Review Article
Genetic diversityamong Tomato(Solanum lycopersicum L.) genotypes: A Review

ABSTRACT

Tomato (*Solanum lycopersicum* L.) is one of the important vegetable crops of the world which belongs to family Solanaceae. Cultivated tomato and wild tomatoes are related to each other which originated from Peru, Ecuador and other parts of South America including the Galapagos Islands. Despite being originated in the Peru-Equador region, it is one of the most popular and widely grown vegetable in India having wide range of variability for various plant characters. For any improvement in tomato a detailed knowledge on genetic variability, heritability, genetic advance, correlation, path coefficient and genetic diversity of various qualitative and quantitative characters and their effect towards yield is essential to achieve highest productivity and production. An improvement in yield and quality in self-pollinated crop like tomato is normally achieved by selecting the genotypes with desirable character combinations that exist in nature or by hybridization. Hence, the information regarding collection of some indigenous genotypes of tomato in order to formulate a breeding plan for its improvement has been reviewed here.

Keywords: Genetic diversity, Variability, Heritability, Genetic advance, Correlation, Path Coefficient and Tomato

INTRODUCTION

Tomato (*Solanum lycopersicum*L. 2n=2x=24) one of the most commercialized vegetables worldwide due to its nutritional properties, is a member of family Solanaceae which contains approximately 100 genera and 2500 species, along with several other crops of agronomic importance such as eggplant, pepper, potato and tobacco [1]. Cultivated tomato and wild tomatoes are related to each other which originated from Peru, Ecuador and other parts of South America including the Galapagos Islands. The centre of tomato domestication and diversification is Mexico [2][3]. Tomatoes are grown as annuals. The plant's growth habit can range from determinate to semi-determinate to indeterminate [4]. Tomatoes are well-known for their flavour, and their soup can also be used as a laxative [5]. For its tremendous nutritional value, the tomato is commonly known as the poor man's orange [6]. Due to its widespread consumption, it outperforms all other vegetables in terms of total contribution of vital nutrients to the diet [7]. It is high in vitamin C (20 mg), vitamin A (270 IU for green and up to 900 IU for ripe fruits) and minerals like Phosphorus (27 mg), Iron (0.5 mg), and Calcium (13 mg). A consumption of roughly 100 mL of tomato juice provides 20% of the recommended daily dose of vitamin A [8]. Clinical studies have indicated that tomatoes can help in prevention of cardiovascular illnesses [9][10] and can also reduce the incidence of rectal, colon, and stomach cancer. The antioxidant lycopene, the most abundant form of carotenoid, is responsible for the fruit's red colour, which significantly lowers the risk of prostate cancer [11][12]. Tomato is one of the most important vegetable crops in the world with annual value exceeding 90 billion USD [13]. India is the world's second-largest tomato producer after China, with 0.830 million hectares under cultivation, 20.300 million metric tonnes of annual production, and an overall average productivity of 24.44 tonnes per hectare [14].
According to Singh *et al*. (2013)[15], the first necessity for plant breeders to impart genetic improvement to a crop is genetic variability. A thorough understanding of the existing genetic diversity is required to begin a crop improvement project. Emphasising the importance of partitioning the observed variability into heritable (additive variance) and non-heritable (non-additive variance) traits using appropriate genetic parameters like genotypic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance is highlighted by the nature of interaction of genotypes and environmental variation in such a population. The genotypic and phenotypic coefficients of variation can be used to detect the amount of variability in genotypes, whereas heritability and genetic advance can be used to determine the influence of the environment on character expression and the extent to which improvement is possible after selection [16]. The statistical tools like correlation and path coefficients aid in determining the degree of association between fruit yield and its attributing traits. Path analysis separates the direct and indirect impacts of a character's relationship. Correlation and path coefficients help a breeder to select efficient traits for targeted improvement while also allocating resources in a crop improvement programme. The knowledge of genetic diversity, its nature and degree are useful for any heritable crop improvement programme. It asses the relative contribution of different components into both inter and intra-cluster levels.

GENETIC VARIABILITY

The success of any breeding programme largely depends upon the presence of genetic variability within the breeding material as it determines the pace and quantum of genetic improvement in concerned crop plant. The degree of variability can be easily predicted through coefficient of variation which is further divided into genotypic coefficient of variation (GCV) and phenotypic coefficients of variation (PCV). The research pertaining to genetic variability studies on tomato have been reviewed below:

Saini *et al.* (2013)[17] investigated the yield and fruit characteristics of 35 tomato genotypes. Plant traits such as the number of fruits per plant, fruit weight, yield per plant, and polar diameter had moderate to high GCV and PCV. Shanker *et al.* (2013)[18] conducted an experiment and high estimates of PCV and GCV were obtained for plant height, titrable acidity, ascorbic acid, average fruit weight, number of fruits per cluster, yield per plant and lycopene indicated a good deal of variability in those characters. In a study by Singh *et al.* (2015)[19], it was observed that high magnitude of GCV and PCV is found for average fruit weight followed by unmarketable fruits per plant, fruit yield per plant, plant height, number of locules per fruit, number of primary branches per plant, pericarp thickness, marketable fruits per plant and number of fruits per plant. It increases the possibility of obtaining higher selection response in respect of above traits. Ligade*et al.* (2017)[20] investigated the genetic variability in yield contributing characters in twenty tomato genotypes and found plant height, number of fruits per plant, average fruit weight, fruit yield per plot, fruit yield per plant, TSS, ascorbic acid, pericarp thickness and number of locules per fruit all showed high GCV and PCV in tomato crop. A study conducted by Kumar and Singh (2018)[21] to find out genetic variability in thirty tomato genotypes indicated the highest values for GCV and PCV in the number of locules per plant, followed by pericarp thickness, plant height, primary branches per plant, fruit diameter, and TSS. Meena *et al.* (2018) [22] reported that high to moderate GCV and PCV for fruit yield per plant, ridges on fruit, average fruit weight, branches per plant, fruits per cluster, flowers per cluster, locules per fruit and clusters per plant. Chaudhari *et al.* (2019)[23] studied 260 minicore accessions of tomato for genetic variability and recorded high GCV and PCV for the traits such as number of fruits per plant, test seed weight, average fruit weight, yield per plant, plant height and number of locules per fruit. However, moderate GCV and PCV was recorded for total soluble solids among the minicore accessions. An experiment conducted by Hussain *et al.* (2021)[24] reported high PCV and GCV for fruits per plant, average fruit weight, fruit yield per hectare, total sugars, titratable acidity and ascorbic acid content, indicating the additive genetic effect. For their improvement, phenotypic selection could be achieved by simple selection. Mahebub*et al.* (2021) [25]evaluated 45 genotypes for genetic variability in tomato and reported high GCV and PCV for average fruit weight followed by number of primary branches per plant at 30 DAT number of locules per fruit and pericarp thickness whereas moderate GCV and PCV were observed for fruit diameter, titratable acidity, ascorbic acid content, number of primary branches per plant at 60 DAT, total sugar, number of primary branches per plant at 90 DAT, reducing sugar and total soluble solids. Pooja *et al.* (2022)[26] studied forty-one genotypes in tomato and high GCV and PCV were observed for average fruit weight, fruit volume, yield per plant, number of fruits per plant, yield per plot, number of locules per fruit, yield per hectare, ascorbic acid, pericarp thickness and titratable acidity. Mahurtale*et al*. (2023)[27] reported that moderate degree of genetic variability were observed in days to 50% flowering, days to first flowering, plant height at 60 and 90 days after transplanting (DAT), count of primary branches per plant at 60 and 90 DAT, stem girth at 60 and 90 DAT, fruit length, fruit diameter, average fruit weight, days to first maturity, total yield per plant, fruit yield per plot, and total soluble solids, as suggested by their GCV and PCV values. A study by Panchbhai and Kulkarni (2023)[28] reported that considerable genetic variability was noticed for the characters like plant height, number of fruits per plant, average fruit weight, days to 50% flowering and yield per hectare. This indicated importance of these characters for the selection of superior genotypes. Srinivasulu *et al*. (2024) [29]reported that number of fruits per plant had the highest phenotypic and genotypic coefficients of variability, followed by lycopene content, fruit yield per plot, number of locules per fruit, fruit length and diameter.

HERITABILITY AND GENETIC ADVANCE

The concept of heritability comes into play while determining whether the phenotypic differences found among various individuals are new to genotypic differences or simply a result of environmental factors. The potentiality of selection at any given level of selection intensity is regarded as genetic advance. Heritability when studied in combination with genetic advance becomes a more reliable parameter and it provides assistance to breeders in allocating their resources efficiently towards important characters and making greater improvements in lesser time. The research pertaining to heritability and genetic advance on tomato have been reviewed below:

Saini *et al.* (2013)[17] reported high to moderate values for heritability and genetic advance for number of fruits per plant, yield per plant, polar diameter, fruit weight, number of flower-clusters per plant, number of fruit-clusters per plants, polar diameter and equatorial diameter. Shanker *et al.* (2013)[18] conducted an experiment on twenty-four hybrids along with their 11 parents and find out high heritability coupled with high genetic advance as per cent of mean was observed for number of primary branches per plant, plant height, number of fruits per cluster, fruit length, fruit width, average fruit weight, number of locules per fruit, pericarp thickness, titrable acidity, ascorbic acid, lycopene and shelf life. Hence, simple selection based on phenotypic performance of these traits would be more effective. Sherpa *et al.* (2014)[30] compared seventeen exotic tomato genotypes and observed that plant characters such as plant height, polar diameter, number of fruits per plant, fruit weight, pericarp thickness, total soluble solids, titratable acidity, ascorbic acid content, and fruit yield per plant had high heritability combined with high genetic advance, suggesting a preponderance of additive gene action and thus good response to selection. Singh *et al.* (2015)[19] observed high heritability along with high genetic advance in per cent of mean average fruit weight followed by unmarketable fruits per plant, fruit yield per plant, plant height, number of locules per fruit, number of primary branches per plant, pericarp thickness, marketable fruits per plant and number of fruits per plant. Rai *et al.* (2016)[31] revealed that high estimates of heritability and genetic gain were observed for average fruit weight, number of fruits per plant, locular wall thickness and lycopene content. An experiment conducted by Ligade*et al.* (2017)[20] reported high heritability associated with high genetic advance for plant height, number of fruits per plant, average fruit weight, fruit yield per plot, fruit yield per plant, TSS, ascorbic acid, pericarp thickness, and number of locules per fruit, demonstrating additive gene action. A study on tomato by Aralikatti*et al.* (2018)[32] reported high heritability along with high estimates of genetic gain was observed for number of fruits per cluster, number of seeds per fruit, average fruit weight, fruit yield per plant and fruit yield per hectare. Thus, indicating direct selection for these traits as a criterion for improvement. Dutta *et al.* (2018)[33] investigated 53 genotypes for genetic variability that provides high range of heritability as well as genetic advance occurs in plant height, primary branches/ plant, fruits per plant, fruit weight, polar diameter of fruit, equatorial diameter of fruit, pericarp thickness, ascorbic acid content of fruit. Meena *et al.* (2018)[22] reported highest heritability and genetic advance was recorded for fruit yield per plant, ridges on fruit, total soluble solids, flowers per cluster, pericarp thickness, fruits per plant, fruits per cluster, clusters per plant and branches per plant. Badhani*et al.* (2019)[34] reported high heritability with high genetic gain for marketable fruit yield and lycopene content, indicating that there is more scope for improvement through selection. A study on tomato by Chaudhari *et al.* (2019)[23] reported high heritability with high estimates of genetic gain were observed for plant height, number of branches per plant, number of fruits per plant, number of locules per fruit, average fruit weight, total yield per plant and test seed weight. Hussain *et al.* (2021)[24] working on tomato reported that high heritability and genetic advance as percent mean was observed for fruits per plant, average fruit weight, fruit yield per hectare, total sugars, titratable acidity and ascorbic acid content, indicating the additive genetic effect. For their improvement, phenotypic selection could be achieved by simple selection. Mahebub*et al.* (2021)[25] working on tomato reported highest estimates of heritability as well as genetic advance as per cent of mean for the characters average fruit weight, lycopene content, fruit firmness, shelf life, seed: pulp ratio, number of locules per fruit , pericarp thickness, fruit diameter, ascorbic acid content, fruit length, number of primary branches per plant at 30 DAT, total sugars, reducing sugars, titratable acidity, total soluble solids, days to 50 percent flowering, number of primary branches per plant at 90 DAT, fruit yield per plant, plant height 60 DAT, number of primary branches per plant at 60 DAT, plant height 30 DAT, plant height 90 DAT, fruit pH. Raut *et al.* (2021)[35] studied sixty diverse genotypes for 24 characters and found high heritability with high genetic advance as per cent of mean was observed for plant spread, polar diameter, fruit pH, pericarp thickness, fruit color, lycopene, equatorial diameter, titrable acidity, ascorbic acid, fruit firmness, average fruit weight, number of fruits per plant. Pooja *et al.* (2022)[26] studied forty-one genotypes in tomato and high heritability and genetic advance over mean were recorded for fruit length, average fruit weight, fruit diameter, fruit volume, number of fruits per plant, number of locules per fruit, yield per plant, yield per plot, yield per hectare, TSS, ascorbic acid content of fruit, number of fruits per plant, lycopene content, titratable acidity, lycopene content, pericarp thickness and firmness. Sahoo *et al*. (2022)[36] reported that characters such as average fruit weight, number of flowers per plant, plant height, number of locules per fruit, number of fruits per plant showed a high degree of heritability and moderate genetic advances was witnessed for the plant height and average fruit weight. Mahurtale*et al*. (2023)[27]reported that both high heritability and substantial genetic advancement in percentage of means were observed in days to first flowering, plant height at 60 and 90 days after transplanting (DAT), count of primary branches per plant at 60 and 90 DAT, stem girth at 60 and 90 DAT, fruit length, fruit diameter, average fruit weight, days to first maturity, total yield per plant, fruit yield per plot, and total soluble solids. A study by Panchbhai and Kulkarni (2023)[28] reported that high heritability combined with high genetic advance as a percentage of mean demonstrated the presence of additive gene action for the characters like plant height, number of fruits per plant, average fruit weight, days to 50% flowering and yield per hectare, which can be exploited for yield enhancement through phenotypic selection.Srinivasulu *et al*. (2024)[29] reported that traits such as lycopene content, number of fruits per plant, fruit yield per plot, fruit length and diameter and number of locules per fruit observed high heritability in conjunction with high genetic advance as a percent of mean. It showed that these traits are strongly influenced by additive gene action. Days to 50% flowering and days to red fruit stage have high heritability and moderate genetic advance as per cent of mean values, respectively, suggesting non-additive gene action.

CORRELATION STUDY

The correlation coefficient analysis is a bivariate analysis that measures the strength of association between two plant characters and the direction of their relationship. The correlation coefficient measures the degree of dependency between two parameters signifying the importance of traits which are to be focused in crop improvement programmes. The literature relating to correlation among different traits have been reviewed below:

Kumar *et al.* (2013)[37] reported that yield was significantly and positively associated with number of fruits per plant and number of fruits per cluster. Srivastava *et al.* (2013)[38] in their association study reported that yield per plant had significantly positive correlation with plant height, average fruit weight, number of fruits per plant and days to 50% flowering, indicating yield can be increased by selection based on these traits. Premalakshmi*et al.* (2014)[39] revealed that number of fruits per plant had positively significant association with fruit yield per plant. Meitei *et al.* (2014)[40] investigated forty-five tomato genotypes and concluded that fruit yield per plant was positively correlated with fruit diameter, single fruit weight and yield per hectare. Meena and Bahadur (2015)[41] observed a significantly positive correlation among fruit yield and fruit weight, number of fruits per plant at genotypic and phenotypic level. Kumar *et al.* (2015)[42] revealed that yield per plant had a significantly positive association with the plant height, primary branches per plant, number of fruits per plant and average fruit weight whereas, significantly negative correlation was there for days to 50% flowering both at genotypic and phenotypic level. Rathod *et al.* (2016)[43] carried out correlation and path analysis forty-three genotypes for yield and quality characters. The association studies showed that average fruit weight was positively and significantly correlated with equatorial diameter and ascorbic acid with titrable acidity of fruits at genotypic and phenotypic levels. Rawat *et al.* (2017)[44] studied fifty-nine genotypes of tomato during the year 2014 and 2015 and found that fruit yield was significantly and positively correlated with number of fruits per plant followed by average fruit weight while it was significantly and negatively correlated with days to first fruit ripening and days to 50% flowering. Kumar and Singh (2018)[21] reported that fruit yield per plant was positively correlated at genotypic and phenotypic level with number of flowers per plant, number of fruits per cluster, fruit diameter, fruit length, average fruit weight, number of locules per fruit and seed yield per plant. Mishra and Nandi (2018)[45] performed the association studies in fifty-five tomato genotypes and inferred a positive association between ascorbic acid content and days to first flowering, days to 50% flowering, number of fruits per plant, length of fruits, pericarp thickness of fruit, number of locules per fruit and fruit TSS. Ritonga *et al.* (2018)[46] investigated eighteen genotypes for character association studies. The result showed that fruit weight, fruit length and fruit diameter had significant positive correlation coefficient and fruit weight and fruit diameter had direct positive effect on fruit yield per plant. It is, therefore, recommended that fruit weight, fruit length and fruit number per plant should be given due importance in selection to develop shading tolerance variety in tomato. Roy *et al.* (2018) [47]performed correlation in twenty genotypes of tomato and observed number of primary branches, flowers per plant, plant height, fruits per plant, average fruit weight per plant were positively correlated with yield per plant. Singh *et al.* (2018)[48] reported that fruit yield per plant exhibited positive correlation with average fruit weight and titrable acidity at both genotypic and phenotypic levels. Total soluble solids found positive correlation with total phenolic content, total antioxidant, lycopene content and total carotenoid content whereas negative correlation with titrable acidity. Madhavi *et al.* (2019)[49] reported significantly positive correlation for fruit yield per plant with number of flowers per cluster, number of branches per plant, fruit length, fruit width and average fruit weight. However, significantly negative correlation was found for yield per plant with days to 50% flowering, number of locules per fruit and titrable acidity. Alam and Amitava (2019)[50] revealed that plant characters *viz.* primary branches per plant, number of fruits per plant and average fruit weight showed a positive and significant correlation to the fruit yield per plant at genotypic and phenotypic levels. Behera *et al.* (2019)[51] conducted an experiment using forty advance lines of tomato and highest positive correlation was reported from the pooled analysis of correlation between yield and numbers of truss per plant followed by number of fruits per plant and number of fruits per truss at both genotypic and phenotypic levels respectively. An experiment on tomato by Alam *et al.* (2019)[52] revealed a positive and highly significant correlation between the yield per hectare and yield per plant, average fruit weight, number of locules per fruit and pericarp thickness. Sriom*et al.* (2020)[53] revealed that number of fruits per plant, plant height, primary branches per plant and fruit length has positive significant and desirable association with fruit yield of tomato and yield could be increased by selecting these traits. A study on tomato by Gill *et al.* (2021)[54] reported that yield per hectare exhibited a significantly positive association, at both genotypic and phenotypic levels, with number of marketable fruits per plant, number of branches per plant, plant height at maturity, days to 50% flowering, weight of marketable fruits per plant, total number of fruits per plant, pericarp thickness, polar diameter and fruit firmness. Dumi *et al.* (2021)[55] reported that fruit per hectare expressed highly significant and positive correlation with fruit weight, number of fruits per plant and number of primary branches and plant height and days to first fruit set showed positive correlation which implies that these characters were the primer contributing factors to fruit yield.Maurya *et al.* (2020)[56] investigated sixteen genotypes of tomato and found that fruit width, fruit length, average fruit weight, number of locules per fruit and number of seeds per fruit showed significant positive association with yield (q/ha).Patel and Kumar (2021)[57]reported that fruit yield per plant was positively correlated with number of primary branches per plant, equatorial diameter, polar diameter, number of fruits per plant, average fruit weight, total soluble solid, days to first flowering and titrable acidity. Sahoo *et al*. (2022)[36] reported that the number of branches per plant, the number of flowers per plant and the number of fruits per plant were positively correlated (genotypic and phenotypic) with the tomato fruit yield. The higher magnitude of positive and significant association of the number of branches per plant, number of flowers per plant, number of fruits per plant with fruit yield suggested their importance as principal yield components in influencing the yield of the plant. A study by Panchbhai and Kulkarni (2023a)[58] reported that both genotypic and phenotypic correlation possessed highly significant and positive correlation with plant height, number of branches per plant, number of fruits per plant, average fruit weight, yield per hectare (t) with yield per plant (kg). However, it showed negative significant correlation with days to 50% flowering, fruit color and days to first harvest. Number of fruits per plant and average fruit weight exhibited positive significant correlation with plant height, number of branches per plant.

PATH COEFFICIENT ANALYSIS

Path analysis examines the relationship between a dependent variable and independent variables contributing towards the former. Path coefficient analysis divides the magnitude of association between characters into direct and indirect effects. Contrary to correlation coefficients it can measure relative importance of several characters contributing to yield at the same time. The literature relating to path analysis have been reviewed below:

Kumar *et al.* (2013)[37] reported that fruit weight had the most positive direct effect on yield per plant followed by number of fruits per plant, fruit diameter, and number of fruits per cluster. Direct selection on the basis of fruit weight, number of fruits per plant, fruit diameter, and number of fruits per cluster is reliable for yield improvement in tomato. Srivastava *et al.* (2013)[38] observed that average fruit weight, number of fruits per plant and number branches per plant had a positive direct effect on yield per plant whereas, plant height and number of fruits per cluster showed negative direct effects. Meitei *et al.* (2014)[40] investigated forty-five tomato genotypes and reported direct positive effect of fruit diameter, single fruit weight, number of fruits per plant and fruit clusters per plant towards the fruit yield per plant. Meena and Bahadur (2015)[41] observed a high direct positive genotypic effect and phenotypic effect of fruit weight over the fruit yield per plant. Rathod *et al.* (2016)[43] observed highest positive indirect effect of plant height on fruit yield per plant *via* average fruit weight and number of fruits per plant. Rawat *et al.* (2017)[44] observed that number of fruits per plant and average fruit weight exhibits maximum values for direct effect from path analysis on fruit yield for 2014 and 2015 respectively, under a two-year trial. Kumar and Singh (2018)[21]studied cause and effect relationship and revealed that number of seeds per fruit, number of clusters per plant, fruit diameter and number of fruits per plant exerted positive direct effects on fruit yield per plant at genotypic level. However, at phenotypic level, maximum exerted positive direct effects on fruit yield per plant was number of seeds per fruit. So, by improving these traits yield can be significantly increased. Mishra and Nandi (2018)[45] performed an experiment on fifty-five tomato genotypes and positive direct effects were observed in path analysis for ascorbic acid content to the number of fruits per plant and number of locules per fruit. A study on tomato by Ritonga *et al.* (2018)[46] investigated eighteen genotypes and reported that fruit weight and fruit diameter had direct positive effect on fruit yield per plant. It is, therefore, recommended that fruit weight and fruit diameter should be given due importance in selection to develop shading tolerance variety in tomato. Roy *et al.* (2018)[47] reported that flower per plant exhibited highest positive direct effect on average yield per plant and days to fifty per cent flowering showed lowest positive direct effect on average yield per plant. The traits *viz*, number of secondary branches, full flowering, plant height, fruits per plant was shown to have positive direct effect over the yield per plant. Singh *et al.* (2018)[48] reported that average fruit weight exhibited very high positive direct effect on fruit yield per plant followed by number of fruits per plant, days to first fruit setting and equatorial fruit diameter. A study on tomato by Madhavi *et al.* (2019)[49] observed positive direct effects of number of branches per plant, fruit width, average fruit weight, pulp yield and pericarp thickness over the fruit yield per plant. Alam and Amitava (2019)[50] revealed that number of secondary branches per plant, average fruit weight, number of fruits per plant and days to 50% flowering had direct positive effects over fruit yield per plant. Alam *et al.* (2019)[52] indicated that yield per plant had highest positive direct effect and fruit breadth had highest negative direct effect towards yield per hectare. Sriom*et al.* (2020)[53] revealed highest positive direct effect on fruit yield per plant was exerted by number of fruits per plant followed by average fruit weight, plant height, pericarp thickness, fruit circumference, number of locules per fruit and harvest duration. Gill *et al.* (2021)[54] reported that the weight of marketable fruits per plant, total number of fruits per plant, yield per plant and equatorial diameter of fruits were the most propitious characters influencing the dependent variable *viz.* yield per hectare directly as well as indirectly. Dumi *et al.* (2021)[55] reported that fruit yield per plant had highest positive direct effect at both genotypic and phenotypic levels on fruit yield per hectare. This indicated that fruit yield per plant is one of the most important characters in influencing fruit yield per hectare. Number of fruits per plant showed positive high to moderate indirect effect on fruit yield per hectare via fruit weight, days to first fruit maturity and days to first fruit harvesting. Fruit yield per plant exhibited very high to moderate indirect contribution on fruit yield per hectare via number of fruits per plant, number of primary branches and plant height. Maurya *et al.* (2020)[56] observed high positive direct effect towards yield *via.* days to 50% flowering, total soluble solids and average fruit weight. An experiment by Patel and Kumar (2021)[57]revealed positive direct effect for plant height at maturity, number of primary branches per plant, days to first flowering, days to fruit maturity at physiological stage, polar diameter, number of locules per fruit, number of fruits per plant, average fruit weight, total soluble solids, titrable acidity and ascorbic acid on fruit yield per plant and for yield improvement, selection of these characters would be more reliable. Sahoo *et al*. (2022)[36] reported that the number of fruits per plant, average fruit weight and the number of branches per plant had a positive direct effect on yield, which indicates that these characters have a direct influence on yield. A study by Panchbhai and Kulkarni (2023a)[58] reported that highest positive direct effects was recorded by yield per hectare (t) followed by number of fruits per plant, number of branches per plant, number of locules per fruit, pericarp thickness and days to first harvest on yield.

GENETIC DIVERSITY

Genetic divergence of yield and yield attributing traits would be of most useful while planning any crop improvement programme. D^2 statistics developed by Mahalanobis (1936)[59] provides a measure of magnitude of the extent of diversity among genotypes under comparison. Suitable parental lines for heterosis breeding programme can be selected by grouping of genotypes based on D^2 analysis it can further help in development of improved varieties for commercial cultivation. The literature relating to genetic diversityhave been reviewed below:

Qumer Iqbal *et al.* (2014)[60] investigated forty-seven tomato genotypes for seven traits. Cluster analysis grouped all forty-seven genotypes into five divergent clusters. The genotypes in clusterII and cluster indicated uniform maturity and higher yield. The D^2 statistics confirmed highest distance between cluster III and cluster V while maximum similarity was observed in clusterII and clusterIII. It is therefore recommended that crosses between genotypes of clusterII and clusterV with those of cluster-I and cluster-III may exhibit heterosis in F1 for hybrid breeding and selection of superior genotypes in succeeding generations for cross breeding programme. Dar *et al*. (2015)[61] investigated sixty genotypes of tomato and D^2 statistics revealed that β-carotene contributed maximally towards the genetic divergence followed by ascorbic acid, total soluble solids, alcohol insoluble solids, pericarp thickness, lycopene content and polygalacturonase activity. Sixty genotypes were grouped into twenty clusters. Fourteen clusters were monogenotypic and cluster I possessed highest number of genotypes numbering twenty-five. Out of twenty clusters, cluster VII is promising for minimum polygalacturonase activity and high average fruit weight, cluster VIII had highest fruit yield per plant, number of locules per fruit and yield per hectare and cluster XVII was superior for ascorbic acid. However, cluster XX was found promising for β-carotene, lycopene content and number of fruits per plant. The highest inter cluster D^2 values were estimated between clusters XII and XX, followed by clusters XI and XX, clusters VII and XX, and clusters XV and XX, it indicates that there is enough scope for the improvement of tomato by hybridization and selection. Henareh*et al.* (2015)[62] evaluated ninety-seven tomato landraces collected from Turkey and Iran for twenty-one characters. Group I contained 29 genotypes. These genotypes had length and width of leaf, length of fruit and pericarp thickness more than other genotypes and most early maturing genotypes were in this group. In cold climatic conditions, early maturing genotypes should be cultivated. In group II with 22 genotypes, the yield was higher than other groups in these genotypes. Genotypes of third group have 50% of the traits studied were dominant compared with genotypes of other groups. Most genotypes with large fruit size were observed in this group. In fresh market tomato, fruit size has significant effect on its marketability. Large number of traits such as the number of flowers per inflorescence, number of fruits per plant, number of days to 50% fruit maturity, fruit set per cluster and TSS was viewed for genotypes in group IV. All genotypes of this group were cherry tomatoes. Fruit Traits like TSS is particularly important to the processing industry and has received more attention than other fruit traits. The acidity of the fifth group genotypes was more than genotypes of other groups. Acidity influences the storability of processed tomato. Higher acidity with lower pH reduces the risk of pathogen growth in tomato products. Kumar *et al*. (2016)[63] evaluated forty genotypes for nineteen characters which were grouped into seven clusters. Cluster II had highest (24) genotypes which was followed by cluster I (2) and VII (2) while cluster III, IV and V had one genotype. 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 intercluster distance. Cluster III and VII had maximum mean values for number of fruits per plant, average fruit weight and fruit yield per plant while genotypes belonging to clusters IV and VI showed minimum values. Therefore, cross made between these genotypes were expected to give maximum heterosis. Sahoo *et al*. (2022)[36] reported that largest group (Cluster IV) included 7 genotypes followed by cluster XI comprising 5 genotypes. Cluster I and XV include 3 genotypes in each cluster, cluster II, III, V, VI, VII, VIII, IX, X, XII, XIII, XIV, XVI and XVII with 2 genotypes in an individual cluster whereas, clusters like XVIII and XIX have only one genotype in an individual cluster. The minimum intracluster distance and maximum intracluster distance were observed in cluster II and cluster XVIII, 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.

CONCLUSION

The literature reviewed in this paper accentuated the variability, heritability, genetic advance, correlation, path analysis and genetic diversity available in tomato genotypes. The scope for the selection of desirable genotypes offered by the studies on the extent of variability available in the germplasm and subsequent estimates of heritability, genetic gain and inter relations among the different characters helps in effective selection. However, if selection of genotypes is not responsive, further, genetic divergence helps in selection of superior parents for hybridization programme that results in development of better hybrids and desirable recombinants. Hence, the present investigation was planned to evaluate the introduced and available germplasm of tomato crop.

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