

## VARIABILITY OF MORPHOLOGICAL AND NUTRITIONAL TRAITS OF TOMATO GERMPLASM

M. S. Rahman<sup>1</sup>, S. Parveen<sup>2</sup>, R. Akter<sup>1</sup>, A. Y. Hossain<sup>1</sup>, K. M. K. Huda<sup>2</sup>, M. S. A. Banu<sup>3</sup>, M. A. I. Arif<sup>4</sup> and M. H. Rashid<sup>2\*</sup>

### ABSTRACT

Genetic variability provides an important basis for selection of suitable genotypes in breeding program. In the present investigation, genetic variability of yield and important morphological and nutritional traits were studied in forty-eight genotypes of tomato. High estimates of PCV and GCV were obtained for ash content, flowers per cluster, fruits per cluster, fruit length, pH of tomato juice, shelf-life of fruit and single fruit weight indicated a good deal of variability present in the characters. Again, high heritability coupled with high genetic advance were observed in fruit length, seeds per fruit, primary branch, secondary branch, shelf-life of fruit, single fruit weight, width of fruit and yield per plant. Thus, the variability and high heritability signify that selection would be effective for improvement of these traits in tomato.

**Keywords:** genetic advance, heritability, morphological, tomato, trait, variability

### INTRODUCTION

A significant impact of globalization on horticultural crops has been increasing. As a results, the demand for quality improvement and the wider adoption of quality standards for fruit, vegetable and salad commodities are increasing. As an important source of minerals, vitamins and organic acids, tomato (*Solanum lycopersicum* L.) is one of the most important Solanaceae vegetable crops grown universally. According to FAO, tomato cultivating area is approximately 5,051,983 hectares in the world and a production of 186,821 million kilos of tomatoes were produced globally in 2020 (<https://www.hortidaily.com/article/9387133/>). A wide range of variability in tomato is available which provide a great scope for improving of yield through a systematic and planned selection breeding program. The yield is complex character and dependent on many other morphological traits which are mostly inherited quantitatively (Hasan *et al.*, 2020; Hossin *et al.*, 2016). It is important to examine the contribution of each of the trait in order to give more attention to those having the greatest influence on seed yield (Tuncturk, 2007). Importance of genotypic and phenotypic variability, heritability and character association have investigated by many scientists (Khan and Mahmud, 2021; Saleem *et al.*, 2013; Yadeta Dabalo *et al.*, 2020) for genetic improvement (Ghosh & Gulati, 2001) of tomato. They also showed that high heritable traits were under the control of additive genes. These implies that selection based on phenotypic performance could be applied for improvement of tomato. The present investigation was conducted to determine the extent of genetic variability, genetic heritability and genetic advance of different characters in 48 genotypes of tomato. The objectives of this present research work was to know the yield potentiality of genotypes, to assess the genetic variability among the genotypes.

### MATERIALS AND METHODS

#### Experimental site

The present research work was carried out in the experimental farm, Sher-e-Bangla Agricultural University, Dhaka. The location of the site was 23° 74' N latitude and 90° 35' E longitude with an elevation of 8.2 meter above sea level. The pH is 6.1 and organic carbon content was 0.82%.

---

<sup>1</sup>IUBAT-International University of Business Agriculture and Technology, <sup>2</sup> Faculty, <sup>3</sup>MS student, Dept. of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, <sup>4</sup> Senior Scientific Editor, Bangladesh Agricultural research Council, Farmgate, Dhaka, Bangladesh

## Plant materials

Forty-eight tomato germplasm were used in this experiment (Table 1). The physically healthy seeds were collected from Plant Genetic Resources Centre (PGRC) of Bangladesh Agricultural Research Institute (BARI) and from local farmer's field.

**Table 1. Forty eight tomato germplasm used in the study**

S.L.	Genotype	Group	S.L.	Genotype	Group	S.L.	Genotype	Group
1	BD-10122	G1	17	BD-7291	G17	33	BARI Tomato-8	BT-8
2	BD-10124	G2	18	BD-7292	G18	34	BD-7276	G28
3	BD-7750	G3	19	BD-7298	G19	35	BD-10123	G29
4	BD-7752	G4	20	BD-7301	G20	36	BD-7748	G30
5	BD-7754	G5	21	BD-10125	G21	37	BD-9011	G31
6	BD-7755	G6	22	BD-10126	G22	38	Local Kustia-1	LK -1
7	BD-7751	G7	23	BD-10127	G23	39	BD- 7290	G32
8	BD-7756	G8	24	BD-10128	G24	40	BD-7762	G33
9	BD-7757	G9	25	BD-9010	G25	41	BD-7279	G34
10	BD-7759	G110	26	BARI Tomato-2	BT-2	42	BD-10321	G35
11	BD-7760	G11	27	BARI Hybrid-4	BH-4	43	BARI Tomato-3	BT- 3
12	BD-7761	G12	28	BARI Hybrid-5	BH-5	44	BARI Tomato-7	BT-7
13	BD-7285	G13	29	BARI Tomato-11	BT-11	45	BARI Tomato-9	BT-9
14	BD-7270	G14	30	BARI Tomato-14	BT-14	46	BARI Tomato-15	BT-15
15	BD-7281	G15	31	BD-7258	G26	47	Local Jossore - 2	LJ-2
16	BD-7287	G16	32	BD-7289	G27	48	Local Jossore - 3	LJ-3

## Field experiment

The experimental plot was prepared by ploughing with proper tiller. The weeds and other unwanted plant materials were removed from the field during the land preparation. Proper laddering was done to bring the soil at proper tilth condition. A Randomized Complete Block Design (RCBD) was used in the experiment with three replications. The field was divided into three main blocks and each blocks were subdivided into 48 plots. Genotypes were randomly assigned into 48 plots in each block. The plot size was 37.71 m × 15 m. Block to block and plot to plot distance were 1 m and 0.5 m respectively. The seed-sowing was carried out on 13 November 2013 in the seedbed. The 25-day old seedlings were transplanted into the main field. Intra and inter row distance were maintained at 0.6 m and 0.5 m respectively.

Standard agronomic practices were followed whenever necessary. Fruits were picked on the basis of maturity, size, color and age. Data were recorded on individual plant basis from 10 randomly selected plants. Observations were recorded on various plant traits i.e. plant height, number of primary branches per plant, number of secondary branches per plant, number of flowers per cluster, number of fruits per cluster, length of fruit, width of fruit, individual fruit weight, yield per plant, shelf life, number of seeds per fruit, pH of juice, % of ash, % of protein, % of vitamin C, % of brix and % of chlorophyll.

## Statistical analysis

The data were analyzed for different components. Mean, range, co-efficient of variation (CV) was estimated using MSTAT computer programme. Phenotypic and genotypic variances were estimated by the formula used by Johnson *et al.*, 1955. Genotypic and phenotypic co-efficient of variation were estimated according to Burton, 1952 and Singh RK, 1985. Heritability and genetic advance were calculated using the formula by (Hanson *et al.*, 1956; Jain & Allard, 1960; Johnson *et al.*, 1955) Genetic advance in percent of mean was calculated by (Comstock & Robinson, 1952).

## RESULTS AND DISCUSSION

**Analysis of variance:** The analysis of variance indicated that there were highly significant differences

among the tested genotypes for all the studied characters (Table 1). The results suggested the presence of inherent genetic differences with respect of various traits among the genotypes which can be exploited through selection. Similar results were noticed by Kumar *et al.* (2013) and Meena and Bahadur, (2015).

For the development of potential plant material of tomato through selection and breeding, availability of variation in the desired characters is imperative for vegetable breeder. In present investigation, simple analysis of variance for different morphological characters of tomato revealed significant variability. These results indicated that variation in these morphological characters may due to the effect of additive genetic component as described by Hayman (1954) and the variation would be helpful for the development of desired plant architecture in tomato. However, a detailed study for the genetic components of variation is essential to confirm the output of analysis of variance.

### **Variability analysis**

From the mean value it was found that the highest percentage of ash content (1.15) was observed in G3 while the lowest percentage of ash 0.27 was observed in G26 (Table 2). On the other hand, the highest percent of protein was found in G29 and the lowest was G6. The range of percent of protein was 0.67 – 3.98. Genotypes G9 and G15 contained the highest (26.35%) and the lowest (3.57%) vitamin-C respectively (Table 2). The highest percentage of brix was found in BT-7 (2.97 %) and the lowest was in G8 (6.76 %). Out of the forty-eight genotypes of tomato indicated that the highest flower per cluster was found in G12 the lowest was in BT-2. G11 was the genotype which contains the highest percentage of fruit per cluster (10.11) and the lowest was in BT-2 (2.75) Table 3.

The highest and lowest length of fruit was found in BT-15 and G20, respectively. The range of the length of fruit was 22.93 – 56.26 (Table 3). From the result it was indicated that the highest number of seeds per fruit were found in G14 and the lowest was in G11. The range of number of seeds from per fruit was 150.51- 16.59. Numbers of seeds play a vital role to keep up their progeny. The size of the fruit was the biggest in the genotype G16. The highest pH of tomato juice was found G21 the lowest was in G23. The range of pH was 3.82 – 4.4. The pH is the parameter for acidic or alkali determination. The highest percentage of chlorophyll was found in Local Jessore-3 plant leaf the lowest was in G21. Chlorophyll is the main element for photosynthesis and ultimate result of photosynthesis is the partitioning of photosynthates toward yield (Table 2). The tallest plant was found in G2 and the lowest was in LJ-2. The maximum number of primary branches per plant (21.85) and number of secondary branches per plant (17.42) were recorded in G23 and G4 respectively and the minimum number of primary branches per plant (3.4) and number of secondary branches per plant (3.1) were recorded in G9 and BT-11, respectively.

Form the experiment, the highest shelf-life was found in the genotype BT-11 and the lowest was in G16. BT-11 is suitable for preservation of tomato naturally. The result revealed that the highest individual fruit weight was found in the genotype BT-15 (87.93 g) and the lowest was in BT-11(6.84 g). The forty-eight genotypes of tomato indicated that the highest width of fruit was found in BD-7287 and the lowest was in BT-11. Mean performance of the forty-eight genotypes of tomato indicated that the highest yield per plant was found in G13 (4.59 kg per plant) and the lowest was in G34 (1.02 kg per plant). Genotype G9 was shown low yield potential but it may be pioneer because it is very much similar to BT-11 which was a cherry type tomato.

The BD-7285, BD-7759, BT-11 and BD-10123 showing wide range of variation provide ample scope for selecting the desirable types. The characters which showed wider range were also characterized by higher magnitudes of PCV and GCV. Therefore, coefficient of variation is more reliable as it is the independent unit of measurement.

### **Heritability**

The phenotypic variance was considerably higher than the genotypic variance for all the characters studied (Table 3). Deshmukh *et al.* (1986) reported that phenotypic co-efficient of variation was higher

**Table 2. Mean performance in percentage of antioxidant, nutritional and chlorophyll of forty eight tomato genotypes**

<b>Genotype</b>	<b>% Ash</b>	<b>% protein</b>	<b>% vit C</b>	<b>% brix</b>	<b>% chlorophyll</b>
G1	0.56	2.72	11.04	5.57	50.33
G2	0.96	1.81	19.17	6.16	57.46
G3	1.15	3.24	9.13	4.17	49.72
G4	0.53	2.28	8.67	3.76	55.71
G5	0.64	1.45	13.79	4.21	54.17
G6	0.56	0.67	14.66	3.67	50.75
G7	0.63	1.89	10.54	4.07	57.33
G8	0.61	1.03	8.76	2.97	61.84
G9	0.84	2.18	26.35	3.53	55.23
G11	0.29	1.33	8.13	3.09	55.67
G11	0.71	1.89	10.69	4.99	55.8
G12	0.58	0.86	17.79	3.23	53.33
G13	0.48	1.47	10.93	4.43	54.68
G14	0.33	1.6	6.66	5.37	53.75
G15	0.49	1.82	3.57	4.73	54.33
G16	0.90	1.36	7.37	5.31	51.54
G17	1.03	2.27	8.97	4.61	51.33
G18	0.91	2.43	5.39	5.23	55.99
G19	0.69	1.03	21.99	3.33	53.67
G20	0.51	1.17	10.38	3.97	61.33
G21	0.99	2.23	17.2	4.63	47.37
G22	0.61	1.19	19.64	5.81	57.63
G23	0.63	1.97	11.37	4.97	58.67
G24	0.68	1.70	25.47	4.03	50.33
G25	0.85	1.89	14.23	5.87	58.47
BT-2	0.54	1.56	10.34	4.35	62.50
BH-4	0.52	1.05	9.42	3.32	57.54
BH-5	0.53	1.62	10.43	4.74	55.27
BT-11	0.36	1.04	4.74	5.05	60.81
BT-14	0.33	1.50	5.19	4.72	59.97
G26	0.27	1.35	15.52	5.07	54.64
G27	0.58	1.92	17.96	6.33	57.18
BT-8	0.60	1.35	16.27	4.99	56.83
G28	0.59	2.04	12.57	5.51	55.78
G29	0.97	3.98	15.71	5.30	48.61
G30	0.65	1.36	9.39	3.63	53.55
G31	0.83	1.72	13.75	5.03	59.22
LK -1	0.63	1.02	20.03	3.83	51.88
G32	0.47	1.84	13.53	5.87	57.84
G33	0.67	0.81	11.64	4.39	53.53
G34	0.9	2.59	9.05	6.58	52.41
G35	0.72	0.96	7.29	5.84	54.82
BT- 3	0.66	1.73	11.87	5.04	49.17
BT-7	0.3	1.53	5.35	6.76	59.92
BT-9	0.65	1.72	11.48	5.13	55.34
BT-15	0.56	1.16	8.846	4.05	60.16
LJ-2	0.69	1.59	11.87	6.07	57.87
LJ-3	0.54	1.25	13.59	6.15	64.27
Mean	0.64	1.67	12.24	4.78	55.53
Max	1.15	3.98	26.35	6.76	64.27
Min	0.27	0.67	3.57	2.97	47.37
<b>CV(%)</b>	<b>3.16</b>	<b>1.19</b>	<b>28.23</b>	<b>3.11</b>	<b>2.11</b>

than the genotypic co-efficient of variation. Relatively high phenotypic variation was observed in plant height (11.79), p<sup>H</sup> of tomato juice (106.65), flower/cluster (146.625) and % of vit-C (106.235) which

**Table 3. Mean performance of twelve morphological characters of forty eight tomato genotypes**

Genotype	No. of flowers / cluster	No. of fruits / cluster	Fruit length	No. of seeds / fruit	pH of tomato Juice	Plant height (cm)	No. of primary Branch	No. of secondary Branch	Shelf life (day)	Individual weight of fruit (gm)	Width of Fruit (mm)	Yield /plant (kg)
G1	7.3	4.63	26.53	118.74	3.97	141.2	7	10.26	15.2	12.22	32.49	2.53
G2	6.11	4.37	26.15	99.5	4.23	186.22	10	11.2	15.23	9.63	30.62	2.44
G3	6.92	4.47	41.07	64.7	4.10	78.23	7.76	8.23	9.56	45.24	47.31	2.41
G4	7.64	5.9	46.91	98.75	3.91	75.51	13.47	17.42	13.7	39.07	40.47	2.23
G5	7.18	5.5	48.82	138.71	3.91	102.3	11.51	8.23	14.33	63.45	60.12	2.37
G6	7.47	6.26	42.69	114.91	3.93	102.62	10	15.42	12.56	44.46	46.89	2.38
G7	5.36	3.38	39.91	92.91	3.89	85.68	6.43	8.06	9.19	24.56	31.35	2.29
G8	6.06	4.64	41.27	75.54	4.19	68.44	8.51	11.25	13.68	21.24	36.85	1.57
G9	12.14	10.00	25.36	42.24	4.06	86.47	3.4	11.37	11.53	10.22	21.12	1.61
G11	10.15	8.53	26.83	31.51	3.95	87.23	10.31	10.51	8.44	14.65	28.57	3.66
G11	12.23	10.11	29.14	16.59	4.06	95.29	6.11	12.26	8.74	17.07	28.22	2.46
G12	4.97	3.55	43.41	69.37	4.16	47.65	8.11	11.2	9.15	39.24	40.16	2.24
G13	5.63	3.77	25.92	61.81	4.01	116.63	11.37	14.41	8.75	13.63	28.59	4.59
G14	8	6.43	32.24	150.51	4.04	156.54	12.56	11.55	11.3	14.23	33.54	2.56
G15	6.24	4.44	23.68	50.16	4.14	54.93	10.14	10.21	10.25	9.44	26.76	1.72
G16	6.27	4.57	33.32	141.44	4.06	142.41	9.52	11.39	4.62	15.23	134.24	2.59
G17	6.77	4.61	55.43	131.57	4.17	176.51	10.14	9.52	6.36	14.73	23.30	2.68
G18	6.80	4.68	28.43	128.9	4.04	150.46	9.67	9.44	5.73	18.24	31.32	2.30
G19	7.32	5.51	37.83	63.81	4.11	47.25	9.1	10	12.64	30.00	35.27	1.58
G20	7.02	4.49	22.93	59.91	4.06	95.38	7.33	7	7.54	12.94	23.53	1.63
G21	9.96	8.25	24.61	134.35	4.4	158.62	11.59	12.32	5.57	13.43	26.44	2.33
G22	7.45	5.35	32.05	61.99	4.07	143.47	8.45	9.39	7.49	16.07	25.54	2.15
G23	6.75	4.52	25.53	100.7	3.82	150.34	21.85	14.58	6.58	11.21	29.41	2.39
G24	7.25	5.17	43.04	90.99	4.11	89.3	8.61	8.46	5.48	46.13	38.68	1.95
G25	6.81	4.21	36.04	92.65	4.12	78.48	11.52	10.37	6.68	26.83	35.21	1.56
BT-2	4.11	2.75	45.85	91.92	3.94	67.24	9.66	15.66	8.44	70.316	88.30	3.41
BH-4	6.79	4.38	40.46	58.14	4.05	78.56	10.33	11.35	11.60	43.33	46.23	3.92
BH-5	5.25	3.32	44.81	50.27	4.12	72.54	9.50	11.5	9.21	38.64	45.17	1.93
BT-11	11.97	9.89	26.68	26.32	4.06	78.53	10.41	8	20.41	6.84	19.71	2.39
BT-14	5.95	4.78	41.37	54.9	4.15	105.62	7.23	3.1	13.26	11.83	50.37	1.29
G26	7.11	5.47	41.93	97.36	3.95	67.44	9.47	15.29	7.37	12.23	31.52	1.43
G27	6.85	4.55	23.92	40.08	4.24	119.5	10.67	11.51	8.22	9.43	30.61	1.38
BT-8	6.036	3.77	41.73	60.13	4.35	103.56	6.52	4.39	13.38	49.43	54.56	1.09
G28	6.47	3.99	32.37	55.14	3.91	125.56	13.44	8.57	10.42	22.84	21.38	1.36
G29	6.75	4.79	23.67	77.30	4.22	150.41	9.56	10	10.21	36.15	31.46	2.30
G30	5.53	3.44	42.19	77.74	4.05	61.48	7.48	13.41	5.64	70.24	39.22	2.88
G31	4.78	3.00	38.87	71.92	4.14	132.48	7.41	7.52	7.29	32.14	40.27	3.06
LK -1	5.92	3.77	44.37	74.71	4.14	70.53	7.44	8.34	12.1	47.24	32.25	1.37
G32	5.78	3.66	30.80	110.72	3.95	132.26	7.60	10.50	10.4	30.13	37.32	1.83
G33	6.49	4.33	30.94	84.62	4.03	118.45	9.51	8.38	7.55	17.61	30.88	1.74
G34	5.77	4.22	26.25	60.73	3.85	168.34	9.60	7.52	9.53	13.26	34.53	1.02
G35	7.03	5.15	29.18	126.72	4.05	150.63	3.48	6.47	11.15	35.24	41.59	1.30
BT- 3	8.3	6.11	45.47	51.81	3.95	113.46	9.61	3.64	10.18	44.84	46.52	1.78
BT-7	6.34	3.77	48.07	79.80	4.18	124.45	13.53	4.32	10.18	81.63	41.43	1.44
BT-9	6.76	5.55	52.04	46.30	4.23	75.63	9.32	11.50	9.35	47.83	31.73	1.07
BT-15	7.5	5.76	<b>56.26</b>	60.26	4.04	93.55	10.25	7.11	11.6	<b>87.93</b>	47.42	1.92
LJ-2	6.29	4.59	32.25	73.63	3.95	<b>9.56</b>	11.43	7.36	10.59	33.24	38.17	1.45
LJ-3	6.25	4.58	38.42	51.81	4.15	10.38	11.68	5.48	11.35	50.24	42.52	2.15
Mean	7.00	5.06	36.19	79.47	4.07	103.07	9.57	9.90	9.99	30.75	38.73	2.12
Max	12.23	10.11	56.26	150.51	4.4	186.22	21.85	17.42	20.41	87.93	134.24	4.59
Min	4.11	2.75	22.93	16.59	3.826	9.56	3.4	3.1	4.62	6.84	19.71	1.02
CV(%)	10.86	9.55	0.13	0.11	1.33	0.24	5.21	5.29	1.82	0.09	10.42	11.15

indicated large environmental influence on these characters. Characters like yield/plant and plant height showed low genotypic and phenotypic coefficient of variation indicated that the genotype has considerable variation for these traits. Moderate genotypic and phenotypic co-efficient of variation was

observed in % of protein, chlorophyll contain of the leaf, number of primary branches/plant, number of secondary branches/plant and width of fruit which indicated moderate variability were present among the genotype for these characters. % of ash, flower/cluster, length of fruit, pH of tomato juice and shelf life showed high genotypic and phenotypic co-efficient of variation indicated that the genotype were highly variable for this trait (Table 2). The phenotypic (PCV) and genotypic coefficient of variation (GCV) were high for % of ash (476.12%, 270.75%), pH of tomato juice (253.72%, 167.35%), flower/cluster (173.01%, 110.39%), and length of fruit (123.40%, 112.35%) which suggested existence of broad genetic base and would be amenable for further selection. The estimated of PCV were generally higher than the respective GCV for all the characters under study denoting environmental factors influencing their expression to some degree or other.

Fruit length, no. of seed/fruit, primary branches, secondary branches, self-life, individual fruit weight, width of fruit and yield per plant showed high heritability with high genetic advance and high genetic advance in percentage of mean revealed the possibility of predominance of additive gene effects and selection might be effective. The protein content showed low heritability with low genetic advance which indicated that the character is highly influenced by environmental effects and selection would not be effective. Low heritability accompanied with high genetic advance found in % of vit. C revealed that the character is governed by additive gene effects. The low heritability is being exhibited due to high environmental effects. Selection may be effective such cases.

**Table 4. Estimation of genetic parameters of 48 tomato germplasm**

Characters	GV	PV	PCV	GCV	h <sup>2</sup> b (%)	GA	GAPM
% of Ash	3.03	9.37	476.12	270.75	0.32	203.91	317.17
% of protein	0.06	0.20	27.16	14.07	0.27	25.02	15.01
% of Vit - C	4.87	106.24	84.18	18.01	0.05	97.23	7.94
% of Brix	0.23	0.76	17.69	10.14	0.32	57.26	11.98
Chlorophyll (%)	42.16	82.22	16.29	11.66	0.51	957.72	17.20
Flower per cluster(no.)	59.69	146.63	173.00	110.39	0.40	1015.55	145.09
Fruit per cluster (no.)	11.56	21.74	92.07	67.14	0.53	510.74	100.86
Length of fruit (mm)	1653.29	1994.52	123.40	112.35	0.83	7625.99	210.76
Seed per fruit (no.)	727.98	950.63	38.79	33.95	0.77	4863.86	61.20
pH of tomato juice	46.4	106.65	253.72	167.35	0.43	925.56	227.39
Plant height (cm)	1.7	11.79	3.33	1.26	0.14	101.99	0.99
Primary branches per plant (no.)	78.91	96.04	57.94	52.52	0.82	1658.72	98.07
Secondary branches per plant (no.)	9.84	11.08	18.80	17.72	0.89	608.97	34.40
Shelf life of tomato (ambient tem.)	338.68	426.53	206.54	184.05	0.79	3378.15	337.85
Individual weight of fruit(g)	358.05	448.58	68.88	61.54	0.79	3482.5	113.26
Width of fruit (mm)	377.43	470.64	56.00	50.18	0.80	3583.9	92.52
Yield per plant (g)	396.80	492.69	1.047	0.96	0.80	3682.57	1.74

Variability is one of the most important hallmark for any breeding program. The further progress of any breeding program depends on the amount and nature of variability (Kumar *et al.*, 2013). GCV values lower than the corresponding PCV values indicated that the traits reacted with the environment. On the other hand, low or very low differences between PCV and GCV values of the traits implies that less environmental effects of those traits (Aker *et al.*, 2020). The results of PCV and GCV in the present study are partially accordance with Ara *et al.* (2009); Khan *et al.* (2012); Kumar *et al.* (2013), Rahman *et al.* (2015) and Tripathy and Mallikarjunarao (2020).

High heritability coupled with high genetic advance were found for length of fruit, seed per fruit, primary branches per plant, secondary branches per plant, shelf life of tomato, individual weight of fruit, width of fruit, and yield per plant. This is due to the additive gene effect and the selection contingent on phenotypic make up could be achieved by pure line or mass selection or bulk or single seed descent method following hybridization and selection in early generation (Reddy *et al.*, 2013).

## CONCLUSION

Fruit length, no. of seed per fruit, primary branches, secondary branches, shelf-life, individual fruit weight, width of fruit and yield per plant showed high heritability with high genetic advance and high genetic advance in percentage of mean which revealed the possibility of predominance of additive gene effects and selection might be effective. The protein content showed low heritability with low genetic advance which indicated that the character is highly influenced by environmental effects and selection would be effective. Low heritability accompanied with high genetic advance found in % of vit. C revealed that the character is governed by non-additive gene effects.

**Acknowledgement:** The work was supported by Sher-e-Bangla Agricultural University Research System (SAURES).

## REFERENCES

- Ara, A., Narayan, R., Ahmed, N., and Khan, S.H. 2009. Genetic variability and selection parameters for yield and quality attributes in tomato. *Indian J. Hort.*, 66(1): 73-78.
- Burton, G.W. 1952. Quantitative inheritance in grasses. Pro. VI Int. Grassl. Cong., 1952: 277-283.
- Comstock, R.E. and Robinson, H.F. 1952. Estimation of average dominance of genes. *Heterosis*. 2: 494-516.
- Deshmukh, S.N., Basu, M.S. and Reddy, P.S. 1986. Genetic variability, character association and path coefficient of quantitative traits in Virginia bunch varieties of groundnut. *Indian J. Agric. Sci.*, 56: 816-821.
- Ghosh, S.K. and Gulati, S.C. 2001. Genetic variability and association of yield components in Indian mustard (*Brassica juncea* L.). *Crop Res. Hisar.*, 21: 345-349.
- Hanson, C.H., Robinson, H.F. and Comstock, R.E. 1956. Biometrical studies of yield in segregating populations of Korean lespedeza 1. *J. Agron.*, 48(6): 268-272.
- Hasan, N., Choudhry, S. and Laskar, R.A. 2020. Studies on qualitative and quantitative characters of mutagenised chili populations induced through MMS and EMS. *Vegetos*. 33(4): 793-799.
- Hayman, B.I. 1954. The theory and analysis of diallel crosses. *Genetics.*, 39: 789-809.
- Hossain, A.Y., Harun, U.R.M., Parveen, S., Rahman, M.S., Akter, R. and Rahim, M.A. 2016. Evaluation of Breeding Potential of Tomato Germplasm using D<sup>2</sup> analysis. *Adv. Biores.*, 7(4): 217-222.
- Jain, S.K. and Allard, R.W. 1960. Population studies in predominantly self-pollinated species, I. Evidence for heterozygote advantage in a closed population of barley. *PNAS U.S.A.*, 46(10): 1371.
- Johnson, H.W., Robinson, H.F. and Comstock, R.E. 1955. Estimates of genetic and environmental variability in soybeans. *J. Agron.*, 47(7): 314-318.
- Khan, S. and Mahmud, F. 2021. Genetic Variability and Character Association of Yield Components in Maize (*Zea mays* L.). *Am. J. Plant Sci.*, 12(11): 1691-1704.
- Kumar, D., Kumar, R., Kumar, S., Bhardwaj, M.L., Thakur, M.C. and Kumar, R. 2013. Genetic variability, correlation and path coefficient analysis in tomato. *Intl. J. Veg. Sci.*, 19:313-323.
- Meena, O.P. and Bahadur, V. 2015. Genetic association analysis for fruit yield and its contributing traits of indeterminate tomato (*Solanum lycopersicum* L.) germplasm under open field condition. *J. Agric. Sci.*, 7(3): 148-163.
- Rahman, M.S., Parveen, S., Rashid, M.H.U., Akter, R., Hossain, A.Y. and Robbani, M.G. 2015. Correlation and path coefficient analysis of tomato germplasms. *Intl. J. App. Sci., Biotech.* 3(2): 223-226.
- Reddy, B.R., Reddy, D.S., Reddaiah, K. and Sunil, N. 2013. Studies on genetic variability, heritability and genetic advance for yield and quality traits in Tomato (*Solanum lycopersicum* L.). *Int. J. Curr. Microbiol. App. Sci.*, 2(9): 238-244.

- Saleem, M.Y., Iqbal, Q. and Asghar, M. 2013. Genetic variability, heritability, character association and path analysis in F<sub>1</sub> hybrids of tomato. *Pak. J. Agric. Sci.*, 50(4): 649–653.
- Singh R.K.C.B. 1985. Biometrical method in quantitative genetic analysis. Kalyani Publishers, Ludhiana, New Delhi, 54-57 pp.
- Tripathy, B. and Mallikarjunarao, K. 2020. Variability in tomato (*Solanum lycopersicum* L.): A review. *J. Pharmacog. Phytochem.*, 9(4): 383-388.
- Tuncturk, M. and Ciftci, V. 2007. Relationships between yield and some yield components in rapeseed (*Brassica napus* spp. *Oleifera* L.) cultivars by using correlation and path analysis. *Pak. J. Bot.*, 39(1): 81–84.
- Yadeta, D., Chandra, S.S. and Weyessa, B. 2020. Genetic variability and association of characters in linseed (*Linum usitatissimum* L.) plant grown in central Ethiopia region. *Saudi J. Biol. Sci.*, 27(8): 2192–2206.