GENETIC VARIABILITY IN CUCUMBER (*CUCUMIS SATIVUS* L.) : A REVIEW

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Abstract

Cucumber is one of the most important member of cucurbitaceae family. It is thought to be originated from India and China, is considered as secondary center of diversity. Inspite of being native of Indian sub-continent and endowed with enormous variability for various plant characters, cucumber remain underutilized in context of its economic potential and breeding value. There is huge scope to work on cucumber improvement in India. For any crop improvement programme, aimed to achieve maximum productivity, a detailed knowledge of facts such as genetic variability, genetic diversity, heritability, genetic advance, correlation and path coefficient of various quantitative traits and their contribution towards yield is essential. Studies in this direction are very less and can not to be generalized for every climatic condition and with other genetic materials. Hence, the information in a collection of some indigenous genotypes of cucumber in order to formulate a sound breeding plan for its improvement has been reviewed here.

Key word: Correlation, Genetic diversity, cucumber, Path coefficient, Variability.

Introduction

Success of any breeding programme depends much on genetic diversity available to the breeders and the judicious selection of parents. The success of breeding programme is achieved by the efficient utilization of heritability and variability available in the population. The importance of genetic diverse genotypes as a source of obtaining transgressive seggregants with desirable combinations have been realized by several workers (Kurian and Peter, 1994). Mahalanobis (1936) has been used gernelized distance as an efficient tool in quantitative estimation of genetic diversity and a rational choice of potential parents for a breeding programme. Knowledge of interrelationship between yield and its components is obvious for efficient selection of desirable plant type. Unlike the correlation coefficient values, which measure the extent of relationship, path coefficient (Wright, 1921; Dewey and Lu, 1959) measure the magnitude of direct and indirect effects of characters on complex dependent characters like yield and thus enable the breeders to judge best about the important component characters during selection.

2.1 Genetic variability, heritability and genetic advance for yield and its contributing traits

Genetic variability is an obvious feature of considerable importance in crop improvement. It is the basic necessity for any breeding programme to be successful. The knowledge of existing variability with respect to yield and yield attributing traits in the germplasm of a crop is the basic requirement in order to select the desirable types. Vavilov (1951) for the first time perceived the importance of genetic variability and advocated that the wide range of variability provides better scope of selecting desired genotypes. According to Allard (1960), heritability is the proportion of observed variability which is due to genetic causes, the remainder being due to the environmental cause. Heritability of a character indicates the extent to which the character can be transmitted from one generation to another (Balouch *et al*., 2003) and is a valuable tool to predict the magnitude of genetic gain that follows selection for a character (Adeniji and Kehinde, 2003).

Gulam *et al.* (2006) observed significant differences among all the twenty five genotypes for all the character studied. The coefficient of genotypic and phenotypic variability were moderate to high for all the characters with high broad sense heritability and expected genetic gain, except fruit width, which showed moderate heritability. Whereas Kanwar and Rana (2006) observed that all the character showed a wide range of values except days to first picking and fruit circumference. Phenotypic variability was high for node at which first female flower appears, sex ratio, yield per plant, number of fruits and vine length in cucumber.

Kumar *et al.* (2008) observed highly significant differences for all the traits under study. A wide range of variability along with estimates of PCV and GCV was observed for days to 1st female flower anthesis followed by number of primary branches per plant and number of fruits per plant. High heritability and high expected genetic gain were observed for days to 1st female flower anthesis followed by number of primary branches per plant and number of fruits/plant, indicates that these characters had additive gene effect and therefore, these are more reliable for effective selection in cucumber. Whereas Mehdi and Khan (2009) found wide range of phenotypic variation along with high heritability in cucumber. The characters namely, fruit girth, fruit length, fruit weight, number of fruit per plant and fruit yield per plant showed high GCV and high heritability along with high genetic advance revealing that these characters are controlled by additive gene. Yadav *et al.* (2009) observed existence of considerable amount of genetic variability for all the traits except cavity of fruit at edible stage in cucumber. The maximum phenotypic and genotypic coefficient of variation was observed for number of days to first female flower anthesis. Bisht *et al.* (2010) found significant differences among the genotypes for all the characters except internodal length. Phenotypic coefficient of variation and genotypic coefficient of variation were found high for number of fruits per plant. Highest heritability in broad sense was recorded for number of fruits per plant and number of nodes on main shoot. Hossain *et al.* (2010) recorded highest GCV in yield per plant whereas number of fruits per plant, fruit length, number of lateral shoots, average fruit weight, petiole length, node order at which male and female flowers opened was recorded. Gaikwad *et al.* (2011) observed high degree of variation in respect of all the characters studied. The estimates of genotypic coefficient of variation were slightly low as compared to estimates of phenotypic coefficient of variation, indicating the effect of environment. Kumar *et al.* (2011) observed high variability for number of female flowers per vine

followed by number of male flowers per vine and number of branches per vine. High PCV and GCV were recorded for number of misshaped fruits per vine Singh *et al.* (2011) found maximum variability in yield per vine followed by fruit weight, vine length, fruit length in parents.

Ullah *et al.* (2012) reported that the estimates of genotypic coefficient of variation and phenotypic coefficient of variation were high for yield per plant, fruit per plant, fruit weight and fruit length. Veena *et al.* (2012) found that genotypic coefficient of variation and phenotypic coefficient of variation were highest for node at first female flower appearance followed by node at first male flower appearance, yield per plant, seed cavity breadth, average fruit weight and number of fruits per plant.

Basavarajeshwari, (2014) observed high genotypic coefficient of variation and phenotypic coefficient of variation for vine length (cm), number of primary branches on 75 days after sowing (DAS) and nodes upto first female flower. High heritability coupled with high genetic advance over mean was observed for the characters *viz.,* vine length (cm), nodes upto first female flower and hence these traits can be improved by selection. Vidhya and Kumar (2014) in their study on cucumber recorded high heritability with high genetic advance as per cent of mean for ripe fruit weight per vine.

Pal *et al.*, (2016) in their study on cucumber recorded high GCV for yield per plant followed by anthracnose severity and number of marketable fruits per plant. These confirm presence of sufficient variability in the germplasm, predominance of additive gene action and high transmissibility of the characters. Therefore, direct selection will be rewarding depending upon these traits. Pushpalatha *et al.*, (2016) in their study on twenty four diverse cucumber genotypes found high phenotypic and genotypic coefficient of variation for yield per plant followed by fruit flesh thickness and number of fruits per plant. High heritability, coupled with high genetic advance as per cent mean, was recorded for all the characters studied except days to first female-flower opening, days to 50% flowering and days to first-fruit harvest, indicating a scope for improvement through selection.

2.2 Correlation and path coefficient studies:

Correlation coefficient is a statistical measure to determine the extent of association, whether positive or negative, between various plant characters and thus, helps to identify the character on which selection can be imposed for improvement in associated characters. Path coefficient analysis is simply a standardized partial regression coefficient, which splits the correlation into

direct and indirect effects. In other words, it measures the direct and indirect contribution of various independent characters on a dependent character. The concept of path analysis was developed by Wright (1921) and the technique was first used by Dewey and Lu (1959) that helps in determining yield contributing characters thus, useful in indirect selection. Correlation coefficients along with path coefficients together provide more reliable information, which can be effectively predicted in crop improvement program. If the correlation between yield and a character is due to direct effect of a character, it reveals true relationship between them and direct selection for the trait will be rewarding for yield improvement. However, if the correlation coefficient is mainly due to indirect effect of the character through another component trait, indirect selection through such trait will be effective in yield improvement.

Kumar *et al*. (2008) revealed that number of primary branches per plant, and number of fruits per plant should be considered for making selection for yield in cucumber.

Mehdi and Khan (2009) found that fruit yield per plant exhibited significant positive correlation with fruit weight and number of fruit per plant at both genotypic and phenotypic levels. Average fruit weight exhibited significant positive correlation with fruit length where as fruit length has negative correlation with number of fruits per plant in cucumber. Whereas, Hossain *et al*. (2010) revealed that yield per plant of cucumber had high positive and significant association with fruit length and diameter, average fruit weighty and number of fruits per plant.

Kumar *et al*. (2011) revealed that fruit yield was positively correlated with total number of fruits per vine followed by number of good fruits per vine and average fruit weight. Path analysis revealed that the total number of fruits per vine had maximum positive direct effect on yield followed by number of branches per vine and number of nodes per vine whereas, negative and maximum direct effect on yield was observed for days to first female flower followed by number of good fruits per vine and fruit diameter. Ullah *et al*. (2012) reported that fruit diameter, fruits per plant, leaf per plant, fruit weight and flesh thickness showed positive and significant correlation with fruit yield. Days to harvest showed negative correlation with yield indicating that early maturing varieties showed lower yields while the late maturing varieties had higher yields in cucumber. Golabadi *et al*. (2013) estimated significant correlation between total fruit yield per picking and fruit number per picking which revealed importance of fruit number for predicting of fruit yield in cucumber. Innark *et al*. (2013) observed that yield of cucumber was significantly and positively

correlated with fruit weight, flesh pith length, fruit length, harvesting period, and number of fruits per plant. Hasan *et al*. (2015) reported fruits per plant and fruit weight of cucumber had maximum positive direct effect on yield.

Pal *et al*. (2017) recorded that yield per plant had positive significant association with average fruit weight, fruit length and diameter, marketable fruits per plant, harvest duration, vine length, primary branches per plant, whereas, yield per plant had negative significant correlation with node number bearing first female flower, days to first harvest, total soluble solids and severity of four foliar diseases. Path analysis provided a clear picture that, harvest duration had maximum positive direct effect, followed by marketable fruits per plant while, days to first harvest had maximum negative direct effect followed by severity of downy mildew on yield per plant.

2.3 Genetic diversity studies:

Genetic diversity in the available gene pool is the source of variation, which is raw for the improvement work. For effective conservation and utilization of cucumber genetic resources, a clear understanding of genetic diversity and relationships of varieties is essential. Precise information on the nature and degree of genetic divergence of the parents is the prerequisite for an effective breeding program. Genetic diversity is a useful tool in quantifying the degree of divergence in a biological population at genotypic level and to assess relative contribution of different components to the total divergence both at intra and inter-cluster levels (Jatasara and Paroda, 1978).

Kanwar and Rana (2006) carried out divergence analysis in 26 genotypes of cucumber. They grouped the genotypes into 5 clusters. Cluster number I, II, III, IV and V contained 11, 3, 5, 2 and 5 genotypes, respectively which are independent of geographical distribution. The genotypes in cluster I had maximum intra-cluster distance whereas Inter-cluster distance was maximum between the clusters I and II suggesting wide diversity between the group. Highest yield per plant was recorded in cluster no. IV followed by cluster number III. Cluster number I and III may be employed for improvement programme in cucumber.

Sharma and Sharma (2006) grouped the thirty one genotypes of cucumber in cluster analysis, collected from different sources in India, into seven clusters. The genotypes Jorji Local, Bengal 60, JJL and Derabassi Local were promising in terms of yield per plant and fruit length, while gyn-2, Gyn-3 and Gyn-4 were superior for number of fruits per plant. However, genotypes Chakkimore Local, Farukabad Local, Chamoli Local and Chamba

Local were promising for average fruit weight and fruit breadth. Whereas Tomar *et al*. (2008) grouped the genotypes into seven clusters on the basis of relative magnitude of D² values. The maximum intra cluster distance was observed between cluster II and V whereas, cluster III and VII displayed lowest distance. Cheema *et al*. (2011) in their study revealed that total 11 principal component were formed out of which five principal components (PCs) contributed 82.79% of the total variability. Genotypes were grouped into four clusters, with 14 genotypes in cluster 1, 26 in cluster 2, 3 in cluster 3, and 2 in cluster 4 based upon similarities and dissimilarities.

Gaikwad *et al*. (2011) study genetic diversity in 18 genotypes of cucumber for various characters revealed substantial differences for all the characters. The accessions were grouped into 8 clusters with Cluster-A and Cluster-B comprising of 5 genotypes each followed by Cluster F (3). The maximum intercluster distance was observed between F and H.

Manohar and Murthy (2011) revealed that the original set of thirty variables was reduced by PCA to twenty eight, which accounted for about 74% of the total genetic diversity by 6 PC's. While the first two PC's explained 46% of the total variation. Cluster analysis revealed that total seven clusters were formed. Golabadi *et al*. (2012) in their study grouped the genotypes into four distinct groups. Genotypes in group number two had the highest total fruit yield per pickling. Therefore, selection of superior genotypes in view point of desirable morphologic traits, with high genetic distance could be selected for hybridization programs and recognition of best genotypes for different traits to produce new elite hybrids in cucumber.

Punitha *et al*. (2012) revealed that total cucumber genotypes were grouped into seven clusters which confirm the presence of wide genetic diversity through the formation of seven clusters. The clustering pattern showed the lack of parallelism between geographic and genetic diversities. Among the clusters, intercrossing the genotypes in the cluster I, II, IV and V had high mean values for many characters studied is likely to result in an enlargement of spectrum of variability facilitating the selection for higher yield. Afroz *et al*. (2013) revealed that the first two axes accounted for 67.39% of the total variation among the fourteen characters studied. As per cluster analysis, the genotypes were grouped into four clusters consisting 5, 3, 8 and 6 genotypes which revealed that considerable diversity is existed among the genotypes. Highest intra cluster distance was found in cluster III and lowest in cluster IV whereas the highest inter-cluster

distance was observed between cluster II and cluster III and lowest between cluster I and cluster IV. Kumar *et al*. (2013) at Solan conducted an experiment on thirty diverse genotypes of cucumber to assess the genetic diversity. They grouped the genotypes into 4 clusters and the highest inter cluster distance was recorded between cluster-II and III. The diverse genotypes characterized by maximum inter cluster distance will differ in phenotypic performance and therefore, selection of divergent parents should be based on these cluster distances to obtain favourable hybrids and transgressive segregants in cucumber.

Hasan *et al*. (2015) grouped the cucumber genotypes into three different clusters. Results revealed that the highest inter-cluster distance was observed between cluster I and II whereas lowest inter-cluster distance was observed between the clusters I and III.

Kumar *et al*. (2015) characterized the genotypes into four principal component based on their total variation (83.72%). The first principal component accounted for more than 48% of the total variation and was the combination of number of marketable fruits per plant, fruit length, harvest duration, total soluble solids, seed germination, seed vigour index-I and II and yield per plot. The second, third and fourth principle components contributed only 15.27%, 13.50% and 6.72% of total variations, respectively. Whereas, Nwofia *et al*. (2015) in their experiment observed that PC1, PC2 and PC3 with eigen-vector value loads greater than unity accounted for the cumulative variance of 70%, which exhibited the degree of influence the plant characters had on fruit yield of cucumber. Rahman *et al*. (2016) revealed that the first principal axis largely accounted for the variation among the genotypes which alone contributed 25.65% of the variations. They grouped 64 genotypes of muskmelon into six clusters to indicate the existence of considerable diversity among the genotypes. The highest inter genotypic distance was observed between the genotypes BD2303 and BD2313 followed by the genotypes BD2303 and BD2314.The highest intra cluster distance was computed for cluster III followed by cluster I. Cluster VI showed the least intra cluster distance which indicated that the genotypes in this cluster were more or less homogeneous. The inter cluster distances were larger than the intra cluster distances suggesting wider genetic diversity among the genotypes of different clusters.

Conclusion

The literature reviewed in this paper highlighted the genetic divergence and variability available in cucumber genotypes. Knowledge of association between yield and

its components is very useful for efficient selection of desirable plant type. Therefore, genetically divergent genotypes could be utilized for crop improvement in cucumber.

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