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Pradipta Dutta
Department of Vegetable Crops, BCKV, Mohanpur, Nadia West Bengal, India

Sourav Hazari
Department of Genetics and Plant Breeding, BCKV, Mohanpur, Nadia, Nadia West Bengal, India

Chandan Karak
Department of Vegetable Crops, BCKV, Mohanpur, Nadia West Bengal, India

Sohini Talukdar
Department of Genetics and Plant Breeding, BCKV, Mohanpur, Nadia, Nadia West Bengal, India

Correspondence
Pradipta Dutta
Department of Vegetable Crops, BCKV, Mohanpur, Nadia West Bengal, India

Study on genetic variability of different tomato (*Solanum lycopersicum*) cultivars grown under open field condition

Pradipta Dutta, Sourav Hazari, Chandan Karak and Sohini Talukdar

Abstract
The present investigation was carried out at the Central Research Farm, Gayeshpur, Bidhan Chandra Krishi Viswavidyalaya (BCKV) during 2017-18 period. The 53 genotypes were grown in RBD with 3 replications, in each replication there were 20 plants. Very high variance (Mean sum of squares for genotype) was recorded for some characters viz., fruit weight (1259.37), fruit number per plant (1124.65), plant height (551.28) and flower cluster per plant (192.55) indicated very wide range for these characters concerned. This investigation provides that high range of heritability occurs in plant height, primary branches/ plant, fruits per plant, flower cluster per plant, fruit weight, polar diameter of fruit, equatorial diameter of fruit, pericarp thickness, ascorbic acid content and ß carotene content of fruit. Thereby, suggesting that study on the genetic diversity of the wide range of genotypes for the selection of promising parental lines.

Keywords: tomato, GCV, PCV, heritability, genetic advance

Introduction
Solanaceous crop tomato is one of the most widely grown vegetable in India. The origin of this crop is tropical America and grown as autumn-winter, winter and spring-summer crop in our country but due to high temperature and rains, tomato cannot be grown commercially in the North West Indian plains from July to October. At present, in terms of area as well as total vegetable production, Uttar Pradesh is the leading state in the country.
Bihar, Karnataka, Orissa, Maharashtra, Himachal Pradesh, West Bengal and Gujarat are major tomato growing states. Export quality tomato production is mainly confined at Pune, Nasik and Bangalore region. It is a day neutral and self-pollinated crop, but sometimes cross pollination can be occurred.
The crop can resist heat, drought and can tolerate wide range of soil and climatic condition. Optimum temperature for tomato cultivation is 20-24°C. Night temperature is more important for better fruit set in tomato. Optimum night temperature for fruit set is 15-20°C (Thamburaj and Singh, 2004) [16].
The scope of crop improvement depends upon the genetic diversity of the initial plant material. Variability may be occurred due to genetic and environmental causes. The most important aspect of genetic constitution is the heretible variability and more particularly its genetic component, which has a close bearing on its response to selection.
Information generated from the studies of character association serve as the most important indicator (plant character) that ought to be considered in the selection programme. Such studies would also help us to know the suitability of multiple characters for indirect selection because selection for one or more traits results in correlated response in several other traits (Searle, 1965) [12].

Materials and Methods
The experimental material consisting of 53 genotypes of tomato (Berika, BCT-17 RHR 33-2, Ruby BCT-7, H-88, BCT-46 (Path Local), NR-MUTANT, Silet-2, BCT-21 NOT-7, BCT-111RIN, BCT-36 COMLCR-6, CLN-213-111, OGC, BCT-27-1, CLN-2116-3, Hp, CLN-2116-B, NIMPTH(Non-pigmented), BCT-18 RIIR-872, BCT-14(Arka Abha), B-Mut-3, CIDII-1, BCT-37 COMLCR-14, P-Mut-5, Non Mutant-1, EC-241148, BCT 51 Agata, CLN-2001-A-4, BCT-15(H-24), CLN-2116-5, Path, CLN-2001 AR, BCT-48, P-Mut-11,

CLN-21141-1, TTL-2, BCT-59, CLN-2026-D, CLN-2001A-8, ALISHA/CR, CLN-2016-4, COMALCR-8, ACAL-1, Coochbehar local, CLN-2114-1, BCT, 115-DG, BCT-28IC 229060, BCT-25- EC-24148, S. *pimpinellifolium*, BCT-107, LC514013, BCT-20(PART T3), S. cheesmanii, CLN-2016-R) were evaluated at Central Research Farm, Gayeshpur, Bidhan Chandra Krishi Viswavidyalaya during 2017-18 period. The genotypes were grown in RBD with 3 replications, in each replication there were 20 plants. The spacing was 60 X 60 cm to study different morphological characters. To record the data on different characters five random plants per replication in each genotype were selected. The ANOVA was calculated as per Panse and Sukhatme (1967) [10]. The genotypic (GCV) and phenotypic (PCV) coefficients of variations were calculated as per Burton (1952) [2] and De Vane (1953) [3]. The estimated genetic advance was estimated according to Johnson *et al*. (1955) [6].

Results and Discussion

Measures of variation

Variation can arise from both genotypic (i.e. real heritable difference) and environmental (non-heritable) factors. All the biometrical calculations related to genetic variability were based on the data of all the 17 characters recorded through evaluation of 53 genotypes.

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 even at 1% level of significance (Table 1) 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 Singh *et al.* (2006) [14], Haydar *et al.* (2007) [4] and Meena *et al.* (2015) [9].Very high variance (mean sum of squares for genotype) was recorded for some characters viz., fruit weight (1259.37), fruit number per plant (1124.65), plant height (551.28) and flower cluster per plant (192.55) indicated very wide range for these character concerned.

Table 1: Analysis of variance for different characters of tomato

Character	Mean sum of squares		
	Genotypes	Replication	Error
Plant height(cm)	551.28**	6.64	9.45
Primary branches /Plant	41.23**	2.99	2.76
Days to 1st flowering	18.68**	0.748	4.12
Flower cluster/Plant	192.55**	7.25	11.56
Flower/Cluster	3.762**	0.47	0.51
Fruits / plant	1124.65**	132.56	28.36
Fruit weight (g)	1259.37**	105.24	79.25
Equatorial diameter (cm)	2.33**	0.21	0.15
Polar diameter (cm)	3.05**	0.018	0.20
Pericarp thickness(mm)	8.98**	0.27	0.11
TSS	0.94**	0.072	0.017
Total sugar content	0.31**	0.031	0.007
Reducing sugar	0.54**	0.087	0.007
Titrable acidity	0.29**	0.021	0.003
Ascorbic acid	48.54**	0.228	0.27
Lycopene	1.74**	0.189	0.047
Beta carotene	0.78	0.358	0.39
DF	53	2	106

Test the significance

*significant at 5%, **significant at 1%, DF- Degree of freedom.

Table 2: Genetic variability parameters for fruit yield, yield components and fruit quality characters of tomato

Characters	Mean	Coefficient of variation(C.V.)	Phenotypic Coefficient of variation (PCV)	Genotypic Coefficient of variation (GCV)	Heritability in broad sense%(H)	Genetic Advance (GA) at 5%	Genetic Advance (GA)% of Mean (5%)
PH	84.35	5.68	186.96	184.39	97.81	31.25	42.98
PBP	8.56	14.52	133.56	145.29	58.69	7.42	68.25
DFF	29.58	5.08	75.12	34.51	49.58	5.91	12.48
FCP	15.26	14.25	145.29	134.75	71.26	11.49	125.73
FC	7.15	15.47	75.18	50.28	74.42	2.67	28.49
NFP	62.77	8.570	267.23	164.24	92.55	31.94	67.48
AFW	81.45	13.35	230.27	207.32	64.91	30.02	41.97
EDF	3.99	8.98	43.82	35.72	78.68	1.21	33.75
PDF	4.19	9.87	46.94	42.56	98.71	1.58	42.26
PT	6.14	5.67	78.75	73.4	97.57	3.87	62.37
LNPF	3.43	2.42	55.26	53.82	99.61	1.87	60.08
TSS	4.35	2.83	23.89	25.60	97.43	1.65	25.32
TS	1.56	6.95	25.04	24.34	90.28	0.48	32.84
RS	1.77	5.23	37.81	34.27	97.41	0.93	53.45
TA	0.24	12.74	24.80	22.18	80.00	0.23	94.57
AA	15.78	3.45	107.89	104.65	98.32	8.15	56.82
LY	2.11	11.28	48.42	47.56	91.24	1.66	68.79
βC	0.68	98.76	85.96	28.28	10.52	0.16	23.11

Where, PH = Plants height (cm), PBP = Primary branches per plant, DFF = Days to first flowering, FCP = Flower cluster per plant, FC = Flower per cluster, NFP = Number of fruits per plants, AFW = Average fruit weight (g), EDF = Equatorial diameter of fruit (mm), PDF = Polar diameter of fruit (mm), PT = Pericarp thickness (mm), LNPF = Locule number per fruit, TSS = TSS content (º Brix), TS = Total sugar content (%), RS = Reducing sugar content (%), TA = Titrable acidity (%), AA = Ascorbic acid (mg/ 100 g fresh), LY = Lycopene content (mg/ 100 g fresh), βC = β carotene content (mg/ 100 g fresh).

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. The genotypic coefficient of variation (GCV) helps to measure the range of genetic variability in the character and provides a measure to compare the genetic variability present in various characters.

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 2), 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. Such inference could also be drawn from the magnitude of low to moderate coefficient of variation for the characters. Hence, the characters could be improved following different phenotypic selections like directional, disruptive and stabilized selections.

The characters which showed very high genotypic and phenotypic coefficients of variation were plant height, primary branches per plant, number of fruits per plants, average fruit weight, flower cluster per plant, ascorbic acid and β carotene content in the fruits (Table 2). These findings corroborated with the earlier reports for fruit weight, TSS and plant height (Ara *et al*., 2009) [1]; plant height, fruits per plant and fruit weight (Tasisa *et al*., 2011; Meena *et al*, 2015) [15, 9]. High to moderate magnitude of GCV and PCV generally indicated of ample scope for improvement through selection. The present findings clearly suggested the worth of plant height, primary branches per plant, flower cluster per plant, fruit number per plant, locule number per fruit, ascorbic acid and lycopene content in the fruits for the study of genetic variability in tomato.

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 (Mangi *et al.*, 2010) [8]. So, for the evaluation of relative magnitude of the effect of genes and environments on total phenotypic variability heritability is important. For this reason, Burton (1952) [2] and Burton and De Vane (1953) [3] suggested that genetic coefficients of variability along with heritability estimates would provide a reliable indication of expected degree of improvement through selection.

The estimates of heritability were high ranging from 58 to 98 percent for plant height, primary branches/ plant, fruits per plant, flower cluster per plant, fruit weight, polar diameter of fruit, equatorial diameter of fruit, pericarp thickness, ascorbic acid content and ß carotene content of fruit (Table 2) which gives information that selection is based on phenotypic expression as there was major role of genetic constitution in the expression of these characters.

Broad sense heritability estimates were moderately low for flower number per cluster (71.26%), primary branches per plant (58.69%), days to first flowering (49.58) and it was very low (10.52%) for ß carotene content of fruit. The broad sense heritability estimates the present investigation with the earlier reports for different characters like, plant height, number of branches per plant, days to flowering, flowers per plant, fruits per plant, fruit weight, fruit yield per plant, TSS content, etc. (Kumar *et al.*, 2013; Singh *et al*., 2006; Haydar *et al.* 2007; Islam *et al.*, 2012; Saleem *et al*., 2013; Meena *et al*., 2015) [7, 14, 4, 5, 11, 9].

The overall estimated scenario of broad sense heritability for different character indicates very high efficiency of selection for plant height, primary branches/ plant, flower cluster per plant, flowers per cluster, fruits per plant, fruit weight, equatorial diameter of fruit, polar diameter of fruit, pericarp thickness, locule number per fruit, total soluble solids content, reducing sugar content, total sugar content, ascorbic acid content, tritrable acidity and lycopene content of fruit. However, heritability value alone cannot provide information on amount of genetic progress that would result from selection of best individuals.

Genetic advance

Genetic advance (GA) is the improvement in performance of the selected lines over the original population. The estimate of genetic advance as percent of mean showed a wide range from low of 12.48% for days to flowering to 126.64% for flower per cluster (Table 2). Genetic advance as percent of mean was high ranging from 23.11 to 125.73 percent for most of the characters viz., plant height, primary branches per plant, flower cluster per cluster, fruit number per plant, fruit weight, pericarp thickness, locule number per fruit, reducing sugar content, tritrable acidity, ascorbic acid content and lycopene content in fruit. Earlier reports of high genetic advance as percent of mean for fruit yield per plant (Shashikanth *et al.*, 2010) [13]; fruit weight (Islam *et al.* 2012) [5]; fruit weight, yield per plant (Kumar *et al.*, 2013) [7], fruit weight and ascorbic acid content (Meena *et al*., 2015) [9] agreed well to the present findings.

The present findings supported by earlier reports suggested that selection would be rewarding for improvement of the characters particularly plant height, primary branches per plant, flower cluster per cluster, fruit number per plant, fruit weight, locule number per fruit, pericarp thickness, reducing sugar content, tritrable acidity, ascorbic acid content and lycopene content in fruit which exhibited very high genetic advance as percent of mean.

Heritability and genetic advance

It is not necessarily true that high heritability would always exhibit high genetic advance. High heritability along with high genetic advance were recorded for plant height, fruit number per plant, equatorial diameter of fruit, polar diameter of fruit, pericarp thickness, locule number per fruit, TSS content, total sugar content, reducing sugar content, ascorbic acid content and lycopene content in fruit. The parallelism of the magnitude of heritability and degree of genetic gain happens due to the additive gene playing a predominant role (Panse, 1967) [10] and therefore, these were more reliable for effective selection. Similar finding were also reported by Singh *et al.* (2006) [14] for number of fruits per plant, fruit weight, plant height and fruit diameter and Meena *et al*., (2015) [9] for plant height. Hence, early generation selection would be helpful for improving these characters.

Low heritability with low genetic advance was recorded for primary branches per plant, days to first flowering, flower cluster per plant, flower per cluster, average fruit weight, equatorial diameter of fruit, titrable acidity, β carotene content. High heritability and moderate genetic advance was recorded for polar diameter of fruit, pericarp thickness, locule number per fruit and high heritability and low genetic advance was recorded for TSS content of fruit and equatorial diameter of fruit (Table 2). High genetic advance and low heritability was recorded for Flower cluster per plant.These combinations of genetic parameters might be attributed to non-additive gene action for the control of these characters (Ara *et al*., 2009) [1]. This result was in agreement with the earlier reports of Meena *et al.*, (2015) [9] for TSS and number of flower clusters per plant. Hence, improvement of the characters viz., equatorial and polar diameter of fruit, first flower, flowers per cluster, TSS and β carotene content of

fruit needs selection over several successive years, preferably across locations.

Fig 1: General view of evaluation block of tomato

Summary and Conclusion

The evaluation of 56 genotypes of tomato indicated a widely divergent genotypes need to be utilized to develop promising and high yielding hybrids. Number of fruits per plant, average fruit weight, equatorial diameter of fruit, ascorbic acid and lycopene contents of fruit emerged as important characters for developing plants with higher fruit yield and enhanced quality in tomato. The biggest fruited genotype emerged from this study was CLN-2116-3 (133.54g). The genotype with the fruits of thickest pericarp was BCT 20 (9.23 mm). The genotype with the fruits containing highest ascorbic acid was CLN-213-11-1 (21.26 mg / 100g fresh). The genotype with the fruits containing highest lycopene was BCT-48 (2.53 mg / 100g fresh). Generation selection would be helpful for improving the characters viz., plant height, primary branches per plant, flower cluster per cluster, fruit number per plant, fruit weight, pericarp thickness, loculenumber per fruit, reducing sugar content, tritrable acidity, ascorbic acid content and lycopene content in fruit. Deferred selection would be applicable for equatorial and polar diameter of fruit, first flower, flowers per cluster, TSS and β carotene content of fruit.

References

1. Ara A, Narayan R, Ahmed N, Khan SH. Genetic variability and selection parameters for yield and quality attributes in tomato. Indian J. Hort. 2009; 66:73-78.
2. Burton GW. Quantitative inheritance in grass. Proc. 6th Inter. Grassland Congr. 1952; 1:277-283.
3. Burton GW, De Vane EH. Estimating heritability in tall fescue (*Festuca arundiancea*) from replicated clonal material. Agron. J. 1953; 45:478-481.
4. Haydar A, Mandal MA, Ahmed MB, Hannan MM, Karim R, Razvy MA, *et al*. Studies on genetic variability and interrelationship among the different traits in tomato (*Lycopersicon esculentum* Mill.). Middle-East J. Sci. Res. 2007; 2(3, 4):139-142.
5. Islam MS, Mohanta HC, Ismail MR, Rafii MY, Malek MA. Genetic variability and trait relationship in cherry tomato (*Solanum lycopersicum* L. var. *cerasiforme* (Dunnal) A. Gray). Bangladesh J. Bot. 2012; 41:163-167.
6. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybean. Agron. J. 1955; 47:314-318.
7. Kumar D, Kumar R, Kumar S, Bhardwaj ML, Thakur MC, Thakur KD, *et al*. Genetic variability, correlation and path coefficient analysis in tomato. Intern. J Veg. Sci. 2013; 19:313-323.
8. Mangi SA, Sial MA, Ansari BA, Arian MA, Laghari KA, Mirbahar AA. Heritability studies for grain yield and yield components in F3 segregating generation of spring wheat. Pak. J Bot. 2010; 42(3):1807-1813.
9. Meena OP, Bahadur V, Jagtap AB, Saini P, Meena YK. Genetic variability studies of fruit yield and its traits among indeterminate tomato genotypes under open field condition**.** African J Agril. Res. 2015; 10:3170-3177.
10. Panse, Sukhatme. Genetics of quantitative characters in relation to plant breeding. Indian J Genet. 1967; 28:225-229.
11. Saleem MY, Iqbal Q, Asghar M. Genetic variability, heritability, character association and path analysis in F_1 hybrids of tomato. Pak. J. Agri. Sci. 2013; 50:649-653.
12. Searle SR. The value of indirect selection. I. Mass Selection. Biometrics. 1965; 21:682-708.
13. Shashikanth BN, Hosamani RM, Patil BC. Genetic variability in tomato (*Solanum lycopersicon* [Mill]. Wettsd.) Karnataka J Agric. Sci. 2010; 23:536-537.
14. Singh PK, Singh B, Singh JP, Singh S. Combining ability in tomato (*Solanum lycopersicon* Gul (Mill.) Wettsd). Veg. Sci. 2006; 33(1):85-87.
15. Tasisa J, Belew D, Bantte K, Gebreselassie W. Variability, heritability and genetic advance in tomato (*Lycopersicon esculentum* Mill.) genotypes in West Shoa, Ethiopia. Am-Euras J Agric. 2011; 11:87-94.
16. Thamburaj S, Singh N. Textbook of vegetables, tuber crops and spices. New Delhi, ICAR, 2004, 10-29.