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Barsha Tripathy
Department of Horticulture,
Centurion University of
Technology and Management,
Paralakhemundi, Odisha, India

K Mallikarjunarao
Department of Horticulture,
Centurion University of
Technology and Management,
Paralakhemundi, Odisha, India

Corresponding Author:
Barsha Tripathy
Department of Horticulture,
Centurion University of
Technology and Management,
Paralakhemundi, Odisha, India

Variability in tomato (*Solanum lycopersicum* L.): A review

Barsha Tripathy and K Mallikarjunarao

Abstract

Tomato (*Solanum lycopersicum* L.) is one of the important vegetable crops of the world which belongs to family Solanaceae. It is believed that this crop is native to Peru Equador region. Despite being originated in the Peru Equador region, it is one of the most important, popular and widely grown vegetable in India having wide range of variability for various plant traits. For any improvement in tomato a detailed knowledge on genetic variability, heritability, genetic advance, correlation, path coefficient and genetic diversity of various quantitative and qualitative characters and their effect towards yield is essential to achieve highest production and productivity. Studies in this aspect can not to be theorized for every genetic materials and climatic condition. Hence, the information below provides a sound breeding plan for the improvement of tomato.

Keywords: Tomato, variability, correlation, path coefficient, genetic diversity

Introduction

The success of any breeding programme mainly depends on the extent and magnitude of variability existing in the population. Therefore, a thorough and adequate knowledge of genetics of various characters is very much essential in vegetable breeding programme for improvement of both qualitative and quantitative traits. A wide range of variation provides better scope for selecting a desirable genotype. The nature and extent of genetic variability, degree of transmission of desirable characters and the actual expected genetic gain for the character in a population determine the efficiency of selection (Golani *et al.*, 2007) ^[10]. Correlation and path coefficient analysis are helpful tools to ascertain the real components of yield, which is a complex character. Any crop improvement is intended to improve the yield considering all other related components, which directly or indirectly contribute for its improvement. For any heritable crop improvement programme the knowledge of genetic diversity, its nature and degree is useful. In quantifying the degree of divergence at genotypic level between biological populations D² analysis is regarded as a helpful tool. It assess the relative contribution of different components into both inter and intra-cluster levels. Hence, genetic variability in relation to fruit yield and its attributes is the main concern for any breeder.

Genetic variability

The basic understanding of genetic variability is a prerequisite for planning of any crop improvement programme. Generally, the variability that exists in the population is measured by genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). Literature pertaining to genetic variability studies on tomato is presented below.

According to Ara *et al.* (2009) ^[3], fruit yield plant⁻¹, number of primary branches plant⁻¹ and number of fruits plant⁻¹ recorded high GCV and PCV. They also observed moderate GCV and PCV for characters like average fruit weight, TSS, vitamin C content, plant height, pericarp thickness and number of fruits cluster⁻¹.

In a study on tomato by Khan *et al.* (2012) ^[15], it was found that PCV and GCV were high in tomato for fruit weight, fruits plant⁻¹, fruit yield plant⁻¹ and plant height. Similarly, Manna and Paul (2012) ^[15] observed that GCV and PCV, respectively were high (>30%) for locules, fruit plant⁻¹ followed by fruit weight, moderate (20-30%) for total acid %, fruits plant⁻¹, vitamin C content, fruit yield plant⁻¹, fruit length and pericarp thickness whereas low (<20%) for fruit width and TSS.

Kumar *et al.* (2013) ^[17] observed that GCV was high for fruit yield plant⁻¹, fruit weight, number of fruits plant⁻¹ and plant height. Moderate GCV was noticed for pericarp thickness, fruit diameter, fruit length, number of fruits cluster⁻¹, number of locules fruit⁻¹.

The GCV was found low for days to 1st harvest, harvest duration and TSS. On the other hand highest GCV was observed for number of fruits plant⁻¹ (Agarwal *et al.*, 2014)^[1]. PCV values were slightly higher for all the traits as compared to GCV but the difference between GCV and PCV values were low indicating less influence of environmental condition on these traits. Similarly, Kumar *et al.* (2014)^[20] while evaluating 21 thermo tolerant tomato genotypes observed that PCV was higher than the corresponding GCV in most of the traits. High PCV was observed for fruit yield plant⁻¹, whereas high GCV was revealed for yield plant⁻¹ and total chlorophyll content.

Meitei *et al.* (2014)^[27] reported high GCV for fruits plant⁻¹, fruit yield plant⁻¹, single fruit weight and fruit yield ha⁻¹ in tomato.

A study by Meena and Bahadur (2015)^[26] also reported high estimates of PCV and GCV for plant height. Basavraj *et al.* (2015)^[5] reported highest GCV for average fruit weight followed by number of fruits plant⁻¹, TSS, branches plant⁻¹, plant height, yield plant⁻¹, equatorial diameter, polar diameter, number of locules fruit⁻¹ and number of fruits cluster⁻¹. They also observed highest PCV for average fruit weight followed by number of fruits plant⁻¹, equatorial diameter, yield plant⁻¹, number of branches plant⁻¹, TSS, polar diameter, fruits cluster⁻¹ and number of locules fruit⁻¹.

A study carried out by Singh *et al.* (2015)^[40] observed high magnitude of GCV and PCV for fruit yield plant⁻¹ followed by number of locules fruit⁻¹, number of fruits plant⁻¹, average fruit weight, plant height and number of primary branches plant⁻¹.

Hasan *et al.* (2016)^[12] reported that PCV was higher than the GCV for plant height, primary branches plant⁻¹, days to 1st flowering, days to 50% flowering, days to 1st harvest, individual fruit weight and fruits plant⁻¹ indicating the influence of environment for the expression of these characters.

A study on tomato by Kumar *et al.* (2016)^[19] reported higher PCV and GCV values for fruits plant⁻¹, number of clusters plant⁻¹, number of seed fruit⁻¹, polar diameter, fruit weight, test weight, plant height, number of fruits cluster⁻¹, number of primary branches plant⁻¹, locule number, flowers cluster⁻¹ and equatorial diameter. Number of fruits plant⁻¹, average fruit weight, fruit yield plant⁻¹, locular wall thickness and lycopene content recorded high estimates of heritability and GA (Rai *et al.*, 2016)^[33] in 56 genotypes of tomato.

In tomato Bhandari *et al.* (2017)^[6] reported maximum estimate of PCV and GCV for number of seeds fruit⁻¹ followed by average fruit weight, plant height and total number of fruits plant⁻¹.

An experiment conducted by Ligade *et al.* (2017)^[22] reported high values of GCV and PCV for characters viz., number of fruits plant⁻¹, number of locules fruit⁻¹, average fruit weight, fruit yield plant⁻¹, marketable fruit yield plot⁻¹ which indicated the presence of high genetic variation in the population.

A study conducted by Mamatha *et al.* (2017)^[24] to find out the genetic variability in F₂ population of Utkal Raja x Arka Sourabh indicated higher estimates of PCV and GCV for the traits like number of clusters plant⁻¹, plant height, average fruit weight, number of branches at peak harvest stage, days to 1st flowering, number of fruits plant⁻¹, and yield plant⁻¹. Moderate PCV and GCV were found for TSS.

Patel *et al.* (2017)^[31] found that GCV and PCV were high for number of fruits plant⁻¹, average fruit weight, fruit yield plant⁻¹, number of primary branches plant⁻¹ and plant height at maturity.

However, Savitharamma (2017)^[37] working on F₄ segregating population of the cross EC771612 × LA 2657 observed high GCV and PCV along with narrow difference between GCV and PCV for fruits plant⁻¹, fruit diameter, plant height, number of clusters plant⁻¹ and fruit yield plant⁻¹ indicating less influence of environment on expression of these characters.

Heritability and Genetic advance

In general heritability refers to the degree to which the variability of quantitative character in a population is transmitted to the progeny. Genetic advance (GA) is a product of heritability and infers the potentiality of selection intensity. GA when considered along with heritability gives reasonable assessment of the resultant effects of selection in breeding populations (Johnson *et al.*, 1955)^[14].

Kour *et al.* (2008) observed high heritability for fruits plant⁻¹ and plant height in F₁ and F₂ generations. A study on tomato carried out by Ara *et al.* (2009)^[3] reported high values of GCV, heritability and higher value of GA for fruit yield plant⁻¹, number of fruits plant⁻¹, number of primary branches plant⁻¹ and average fruit weight.

Khan *et al.* (2012)^[15] reported high and moderate to high heritability and GA for fruit weight, number of locules fruit⁻¹, fruit length, number of fruits plant⁻¹, pericarp thickness and vitamin C which suggested the predominance of additive gene action.

Kumar *et al.* (2013)^[17] observed high heritability estimates for characters like number of fruits plant⁻¹, fruit weight, days to 1st harvest, plant height, fruit length, pericarp thickness and fruit yield plant⁻¹, number of fruits cluster⁻¹, fruit diameter, number of locules fruit⁻¹, harvest duration and TSS. High heritability with high GA was observed in traits like plant height, individual fruit length, fruit weight and fruits plant⁻¹.

High GCV, heritability and GA were observed for average fruit weight and number of fruits plant⁻¹ (Agarwal *et al.*, 2014)^[1].

Basavraj *et al.* (2015)^[5] reported high heritability associated with high GA for number of branches plant⁻¹, number of clusters plant⁻¹, average fruit weight, number of locules fruit⁻¹, equatorial and polar diameter of fruit.

Singh *et al.* (2015) reported high GA with high heritability (>15%) for characters like number of primary branches plant⁻¹, height of the plant, average fruit weight, pericarp thickness, length of the fruit, number of fruits per plant, number of locules per fruit, fruit yield plant⁻¹, marketable fruits plant⁻¹ and TSS.

Hamisu *et al.* (2016) working on tomato under high stress (heat) condition reported highest broad sense heritability for number of clusters plant⁻¹, days to 50% flowering, days to 50% flowering, number of flowers cluster⁻¹, days to 50% flowering, number of fruit plant⁻¹, length of the fruit, diameter of the fruit, fruit yield plant⁻¹, fruit shape index and moderate for height of the plant, number of flowers plant⁻¹, number of branches plant⁻¹, fruit set percentage and leaf chlorophyll content.

Similarly, Hasan *et al.* (2016)^[12] observed maximum heritability with high GA for characters like height of the plant, weight of the fruit, fruits plant⁻¹ indicating that these characters were under additive genetic effects. High heritability with low GA was observed for traits like primary branches plant⁻¹, days to 50% flowering, days to 1st flowering, days to 1st harvest, fruit diameter, yield plant⁻¹, days to last harvest, TSS and ascorbic acid content. However, Kumar *et al.* (2016)^[19] working on tomato reported high GA

with high heritability as % of mean for traits like fruits plant⁻¹, weight of the fruit and number of seeds fruit⁻¹.

Bhandari *et al.* (2017) [6] observed that fruit yield plant⁻¹ recorded the high heritability succeeded by fruits cluster⁻¹ in tomato. Similarly, research was conducted by Mamatha *et al.* (2017) [24] to find out the genetic variability in F₂ population of cross Utkal Raja x Arka reported high GA along with higher heritability as % mean for plant height, days to 1st flowering, average fruit weight, fruits per plant and yield plant⁻¹ indicating supremacy of additive gene component which implies much scope for enhancement of these traits by simple selection in the next generations.

Similarly, Savitharamma (2017) [37] observed high heritability coupled with high GA as % mean for fruits plant⁻¹, plant height and flower clusters plant⁻¹ and fruit yield plant⁻¹ indicating the involvement of additive gene action for expression of these traits in the crosses studied.

Correlation study

Association of characters, important from economic point of view and is determined statistically by correlation coefficient. This helps in selecting the component characters which are quite useful as a basis of selection. Correlation investigations between fruit yield and its components provides information of involvement of those characters to yield which will help in outlining and implementing any crop improvement programme. Thus, the review pertaining to correlation among different traits is presented below.

Hidayatullah *et al.* (2008) reported that fruits plant⁻¹ and number of pickings had positive correlation with weight of the fruit per plant. Fruits plant⁻¹ had negative correlation with number of locules, weight of a single fruit, size of the fruit, and pericarp thickness. Fruit length had positive correlation with diameter of the fruit, weight of a single fruit and pericarp thickness.

A study by Ara *et al.* (2009) [3] reported that the yield of the fruit per plant exhibited high positive significant correlation with height of the plant, size of the fruit, primary branches per plant and fruits per plant at both genotypic and phenotypic levels. Similarly, Sharma *et al.* (2009) [39] reported positive phenotypic and genotypic association of fruit yield with fruits plant⁻¹, fruit weight with plant height and negative with locules fruit⁻¹.

A Study by Manna and Paul (2012) [15] on tomato reported that yield of the fruit plant⁻¹ was significantly and positively correlated with weight of the fruit, length of the fruit, thickness of the pericarp and fruits plant⁻¹. Similarly, Kumar *et al.* (2013) [17] reported yield of the fruit per plant was positively and significantly associated with fruits plant⁻¹ at both genotypic and phenotypic levels and fruit cluster number plant⁻¹ only at the genotypic level. Fruit weight was positively and significantly correlated with pericarp thickness, length of the fruit and diameter of the fruit whereas, it is significantly and negatively correlated with fruits per plant at both genotypic and phenotypic level.

However, Monamodi *et al.* (2013) [36] working with determinate tomato reported positive and significant association between yield of the fruit and number of trusses plant⁻¹ with plant height and fruits plant⁻¹, respectively.

They also reported that three components, marketable fruits, weight of a single fruit and number of fruits truss⁻¹ were potential selection criteria for improving determinate tomato fruit yield.

Reddy *et al.* (2013) [36] observed that fruits cluster⁻¹ and Ascorbic acid had positive significant association with days to

50% flowering and primary branches plant⁻¹ whereas, days to last fruit harvest had negative association with primary branches plant⁻¹.

Similarly, number of fruits plant⁻¹ and width of the fruit had positive and significant correlation with yield of fruits plant⁻¹.

Correlation studies by Kiran (2014) revealed strong inheritant association between fruit yield plant⁻¹ with fruit bunches plant⁻¹, length of the fruit, number of fruits plant⁻¹, average weight of the fruit and girth of the fruit, plant height with TSS and primary branches plant⁻¹, primary branches plant⁻¹ with fruits bunch⁻¹ and fruits plant⁻¹, fruits bunch⁻¹ with fruits plant⁻¹, average weight of the fruit with locules fruit⁻¹, locules fruit⁻¹ with girth of the fruit and fruit length with girth of the fruit.

However, Shankar *et al.* (2014) reported significant and positive phenotypic and genotypic correlation of yield plant⁻¹ with pericarp thickness, length of the fruit, average weight of the fruit, fruit width and flowers cluster⁻¹.

Basavraj *et al.* (2015) [5] reported that fruit yield was positively and significantly correlated with yield of fruits plant⁻¹, average weight of the fruit and fruits plant⁻¹ whereas, number of flowers cluster⁻¹ and TSS were negatively correlated with fruit yield.

Rahman *et al.* (2015) reported higher genotypic correlation coefficient than phenotypic correlation coefficient which indicated the subdued effect of the environment.

Hasan *et al.* (2016) [12] suggested that yield plant⁻¹ had positive significant correlations with fruit clusters plant⁻¹ and weight of individual fruit whereas, significant negative correlation was observed with primary branches plant⁻¹.

Kumar *et al.* (2016) [19] reported that fruit yield had positive significant correlation with fruits cluster⁻¹ and fruits plant⁻¹.

Genotypic and phenotypic correlation coefficient studies carried out by Ambresh *et al.* (2017) in population of Vaibhav x Anaga cross (recombinant inbred lines). They reported that fruit yield plant⁻¹ had positive correlation with average weight of the fruit, height of the plant, branches plant⁻¹, fruits plant⁻¹, TSS and locules fruit⁻¹ at both phenotypic and genotypic level.

Similarly, average fruit weight was negatively and significantly correlated with fruits per plant, both at the phenotypic and genotypic level. Branches plant⁻¹ was negatively correlated with TSS.

A study by Rasheed *et al.* (2017) involving total of eight parents and 15 F₁s revealed that branches plant⁻¹, height of the plant, clusters plant⁻¹, fruits cluster⁻¹, flowers cluster⁻¹, fruit set% cluster⁻¹ and weight of a single fruit showed significant correlation with yield of fruit plant⁻¹ at genotypic level and highly significant at phenotypic level and these characters could be used as selection criteria for enhancement of yield plant⁻¹ in tomato.

In a study on tomato conducted by Rawat *et al.* (2017) fruit yield was positively and significantly correlated with fruits cluster⁻¹ and average weight of the fruit while it was negatively and significantly correlated with days to 50% flowering and days to 1st fruit ripening. The average weight of the fruit and fruits per plant exhibited significant positive correlation and direct effect on yield of fruit and emerged as predominant components that contributed to fruit yield.

Similarly, Savitharamma *et al.* (2017) [37] working on genetic parameters in F₄ segregating population of the cross EC 771612 × LA 2657 reported that characters like fruits plant⁻¹, plant height, fruits cluster⁻¹, clusters plant⁻¹ and fruit diameter exhibited positive significant relation with yield of the fruit among F₄ segregants.

Path coefficient analysis

Path analysis was originally developed by Wright (1921), who defined the path coefficient as the ratio of standard deviation of the effect due to a given cause (independent variable) to the total standard deviation of the effect (dependent variable). As the study of simple correlation does not provide an exact picture of relative importance of indirect and direct influence of each of the component character towards the desired character. So, this can be overcome by following path coefficient analysis technique by further separating the correlation coefficient into indirect and direct effects. The available literature on path analysis of yield with other component traits in tomato is briefly reviewed as follows:

Ara *et al.* (2009) [3] observed that days to 1st picking had maximum positive direct effect on yield of the fruit followed by fruits plant⁻¹, average weight of the fruit, duration of harvest, flowers cluster⁻¹ and height of the plant. They suggested that characters viz., minimum days to 1st more number of fruits plant⁻¹, fruit picking, average fruit weight, fruit size, plant height extended harvest duration and number of primary branches plant⁻¹ should be given importance over other characters for selecting genotypes with higher yields. Contrary, Mohanty (2003) reported that fruits plant⁻¹ had the maximum direct effect positively on yield of the fruit followed by days to 1st harvest and average weight of the fruit.

Manna and Paul (2012) [15] reported that TSS, locules fruit⁻¹, fruits plant⁻¹, length of the fruit, weight of the fruit, pericarp thickness and vitamin C content had direct positive effect on fruit yield whereas, total acid content and width of the fruit had high negative effect on yield of fruit.

Path analysis study by Kumar *et al.* (2013) [17] reported that weight of the fruit had most direct positive effect on yield plant⁻¹ followed by fruits cluster⁻¹, fruits plant⁻¹ and diameter of the fruit at the genotypic level. The most positive indirect effects of fruit diameter, fruit length, pericarp thickness were *via* fruit weight to affect yield plant⁻¹.

Path coefficient analysis study by Monamodi *et al.* (2013) [29] showed that marketable fruit number and weight of a single fruit were directly related to fruit yield with direct effect of 0.752 and 0.446, respectively.

Similarly, Reddy *et al.* (2013) [36] revealed that ascorbic acid, fruits per plant, height of the plant, width of the fruit and length of the fruit had high direct positive effects on fruit yield plant⁻¹. High negative direct effects on fruit yield per plant had been observed for primary branches per plant, days to 50% flowering, clusters plant⁻¹, flowers cluster⁻¹ and days to 1st fruit harvest, days to 1st fruit set and fruit weight.

Path analysis study by Kiran (2014) [20] showed that fruits plant⁻¹, average weight of the fruits, number of locules fruit⁻¹, length of the fruit, number of bunches plant⁻¹ and plant height had positive direct effect on fruit yield.

However, Shankar *et al.* (2014) working on 37 genotypes of tomato for phenotypic and genotypic path coefficient analysis disclosed that positive direct effect was exerted by flowers cluster⁻¹, thickness of the pericarp, shelf life whereas, days to 50% flowering reported negative direct effect.

Hasan *et al.* (2016) [12] observed maximum positive direct contribution towards yield was through individual fruit weight whereas, plant height showed negative direct contribution towards yield.

Path analysis studies by Rasheed *et al.* (2017) revealed that height of the plant, branches plant⁻¹, flower clusters plant⁻¹, flowers cluster⁻¹, weight of the fruit and fruit set % cluster⁻¹ directly contributed to yield improvement.

Rawat *et al.* (2017) revealed that the number of fruits per plant had maximum direct positive effect on yield followed by average weight of the fruit.

Genetic Diversity

The information on genetic divergence of various traits particularly of those contributing to yield and quality would be of most useful while planning any crop improvement programme. D² statistics developed by Mahalanobis (1936) provides a measure of magnitude of the extent of diversity among genotypes under comparison. Grouping of genotypes based on D² analysis will be useful while choosing suitable parental lines for heterosis breeding programme and it can further help in development of improved open pollinated varieties for commercial cultivation.

Arun *et al.* (2003) studied the genetic divergence for quantitative traits and grouped the genotypes into 15 clusters, indicating the presence of a wide range of genetic diversity among the genotypes.

Reddy *et al.* (2013) [36] conducted a study on genetic divergence analysis using 19 exotic genotypes of tomato following Mahalanobis D² statistics. They found considerable genetic diversity among the genotypes with respect to 18 quantitative characters. They also reported 92.40% to the total divergence was contributed by plant height, fruit weight and fruits plant⁻¹. The potent factors in differentiating the germplasm of tomato under study were fruit weight, fruits plant⁻¹ and plant height.

Chernet *et al.* (2014) used Mahalanobis D² to estimate genetic distance between pair of clusters. In the study they grouped 36 genotypes into six distinct clusters. Maximum and minimum distance was recorded between clusters IV and V and cluster II and III, respectively. This indicated that hybridization can be carried out among genotypes from any pair of clusters and subsequent selection can be made from segregating generations.

However, Nalla *et al.* (2014) grouped 27 genotypes into nine clusters. Cluster I, had maximum number of genotypes (16) followed by cluster III (3) and VII (2). However, cluster II, IV, V, VI, VIII and IX were having one genotype each. Maximum intra-cluster and inter-cluster distance was recorded within cluster III and between cluster VI and VII respectively. Cluster VIII with single genotype ranked first and contain the potential genotype. High plant height was registered by cluster VIII and II. Less number of days to 50% flowering was taken by the genotypes of clusters V and VIII. Cluster III registered high average fruit weight, fruit yield plant⁻¹ and ascorbic acid. High number of fruits plant⁻¹ was recorded in Cluster IX.

As per a study carried out by Kiran (2014), 45 genotypes were grouped into nine clusters using D² statistics. Cluster VIII, the largest group included nine tomato genotypes (IIVR SEL-2, BT-428-3, BT-306-1-2, BT 224-3-1, BT-305-2-4-2, BT-3, BT-101, Arka Saurabh and BT-136), Cluster I comprised of eight tomato genotypes (BT-442-2, BT-437-1-2, BT-429-2-2, BT-413-1-2, BT-429-1-1, BT-215-3-3-1, BT- 317 and BT-106), Cluster III included seven tomato genotypes (BT-12-2, BT-507-2-2, BT-506-1, BT112-1, BT-508-1-1, Megha Tomato and BT-21-2), Cluster IV comprised of six tomato genotypes (BT-433-2-1, Arka Vikash, BT-17-2, BT-433-3-2, BT-18 and Utkal Pragyan). Similarly, Cluster IX comprised of five tomato genotypes such as (Utkal Pallavi ,Utkal Urbashi, Utkal Raja, BT-218 and BMZ-21) whereas Cluster II had four tomato genotypes (BT-22-4-1, BT-19-1-1-1, BT-19-1-1 and BT-207-2). Remaining three clusters i.e. cluster V

(BT-21 and BT-17), cluster VI (BT-17-2 (5) and Utkal Deepti) and Cluster VII (BT-12-3-2 and Utkal Kumari) comprised of two tomato genotypes each. Out of which cluster VI and cluster III were more divergent consisting of two and seven genotypes. Plant height contributed maximum towards genetic diversity followed by average fruit weight, number of fruits plant⁻¹ and yield plant⁻¹.

A study was carried out by Ullah *et al.* (2015) with 20 genotypes of tomato. Based on D² values of 11 yield related characters, the genotypes were grouped into five clusters. Maximum six number of genotypes were present in cluster II (TM 368, TM 371, TM 384, TM 388, TM 360 and TM 528) followed by five in cluster IV (TM 356, TM 382, TM 410, TM 422 and TM 423), four in cluster III (TM 390, TM 392, TM 419 and TM 409), 3 in cluster I (TM 361, TM 403 and TM 386) and 2 genotypes in cluster V (TM 377 and TM 349). Clustering pattern revealed that there was no association between genetic divergence and geographical distribution of genotypes. Cluster I had highest intra cluster distance, while cluster III and I had maximum inter cluster distance followed by III and V. As per their study the characters which contributed maximum to genetic divergence were fruit weight, plant height and fruits plant⁻¹.

Dar *et al.* (2015) grouped 60 genotypes into 20 clusters in tomato. They reported 14 clusters to be solitary and cluster I had 25 numbers of genotypes. Out of 20 clusters, cluster VII had high average fruit weight and cluster VIII had highest number of locules fruit⁻¹, fruit yield plant⁻¹ and yield ha⁻¹ and cluster XVII was superior for ascorbic acid. Similarly, cluster XX was found promising with respect to number of fruits plants⁻¹. The highest inter cluster D² values were estimated between clusters XII and XX followed by clusters XI and XX, clusters VII and XX, and clusters XV and XX which predicted enough scope for the improvement of tomato crop by hybridization and selection.

Bhattarai *et al.* (2016) demonstrated a high level of morphological diversity within 71 germplasm of tomato and were grouped into six distinct clusters. Genetic divergence analysis was carried out by Lekshmi *et al.* (2016) for polyhouse tomato using Mahalanobis D² statistics in 40 tomato genotypes which were grouped into eight clusters. Cluster I was the largest cluster with 24 genotypes followed by cluster II (10) and all other clusters had one genotype each. The highest intra-cluster distance was noticed in cluster II followed by cluster I. Clusters VII and VIII recorded highest inter-cluster distance followed by clusters IV and VIII.

Similarly, about 40 genotypes were evaluated for 19 characters which were grouped into seven clusters by Kumar *et al.* (2016)^[19]. Cluster II had highest (24) genotypes which was followed by cluster I (2) and VII (2) while cluster III, IV and V were solitary. Highest intra-cluster distance was seen in cluster VII followed by clusters VI and II which were identified genetically diverse. Cluster II and VI noticed maximum and cluster III and IV reported minimum inter-cluster distance. Cluster III and VII had maximum mean values for average fruit weight, number of fruits plant⁻¹ and fruit yield plant⁻¹ while genotypes belonging to clusters IV and VI showed minimum values. Therefore, crossing between these genotypes were expected to give maximum heterosis.

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