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Heritability and genetic advance in F_5 segregating generation of Tomato (*Solanum lycopersicum* L.)

Muhammad Usman*[1], Sardar Ali[1], Muhammad Ismaeel[2], Muhammad Shabir[3], Rooh Ullah[3] , Hanif Raza[4]

[1]*Department of Plant Breeding & Genetics, The University of Haripur, Haripur, Pakistan*

[2]*Agricultural Research Station, Swabi, Khyber Pakhtumkhwa, Pakistan*

[3]*Department of Environmental Sciences, The University of Haripur, Haripur, Pakistan*

[4]*Agricultural Research Institute, Tarnab, Peshawar, Pakistan*

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Key words: Tomato, F_5 segregating generation, Heritability, Genetic advance, GCV, PCV

Abstract

The present study investigated the yield and its contributing attributes among F_5 segregating tomato lines so as to find degree of genetic variability, heritability, and genetic advance. This research study was conducted using a randomized complete block design (RCBD) during season 2018-2019 at Agricultural Research Station Swabi, Khyber Pakhtunkhwa. The experimental material (23 segregating lines and 2 parental genotypes) were characterized for morphological days to first flowering, days to fruiting, plant height, stem diameter, cluster per plant, flowers per cluster, fruits cluster^{-1}, fruits per plant, yield hectare$^{-1.}$ Analysis of variance regarding morphological attributes showed highly significant differences (*P≤ 0.01)* among tomato F_5 segregating lines. Minimum days to first flowering and days to fruiting were recorded for ST-12, ST-14, ST-17 with values of (50.00), (78.33) each, respectively. Maximum plant height, stem diameter, clusters per plant, flowers per cluster, fruit per cluster, fruits per plant, single fruit weight were observed for ST-20, ST-17, ST-12, ST-21, Roma, ST-12, ST-8, Roma with values of (105.38), (1.69), (29.33), (6.18), (6.00), (150.27), (81.41). Very little differences were observed between phenotypic coefficient of variation and genotypic coefficient of variation for all traits except cluster plant^{-1} and fruits plant^{-1} indicating that most of the traits were less influenced by environmental factors for their phenotypic expression. All traits had high h^2 but only fruit plant^{-1} (0.37), single fruit weight (0.58), yield ha^{-1} (0.39) were found to be moderate and clusters plant^{-1}(0.12) had low h^2. Low genetic advance (20.0) was recorded for all traits except yield. Moderate to low genetic advance suggests the action of both additive and non-additive genes and favorable influence of environment in the expression. Desired morphological characterization on the basis of the yield attributing traits to fruit yield showed these lines ST-1, ST-2, ST-4, ST-5, ST-6, ST-7, ST-9, ST-11, ST-12, ST-14, ST-17, ST-18, ST-19, ST-21, could further be used for the development of improved varieties in future tomato breeding program.

* **Corresponding Author:** Muhammad Usman ✉ usmankhan6191@gmail.com

Introduction

Tomato (*Solanum lycopersicum* L.) is an economically important crop worldwide. It has a diploid genome with 12 chromosome pairs and belongs to solonaceace family. It is one of the most important vegetable crop grown in every corner of the world. Worldwide total area and production of tomato was 50305.45 thousand hectare and 180766.329 thousand tonnes (FAO, 2019) respectively. Total production of tomato in Pakistan was about 551.0 thousand tones; whereas, area under cultivation was about 58.4 thousand hectares. In Khyber Pakhtunkhwa 118.8 thousand tones were produced on an area of 12.5 thousand hectare. Sindh is the largest producing province of tomato, in the country with the production of 182.2 thousand tones on an area of 25.0 thousand hectares, followed by Balochistan, Khyber Pakhtunkhwa and Punjab (PBS, 2018). Selection is the most decisive stage after hybridization where breeders have to select or reject the lines in the segregating generations. Therefore, the major problem faced by plant breeders in trying to improve self-pollinated crop is the identification of genotypes having high yield potential in the segregating generations**.** In breeding generations, F_2 through F_6 are the critical stages for selection and evaluation of the segregate. The breeders have to evaluate the segregating lines during these stages and selection is made at each successive stage. (Mehboob *et al.*, 2018).

The genetic variability is the raw material of vegetable breeding industry on which acts to evolve superior genotypes. The higher amount of variation present for a character in the breeding materials, greater is the scope for its improvement through selection. In tomato, yield is the cumulative effect of many component characters individually contributing towards yield. The knowledge of association of fruit yield with its component traits helps in success in a breeding program(Singh *et al.,* 2002). However, genetic variation is the true heritable variation which is not influenced by the environmental effects. Phenotypic and genotypic coefficients of variation measure the amount of variability present in a population. (Ismaeel *et al.,* 2019). PCV, GCV, heritability and genetic advance reveal that selection for fruits plant^{-1}, fruit weight, would be effective for improvement of fruit yield. (Manna and Paul 2012).

Heritability is the level of genotypic variance to the aggregate phenotypic variance, which contains both genetic and environmental variance. Genetic advance is the enhancement in the mean phenotypic estimation of the chose plants over the parental populace. Genetic advance gives evidence on expected gain resultant from determination of higher individuals. Evaluation of heritability alongside genetic advance blend is valuable in predicating the increase beneath choice than heritability alone (Iqbal *et al.,* 2018). Selection for the traits having high heritability coupled with genetic advance is likely to accumulate more additive genes leading to further improvement of their performance. The characters showed high heritability along with moderate or low genetic advance which can be improved by inter mating superior genotypes of segregating population developed from combination breeding (Patel *et al.*, 2015).

Among st the several reasons of low production of tomato the two reasons appear to be reasonable, firstly locally developed varieties are not available and secondly the non-existence of local tomato seed industry. This expensive seed supply of tomato necessitates the vegetable breeders to breed varieties/hybrids having great yield potential under local environments. There is pressing need to increase the productivity to fulfill the increasing demand. Therefore, this research is motivated to study tomato segregating lines for the identification of superior Lines, which will finally help in development of potential advance lines

Materials and methods

The present study was performed to estimate heritability and genetic advance in F_5 segregated tomato lines at Agricultural Research Station (ARS) Swabi during 2018-2019. The experimental material comprised 25 tomato genotypes (23 segregated lines and 2 parental genotypes) which were replicated thrice in a randomized complete block design (RCBD). The F_5 23 segregating lines and two prenatal genotypes were provided by the Agricultural Research

Station (ARS), Swabi (lat. 34°7′ 12.55 ″N, long. 72°28′ 12.55″ E), Khyber Pakhtunkhwa, Pakistan. Each genotype was established in 3 rows with a length of 3m. Row-row and plant-plant distances of 60.0cm and 50.0cm, respectively were kept. Cultural practices i.e. fertilizer application, weeding and control of biotic factors were carried out in all experimental plots.

Table 1. Tomato F_5 segregating lines of the cross Roma x KHT-5 used in the study.

SN	Entry	Pedigree/Selection History
1	ST-1	Roma/KHT5-HARS2013-PS3-MS18-NS-27
2	ST-2	Roma/KHT5-HARS2013-PS6-MS20-NS-30
3	ST-3	Roma/KHT5-HARS2013-PS23-MS45-NS-06
4	ST-4	Roma/KHT5-HARS2013-PS45-MS36-NS-34
5	ST-5	Roma/KHT5-HARS2013-PS48-MS40-NS28
6	ST-6	Roma/KHT5-HARS2013-PS50-MS35-NS37
7	ST-7	Roma/KHT5-HARS2013-PS52-MS30-NS45
8	ST-8	Roma/KHT5-HARS2013-PS65-MS54-NS49
9	ST-9	Roma/KHT5-HARS2013-PS71-MS68-NS68
10	ST-10	Roma/KHT5-HARS2013-PS74-MS61-NS65
11	ST-11	Roma/KHT5-HARS2013-PS79-MS45-NS62
12	ST-12	Roma/KHT5-HARS2013-PS81-MS49-NS69
13	ST-13	Roma/KHT5-HARS2013-PS85-MS70-NS70
14	ST-14	Roma/KHT5-HARS2013-PS90-MS75-NS63
15	ST-15	Roma/KHT5-HARS2013-PS99-MS63-NS35
16	ST-16	Roma/KHT5-HARS2013-PS105-MS67-NS29
17	ST-17	Roma/KHT5-HARS2013-PS115-MS75-NS72
18	ST-18	Roma/KHT5-HARS2013-PS120-MS80-NS43
19	ST-19	Roma/KHT5-HARS2013-PS123-MS71-NS33
20	ST-20	Roma/KHT5-HARS2013-PS128-MS39-NS46
21	ST-21	Roma/KHT5-HARS2013-PS130-MS35-NS37
22	ST-22	Roma/KHT5-HARS2013-PS135-MS46-NS56
23	ST-23	Roma/KHT5-HARS2013-PS141-MS47-NS53
24	Roma	Local adopted variety
25	KHT-5	Local adopted variety

Tomato genotypes used in the study are listed in Table 1. All the 25 genotypes were sown in January 2019 for raising nursery. Seedbed was prepared taking after standard cultural practices, while the seed bed had the soil texture of sandy light, well drained and high in organic matter. Farmyard manure was connected at the rate of 15 tones ha^{-1} whereas (NPK) of 100:80:60kg per hectare were used during seed bed preparation and at 1st irrigation. In order to keep the block, weed free, mechanical weeding was done from translation till harvest. Transplantation of the seedlings was carried out into well prepared fields plots rich in organic matter after 5 weeks from nursery at the evening time so that to reduce the risk of transplant shock.

The morphological data were collected on ten characteristics days to first flowering, days to fruiting, plant height, stem diameter, fruits $plant^{-1}$, clusters $plant^{-1}$, flowers $cluster^{-1}$, fruits $cluster^{-1}$, single fruit weight, yield $hectare^{-1}$ were observed on a plot basis and measured from representative plants and the average result was obtained . Ten to fifteen plants were randomly selected from each category: genotype and replication and labeled.

Data collected were subjected to the analysis of variance (ANOVA) procedure to trial the null hypothesis of no differences among different tomato isolated lines by following formula as used by (Ismaeel *et al.,* 2019). Genotype implies for each variable were further isolated and compared by utilizing the least significant differences (LSD) test at a 5% level of probability. henotypic and genotypic variances, genotype coefficient of variation and phenotype coefficients of variation were calculated by utilizing the method of Burton and Devane (1953). Heritability (broad sense) and genetic advance were computed by using the following formula as used by Ahmad *et al*, (2018), Singh & Choudary (1985) in their study.

Results

Measures of variation

Variation can arise from both genotypic and environmental factors. All the biometrical calculations related to genetic variability were based on the data of all the 10 characters recorded through evaluation of 25 genotypes.

Days to first flowering

Significant differences ($P\leq 0.01$) were observed among tomato genotypes for all traits (Table 2). Very high mean square values were recorded for traits viz., Day to first flowering (70.7200), days to fruiting (45.5256), plant height (636.967), stem diameter (0.07734), clusters per plant (55.7292), Flowers per cluster (1.36528), fruits per cluster (0.93154), fruits per plant (1830.01), single fruit weight (420.438) and yield ha^{-1} (3363.36). Cruel values for days to first flowering extended from 50.0 to 68.0 days with an overall cruel value of 63.64 days. Minimum days to first flowering were obtained for ST-12 (50.00 days) followed by ST-7 (52.67 days), KHT-5 (55.33), ST-22 (61.00). Maximum days to first flowering were

obtained for ST-14 (68.00 days) as shown in (Table 4). Genetic variance (20.48) was less than the phenotypic variance (22.69) whereas; environmental variance value was 2.21 which indicated that the traits were under genetic control. Low PCV (7.12%) and GCV (7.47%) values were observed among F_5 populations of tomato. High broad sense heritability (h^2_{bs}) and low genetic advance were recorded with values of 0.90 and 7.54, respectively (Table 3).

Table 2. Mean squares for morphological traits of tomato studied during 2018-19.

	Mean square			
Traits	Reps	Genotypes	Error	CV (%)
Degree of freedom	02	24	48	
Days to First Flowering	3.8800	70.7200**	2.2133	2.34
Days to Fruiting	5.8533	45.5256 **	2.9506	2.15
Plant Height	15.045	636.967**	66.188	11.31
Stem Diameter	0.00802	0.07734**	0.01223	7.33
Clusters Plant^{-1}	13.0985	55.7292**	9.7990	22.41
Flowers Cluster^{-1}	0.04534	1.36528**	0.58772	14.77
Fruits Cluster^{-1}	2.35375	0.93154**	0.48184	15.97
Fruits Plant^{-1}	79.36	1830.01*	307.74	29.14
Single Fruit Weight	134.689	420.438**	72.975	13.78
Yield Ha^{-1}	194.80	3363.36**	1134.48	19.29

Table 3. Genetic, environmental and phenotypic variance, phenotypic and genotypic coefficient of variations along with heritability and genetic advance for morphological traits of tomato studied during 2018-19.

Traits	Vg	Ve	Vp	h²(bs)	PCV	GCV	G.A
Days to first flowering	20.48	2.21	22.69	0.90	7.12	7.47	7.54
Days to fruiting	25.69	2.95	28.64	0.90	6.68	6.34	8.47
Plant height	1.91	66.19	68.1	0.67	11.47	1.92	0.44
Stem diameter	0.50	0.012	0.512	0.98	47.01	46.36	1.23
Cluster plant^{-1}	1.39	9.79	11.18	0.12	23.91	8.45	0.71
Flower cluster^{-1}	1.53	0.59	2.12	0.72	28.13	23.89	1.85
Fruit cluster^{-1}	1.29	0.48	1.77	0.73	30.57	26.21	1.74
Fruit plant^{-1}	82.51	307.74	225.23	0.37	24.93	15.08	9.77
Single fruit weight	3.66	72.98	69.32	0.58	13.43	3.08	0.78
Yield hectare^{-1}	319.95	1134.48	814.53	0.39	16.34	10.24	19.59

Days to fruiting

Days to fruiting . The mean value for days to fruiting varied from 68.00 to 85.00 days. The minimum days to fruiting were observed for Kht-5 (68.00 days) followed by Roma (72.00days), ST-17, ST-14, ST-9 (78.33 days), ST- 16, ST-15, ST-5, ST-6 and ST-8 (78.67 days). The maximum days to fruiting were recorded for ST-2, ST-12, ST-22 (85.00 days) (Table 4).

Table 4. Mean values of Day s to first flowering (DFF), day sto fruiting (DFr), plant-height (PH) comparison of 25 tomato genotypes studied during 2018-19.

SN	Genotype	DFF	DFr	PH
1	R ×K (ST_1)	63.00 b	83.00 a-b	62.12 f-i
2	R ×K (ST_2)	61.00 b	85.00 a	71.65 d-f
3	R ×K (ST_3)	66.00 a	80.00 c-e	54.03 h-i
4	R ×K (ST_4)	66.00 a	80.00 e	67.94 e-g
5	R ×K (ST_5)	67.33 a	78.67 e	66.00 e-h
6	R ×K (ST_6)	67.33 a	78.67 e	75.53 d-e
7	R ×K (ST_7)	52.67 d	82.33 a-c	74.83 d-f
8	R ×K (ST_8)	67.33 a	78.67 e	68.79 e-f
9	R ×K (ST_9)	67.67 a	78.33 e	65.53 e-h
10	R ×K (ST_{10})	66.00 a	80.00 c-e	63.90 e-i
11	R ×K (ST_{11})	62.33 b	83.67 a-b	64.00 e-i
12	R ×K (ST_{12})	50.00 e	85.00 a	71.44 d-f
13	R ×K (ST_{13})	67.00 a	79.00 d-e	68.90 e-f
14	R ×K (ST_{14})	68.00 a	78.33 e	61.82 f-i
15	R ×K (ST_{15})	67.67 a	78.67 e	55.42 g-i
16	R ×K (ST_{16})	67.67 a	78.67 e	51.69 i
17	R ×K (ST_{17})	67.67 a	78.33 e	69.33 e-f
18	R ×K (ST_{18})	63.00 b	81.67 b-d	70.26 d-f
19	R ×K (ST_{19})	63.00 b	81.67 b-d	51.17 i
20	R ×K (ST_{20})	63.00 b	83.00 a-b	105.38 a
21	R ×K (ST_{21})	61.67 b	84.33 a-b	98.03 a-b
22	R ×K (ST_{22})	61.00 b	85.00 a	83.24 c-d
23	R ×K (ST_{23})	67.33 a	78.67 e	92.11 a-c
24	Roma	62.00 b	72.00 f	90.00 b-c
25	Kht-5	55.33 c	68.00 g	95.00 a-c
	$LSD_{(0.05)}$	2.4424	2.8199	13.356

For days to fruiting the genetic and environmental variances were 25.69 and 2.95 while phenotypic variance was 28.64. High broad sense heritability followed by low genetic advance values were obtained value of 0.90 and 8.47. The magnitude of GCV and PCV values were 6.34% and 6.68%. (Table 3).

Plant height (*cm)*

Data transcribed on plant acme pretence that highly significant differences (*P≤0.01)* among tomato genotypes (Table 1). The mean data ranged from 105.38 to 51.17cm with average value of 71.92cm. Maximum plant height were observed for ST-20(105.38) followed by ST-21 (98.03), ST-25 (95.00), ST-23 (92.11). Minimum plant height was observed for ST-19 (51.17) followed by ST-16 (51.69), ST-3 (54.03), ST-15 (55.42) as shown in (Table 4). For plant height genetic variance, phenotypic, environmental variances, were recorded 1.91, 68.1 and 66.19 respectively. Moderate PCV value (11.47%) and low GCV (1.92%) was observed among tomato genotypes as shown in (Table 3). High heritability (bs) and genetic advance were obtained with values of 0.67, and 0.44.

Stem diameter (*cm)*

Analysis of variance indicates highly significant differences (*P≤0.01*) among tomato genotypes for stem diameter (Table 2). Mean information extended from 2.04 to 1.26mm with average value 1.51cm. Maximum stem diameter was observed for Kht-5 (2.04cm) followed by ST-17 (1.69cm), Roma (1.65cm), ST-16 (1.64cm) while minimum stem diameter was observed for ST-19 (1.26cm) followed by ST-4 (1.27mm), ST-2c(1.34cm) and ST-22 (1.34cm) as shown in (Table 5).

Genetic, phenotypic and environmental variances values for stem diameter were 0.50, 0.51 and 0.012. High heritability (bs) and low genetic advance with values of 0.98 and 1.23 were recorded among tomato genotypes for stem diameter. High values of GCV and PCV were obtained with value of 46.36% and 47.01% as shown in Table 3.

Clusters plant^{-1}

Highly significant differences (*P≤ 0.01)* were observed among the tomato genotypes for cluster plant^{-1}. Mean values for cluster plant^{-1} ranged between 29.33 and 9.43 with overall average of 13.97. Maximum number of clusters plant^{-1} were obtained for ST-12(29.33), followed by ST-7 (22.63), ST-4 (16.97), ST-22(16.30) while the minimum data recorded for ST-10 (9.43) followed by KHT-5 (9.73), ST-14 (9.83), ST-3 (10.33), ST-23 (10.63) as shown in (Table 5).

Genetic, phenotypic and environmental variance values were 1.39, 11.18, and 9.79 for cluster plant^{-1}. Low heritability (bs) and genetic advance were observed with values of 0.12 and 0.71. The (PCV) value (23.91) was greater than (GCV) 8.47 as shown in (Table 3).

Flowers cluster^{-1}

Highly significant differences (*P≤0.01)* was observed for flower cluster^{-1}. Mean values for said traits were ranged from 4.11 to 7.00 with an overall mean value of 5.19. Maximum number of flowers cluster^{-1} were observed for Roma (7.00) followed by ST-21 (6.18), ST-22 (6.05), ST-25 (6.00), ST-12 (5.83) while minimum number was recorded for ST-5 (4.11) followed by ST-13 (4.52), ST-16 (4.56), ST-14 (4.57) as shown in (Table 5).

Table 5. Mean values of stem diameter (SD), cluster plant^{-1} (CPP), flowers cluster^{-1} (FPC) and fruits plant^{-1}(FrPC) of 25 tomato genotypes studied during 2018-19.

S.No	Genotypes	SD	CPP	FPC	FrPC
1	R ×K (ST_1)	1.46 d-g	15.90 c-e	5.49 b-e	4.45 b-e
2	R ×K (ST_2)	1.34 e-i	15.17 c-f	5.22 b-f	4.36 b-e
3	R ×K (ST_3)	1.62 b-d	10.33 f-h	4.65 d-f	3.91 c-e
4	R ×K (ST_4)	1.27 h-i	16.97 c	4.68 d-f	3.96 b-e
5	R ×K (ST_5)	1.43 e-i	14.83 c-g	4.11 f	3.94 b-e
6	R ×K (ST_6)	1.59 b-e	14.57 c-h	5.05 b-f	4.79 b-d
7	R ×K (ST_7)	1.39 f-g	22.63 b	5.73 b-e	4.88 a-c
8	R ×K (ST_8)	1.52 b-g	10.93 e-h	5.13 b-f	3.74 d-e
9	R ×K (ST_9)	1.53 b-f	14.33 c-h	4.99 b-f	4.15 b-e
10	R ×K (ST_{10})	1.51 b-g	9.43 h	4.82 c-f	4.30 b-e
11	R ×K (ST_{11})	1.44 e-i	12.73 c-h	4.63 d-f	3.73 d-e
12	R ×K (ST_{12})	1.55 b-f	29.33 a	5.83 a-d	5.07 a-b
13	R ×K (ST_{13})	1.53 b-f	11.43 d-h	4.52 d-f	3.57 e
14	R ×K (ST_{14})	1.45 d-h	9.83 g-h	4.57 e-f	3.92 c-e
15	R ×K (ST_{15})	1.42 e-i	11.77 d-h	4.90 c-f	4.49 b-e
16	R ×K (ST_{16})	1.64b-c	13.17 c-h	4.56 e-f	3.84 c-e
17	R ×K (ST_{17})	1.69 b	12.07 c-h	4.64 d-f	4.02 b-e
18	R ×K (ST_{18})	1.41 f-i	13.83 c-h	5.13 b-f	4.05 b-e
19	R ×K (ST_{19})	1.26 i	14.00 c-h	4.68 d-f	3.79 c-e
20	R ×K (ST_{20})	1.49 c-g	13.13 c-h	5.72 b-e	4.64 b-e
21	R ×K (ST_{21})	1.63 b-d	11.43 d-h	6.18 a-b	4.88 a-c
22	R ×K (ST_{22})	1.34 g-i	16.00 c-d	6.05 a-c	4.91a-c
23	R ×K (ST_{23})	1.49 c-g	10.63 f-h	5.48 b-e	4.57 b-e
24	Roma	1.64 b-c	14.67 c-g	7.00 a	6.00 a
25	Kht-5	2.04 a	9.73 g-h	6.00 a-c	4.66 b-e
	LSD $_{(0.05)}$	0.1816	5.1390	1.2586	1.1396

For flower cluster^{-1} genetic phenotypic and environmental variances, values were 1.53, 2.12 and 0.59. The value of GCV (23.89%) was less than PCV (28.13%). High broad-sense heritability and low genetic-advance were recorded with values of 0.72, and 1.85 (Table 3).

Fruits cluster^{-1}

Analysis of variances showed significantly differences (*P≤0.05)* for fruits cluster^{-1} (Table 2). Mean values varied from 6 to 3.57 with mean value of 4.35 for fruit cluster^{-1}. The maximum number fruit cluster^{-1} were observed for Roma (6.00) followed by ST-12 (5.07), ST-22 (4.91), ST-7, ST-21 (4.88), ST-6 (4.78) whereas; minimum amount were obtained in ST-13 (3.57) followed by ST-11 (3.73), ST-8 (3.74) as shown in (Table 5).

Genetic phenotypic and environmental variances values were recorded for fruits cluster^{-1} 1.29, 1.77 and 0.48. High of GCV and PCV values of 26.21 and 30.57 were observed for this trait.

Higher heritability (bs) and low genetic advance were obtained with values of 0.73, 1.74 (Table 3).

Fruits per plant (*FrPP)*

Fruits plant^{-1} showed highly significant differences (*P≤0.01)* among tomato genotypes. The maxi mum value of fruit plant^{-1} were recorded for ST-12 (150.27) followed by ST-7 (108.73), ST-22 (81.63), ST-1 (70.73) and ST-6 (70.13). Mean values was for fruit plant^{-1} were ranged from 150.27 to 35.13 with mean value 60.19 as shown in (Table 6).

Table 6. Mean values of fruit plant^{-1} (FrPP) and single fruit weight (SFW), yield ha^{-1} (YPH) of 25 tomato genotypes studied during 2018-19.

SN	Genotypes	FrPP	SFW	YPH
1	R ×K (ST_1)	70.73 c-d	55.65 g-i	180.33 b-e
2	R ×K (ST_2)	67.90 c-f	59.44 e-i	211.73 b-c
3	R ×K (ST_3)	41.83 e-f	69.85 a-f	161.33 c-f
4	R ×K (ST_4)	67.27 c-g	54.05 g-i	180.17 b-e
5	R ×K (ST_5)	60.33 c-h	54.67 g-i	193.40 b-e
6	R ×K (ST_6)	70.13 c-e	71.22 a-f	210.50 b-c
7	R ×K (ST_7)	108.73 b	67.59 b-g	232.90 a-b
8	R ×K (ST_8)	40.63 f-h	81.41 a-b	148.10 e-f
9	R ×K (ST_9)	59.73 c-h	69.77 a-f	182.63 b-e
10	R ×K (ST_{10})	39.53 f-h	77.27 a-c	140.10 e-f
11	R ×K (ST_{11})	57.53 d-h	71.93 a-e	174.43 c-f
12	R ×K (ST_{12})	150.27 a	60.32 e-i	270.30 a
13	R ×K (ST_{13})	41.47 e-h	58.33 e-i	139.63 e-f
14	R ×K (ST_{14})	39.00 g-h	74.91 a-d	147.17 e-f
15	R ×K (ST_{15})	50.10 d-h	61.79 d-h	165.13 c-f
16	R ×K (ST_{16})	50.37 d-h	61.86 d-h	159.73 c-f
17	R ×K (ST_{17})	48.20 d-h	66.44 c-g	207.93 b-d
18	R ×K (ST_{18})	54.53 c-h	57.29 f-i	161.40 c-f
19	R ×K (ST_{19})	50.90 d-h	51.37 h-j	121.63 f
20	R ×K (ST_{20})	58.87 c-h	39.46 j	153.10 d-f
21	R ×K (ST_{21})	55.47 c-h	47.32 i-j	158.10 c-f
22	R ×K (ST_{22})	81.63 b-c	38.92 j	179.57 b-e
23	R ×K (ST_{23})	48.57 d-h	47.58 i-j	140.47 e-f
24	Roma	66.27 c-g	81.67 a	193.21 b-e
25	Kht-5	35.13 h	70.00 a-f	152.59 e-f
	LSD (0.05)	28.799	14.024	55.295

Fruits plant^{-1}, environmental and genetic variances were to be 307.74 and -82.51. Medium heritability (bs) and low genetic advance with the values of 0.37 and 9.77 were observed for tomato genotypes. The (GCV) value 15.08 was less than PCV 24.93 value (Table 3).

Single fruit weight (*g)*

Data was recorded on single fruit weight and analysis of variance showed that highly significant differences (*P≤0.01)* are present among the tomato genotypes. Mean values for single fruit weight were extended from 38.92 to 94.67g with mean value of 62.01g. Maximum values single fruit weight were obtained for Roma (94.67 g) followed by ST-9 (81.41), ST-10 (77.27) and ST-14 (74.91) while minimum value for single fruit weight recorded for ST-22 (38.92) followed by ST-20 (39.46) as shown in (Table 6). Phenotypic and genetic variances values were 69.32 and -3.66 whereas; environmental variance was 72.98. The moderate (PCV) and low (GCV) were to be, 13.43 and 3.08 were obtained for single fruit weight. Low heritability (bs) and low genetic advance were recorded with values of 0.053, 0.78 as shown in (Table 3).

Yield hectare^{-1}

Highly significant differences (*P≤0.01)* were ascertained for yield hectare^{-1} among all tomato genotypes (Table 2). Mean data varied from 270.30 to 121.63kgha^{-1} with overall mean of 174.62kgha^{-1}. Maximum yield ha^{-1} was obtained for ST-12 (270.30kgha^{-1}) followed by ST-7 (232.90kgha^{-1}), ST-2 (211.73kgha^{-1}), ST-6 (210.50kgha^{-1}) and ST-17(207.93) while minimum yield ha^{-1} were recorded for ST-19 (121.63) followed by ST-13 (139.63kgha^{-1}), ST-10 (140.10), ST-23 (140.47kgha^{-1}) and ST-14 (147.17kgha^{-1}) as shown in Table 6.

For yield ha^{-1} genetic, phenotypic and environmental variances were recoreded -319.95, 814.53 and 1134.48. Medium heritability (bs) and genetic advance values were obtained 0.39 and 19.59 as given in (Table 3). The moderate GCV and PCV values were 10.24% and 16.34% respectively. High value of heritability is important parameter for betterment through selection due to high variability, thus this traits is likely to show high selection response practice in the studied breeding lines.

Discussion

Analysis of variance

The result on analysis of variances (ANOVA) using randomized block design revealed that the genotypes exhibited highly significant differences for all the characters studied (Table 2), which clearly endorsed

the justification of studying genetic variability of different characters employing these genotypes. This finding was in agreement with the some earlier reports of Ismaeel *et al.* (2019), Mohammed *et al.* (2012), Meena *et al.* (2014), Islam *et al.* (2012), Somraj *et al.* (2017), Hussain *et al.* (2018), Meena *et al.* (2017) and Manna *et al.* (2012).

Phenotypic and genotypic coefficient of variation

The nature and extent of genetic variability is one of the most important criteria in formulating an efficient breeding programme and knowledge of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) is much helpful in predicting the amount of variation present in a given assemblage of genotypes. In the present investigation, the phenotypic coefficient of variations were slightly higher than the corresponding genotypic coefficient of variations for all the characters studied (Table 3), which indicated that the apparent variation was not only due to genotypes but also due to the influence of environment in the expression of the traits. However, the influence of environment for the expression of characters was not very high suggesting appreciable genotypic worth for all the characters.

The characters which showed very high genotypic and phenotypic coefficients of variation were stem diameter, cluster plant^{-1}, flower cluster^{-1} and fruit cluster^{-1}. These findings are accordance with earlier report of Islam *et al.* (2012), Dar and Sharma (2014), Tasisa *et al.* (2011), Anjum *et al.* (2009) and Prema *et al.* (2011). Other traits exhibited moderate to low PCV and GCV were days to first flowering, days to fruiting, plant height, fruit plant^{-1} single fruit weight and yield ha^{-1} among tomato genotypes. High to moderate magnitude of GCV and PCV generally indicated of ample scope for improvement through selection.

Heritability in broad sense

Through Heritability we can understand the idea of the extent of genetic control for the expression of a particular character and the reliability of phenotype in predicting its breeding value and the coverage of which a particular genetic character can be transmitted to the succeeding generations. The estimates of high heritability were observed for days to first flowerng, days to fruiting, plant height, stem diameter, flower cluster^{-1} and fruit cluster^{-1} which are comparative with the discoveries of Ali *et al.*, 2012; Kanneh *et al.*, & Somraj *et al.* (2017) and Ismaeel *et al.* (2019). The heritability estimates in combination with selection response are more reusable than heritability only for promised the resultant outcome of choice in segregating population Joshi *et al.* (2004); Bhardwaj & Sharma, (2005) and Asati *et al.* (2008); Ghosh *et al.,* 2013). Similar results were also reported by Islam *et al.,* 2012 and Sharma *et al.*, 2009 for stem diameter.

Broad sense heritability estimates were moderately low for fruit plant^{-1}, single fruit weight and yield ha^{-1} reported by Meena *et al.* (2015), Mohamed *et al.* (2018) and it was very low for cluster per plant. This results are an agreement with the earlier reports of Dar and Sharma *et al.* (2014).

Genetic advance

Genetic advance (GA) is the improvement in performance of the selected lines over the original population. The estimate of genetic advance were recorded low for all characters viz., days to flowering (Ismaeel *et al.*, 2019), days to fruiting and fruit cluster^{-1} (Somraj *et al.*, 2017), plant height (Ghosh *et al.,* 2013), stem diameter (Sharma *et al.*, 2009), cluster per plant (Dar and Sharma *et al.,* 2014), flower truss^{-1} (Dutta *et al.*, 2018), single fruit weight (Meena *et al.,* 2015) and fruit plant^{-1} except yield ha^{-1} (Elahi *et al.*, 2019) was moderate which are accordance with our present results. Hence moderate to low genetic advance suggested the role of additive and non additive gene. Therefore, the breeder should adopt suitable breeding methodology to utilize both effects simultaneously, since varietal and hybrid development will go a long way in the breeding programme.

Conclusion

The analysis of variance revealed highly significant differences among all genotypes for the characters. High PCV and GCV estimates were recorded for stem diameter, flower per cluster and fruit per cluster which indicating the existence of wider genetic

variability for these genotypes. On the other side, PCV and GCV estimates were moderate to low for traits viz., days to first flowering, days to fruiting, plant height, single fruit weight and yield ha^{-1} suggesting medium to narrow genetic variability.

The PCV was slightly higher than the corresponding GCV for all the traits which might be due to the interaction of the genotypes with the environment to some degree or other denoting environmental factors influencing the expression of these characters. All traits had high heritability but only fruit plant^{-1}, single fruit weight, yield ha^{-1} was found moderate and cluster plant^{-1} were low while less genetic advance except yield ha^{-1} was medium. The characters showing high heritability with low genetic advance indicated the presence of non additive gene action. Hence selection could be postponed for these characters could improved by inter matting of superior genotypes of segregation population from recombination breeding. Desired morphological characterization on the basis of the yield attributing traits to fruit yield showed excellent performance so these lines ST-1, ST-2, ST-4, ST-5, ST-6, ST-7, ST-9, ST-11, ST-12, ST-14, ST-17, ST-18, ST-19, ST-21, could further be used for the development of improve varieties in future tomato breeding program.

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