

Research Article

Evaluation of advanced breeding lines of tomato for fruit quality based on morphophysiological and biochemical traits

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Abstract

Tomato is one of the most important vegetable crops in the world considering its production potential and consumption rate. It serves as an essential source of important nutrients like vitamins C and K, antioxidants, and lycopene, contributing to a balanced and healthy diet. The fruit yield and other yield contributing traits in tomatoes are governed by polygenes and are quantitatively inherited akin to other crops. A study was conducted on tomato (Solanum lycopersicum L.) during Kharif 2020 at the Zonal Agricultural Horticultural Research Station, KSNUAHS, Shivamogga, to assess genetic variability and diversity and to identify superior segregants for shelf life and yield among 40 advanced breeding lines derived from a cross between Red Ball (More shelf life) × Arka Abha (High yield). Out of 16 characters studied, lycopene content, shelf life, pericarp thickness, pulp content, fruit weight, and five other yield contributing traits were positively skewed and were platykurtic, indicating the complementary form of epistasis. A relatively high range of PCV and GCV were observed for almost all the traits considered under study. The lines were clustered into 9 classes based on genetic divergence analysis. Two superior lines, G-32 and G-29 were selected for higher yield and increased shelf life.

Keywords advanced breeding lines, genetic divergence, lycopene content, shelf life, tomato

Introduction

Tomato (Solanum lycopersicum L., 2n = 24) holds significant global importance as a widely cultivated and consumed vegetable crop, belonging to the family Solanaceae. This self-pollinated, day-neutral vegetable thrives in sunny and moderate climates. India ranks second in the total production of tomatoes among other countries (www.nabard.org) [1], which contributes to 778 thousand hectares of area with a production of 19.3 million metric tons. Due to its high consumption rates in developed and developing countries, it is often referred to as a luxury crop. In England, it is commonly known as Love Apple and is cultivated in numerous home gardens as well as by market and truck growers. Furthermore, it serves as a valuable income source for small and marginal farmers, being grown in greenhouses during the offseason.

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However, the tomato's fruit is highly perishable, leading to substantial post-harvest losses caused by natural perishability, precarious transportation and storage conditions, and inadequate packaging. In India, a total post-harvest loss of up to 12.44% of tomatoes was recorded (NABARD, 2021) [1], which scores highest among other vegetable crops. Enhancing its shelf life through advanced post-harvest packaging methods and genetic engineering techniques have proven efficient but are not practical in a farmer's field and requires social acceptance. Therefore, genetic enhancement of major fruit quality characteristics emerges as an ideal and safe approach to improve shelf life. At the same time, fruit yield is a complex polygenic quantitative trait, that results from interactions between various yield components. Selecting multiple characteristics proves more effective than relying solely on yield-based selection. Therefore, understanding the associations between yield and its attributing characteristics becomes crucial for breeders. The vast genetic diversity present in the genus Solanum allows tomatoes to adapt to diverse uses and environments, making it a valuable resource for applied breeding programs. The observed variability in tomato traits can be attributed to genetic and environmental factors and their interactions within populations.

Considering the importance of exploiting genetic variability in segregating populations, an attempt has been made to investigate genetic variability, heritability, and genetic advancement for yield and yield components. Additionally, the study aims to identify high yielding segregants with extended shelf life, surpassing the traits of their parents in the F_4 segregating population of tomatoes derived from the cross Red ball \times Arka Abha.

Methodology

The study was conducted during *Kharif* 2020 at Zonal Agriculture and Horticultural Research Station, Keladi Shivappa Nayaka University of Agricultural and Horticultural Sciences, Shivamogga, Karnataka. The material composed of forty F_4 advanced breeding lines (ABL's) with two parents, Red ball (as female parent with a good shelf life) and Arka Abha (as male having a high yield). The seeds were treated with Captan @ 0.1 per cent before sowing and were raised in portrays. Seedlings of 30 days old were transplanted in the main field at a spacing of 90 cm x 45 cm and a recommended package of practices were followed to raise a healthy crop.

Observations on individual plants and their parents were recorded for nine yield governing traits such as fruit length (mm), fruit width (mm), fruit weight (g), plant height (cm), number of branches per plant, number of flowers per cluster, number of fruits per cluster, fruit yield per plant and number of locules per fruit; four physiological characters such as fruit firmness (kg/cm²), pulp content (%), pericarp thickness (mm) and shelf life; and three biochemical characters such as Total Soluble Solids (TSS), pH, and lycopene content. Lycopene content was analyzed using the spectrophotometric method [2], and fruit firmness and pericarp thickness were estimated using a fruit penetrometer and Vernier caliper, respectively.

Descriptive statistical measures including skewness, kurtosis, and genetic variability were calculated as per Das and Giri [3] using the software SPSS 16.00 and R studio. Genetic divergence between populations was assessed according to Mahalanobis [4] using WINDOSTAT version 9.2.

Results and Discussion

Genetic variability

A wide range of variability was observed among the breeding lines for most traits such as fruit shape, size, pericarp thickness, number of locules per plant (Figure 1), number of clusters per plant, plant height, fruit length, fruit weight, pulp content, TSS, shelf life, and total yield per plant which indicates ample amount of variation available for improvement by selection (Table 1). Line G23 had the maximum number of fruits per cluster (7.20) and recorded the highest fruit yield per plant (1512.90 g). G16 recorded the highest pericarp thickness (8.47 mm) while the highest shelf life of 39.44 days

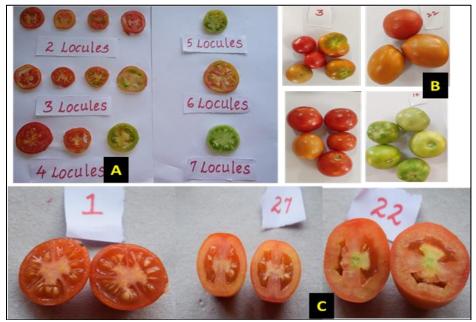


Figure 1. Range of variability among breeding lines for fruit traits (A) No. of locules per fruit (B) Fruit size and Fruit shape (C) Pericarp thickness

was noticed in the line, G11. Among the sixteen fruit biochemical, morpho-physiological, and yield attributing traits evaluated, ten characters exhibited a positive skewness with a platykurtic distribution. These traits included lycopene content, shelf life, number of locules per fruit, pericarp thickness, number of clusters per plant, number of fruits per cluster, fruit length, fruit diameter, fruit weight, and pulp content.

Conversely, five attributes displayed a negative skewness alongside a platykurtic distribution. Notably, the TSS content demonstrated a leptokurtic distribution with positive skewness. Examining the distribution properties, specifically the coefficient of skewness and kurtosis, aids in comprehending the genetic nature and the number of genes governing these traits [5]. The presence of positive skewness with a platykurtic distribution signifies the involvement of a moderate number of genes associated with the traits, characterized by complementary epistasis [6]. On the other hand, negative skewness suggests that inheritance is governed by a larger number of dominant genes with a duplicate type of epistasis. These findings align with the conclusions drawn by Yogendra [7].

The estimates of PCV were found to be higher than GCV for all the characters considered under study (Table 2). The PCV and GCV estimates were comparatively high for shelf life, lycopene content, pulp content, TSS, number of locules per fruit, number of clusters per plant, number of fruits per cluster, fruit weight, and fruit length whereas, the trait, fruit yield recorded high PCV but a lower GCV. This pattern signifies a substantial degree of variability within the examined material, indicating the presence of considerable diversity within the population, suitable for potential selection. These findings align with prior research reports by different researchers [8-11], which similarly reported high PCV values for fruit yield per plant. Furthermore, the difference between the computed GCV and PCV values were relatively minimal, particularly evident in traits like fruit diameter, fruit weight, pulp content, and shelf life. The narrow gap between PCV and GCV estimates for these traits suggests a reduced influence of environmental factors on their expression, thus contributing to a higher degree of heritability.

Heritability (broad sense) offers insight into the extent of observable variation influenced by genetic differences. High heritability coupled with high genetic advance for characteristics such as total soluble solids, pH content, lycopene content, shelf life, number of locules per fruit, pericarp



Table 1. Genetic variability and distribution of 16 traits in advanced breeding lines of tomato

S.N.	Characters	F4 Mean±S.Em	Range		Parental mean		Skewness	Kurtosis	Type of kurtosis
			Min.	Max.	Red Ball	Arka Abha			Kurtosis
1	No. of locules/fruit	3.89 ± 0.26	2.52	7.34	3.00	6.50	1.383	2.394	P
2	No. of clusters/plant	21.75 ± 0.76	12.70	32.10	14.81	21.58	0.136	0.059	P
3	No. of fruits/cluster	4.07 ± 0.33	2.60	7.20	4.30	2.80	1.465	1.750	P
4	Plant height (cm)	96.50 ± 1.56	67.70	128.00	93.45	74.15	-0.037	-0.749	P
5	No. of branches/plant	6.96 ± 0.20	4.50	8.50	6.48	7.83	-0.940	2.337	Р
6	Fruit length (cm)	41.45 ± 2.31	20.88	67.12	57.35	37.32	0.530	-0.193	P
7	Fruit diameter (cm)	38.69 ± 0.43	29.94	54.48	53.81	50.13	0.684	0.604	P
8	Fruit weight (g)	36.45 ± 0.63	15.65	66.84	82.01	49.10	0.500	-0.355	P
9	Pericarp thickness (mm)	6.62 ± 0.14	4.74	8.48	6.79	5.19	0.064	-0.366	Р
10	Firmness (kg/cm ²)	3.84 ± 0.16	2.46	4.92	3.92	1.82	-0.228	-0.898	P
11	TSS (%)	5.42 ± 0.17	3.21	11.39	2.95	3.33	2.305	3.538	L
12	pH content	4.18 ± 0.20	2.65	5.24	5.23	5.09	-0.792	-0.465	P
13	Lycopene (mg/100g)	4.48 ± 0.22	2.36	6.72	1.28	1.01	0.124	-0.630	P
14	Pulp content (%)	26.43 ± 0.85	7.95	49.88	76.81	50.31	0.205	-0.885	P
15	Shelf life (days)	26.18 ± 0.47	15.70	39.56	36.00	19.00	0.429	-0.566	P
16	Yield/plant (g)	1009 ± 55.21	541.97	1512.90	506.31	1110.35	-0.029	0.32	P

Table 2. Estimates of genetic parameters for yield attributing traits in advanced breeding lines of tomato

S.N.	Character	Mean	Vp	Vg	PCV	GCV	h ² _{bs} (%)	GAM (%)
1	No. of locules/fruit	3.89	1.12	0.97	27.19	25.42	87.41	48.97
2	No. of clusters/plant	21.75	34.57	33.40	27.02	26.56	96.62	53.79
3	No. of fruits/cluster	4.07	1.26	1.03	27.59	25.01	82.10	46.67
4	Plant height (cm)	96.50	259.36	254.44	16.68	16.52	98.10	33.72
5	No. of branches/plant	6.96	0.57	0.49	10.89	10.11	86.09	19.32
6	Fruit length (cm)	41.45	130.91	120.16	27.60	26.44	91.78	52.19
7	Fruit diameter (cm)	38.69	29.30	28.93	13.99	13.90	98.72	28.45
8	Fruit weight (g)	36.45	177.27	176.47	36.52	36.44	99.54	74.90
9	Pericarp thickness (mm)	6.62	0.77	0.72	13.26	12.87	94.20	25.75
10	Firmness (kg/cm ²)	3.84	0.47	0.42	17.89	16.92	89.46	32.98
11	TSS (%)	5.42	2.014	1.95	26.14	25.76	97.09	52.28
12	pH content	4.18	0.57	0.48	18.04	16.72	85.84	31.92
13	Lycopene (mg/100g)	4.48	1.24	1.14	24.86	23.82	91.84	47.03
14	Pulp content (%)	26.43	133.75	132.29	43.75	43.51	98.90	89.14
15	Shelf life (days)	26.18	45.18	44.73	25.67	25.54	98.99	52.36
16	Yield/plant (g)	1009	43607.22	37510.10	20.68	19.18	86.02	36.64

thickness, firmness, number of clusters per plant, number of fruits per cluster, plant height, number of branches per plant, fruit length, average fruit weight, pulp content and fruit yield per plant (Table 2), implies the preponderance of additive gene action. This trend also indicates a heightened potential for selecting high-yield genotypes due to the prevalence of additive gene effects. The results are in line with the conclusions drawn by different researchers [12-16], for fruit yield per plant and average fruit weight. The adoption of indirect selection in advanced breeding lines of tomato



production based on both yield per plant and its attributing component traits, especially the number of clusters per plant, number of fruits per cluster, plant height, number of branches per plant, pericarp thickness, fruit weight, and pulp content rather than direct selection for fruit yield per plant, will be highly effective for developing high yielding genotypes.

Genetic divergence

Forty advanced breeding lines of tomatoes were grouped into nine clusters (Table 3). Cluster pattern revealed that cluster I is the largest cluster having 16 genotypes followed by cluster II with 6 genotypes; clusters IV and VII have 5 genotypes each. Cluster III, VIII, and IX were the smallest clusters with 1 genotype each. The results were in accordance with other researchers [11-18]. The intra cluster distance was maximum for cluster VII (G-38, G-40, G-25, G-23, and G-24) followed by cluster VI (G-30, G-14, and G-35). Cluster IV and Cluster VIII have exhibited maximum inter-cluster distances between them, followed by Cluster VI and cluster VIII. Clusters with maximum inter-cluster distance infer the wider genetic diversity between the genotypes while the clusters with minimum inter-cluster distance manifest the narrow genetic diversity among such genotypes. Hence, it is preferable to select the genotypes that fall under the clusters having greater inter-cluster distances for the hybridization purpose to develop high yielding varieties and hybrids. Fruit weight contributed the maximum for the total genetic divergence (33.97%), followed by shelf life and pulp content.

Clusters	No. of genotypes	Cluster members
I	16	G-17, G-19, G-20, G-33, G-36, G-34, G-7, G-22, G-18, G-16, G-4, G-8,
		G-2, G-9, G-13, G-32
II	6	G-27, G-29, G-28, G-39, G-15, G-26
III	1	G-1
IV	5	G-6, G-10, G-31, G-3, G-5
V	2	G-12, G-11
VI	3	G-30, G-14, G-35
VII	5	G-38, G-40, G-25, G-23, G-24
VIII	1	G-21
IX	1	G-37

Table 3. Clustering of advanced breeding lines based on genetic divergence

Reddy et al., [19], Nalla et al., [20], and Ullah et al., [21] have reported the maximum contribution of fruit weight and plant height towards total divergence. Hence, these characters should be given more preference when selecting diverse parents for the hybridization program. On the other hand, characters such as the number of fruits per cluster, fruit length, number of locules per plant, and pH had no contribution towards the genetic divergence (Figure 2).

Selection of superior lines

The advanced breeding lines in F4 were evaluated and selected for shelf life and its contributing characteristics such as pericarp thickness, fruit firmness, and pulp content (Table 4) and also for fruit yield and yield contributing characteristics such as number of clusters per plant, number of fruits per cluster, plant height, and number of branches per plant (Table 5). The parental varieties, Red Ball and Arka Abha, exhibited mean shelf life qualities of 36.00 and 19.00, respectively. Among the identified lines, G-11 (39.45 days) demonstrated significant superiority in shelf life quality compared to both parents. Furthermore, G-11 showcased notably higher values for attributes such as pericarp thickness (6.82 mm) and fruit firmness (3.61 kg/cm²) when compared to the parent Arka Abha. Another distinguished line, G-10, exhibited a substantially extended shelf life of 37.20 days compared to the parent Arka Abha besides having increased pericarp thickness (6.82 mm) and enhanced fruit firmness (4.6 kg/cm²).

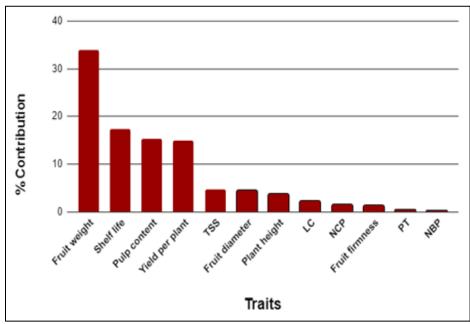


Figure 2. Per cent contribution of various traits towards total divergence LC: Lycopene content, NCP: Number of clusters per plant, PT: Pericarp thickness, NBP: Number of branches per plant

Table 4. List of high yielding genotypes with appreciable shelf life selected based on various shelf life attributing traits in advanced breeding lines of tomato

S.N.	Genotype number	Shelf life(days)	Pericarp thickness(mm)	Firmness (kg/cm²)	Pulp content (%)	Yield per plant(g)
1	G-11	39.45	5.89	3.61	34.85	1114.58
2	G-10	37.20	6.82	4.6	8.745	859.00
3	G-06	35.44	5.89	4.0	11.13	846.22
4	G-31	31.55	5.87	3.82	17.81	948.78
5	G-01	31.22	6.59	4.51	37.75	920.6
6	G-32	30.72	5.57	3.56	40.67	1265.84
7	G-29	29.53	7.37	4.57	10.19	1217.65
8	G-38	28.82	5.12	3.25	27.08	1112.26
9	G-02	28.81	6.59	4.51	38.085	1165.49
10	G-13	28.49	6.71	4.6	17.765	838.48
	Arka Abha	19	5.19	1.82	50.31	1110.35
	Red ball	36	6.79	3.92	76.81	506.31
	CD@5%	1.35	0.42	0.38	12.15	156.94

G-23 and G-04 displayed the highest fruit yield per plant, measuring 1512.90 g and 1311.69 g, respectively. This exceptional yield was attributed to various component characters, including the number of branches per plant, plant height (cm), number of fruits per cluster, and number of clusters per plant. In contrast, two parent varieties, Arka Abha and Red Ball, achieved an average yield of 1110.31 g and 56.31 g, respectively. In addition to the aforementioned four lines, two additional lines demonstrated an enhanced extended shelf life and increased fruit yield within the population. One of these lines, designated as G-32, exhibited a noteworthy mean shelf life of 30.72 days (significantly superior to that of Arka Abha), coupled with an impressive average fruit yield of 1265.84 g, which markedly outperformed both the parent varieties. Another line, G-29, exhibited a remarkable average fruit yield of 1217.65 g per plant, accompanied by an average shelf life of 29.53 days,



Table 5. List of high yielding genotypes selected based on various yield attributing traits in advanced breeding
lines of tomato

S.N.	Genotype number	Plant height(cm)	Number of branches/ plant	Number of fruits/cluster	Number of cluster/plant	Yield per plant(g)
1	G-23	99.30	7.01	7.20	30.60	1512.90
2	G-04	108.10	7.50	3.20	19.30	1311.69
3	G-32	96.10	6.91	3.50	17.10	1265.84
4	G-33	106.60	5.93	5.80	22.60	1230.83
5	G-07	128.00	7.90	3.50	33.62	1224.41
6	G-16	117.70	7.05	3.60	24.70	1222.72
7	G-29	89.00	6.70	6.30	22.10	1217.65
8	G-40	106.30	7.82	5.20	22.38	1207.90
9	G-20	88.30	5.64	4.90	21.60	1193.47
10	G-09	111.40	7.00	3.20	22.20	1188.07
	Arka Abha	74.15	7.83	2.80	21.58	1110.35
	Red ball	93.45	6.48	4.30	14.81	506.31
	CD@5%	4.45	0.56	0.95	2.17	156.94

representing a substantial improvement over the parent varieties Arka Abha and Red Ball, respectively. The superior advanced breeding lines, G-10 and G-11 (high shelf life) as well as G-23 and G-24 (high fruit yield) can be used as donor parents to map QTLs responsible for shelf life and yield. The lines with high fruit yield combined with high shelf life (G-32 and G-29) can be forwarded to F_5 and further generations for testing under different agro climatic conditions over the seasons for testing their stability of performance for the final release as improved varieties for yield and shelf life.

Conclusion

The research findings revealed a significant level of diversity among the advanced breeding lines across nearly all the characteristics examined. Traits like shelf life, pericarp thickness, number of fruits per cluster, average fruit weight, and fruit yield per plant displayed substantial heritability, suggesting a predominance of additive genes that are particularly valuable for phenotypic selection. Utilizing D² analysis, the lines were categorized into nine distinct clusters based on their genetic variation. Among different genotypes, G-11 and G-10 emerged as prime candidates for extending shelf life quality, while G-23 and G-24 showed promise for achieving higher fruit yields. These specific lines could serve as valuable donor parents and potential sources for identifying the quantitative trait loci (QTLs) responsible for enhancing shelf life. Furthermore, two noteworthy lines, G-32 and G-29, were identified for their combination of high fruit yield and extended shelf life, warranting further evaluation in subsequent generations.

Conflict of interest

The authors have no conflict of interest.

References

- [1] NABARD (2021). National bank for agriculture and rural development. www.nabard.org.
- [2] H. K. Lichtenthaler (1987). Chlorophylls and carotenoids: Pigments of photosynthetic biomembranes. Methods in Enzymol., 148: 350-382.
- [3] M. N. Das and N. G. Giri (1986). Design and analysis of experiments, 2nd edn. Wiley, New York.
- [4] P. C. Mahalanobis **(1936)**. On the generalized distance in statistics. Proc. Nat. Inst. Sci., India., **2:** 49-55
- [5] D. S. Robson **(1956)**. The application of K₄ statistics to genetic variance component analysis. Biometrics, 12: 433-444.



- [6] D. Roy **(2000)**. Plant breeding The Analysis and exploitation of variation. PB, Narosa Publishing House. New Delhi. India. pp198.
- [7] K. N. Yogendra **(2011)**. Development of tomato (*Solanum lycopersicum* L.) for extended shelf life through molecular marker approaches. Ph.D. Thesis University of Agricultural Sciences, GKVK, Bengaluru, pp137.
- [8] N. C. Mamatha, H. B. Lingaiah and H. K. Jyoti **(2017)**. Variability Studies in F₂ population of tomato (*Solanum lycopersicum* L.) for yield and other economic traits. Int. J. Pure App. Biosci., **5:** 1093-1096.
- [9] R. K. Meena, S. Kumar, M. L. Meena and S. Verma (2018). Genetic variability, heritability and genetic advance for yield and quality attributes in tomato (*Solanum lycopersicum* L.).J. J. Pharmacogn. Phytochem., 7: 1937-1939.
- [10] K. Eppakayala, S. Pidigam, S. Natarajan, G. Amarapalli and R. R. Komatireddy **(2021)**. Study of genetic variability, heritability and genetic advance for yield and yield parameters in tomato (*Solanum lycopersicum* L.) germplasm. J. Pharmacogn. Phytochem., **10**: 768-771.
- [11] Shweta, B. M. D. Kumar, V. Ellur and S. K. Patil **(2016)**. Assessment of genetic variability and diversity in tomato (*Lycopersicon esculentum* Mill.) germplasm. Green Farming, **7:** 819-823.
- [12] B. Anuradha, P. Saidaiah, K. R. Reddy, S. Harikishan and A. Geetha **(2020)**. Genetic variability, heritability and genetic advance for yield and yield attributes in tomato (*Solanum lycopersicum* L.). Int. J. Curr. Microbiol. App. Sci., **9:** 2385-2391.
- [13] K. Kumari, S. Akhtar, S. Kumari, M. Kumar, K.Kumari, N. K. Singh and A. Ranjan **(2020)**. Genetic variability and heritability studies in diverse tomato genotypes. J. Pharmacogn. Phytochem., **9:** 1011-1014.
- [14] H. Limbani and J. P. Makati **(2020)**. Genetic variability and D² analysis for yield and quality traits in tomato (*Solanum lycopersicum* L.). Int. J. Curr. Microbiol. App. Sci., **9:** 2163-2174.
- [15] M. Akhter, F. N. Apon, M. M. R. Bhuiyan, A. B. Siddique, A. Husna and N. Zeba **(2021)**. Genetic variability, correlation coefficient, path coefficient and principal component analysis in tomato (*Solanum lycopersicum* L.) genotypes. Plant Cell Biotech. Mol. Bio., **9:** 46-59.
- [16] K. K. Namita and P. S. Negi **(2021)**. Genetic variability in tomato cv. Arka Ahuti (*Solanum lycopersicum* L.). J. Plt. Biochem. Biotech., **27**: 68-77.
- [17] B. L. Naveen, K. R. Reddy and P. Saidaiah (2018). Genetic divergence for yield and yield attributes in tomato (*Solanum lycopersicum*). Indian J. Agric. Sci., 88: 1018-1023.
- [18] M. S. Alam, S. Hossain, M. A. Ali, M. G. Hossain and M. F. Islam **(2020)**. Assessment of genetic divergence in tomato (*Solanum lycopersicum* L.) through clustering and principal component analysis. J.Agric. Sci. Eng. Inov., **1:** 10-14.
- [19] B. R. Reddy, H. Begum, N. Sunil and B. V. Rajkumar **(2013)**. Genetic variability studies for yield and quality traits in exotic lines of tomato (*Solanum lycopersicum* L.). Environ. Ecol., **31**: 1881-1883.
- [20] M. K. Nalla, M. K. Rana, S. J. Singh, A. K. Sinha, P. K. Reddy and P. P. Mohapatra **(2014)**. Assessment of genetic diversity through D² analysis in tomato (*Solanum lycopersicon* L.). Int. J. Innov. Appl. Stud., **6:** 431-438.
- [22] M. Z. Ullah, L. Hassan, T. Singha and A. K. Patwary **(2015)**. Genetic divergence in tomato lines (*Solanum lycopersicum* L.). J. Bangladesh Agric. Uni., **13**: 61-64.