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Genetic variability studies of fruit yield and its traits among indeterminate tomato genotypes under open field condition

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The present study was aimed to investigate the yield and its contributing traits among indeterminate tomato genotypes in order to generate information regarding the extent of genetic variability, heritability and genetic advance. The experiment was conducted using a randomized complete block design with three replications at Vegetable Research Farm, Department of Horticulture, SHIATS, Allahabad during 2012-2013 cropping season. The analysis of variance revealed highly significant differences among all genotypes for the characters. Analysis of coefficient of variation revealed that the magnitude of phenotypic coefficient of variation was higher than genotypic coefficient of variation for all traits under study. The leaf curl incidence (39.73 and 39.74) and ascorbic acid (27.62 and 27.67) recorded high genotypic and phenotypic coefficients of variation, indicating higher magnitude of variability for these characters, thus the scope for improvement of these characters through simple selection would be better. The estimates of heritability were high for all the traits and ranged from 95 to 100 percent, suggested that selection based on phenotypic expression could be relied upon as there is major role of genetic constitution in the expression of these characters. High heritability accompanied with high genetic advance were noted for fruit yield per plant (1129.78), plant height (43.37), number of flowers per plant (40.35), number of leaves per plant (25.48) and ascorbic acid (21.68) indicating that these characters are under additive gene effects and that these traits could be considered as reliable indices for selection and higher responses of this trait could be expected from selection.

Key words: Genetic variability, heritability, genetic advance, *Solanum lycopersicum* L., yield, yield traits.

INTRODUCTION

Tomato (*Solanum lycopersicum* L.) occupies the prime position among different vegetables and is an important vegetable cultivated in India (Shankarappa et al., 2008; Narolia et al., 2012). It is a very versatile vegetable for

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culinary purposes (Kumar et al., 2014). Ripe fresh fruits are consumed as salads, in cooked form as stew and utilized in the preparation of various forms of processed products such as juice, paste, powder, ketchup, sauce and canned whole fruits (Grandillo et al., 1999). Unripe green fruits are used for preparation of pickles and chutney (Adebooye et al., 2006; Osekita and Ademiluyi, 2014). All the species of tomato are native to Western South America (Rick, 1976). Tomatoes are the main source of lycopene (an antioxidant), ascorbic acid and ß-carotene and also are valued for its colour and flavor (Krumbein et al., 2006). Lycopene is the principle carotenoid, causing the characteristic red hue of tomatoes (Shi and Le-Maguer, 2000) used in treating various chronic human diseases like cancer, cardiovascular diseases, osteoporosis and diabetes (Bai and Lindhot, 2007). Tomato is an important cash-generating crop for small scale farmers and also provides employment opportunities in production and processing industries. Considering the importance of tomato as one of the potential vegetable crop for domestic consumption as well as export markets, it is important to increase its productivity along with desirable attributes through genetic manipulation.

For improving yield potential of tomato, there is a need of systemic breeding approach. Systematic study and evaluation of tomato genotypes is of great importance for current and future agronomic and genetic improvement of this crop. Furthermore, if an improvement program is to be carried out, evaluation of genotypes is imperative, in order to understand the genetic background and the breeding value of the available genotypes (Agong et al., 2000). In any crop-improvement programme the success of selection as a breeding method is determined by the magnitude of genetic variability for yield and yield components (Dudley and Moll, 1969). The genetic variance of any quantitative trait is composed of additive variance (heritable) and non-additive variance and include dominance and epitasis (non-allelic interaction).

Therefore, it becomes necessary to partition the observed phenotypic variability into its heritable and non-heritable components with suitable parameters such as phenotypic and genotypic coefficient of variation, heritability and genetic advance. In genetic studies, characters with high genotypic coefficient of variation indicate the potential for an effective selection (Sadiq et al., 1986). Determining the components of variability in yield and its components enable us to know the extent of environmental influence on yield, taking into consideration of the fact that yield and its component are quantitative characters that are affected by the environment (Ahmed et al., 2007). Heritability provides an idea of the extent of genetic control for expression of a particular character and the reliability of phenotype in predicting its breeding value and the extent of which a particular genetic character can be transmitted to the successive generations (Mangi et al., 2010). High heritability indicates less environmental influence in the observed variation (Songsri et al., 2008). Heritability value alone cannot provide information on amount of genetic progress that would result from selection of best individuals.

Johnson et al. (1955) reported that heritability estimates along with genetic advance would be more successful in predicting the effectiveness of selecting the best individuals. Genetic advance which estimates the degree of gain in a trait obtained under a given selection pressure is an important parameter that guides the breeder in choosing a selection programme (Hamdi et al., 2003). High heritability and high genetic advance for a given trait indicates that it is governed by additive gene action and, therefore, provides the most effective condition for selection (Nwosu et al., 2014). So, proper evaluation of genetic resources is essential to understand and estimate the genetic variability and heritability. Studies on genetic parameters provide information about the expected response of various characters to selection and it will help in developing optimum breeding procedure. Keeping in view of this, an attempt was made to know the nature and magnitude of genetic variability existing for yield and its contributing traits in the available genotypes of indeterminate tomato.

MATERIALS AND METHODS

Genotype collection and seedling establishment

The experimental materials comprised of nineteen indigenous genotypes of indeterminate growth tomato collected from Indian Institute of Vegetable Research (IIVR), Varanasi and Vegetable Research Station (VRS), Junagadh Agricultural University, Junagadh, Gujarat, India (Table 1). For raising good and healthy seedlings, the seeds were treated with carbendazim using 2.0 g/kg of seed. Afterwards, the seeds of nineteen genotypes of tomato were sown in lines 10 cm apart on the nursery beds.

Establishment of tomato genotypes in field

The present investigation was conducted at Vegetable Research Farm, Department of Horticulture, SHIATS, Allahabad, India during 2012-2013 cropping season. Allahabad is situated at an elevation of 98 m above sea level at 25° 28' N latitude and 81° 54' E longitude. This region has a sub-tropical climate prevailing in the south-eastern part of the state Uttar Pradesh with extremes temperatures, the winter and the summer. During winter, frosts and during summer, hot scorching winds are also not uncommon. The average rainfall is around 1027 mm (40.4 inches) with maximum concentration from July to September. The mean monthly agro-meteorological observations were recorded during the crop season (Figure 1).

The experiment was laid out in a randomized complete block design (RCBD) with three replications. Thirty-days-old seedlings of all genotypes were transplanted in small plots (2.0 m × 2.0 m) in open-field where row-to-row and plant-to-plant spacing was 60 cm × 60 cm that contained 9 plants. All the recommended agronomic package of practices were followed (like staking, earthing up, pruning and training, irrigation, weeding, fertilizers applications), as recommended for commercial tomato production.

Table 1. Lists of genotypes used for the study.

S/N	Name of genotype	Source	S/N	Name of genotype	Source
1.	2011/TOINDVAR-1	IIVR, Varanasi	11.	EC 620430	IIVR, Varanasi
2.	2011/TOINDVAR-2	IIVR, Varanasi	12.	EC 620432	IIVR, Varanasi
3.	2011/TOINDVAR-3	IIVR, Varanasi	13.	EC 620434	IIVR, Varanasi
4.	2011/TOINDVAR-4	IIVR, Varanasi	14.	EC 620437	IIVR, Varanasi
5.	2011/TOINDVAR-5	IIVR, Varanasi	15.	EC 620449	IIVR, Varanasi
6.	2012/TOINDVAR-1	IIVR, Varanasi	16.	AJETA-32	IIVR, Varanasi
7.	2012/TOINDVAR-2	IIVR, Varanasi	17.	ARKA VIKAS	IIVR, Varanasi
8.	2012/TOINDVAR-3	IIVR, Varanasi	18.	ANGOOR LATA	IIVR, Varanasi
9.	2012/TOINDVAR-4	IIVR, Varanasi	19.	2012/GT-1	VRS, JAU, Junagadh
10.	EC 620421	IIVR, Varanasi			

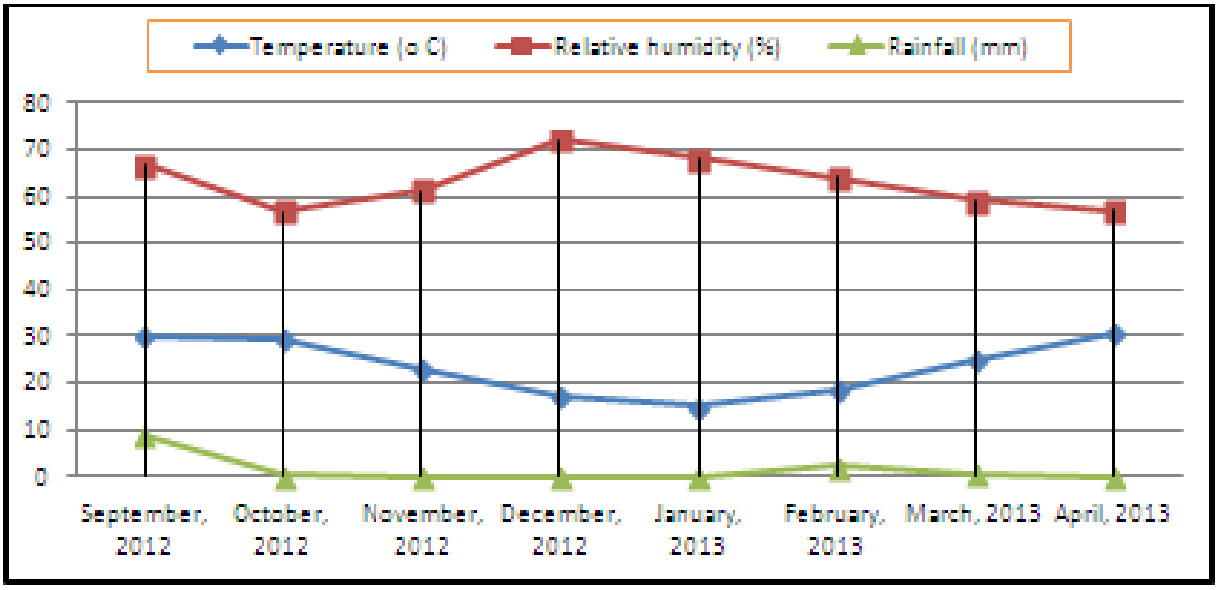

Figure 1. Mean monthly agro-meteorological observations recorded during crop season 2012-2013.

Recording of observations and biochemical analysis

The observations were recorded on a randomly selected five plants from each replication for morphological and biochemical characters viz., (1) plant height (cm), (2) number of branches per plant, (3) number of leaves per plant, (4) days to flowering, (5) number of flower clusters per plant, (6) number of flowers per plant, (7) number of fruits per plant, (8) fruit set percentage, (9) fruit weight (g), (10) radial diameter of fruit (mm), (11) polar diameter of fruit (mm), (12) fruit yield per plant (g), (13) leaf curl incidence percentage (based on the scale given by Joshi and Choudhary (1981), (14) TSS °Brix and (15) ascorbic acid (mg/100 g).

Total soluble solids (TSS) (◦brix)

The total soluble solids of the selected samples were determined with a hand refractometer, Model ATAGO, Tokyo, Japan (0-32° Brix range). The refractometer was washed with distilled water each time after use and dried with blotting paper to avoid contamination.

Ascorbic acid (mg/100 g)

Ascorbic acid was estimated by 2,6-dichlorophenol indophenol method (AOAC, 1975). A two milliliter juice sample was added to an equal volume of 6% metaphosphoric acid in a conical flask and titrated with standard dye solution. The end point was indicated by the appearance of pink colour, which persisted for about 15 s. The dye was standardized with standard stock solution (1 mg/1 ml) of ascorbic acid. The results were expressed as milligrams ascorbic acid/100 g of tomato juice and calculated as follows:

$$\text{Ascorbic acid} = \left[\frac{Y}{X}\right] \times 100$$

Where *Y* is the volume of dye used (ml) in titrating 2 ml juice and *X* the volume of dye used (ml) in titrating 2 ml standard stock solution.

Table 2. Analysis of variance for 15 characters of indeterminate tomato genotypes.

Source of variance	df	Plant height	No. of branches / plant	No. of leaves/ plant	Days to flowering	Flower clusters/ plant	No. of flowers/ plant	No. of fruits/ plant	Fruit set (%)	Average fruit weight	Radial diameter of fruit	Polar diameter of fruit	Fruit yield/ plant	Leaf curl incidence (%)	TSS ° brix	Ascorbic acid
Replication	2	1.69	0.16	0.34	0.006	0.04	0.37	0.08	0.07	1.43	0.42	0.23	5206.96	0.004	0.01	0.17
Treatment	18	1331.66**	11.65**	461.38**	153.96**	24.02**	1159.45**	228.04**	129.30**	225.66**	172.18**	70.06**	912915.31**	257.55**	1.33**	333.75**
Error	36	0.46	0.20	0.60	0.31	0.06	2.06	0.28	0.56	0.36	0.12	0.39	2657.22	0.02	0.01	0.39

** Significant at 0.01%.

Statistical analysis

Analysis of variance was carried out by the method suggested by Panse and Sukhatme (1985). The genotypic and phenotypic coefficients of variation were calculated using the formula of Burton and De Vane (1953). Heritability and genetic advance were calculated according to Allard (1960) and genetic advance as percent of mean was estimated using the method of Johnson et al. (1955).

RESULTS AND DISCUSSION

Analysis of variance

The result on analysis of variances (ANOVA) using randomized complete block design revealed that the genotypes exhibited highly significant differences for all the characters studied (Table 2). Fruit yield per plant (912915.31), plant height (1331.66), number of flowers per plant (1159.45), number of leaves per plant (461.38) and ascorbic acid (333.75) were some of the traits which showed highly significant variation. The significant variation among the genotypes revealed that presence of adequate variability which can be exploited through selection. This is in agreement with the findings of Singh et al. (2006), Dar et al. (2012), Singh et al. (2014), Pandey et al. (2015) and Senapati and Kumar (2015).

Estimation of range and mean

There were high differences observed between the least and highest mean values for all characters studied (Table 3). A wide range of variation was observed for fruit yield per plant (2186.71-4356.49), followed by plant height (120.82-207.27), number of flowers per plant (87.67-153.60), number of leaves per plant (186.83-234.90), radial diameter of fruit (34.72-72.37), and leaf curl incidence percentage (11.39-46.76) indicating their maximum contribution to the total variability observed among the tomato genotypes. This showed the possibility to improve the various desirable traits through direct selection as short term strategy. The wide range of variation obtained may be due to divergent genotypes included in the study. Similar finding were also reported by Haydar et al. (2007), Mehta and Asati (2008) and Kaushik et al. (2011) for fruit yield per plant; Patil et al. (2013) for plant height, yield per plant and fruit diameter.

Estimation of phenotypic and genotypic variability

In the present study, maximum genotypic and phenotypic variance (σ^2_g and σ^2_p), respectively were recorded for fruit yield per plant (303419.38 and 306076.59), plant height (443.74 and 444.20), number of flowers per plant (385.79 and 387.86), number of leaves per plant (153.60 and 154.20), ascorbic acid (111.12 and 111.51), leaf curl incidence (85.84 and 85.87), number of fruits per plant (75.92 and 76.20), fruit weight (75.10 and 75.47) whereas the minimum for TSS (0.44 and 0.46). High genotypic variance indicating more contribution of genetic component for the total variation. Therefore, these characters could be considered and exploited for selection purpose, whereas, high phenotypic variance indicating the strong influence of environmental factors during the growth period for their expression. These results are in accordance of the results obtained by Haydar et al. (2007), Shashikanth et al. (2010) and Mohamed et al. (2012) in tomato.

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 genetic stock. In general, the phenotypic coefficient of variations were slightly higher than the corresponding genotypic coefficient of variations for all the traits studied (Table 3 and Figure 2), which indicated that the apparent variation is not only due to genotypes

Table 3. Range, mean, variance, coefficient of variations, heritability, genetic advance and genetic advance as percent of mean for 15 characters of indeterminate tomato genotypes.

Characters	Range		Mean	GV ($\sigma^2 g$)	PV ($\sigma^2 p$)	CV		h^2 (bs) (%)	GA	GA as % of mean
	Min.	Max.				GCV (%)	PCV (%)		5%	5%
Plant height	120.82	207.27	146.30	443.74	444.20	14.40	14.41	100	43.37	29.64
No. of branches/plant	15.20	22.93	18.37	3.82	4.02	10.64	10.91	95	3.92	21.35
No. of leaves/plant	186.83	234.90	199.16	153.60	154.20	6.22	6.23	100	25.48	12.79
Days to flowering	47.27	73.00	58.53	51.22	51.53	12.23	12.27	99	14.70	25.11
No. of flower clusters/plant	17.53	27.20	22.08	7.99	8.05	12.80	12.85	99	5.80	26.26
No. of flowers/plant	87.67	153.60	125.34	385.79	387.86	15.67	15.71	99	40.35	32.20
Average no. of fruits/plant	41.13	76.23	56.58	75.92	76.20	15.40	15.43	100	17.92	31.67
Fruit set (%)	37.17	61.71	45.53	42.91	43.48	14.39	14.48	99	13.41	29.44
Average fruit weight	34.60	69.67	53.61	75.10	75.47	16.17	16.21	100	17.81	33.22
Radial diameter of fruit	34.72	72.37	53.91	57.35	57.48	14.05	14.06	100	15.58	28.91
Polar diameter of fruit	38.97	54.25	47.75	23.22	23.62	10.09	10.18	98	9.84	20.62
Fruit yield/plant	2186.71	4356.49	3000.71	303419.38	306076.59	18.36	18.44	99	1129.78	37.65
Leaf curl incidence (%)	11.39	46.76	23.32	85.84	85.87	39.73	39.74	100	19.08	81.83
TSS ° brix	2.87	5.60	4.52	0.44	0.46	14.69	14.93	97	1.35	29.77
Ascorbic acid	19.25	51.79	38.16	111.12	111.51	27.62	27.67	100	21.68	56.80

but also due to the influence of environment in the expression of the traits. Similar finding were also reported by Kaushik et al. (2011), Islam et al. (2012), Patil et al. (2013), Saleem et al. (2013) and Senapati and Kumar (2015). In present study, the difference between values of PCV and GCV were less for all traits except number of branches and total soluble solid (TSS). It means that these traits were less influenced by environment and hence, they could be improved by following different phenotypic selections like directional, disruptive and stabilized selections. The leaf curl incidence (39.73 and 39.74) and ascorbic acid (27.62 and 27.67) recorded high genotypic and phenotypic coefficients of variation, indicating higher magnitude of variability for these characters. Similar findings were also reported by Narolia et al. (2012) and for ascorbic acid. The moderate amount of GCV and PCV, respectively were recorded for fruit yield per plant (18.36 and 18.44), fruit weight (16.17 and 16.21), number of flowers per plant (15.67 and 15.71), number of fruits per plant (15.40 and 15.43), TSS (14.69 and 14.93), plant height (14.40 and 14.41), fruit set percentage (14.39 and 14.48), radial diameter of fruit (14.05 and 14.06), number of flower clusters per plant (12.80 and 12.85), days to flowering (12.23 and 12.27), number of branches per plant (10.64 and 10.91) and polar diameter of fruit (10.09 and 10.18). Moderate rate of GCV and PCV are indication of ample scope for improvement through selection. These results corroborate with the findings of earlier researchers for average fruit weight, TSS, plant height (Ara et al., 2009); fruit diameter (Singh, 2009; Kumar et al., 2013); plant height, fruits per plant, fruit weight (Kumar, 2010); fruit yield per plant, fruit diameter (Tasisa et al., 2011).

Estimates of broad sense heritability and genetic advance

Genotypic coefficients of variation do not estimate the variations that are heritable (Falconer, 1960), and estimation of heritability becomes necessary. Genotypic coefficient of variation represents the total genetic variation whereas heritability measures the proportion to which the variability of a character is transmitted to offspring (Lush, 1949). Burton and De Vane (1953) suggested that genetic coefficients of variability, along with heritability estimates, would provide a reliable indication of expected degree of improvement through selection.

Heritability in broad sense is a parameter of tremendous significance to the breeders as its magnitude indicates the reliability with which a genotype can be recognized by its phenotypic

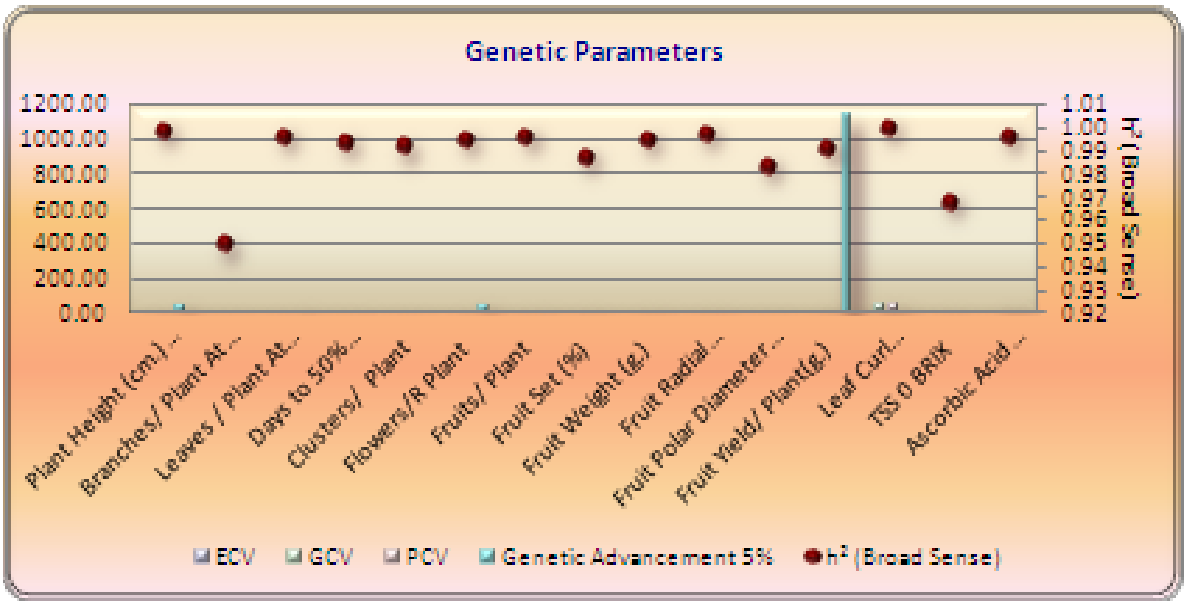

Figure 2. Range, mean, variance, coefficient of variations, heritability, genetic advance and genetic advance as percent of mean for fifteen characters of indeterminate tomato genotypes.

expression. The estimates of heritability were high for all the traits and ranged from 95 to 100 percent, suggested that selection based on phenotypic expression could be relied upon as there is major role of genetic constitution in the expression of these characters. The heritability estimates worked out in the present investigation are in consonance with earlier reports by Haydar et al. (2007) and Mohamed et al. (2012) for plant height, fruit weight, number of branches per plant and days to flowering in different genotypes of tomato; Kumar (2010) for days to flowering, polar diameter, TSS, plant height, fruits per plant, average fruit weight, yield per plant; Saleem et al. (2013) for plant height, fruit yield per plant, number of fruits per plant; Kumar et al. (2006) for fruit weight for all characters studied; Singh et al. (2006) for number of fruits per plant; Saeed et al. (2007) for number of fruits per plant and number of flowers per plant; Mehta and Asati (2008) also found high heritability in broad sense for plant height and TSS; Singh (2009), Kumar et al. (2013) for plant height, number of fruits per plant, fruit diameter, fruit weight, fruit yield per plant; Islam et al. (2012) for fruit weight, days to flowering and number of fruits per plant; Osekita and Ademiluyi (2014) also found high heritability in broad sense for days to flowering and plant height.

The estimate of genetic advance showed a wide range from 1.35 for TSS °B to 1129.78 for fruit yield per plant. Generally, genetic advance as percent of mean (GAM) at 5% selection intensity was high (>20%) for all characters studied except number of leaves per plant. The highest GAM was recorded for leaf curl incidence percentage (81.83), ascorbic acid (56.80), fruit yield per plant (37.65), average fruit weight (33.22), number of flowers per plant (32.20), number of fruits per plant (31.67), showed that these characters are governed by additive genes and selection will be rewarding improvement of such traits. This is in confirmation with the findings of Shashikanth et al. (2010) who reported high GAM for fruits per plant and fruit yield per plant; Islam et al. (2012) for fruit weight and number of fruits per plant; Kumar et al. (2013) for number of fruits per plant, fruit weight, yield per plant.

Heritability coupled with genetic advance is more effective and reliable in predicting the results and the effect of selection (Dudley and Moll, 1969). High heritability accompanied with high genetic advance were noted for fruit yield per plant (1129.78), plant height (43.37), number of flowers per plant (40.35), number of leaves per plant (25.48) and ascorbic acid (21.68) indicating that these characters are under additive gene effects and that these traits could be considered as reliable indices for selection and higher responses of this trait could be expected from selection. This result is in agreement with the findings of Patil et al. (2013) for fruit yield per plant. High heritability with low genetic advance was observed for TSS (1.35), number of branches per plant (3.92) and number of flower clusters per plant (5.80). Since, these characters are governed by non-additive gene action hybridization followed by selection may be used for improvement (Liang and Walter, 1968; Ara et al., 2009).

Similar results were also reported by Singh et al. (2006) for number of branches per plant and TSS. Johnson et al. (1955) has suggested that traits with high heritability coupled with high genetic advance would respond to selection better than those with high heritability and low genetic advance. High heritability and genetic advance as per cent for the trait suggested the possibility of selecting

high yielding cultivars from the present collection (Singh, 2009). The high heritability was associated with high genetic advance as per cent of mean for all the yield contributing characters except number of leaves per plant. The parallelism between the magnitude of heritability and degree of genetic gain has been due to the additive gene playing a predominant role and therefore, these were more reliable for effective selection. Similar finding were also reported by Singh (2009) for number of fruits per plant, fruit weight, plant height and fruit diameter.

Heritability, genetic advance as percent of mean and genotypic coefficient of variation together could provide the best image of the amount of advance to be expected from selection (Johnson et al., 1955). The characters *viz.*, leaf curl incidence percentage and ascorbic acid with high genotypic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance as percent of mean. Similar results were noticed by Singh et al. (2006) for ascorbic acid. Therefore, this observation indicated that these characters are under additive gene effects and more reliable for effective selection.

Conflict of Interest

The authors have not declared any conflict of interest.

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