effect. Cross between Pioneer-2761 × Yaqui (10.87) showed highest better parent heterosis. Parent of pioneer-2761 × Yaqui were of poor × poor GCA effects. Since, SCA effects were found maximum than the corresponding GCA effects; this character was genetically directed towards non-additive gene action. Similar inferences were concluded by Chisti *et al*., (2008), Kumari and Sharma (2012) and EI-Gabry *et al*., (2014) in tomato. Line LA-2711(0.46) and tester 01786 (0.58) were proved as efficient general combiners for fruits per cluster. The cross BL-1174 × Yaqui showed highest heterosis (51.35) and (22.28) over mid and better parents respectively. Parents of BL-1174 × Yaqui were of poor × poor GCA effects. Pioneer-2761 × Yaqui showed highest better parent heterosis (21.26) and were of poor × poor GCA effects. Higher values of Variance due to SCA effect (0.18) than GCA effect (0.03) suggested that fruits per cluster was controlled by non-additive gene actions. Same recordings were found by Chisti *et al*., (2008), Hasan *et al*., (2014) and Javed *et al*., (2022).

Line BL-1174 (6.30) and tester 01786 (8.85) turned out to be good general combiners. Among crosses, the cross BL-1174 × Yaqui were of good × poor GCA effects which showed highest heterosis (48.56) and (31.46) over mid and better parents respectively. Higher value of GCA than SCA value suggested that fruit setting percentage had a genetical control of additive genes as were reported by Farzane *et al*., (2012). As far as number of branches per plant, were concerned; the tester CLN-2413(0.91) was proved as good general combiner. Variance of GCA was observed as (0.04) and was higher than variance of SCA (-0.02) and suggested that number of branches per plant was controlled by additive genes. Conclusions of these type of results in tomato were reported by Saidi *et al*., (2008) EI-Gabry *et al*., (2014) and Hasan *et al*., (2014).

The cross between Pioneer-2761 × 01786 (12.67) was turned out to be good specific combiner and were of poor × poor GCA effects for number of clusters per plant. Cross BL-1174 × Yaqui were of poor × poor GCA effects and showed the highest heterosis (71.01) and (64.15) over mid and better parents respectively. Higher values of SCA effects indicated non-additive gene action for this trait. Similar inferences were drawn by Chisti *et al*., (2008) in tomato. Higher values of SCA for days to first harvest suggested non-additive gene action as were reported by Kumar *et al*., (2013) and Triveni *et al*., (2017).

Line LA-2711(25.66) was proved as best general combiner for plant height. Among tester; the testers BA-1079 (38.76) and CLN-2413 (32.01) turned out to be the best general combiners. LA-2711 × 01786(24.52) was proved as good specific combiner for plant height and were of good × poor GCA effects. The cross between Pioneer-2761 × BA-1079(62.09) showed highest mid parent heterosis (62.09) and were of poor × good GCA effects. For better parent heterosis, the cross between LA-2711 × BA-1079 (25.06) showed highest better parent heterosis and were of good × good GCA effects. GCA was high that depicted that plant height was controlled by additive gene action. In tomato similar results were also reported by Dharva *et al*., (2018). For fruit weight; tester BA-1079 (9.07) turned out to be best general combiner. Cross between PB-LO-017904 × 01786 (11.64) was proved as good specific combiner and showed highest mid parent heterosis (36.23). Parents of PB-LO-107904 × 01786 were of poor × poor GCA effects that reflected higher values of SCA pointing that fruit weight was controlled by non-additive gene action. In tomato similar findings were reported by Kumar and Gowda (2016) and Raj *et al*., (2017).

Line PB-LO-017904 (2.45) and tester BA-1079 (3.47) were proved as good general combiners. Cross between PB-LO-017904 × 01786 (4.48) turned out to be good specific combiner and were of good × poor GCA effects. For mid parent heterosis, the cross LA-2711 × 01786 (14.71) showed the highest value of heterosis over mid parent for fruit length and were of poor × poor GCA effects. Higher value of SCA for this trait pointed towards non-additive gene action. The same outcomes were recorded by Aisayh *et al*., (2016) for a tomato study. For fruit width, the tester BA-1079(3.47) turned out to be good general combiner. The cross PB-LO-017904 × 01786(14.59) showed highest mid parent heterosis and were of poor × good GCA effects. SCA values indicated that there was non-additive gene action. Similar results were reported by Chisti *et al*., (2008) and Mondal *et al*., (2009). For fruits per plant, the tester CLN-2413(13.02) was proved as good general combiner. Higher value of GCA indicated that there was additive gene control. These results were found in line with the findings of Kumari & Sharma (2012) and Izge & Garba (2012). Tester BA-1079 (0.54) was proved as good general combiner for fruit yield per plant. Among crosses, the cross BL-1174 × CLN-2413(59.26) showed highest mid parent heterosis and were of poor × poor GCA effects. GCA (0.03) and SCA (0.04) indicated that this trait had both additive and non-additive type of gene actions. Similar kind of inferences were observed by Savale & Patel (2017) and Dharva *et al*., (2018).

The purpose of studying GCA effects was to find good general combiners of yield and yield related traits. Following parents were found good general combiners i.e., CLN-2413 for flowers per cluster, branches per plant, plant height and fruits per plant.LA-2711 for fruits per clusters and plant height, 01786 for fruits per cluster, fruit setting percentage and fruit width, BL-1174 for fruit setting percentage, BA-1079 for plant height, fruit weight, fruit length, fruit width and yield per plant. PB-LO-17904 for fruit length. Among crosses, following crosses showed good results and were good specific combiners i.e., BL-1174 × BA-1079 for days to first flowering, BL-1174 × Yaqui for flowers per clusters,BL-1174 × Yaqui and Pioneer-2711 × 01786 for clusters per plant, LA-2711 × 01786 for plant height, PB-LO-017904 × 01786 for fruit weight and fruit length.

Conclusion

Two parents were good general combiners for most of the characters i.e. CLN-2413 for flowers per cluster, branches per plant, plant height and fruits per plant and BA-1079 for plant height, fruit weight, fruit length, fruit width and yield per plant and must be exploited in further breeding programs in future. Among the crosses, the following crosses showed good results and were good specific combiners: BL-1174 × BA-1079 for days to first flowering, BL-1174 × Yaqui for flowers per clusters, BL-1174 × Yaqui and Pioneer-2711 × 01786 for clusters per plant, LA-2711 × 01786 for plant height, PB-LO-017904 × 01786 for fruit weight and fruit length and are considered to be best hybrids and may have the potential to be used for commercial exploitation after further evaluation.

Conflict of Interest: The Authors declare that there is no conflict of interest.

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