Review Article

A Review on Genetic diversityamong Tomato(*Solanum lycopersicum* L.) genotypes

ABSTRACT

Tomato (*Solanum lycopersicum* L.) holds significant importance as a vegetable crop worldwide and is classified within the Solanaceae family. 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. Although originating in the Peru-Ecuador region, the tomato has gained immense popularity and widespread cultivation in India, exhibiting significant variability in various plant traits. To enhance tomato cultivation, a comprehensive understanding of genetic variability, heritability, genetic advance, correlation, path coefficient, and genetic diversity of both qualitative and quantitative traits is imperative. Traits showing higher values for genetic variability, heritability and genetic advance shows increased likelihood of achieving a higher selection response for maximizing productivity and yield.High significant positive association and positive direct effect of various yield attributing traits on fruit yield shows that these characters are the prime factors contributing to fruit yield. Improvement in yield and quality of self-pollinated crops like tomato also involves selecting genotypes with favorable trait combinations present in nature or through hybridization. Therefore, this review focuses on gathering information about the collection of indigenous tomato genotypes to formulate a breeding strategy for yield enhancement.

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

1.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 comprehensive grasp of the genetic diversity is fundamental for initiating a crop enhancement endeavor. It underscores the significance of segregating the observed variability into heritable (additive variance) and non-heritable (non-additive variance) traits, employing appropriate genetic parameters like genotypic coefficient of variation, phenotypic coefficient of variation, heritability, and genetic advance. This is crucial due to the interplay between genotypes and environmental variation within such a population. The genotypic and phenotypic coefficients of variation serve to identify the level of variability among genotypes, while heritability and genetic advance aid in assessing the impact of the environment on trait expression and the potential extent of improvement achievable through selection.[16].Statistical techniques such as correlation and path coefficients are invaluable for assessing the relationship between fruit yield and its contributing traits. Path analysis distinguishes between the direct and indirect effects of a trait's association. Correlation and path coefficients enable breeders to identify effective traits for targeted enhancement and allocate resources efficiently in crop improvement programs. Understanding genetic diversity, its characteristics, and extent is indispensable for any heritable crop improvement initiative. It evaluates the relative contributions of various components at both inter and intra-cluster levels.To enhance tomato cultivation, a comprehensive understanding of genetic variability, heritability, genetic advance, correlation, path coefficient, and genetic diversity of both qualitative and quantitative traits is imperative. Traits showing higher values for genetic variability, heritability and genetic advance shows increased likelihood of achieving a higher selection response for maximizing productivity and yield. High significant positive association and positive direct effect of various yield attributing traits on fruit yield shows that these characters are the prime factors contributing to fruit yield.

2.1GENETIC 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 characteristics like the number of fruits per plant, fruit weight, yield per plant, and polar diameter exhibited moderate to high levels of Genetic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV).In the conducted experiment by Shanker *et al.* (2013)[18], notably high estimates of Phenotypic Coefficient of Variation (PCV) and Genetic Coefficient of Variation (GCV) were observed for plant height, titrable acidity, ascorbic acid, average fruit weight, number of fruits per cluster, yield per plant, and lycopene. These findings suggest a substantial amount of variability within these traits. 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. This suggests an increased likelihood of achieving a higher selection response for these 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 at harvest, number of 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 were evaluated for genetic variability, revealing high GCV and PCV for traits like 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 were observed for total soluble solids among the minicore accessions. An experiment conducted by Hussain *et al.* (2021)[24]reported that there were high PCV and GCV values for traits such as fruits per plant, average fruit weight, fruit yield per hectare, total sugars, titratable acidity, and ascorbic acid content, indicating a significant additive genetic effect. For their enhancement, phenotypic selection could be accomplished through straightforward selection methods. 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]noted that a moderate degree of genetic variability was detected in traits such as 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 polar diameter, fruit equatorial diameter, average fruit weight, days to first maturity, total yield per plant, fruit yield per plot, and total soluble solids, as indicated 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 underscores the significance of these characters in determining the superior genotypes. Srinivasulu *et al*. (2024) [29]documented that the number of fruits per plant exhibited the greatest phenotypic and genotypic coefficients of variability, succeeded by lycopene content, fruit yield per plot, number of locules per fruit, and fruit length and diameter that offered more chances for selection for these traits. Low PCV and GCV were stated in the days to red mature fruit stage and days to 50% blooming, recommanding that there is little scope for improvement for these traits.

2.2HERITABILITY AND GENETIC ADVANCE (GA)

The concept of heritability is crucial in discerning whether the observed phenotypic differences among individuals stem from genetic disparities or are merely influenced by environmental factors. Genetic advance, on the other hand, signifies the potential for selection at a given level of selection intensity. When studied alongside heritability, genetic advance becomes a more dependable parameter, aiding breeders in allocating resources efficiently towards key traits and facilitating greater improvements in less time. The research concerning heritability and genetic advance in tomatoes has been reviewed below:

Saini *et al.* (2013)[17] reported high to moderate heritability and GA for yield per plant, number of fruits 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]in an experiment involving twenty-four hybrids and their 11 parent lines, high heritability along with substantial genetic advance as a percentage of the mean was observed for several traits. These included the 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, titratable acidity, ascorbic acid, lycopene, and shelf life. Therefore, it suggests that straightforward selection based on the phenotypic performance of these traits would likely 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, titrable 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.

2.3CORRELATION 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 positively associated with number of fruits per plant and number of fruits per cluster. Srivastava *et al.* (2013)[38] in their association study revealed that yield per plant had significantly positive correlation with plant height at harvest, average fruit weight, number of fruits per plant and days to 50% flowering, indicating yield can be enhanced by selection based on these traits. Premalakshmi*et al.* (2014)[39]stated that number of fruits per plant is positively significantly associated 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]stated that yield per plant had a significantly positive correlation 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 analysis on forty-three genotypes for yield and other characters. The correlation studies stated that average fruit weight was positively and significantly associated with equatorial diameter and ascorbic acid with titrable acidity of fruits at both genotypic and phenotypic levels. Rawat *et al.* (2017)[44] studied fifty-nine genotypes of tomato during the year 2014 and 2015 and found that tomato 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 associated at both genotypic and phenotypic level with number of fruits per cluster, fruit diameter,number of flowers per plant, 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 results showed that fruit weight, fruit length and fruit diameter had high positive correlation coefficient and average fruit weight and fruit equatorial diameter had direct positive effect on fruit yield per plant. It is, therefore, recommended that average fruit weight, fruit equatorial diameter and number of fruits 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 primary branches, number of flowers per plant, plant heightat harvest, fruits per plant, average fruit weight per plant were positively associated with yield per plant. Singh *et al.* (2018)[48] reported that tomato fruit yield per plant showed high positive correlation with titrable acidity andaverage fruit weight at genotypic and phenotypic levels. Total soluble solids also found positive association with total antioxidant, lycopene content, total phenolic contentand total carotenoid content but negative association with titrable acidity of tomato fruit. Madhavi *et al.* (2019)[49] reported significantly positive correlation for fruit yield per plant with fruit equatorial diameter, number of flowers per cluster, branch number per plant, fruit polar diameter and 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 succeeded by fruits number per plant and fruits number per truss at both genotypic and phenotypic levels respectively. An experiment on tomato by Alam *et al.* (2019)[52]stated a highly significant positive correlation between the yield per hectare, average fruit weight, number of locules per fruit, yield per plantand pericarp thickness. Sriom*et al.* (2020)[53]stated that fruits number per plant, plant height at harvest, primary branches per plant and fruit polar diameter has positive significant and desirable association with fruit yield of tomato and yield could be increased by selecting these traits. An experiment on tomato by Gill *et al.* (2021)[54]stated that fruit yield per hectare exhibited a significantly positive correlation, at phenotypic and genotypic 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 association with number of fruits per plant,average fruit weight, number of primary branches, plant height and days to first fruit set showed positive correlation which shows 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, fruit weight, number of locules and number of seeds per fruit observed significant positive association with yield.Patel and Kumar (2021)[57]revealed that tomato fruit yield per plant was highly positively associated with number of primary branches per plant, equatorial diameter, polar diameter, fruits number per plant, fruit weight, total soluble solid, days to first flowering and titrable acidity. Sahoo *et al*. (2022)[36]stated that the branches number per plant, flowers number per plant and the number of fruits per plant were positively associated (genotypic and phenotypic) with the tomato 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 phenotypic and genotypic correlation possessed significant and positive association ofnumber of branches per plant, plant height at harvest, average fruit weight, number of fruits per plant, yield per hectare (t) with yield per plant (kg). This desirable association with fruit yield of tomato could be utilized in enhancing yield by selecting these traits. However, it showed negative significant asociation with fruit color,days to 50% flowering and days to first harvest. These traits play less important role in yield enhancement of tomato genotypes.Fruits number per plant and fruit weight showed positive significant association with plant height, number of branches per plant.

2.4PATH COEFFICIENT ANALYSIS

Path analysis investigates the relationship between a dependent variable and independent variables that contribute to it. It breaks down the association between variables into direct and indirect effects. Unlike correlation coefficients, path analysis can determine the relative importance of multiple variables contributing to a yield simultaneously. Below, the literature on path analysis has been reviewed:

Kumar *et al.* (2013)[37]reported that average fruit weight had the highest positive direct effect on fruit yield per plant, succeeded by the number of fruits per plant, fruit equatorial diameterand the number of fruits per cluster. Therefore, direct selection based on fruit weight, number of fruits per plant, fruit equatorial diameter, and number of fruits per cluster is considered reliable for yield enhancement in tomatoes. Additionally, Srivastava *et al*. (2013)[38]observed that average fruit weight, number of fruits per plant, and number of branches per plant had a positive direct effect on yield per plant, while plant height and the 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 that average fruit weight and the number of fruits per plant show the most substantial positive indirect effects of plant height on fruit yield per plant. Rawat *et al.* (2017)[44] observed that average fruit weight and number of fruits per plant 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]conducted an experiment using 55 tomato genotypes, and the number of fruits per plant and number of locules per fruit showed positive direct impacts in path analysis for ascorbic acid amount. 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 displayed a very high positive direct effect on fruit yield per plant, succeeded by the 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]documented that fruit yield per plant exerted the highest positive direct effect, both at the genotypic and phenotypic levels, on fruit yield per hectare. This highlights the significance of fruit yield per plant in influencing overall fruit yield per hectare. Additionally, the number of fruits per plant demonstrated a positive, ranging from high to moderate, indirect effect on fruit yield per hectare through factors such as fruit weight, days to first fruit maturity, and days to first fruit harvesting. Moreover, fruit yield per plant displayed a very high to moderate indirect contribution to fruit yield per hectare via the number of fruits per plant, number of primary branches, and plant height at harvest.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. Enhancement of yield depends on the selection of these characters for tomato genotypes.

2.5GENETIC DIVERSITY

To assess genetic divergence in yield and yield-related traits is crucial for planning crop improvement programs. The D^2 statistics devised by Mahalanobis (1936) offer a quantitative measure of the magnitude of diversity among compared genotypes. By grouping genotypes based on D^2 analysis, suitable parental lines can be identified for heterosis breeding programs, facilitating the development of improved varieties for commercial cultivation. The literature pertaining to genetic diversity has been reviewed below:

Qumer Iqbal *et al.* (2014)[60] investigated forty-seven tomato genotypes for seven traits. Cluster analysis categorized all forty-seven genotypes into five distinct clusters. Genotypes within cluster II and cluster Vdisplayed uniform maturity and higher production. D^2 statistics confirmed the greatest distance between cluster III and cluster V, while the highest similarity was observed between cluster II and cluster III.It is therefore recommended that crosses between genotypes of clusterII and clusterV with those of cluster-I and cluster-III may exhibit heterosis in F_1 for hybrid breeding and selection of superior genotypes in succeeding generations for cross breeding programme. Dar *et al*. (2015)[61]in the study of sixty tomato genotypes, through D^2 statistics revealed that β-carotene contributed most significantly to genetic divergence, followed by ascorbic acid, total soluble solids, alcohol insoluble solids, pericarp thickness, lycopene content, and polygalacturonase activity. These genotypes were then grouped into twenty clusters, with fourteen clusters being monogenotypic and cluster I containing the highest number of genotypes at twenty-five. Among these clusters, several stood out for specific traits: cluster VII showed promise for minimal polygalacturonase activity and high average fruit weight, cluster VIII exhibited the highest fruit yield per plant, number of locules per fruit, and yield per hectare, while cluster XVII was superior in terms of ascorbic acid content. Notably, cluster XX displayed promise for β-carotene, lycopene content, and number of fruits per plant. The highest inter-cluster D2 values were found between clusters XII and XX, followed by clusters XI and XX, clusters VII and XX, and clusters XV and XX, indicating significant potential for tomato improvement through 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 contained the highest number of genotypes (24), followed by cluster I (2) and VII (2), while clusters III, IV, and V each had one genotype. The highest intra-cluster distance was observed in cluster VII, followed by clusters VI and II, indicating genetic diversity. Clusters II and VI exhibited the maximum intercluster distance, while clusters III and IV showed the minimum. Clusters III and VII had the highest mean values for number of fruits per plant, average fruit weight, and fruit yield per plant, while genotypes from clusters IV and VI displayed the lowest values. Therefore, crosses between genotypes from these clusters were anticipated to yield 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 suggests that hybridization can be conducted among genotypes from any pair of clusters, and subsequent selection can be performed from segregating generations.

3. CONCLUSION

The literature surveyed in the paper above emphasized the diversity, heritability, genetic advance, correlation, path analysis, and genetic diversity present in tomato genotypes. The studies on the extent of variability in the germplasm, along with subsequent assessments of heritability, genetic gain, and relationships among different traits, provide valuable insights for effective selection of desirable genotypes. However, if the selection of genotypes proves unresponsive, further exploration of genetic divergence aids in identifying superior parents for hybridization programs, leading to the development of improved hybrids and desirable recombinants. According to research on genetic diversity, closer genetic relationships are indicated by lower genetic distances, while farther genetic distances are indicative of more distant genetic relationships. In order to produce heterotic hybrids in the first generation of offspring and some potentially transgressive segregants in the F2 generation, hybridization is best suited for clusters with greater genetic separation. Predictions of genetic divergence have been suggested for vegetable crops like tomato in order to give a variety of parents for high-yielding hybrids. It is clear that genetic variety is important for a species ability to adapt and survive. For instance, a species with high genetic diversity will tend to produce a wider variety of offspring, where some of them may become the fit variants. IConsequently, the present investigation was designed to assess both introduced and available germplasm of the tomato crop.

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