REVIEW ARTICLE

VARIABILITY STUDIES IN CUCUMBER (*CUCUMIS SATIVUS* L.)

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Abstract: It is believed that cucumber has been originated from India and is acknowledged that China is the secondary center of diversity. Despite being originated in the Indian sub-continent and having substantial variety of plant traits, the crop remains underutilized with respect to its breeding value and economic potential. Cucumber improvement has a huge scope in India and overseas. A detailed knowledge on genetic variability, heritability, genetic advance, correlation, path coefficient of various quantitative characters and genetic diversity is essential for any crop, to achieve highest productivity. Studies in this aspect are minimal and are not carried out for every genetic materials and climatic condition. Hence, the information below provides a soild breeding plan for the improvement of cucumber crop.

Keyword: Cucumber, Variability, Correlation, Path coefficient, Genetic diversity

INTRODUCTION

Successful breeding plan is accomplished by the following characters such as selection of parents, wide genetic heterogeneity available to the breeders, productive usage of variability and heritability available in the plant population. The significance of genetically distinct genotypes as a means of acquiring transgressive seggregants with beneficial combinations has been noticed by several workers (Kurian and Peter, 1994). Mahalanobis (1936) used normal distance as an important tool in the estimation of genetic diversity quantitatively and a logical choice for capable parents for a breeding programme. Knowing about the relation between the plant yield and yield components is evident for choosing preferred plant types. Path coefficient (Wright, 1921; Dewey and Lu, 1959) estimated the immensity of indirect and direct effects of traits on yield which is the most complex dependent character which help the breeders to choose important component traits during selection where as the values of correlation coefficient, measure the degree of relationship. The heritability indicates the inherent proportion of variation where as the amount of genetic variation present in various desirable traits is indicated by the estimation of genetic coefficient of variation. The heritability estimate suggests the amount of observed variability, which leads to genetic difference. Heritability broadly represents a greater role about the importance of selection, but Johnson *et al.* (1955) had proved that genetic advance and heritability should be mutually considered for authentic conclusion, to represent true inheritance properties. Clear cut knowledge about the diversity and genetic variability within the germplasm lines is essential for crop improvement.

Genetic variability, heritability and genetic advance

Genetic variability is the most important component for crop improvement. It is the basic requirement for any successful breeding programme. To select a desirable type it is necessary to have the sound knowledge on existing variability in the genotypes. According to Vavilov (1951) there is a better scope to select the desired types from wide range of variability. Heritability of a character that indicates to what measure the trait can be transmitted from one generation to another generation (Balouch *et al.*, 2003) and is an prominent tool to foresee the magnitude of genetic gain that follows choosing a trait (Adeniji and Kehinde, 2003). However cucumber has a limited genetic base, with 3-8% of genetic variability.

Genotypic mean sum of squares is highly significant for all the characters which indicates that there was existence of variation in the genotypes (Gaikwad *et al.*, 2011). The expression of the traits depends on the modifying effect of environment which indicates higher Phenotypic coefficient of variation (PCV) than Genotypic coefficient of variation (GCV) for all the characters. Maximum GCV and PCV was seen in PDI followed by first female flower node number, length of fruit, weight of fruit and fruits per vine. High percentage of heritability is observed in all characters. High percentage of heritability along with high evaluation of genetic advance was marked by fruit weight and final vine length. Remaining characters showed high heritability with medium or little genetic advance.

Veena *et al.* (2012) observed that the character days to 1st opening of female and male flower, days to 1st

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fruit harvest, nodes per vine and vine length showed low value of GCV and PCV. Except vine length, node at 1st female flower appears, flesh thickness, yield (per plant, plot and hectare) and fruit weight all other traits noted high heritability. Contradiction to above finding they observed high genetic advance along with high heritability for seed cavity breadth and node at first female flower appearance in cucumber. Whereas, Ullah *et al.* (2012) revealed highest PCV for the traits, yield per plant, length of the fruit, weight of the fruit and fruits per plant. Low PCV was observed in days to flowering and days to harvest. The traits which had high to moderate genetic gain as well as heritability were length of the fruit, weight of the fruit, days to flowering and fruits per plant, showing that these were easily inherited characters.

Kumar *et al.* (2013) observed high PCV, GCV and heritability estimates combined with high genetic gain for yield per plot and seed vigour index-I. Low heritability was reported for higher incidence of angular leaf spot and anthracnose. On the other hand 8 parents and their 28 F_1s and 28 F_2s for ten characters were studied in cucumber by Singh *et al.* (2013). The analysis of variances for parents, F_1s, F_2s, and parents vs F_2s were highly significant to all the characters. Similarly, among parent vs F_1s all the traits exhibited great measure of genetic variability except the length of the vine. The variability among parents, F_1s and F_2s was highest for yield per vine succeeded by fruit weight. In F_1 generation the narrow sense heritability estimates were not found to be highest for any character. Mean percentage of genetic advance was observed moderate for weight of the fruit and yield per vine. Contrary to F_1, in F_2 generation vine yield and fruit weight recorded high heritability with high genetic advance in % of mean and this may be due to greater contribution of additive genetic component in F_2 generation.

Ranjan *et al.* (2015) observed notable significant variation for all the fourteen traits while evaluating forty two indigenous collections of cucumber. The characters namely, seeds per fruit, nodes bearing first female flower and fruits per plant showed high GCV, PCV and heritability estimates along with high genetic gain reflecting that these traits are governed by additive gene effects and more responsive to selection.

Pushpalatha *et al*. (2016) reported a close proximity in the genotypic and phenotypic coefficients of variability, showing little impact of environment on expression of the various traits studied in cucumber. The mean squares were found to be significant for all the characters under study but the variation due to replication was non-significant. They also revealed high phenotypic coefficient of variation (PCV) and Genotypic coefficient of variation (GCV) for fruit flesh thickness, yield per plant, fruits per plant, nodes per plant, average fruit weight, branches per plant, vine length and internodal length. High genetic advance, combined with high heritability as % mean, was noted for all the characters studied except, number of days to 50% flowering, number of days to first fruit harvest and number of days to first female flower opening.

Kumari *et al.* (2017) investigated 19 genotypes of cucumber for twenty one traits to study the magnitude and nature of genetic variability between them. High estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were obtained for traits like number of node at which first pistillate flower appears, length of the fruit and fruit yield (q/ha). High genetic advance coupled with high heritability as mean percentage was recorded for length of the fruit, number of nodes at which first female flower appears followed by yield of the fruit (q/ha), test weight, fruits per plant, average fruit weight, primary branches per vine, nodes per vine.

Shah *et al.* (2017) performed an experiment in summer season and found that the mean sum of square due to treatment had highly significant differences at 1% level for most of the traits except germination rate. Number of nodes bearing first male flower was the single character which recorded highest PCV, GCV and high genetic advance along with high heritability over mean. But according to Shah *et al*. (2018) the analysis of variance (ANOVA) put forth significant differences at 1% for most of the characters other than carbohydrate content, which showed a broad range of variability among the 13 genotypes for all the traits. Carbohydrate content, primary branches per vine, protein content and diameter of seed were reported high differences between PCV and GCV.

Ahirwar and Singh (2018) conducted an experiment during July-October, 2014 and February-June, 2015. The PCV was more than GCV and the difference between GCV and PCV was less for most of the traits showing less impact of the environment in the expression of these characters. During first season and second season, GCV and PCV were highest for length of the fruit and yield respectively. For pooled analysis, in first season PCV was highest for yield but in second season no character had shown high value for it. Deepa *et al*. (2018) while evaluating 30 genotypes of cucumber in Karnataka reported GCV and PCV were high for number of leaves at 90 days after sowing, vine length, inter nodal length, leaf area, fruits per vine, fruit length, branches per vine, average fruit weight, fruit yield per vine, fruit yield per plot and fruit yield per hectare. High heritability combined with moderate to high genetic advance was observed for all the traits except for days to female flowering, first male flowering and percentage of fruit set.

Pradhan *et al.* (2018) observed all the cucumber genotypes showed significant differences for most of the traits. Wider variation was observed for different growth and yield related characters. However, intermodal length, number of fruits per vine, and node of first female bloom recorded low value which showed that there lies minimum variation and very less scope for selection. Greater values of phenotypic coefficient of variation (PCV) as well as genotypic coefficient of variation (GCV) was observed for characters like length of the fruits, branches per vine, fruit weight, node of first male bloom, vine length and downy mildew scoring. High heritability along with high genetic advance over mean was observed in traits like fruit yield per hectare, vine length, and fruit weight. Tamang *et al*. (2018) carried out their experiment at Department of Horticulture, Sikkim University. Highest GCV was found for fruit weight, fruits per plant, vine length, fruit length, and node at which first female flower appeared and primary branches per plant. High heritability coupled with high genetic advance as percentage of mean was observed in fruit yield per plant.

Gangadhara *et al*. (2019) performed their experiment at Division of vegetable crops, IIHR, Bengaluru during winter season. They found that the characters fruit weight, fruit yield per plant, number of fruits and nodal position of first female flower had noted high GCV, PCV and high genetic advance with high heritability. Wide variations between thirty six cucumber genotypes for several horticultural traits were observed by Karthick *et al*. (2019). In their study they reported that the traits like number of nodes bearing first male flower, primary branches, number of female flower, number of male flower, fruits per plant, weight of the fruit, length of the fruit and yield per plant recorded high value for GCV and PCV.

Correlation and path coefficient studies

The statistical measure to determine the extent of association, whether positive or negative among various plant characters and which helps to identify the trait on which selection can be done for crop improvement with associated characters is known as correlation coefficient. A standardized partial regression coefficient, which divides the correlation into indirect and direct effect is known as path coefficient analysis. In another way, it measures the direct and indirect contribution of various independent traits on a dependent trait. The concept of path analysis was given by Wright in the year 1921 and the technique was pioneered by Dewey and Lu in the year 1959 that helps in identifying yield contributing traits thus, helpful in indirect selection. Correlation coefficients in association with path coefficients provide more authentic information, which can be successfully predicted in crop improvement programme. If the correlation between yield and trait is a result of direct effect of the trait, it shows actual relationship between them and direct selection for the trait leads to yield improvement. Though, the correlation coefficient is primarily due to indirect effect of the trait through another important character, indirect selection through such character will be useful in yield improvement.

Kumar *et al*. (2011) while evaluating 30 genotypes of cucumber during *kharif* season observed that all the characters were significant at both genotypic and phenotypic levels. Correlation studies disclosed that yield had negative association with intensity of powdery mildew, days to marketable maturity, angular leaf spot, nodes bearing first female flower and anthracnose. Remaining traits recorded positive association with yield. Path coefficient analysis revealed that average weight of the fruit showed high positive direct effect on yield followed by seed vigour index-II, harvest duration, anthracnose and powdery mildew, serious incidence of angular leaf spot, total soluble solids, and marketable fruits per plant whereas, negative direct effect of seed vigour index-I, fruit length and breadth, days to marketable maturity, seed germination, number of nodes bearing first female flower and fruit length was observed on yield. However, Ullah *et al*. (2012) observed that fruits per plant, fruit diameter, leaf per plant, flesh thickness and weight of the fruit showed positive and significant correlation with fruit yield. Days to harvest reported negative correlation with yield stating that late maturing varieties showed higher yields while the early maturing varieties had lower yields in cucumber.

Veena *et al*. (2013) revealed that 100 fruits per plant, weight of the seed, length of the fruit, average fruit weight, seed cavity length and flesh thickness must be considered for selection for yield in cucumber. Innark *et al*. (2013) observed that along with above character flesh pith length and harvesting period were positively correlated and significantly with yield of cucumber.

According to Hasan *et al*. (2015) there was positive and significant association of weight of the fruit and fruits per plant with fruit yield. Ahirwar *et al*. (2017) observed high positive direct effect of fruit weight and fruits per plant on yield of cucumber which showed the importance of fruit number and its weight for figuring the yield in cucumber.

Pal *et al*. (2017) recorded maximum significant correlation between fruit length and diameter, fruit yield per plant with average fruit weight, marketable fruits per plant, harvest duration, number of primary branches per plant and vine length. Linear relationship between yield per plant and fruit characters suggest that method of selection should be concentrated over fruit characteristics for crop improvement. Whereas, yield per plant had significant negative correlation with days to first harvest, number of nodes bearing first female flower, severity of four foliar diseases and total soluble solids indicating that disease affected varieties and early maturing varieties showed lesser yields in cucumber crop. Path analysis provided an accurate picture that harvest duration, marketable fruits per plant had high positive direct effect. Whereas, days to first harvest followed by severity of downy mildew had high negative direct effect on plant yield. Kumar *et al.* (2018) reported that genotypic correlation is more than phenotypic correlations indicating that the characters were highly heritable. The traits *viz*., primary branches per plant, fruits per plant, weight of the fruit, vine length and fruit length resulted in maximum significant positive association with yield. The path coefficient analysis showed that weight of the fruit, primary branches per plant, fruits per plant, length of the fruit, 100 seed weight, days to last fruit harvest, seeds per fruit, nodes per vine and fruit diameter have direct positive phenotypic and genotypic effect on yield. Fruit yield can be genetically improved by direct selection of the above mentioned yield components. Murtadha and Sanni (2018) reported positive and highly significant genotypic correlation between vine length and fruit yield in dry season. They also found negative association between number of days to flowering and vine length indicated short plant types are obtained if early flowering plants are selected.

Rajawat *et al.* (2018) revealed that fruit yield per vine exhibited positive and significant correlation with branches per vine followed by fruit per vine, female flower per vine, fruit weight, fruit diameter, vine length, vitamin C and TSS. Path analysis study reported maximum positive direct effect on fruit yield per vine, male flowers per vine followed by fruits per vine, fruit weight, vitamin C, female flowers per vine and branches per vine. Whereas, highest negative direct effect on the fruit yield per vine was observed by TSS and nodes of first female flower. Sharma *et al.* (2018) observed that the yield per plot had positive significant relation with average weight of the fruit, marketable fruits per plant, seed vigour index-I harvest duration, and seed germination, whereas significant negative correlations were reported with nodes bearing first female flower, days to marketable maturity, anthracnose and angular leaf spot both at genotypic and phenotypic levels respectively.

On evaluating 15 parthenocarpic gynoecious hybrids lines of cucumber under controlled environment for both quality and yield Gangadhara *et al.* (2019) reported that fruit yield per plant had significant and highly positive association both phenotypically and genotypically with fruits per plant and maximum direct positive effects towards yield was observed by fruits per plant, weight of the fruit and days to fifty percent flowering. Whereas, Bartaula *et al.* (2019) observed high significant and positive correlation of fruit yield with fruit diameter and days to flowering reported negative correlation suggesting that larger the fruit size higher will be the yield while early flowering varieties had lower yields.

Genetic diversity studies:

Genetic diversity is the source of variation in the available gene pool, which is essential for crop improvement. Deep knowledge on genetic diversity and relationships of varieties is essential for effective utilization and conservation of cucumber genetic resources. Clear information on the degree of genetic divergence and nature of the parents is the vital for an effective breeding programme. Genetic diversity is a vital tool to assess relative contribution of different components to the total divergence both at inter and intra-cluster levels and to quantify the degree of divergence at genotypic level in a biological population (Jatasara and Paroda, 1978).

Gaikwad *et al.* (2011) demonstrated an experiment to study genetic diversity in 18 genotypes of cucumber for various traits. They recorded considerable variations for all the characters. The accessions were grouped into eight clusters. Cluster-A and Cluster-B containing five genotypes each followed by Cluster F. Inter-cluster distance was maximum in F cluster and H cluster. High yielding varieties with other desirable characters were developed on inter crossing among the genotypes belonging to Cluster-C, D, F, G and H.

Kumar *et al.* (2013) conducted genetic divergence analysis in 30 genotypes of cucumber. Genotypes are grouped into 4 clusters. Cluster number I, II, III and IV contained 5, 11, 9 and 5 genotypes, respectively. Inter-cluster distance was maximum between clusters II and III whereas, intra-cluster distance was maximum in cluster IV. On the basis of cluster means, higher mean for marketable fruits per plant was exhibited by cluster-III, whereas no superior character was observed in cluster-II.

Hasan *et al.* (2015) at Dhaka demonstrated an experiment by taking seven genotypes of cucumber and arranged them into 3 different clusters. Intra-cluster distance was maximum in cluster I and no intra-cluster distance was reported in cluster II due to solitary genotype. The inter-cluster distances were more than the intra-cluster distances which implied wider genetic diversity within the genotypes of various groups. Cluster I and II reported highest inter-cluster distance whereas, clusters I and III reported lowest inter-cluster distance.

Ahirwar *et al.* (2017) conducted an experiment among fourty four genotypes with 2 checks to study genetic diversity through cluster analysis in two seasons i.e. July-October, 2014 and February-June, 2015. The genotypes were segregated into 7 clusters in two seasons. First cluster and second cluster, cluster IV and VII, cluster III and cluster VII reported maximum distance at inter cluster level during first season, second season and pooled analysis of two seasons respectively. In first season, maximum genotypes were received by cluster II and VI. In second season, by cluster II. However in pooled analysis, maximum genotypes were received by cluster II. Out of ten characters, maximum genetic divergence was contributed by fruit weight in cucumber. Again Ahirwar *et al.* (2017) grouped 46 germplasm of cucumber into 7 non-overlapping clusters. Maximum intra cluster distance is maximum in cluster IV which was followed by cluster II and cluster I. Rest of the clusters recorded ‘0’ value. Maximum inter cluster distance was reported in Cluster IV and cluster VII which was followed by cluster III. However cluster III and cluster VI recorded minimum inter cluster distance.

Pal *et al*. (2017) carried out an experiment on genetic diversity in thirty indigenous genotypes for twenty four characters. Five clusters were formed. The clustering pattern had no parallelism between geographical distribution and genetic diversity, indicating that the parental genotype selection for hybridization will be appropriate based on genetic diversity. More number of genotypes were in cluster III. Cluster II reported maximum Intra-cluster distance whereas, cluster II and cluster V reported highest inter-cluster distance.

Shah *et al*. (2017) revealed presence of greater variability for 13 genotypes of cucumber. Based on the relative magnitude of D^2 values genotypes were grouped into 4 clusters. Maximum inter cluster distance was reported in Cluster II and IV. Cluster I and II reported minimum distance which indicated that existence of less diversity between them. Cluster III was the most diverse. Therefore, genetically divergent genotypes were reported in these clusters. Wider variability may be observed on inter-crossing the genotypes from this cluster and is anticipated to show high yielding transgressive segregants in crop population improvement programme.

Kumar *et al*. (2018) studied 32 genotypes of cucumber during late *kharif* in the year 2016 to identify divergent genotypes. 6 clusters of genetically divergent genotypes were grouped on the ground of D^2 analysis. genetically more divergent genotypes belongs to cluster VI and V and Cluster VI ranked first for characters like length of the fruit, fruits per plant, fruit yield per vine and fruit diameter on the basis of cluster mean. The same cluster also recorded lower mean value for powdery mildew incidence. Hence genotypes belonging to Cluster VI were amenable for exploitation in future crop improvement.

Sharma *et al*. (2018) grouped total cucumber genotypes into 5 clusters. Maximum (12) numbers of genotypes were in Cluster II, whereas cluster V had minimum (3) genotypes. Cluster IV reported highest intra cluster distance and cluster III reported minimum. Similarly, cluster III and cluster IV computed highest inter-cluster distance. Cluster III and IV genotypes can be hybridized for getting superior hybrids.

CONCLUSION

The review literature cited in this paper throw a light on genetic variability, character association and genetic diversity present in cucumber genotypes. This knowledge is very helpful for the choosing desirable plant type. Therefore, genetically divergent genotypes can be used in upcoming breeding programmes in Cucumber.

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