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Genetic variability and divergence in okra [*Abelmoschus esculentus* (L.) Moench.]: A review

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Abstract

Okra is an important vegetable crop widely grown in the tropical and subtropical regions of the world (Tindall, 1983). Cultivated okra has significant variations in the chromosome numbers but most frequent observed chromosome number is $2n = 130$ (Joshi and Hardas, 1956) and it belongs to the family Malvaceae. The centre of origin of okra remains unclear, but their centre of genetic diversity includes West Africa, India and Southern Asia (Hamon and Van Sloten, 1998). Okra is said to be very useful against genito-urinary disorders, spermatorrhoea and chronic dysentery (Nadkarni, 1927). Okra is an often cross pollinated crop, heterosis is being exploited in form of development of hybrids. Hence, genetic divergence is an important tool while selecting the parents for hybrid breeding. Divergence analysis is more authentic and powerful tool for systematic identification of the diverse genotypes for hybridization purposes (Mahalanobis, 1936). To develop high yielding varieties, genetic diversity is an important tool to select genetically diverse parents with high yield and wider adaptability in breeding programme. Progress of any breeding programmes depends to a great extent on the availability of genetic variability for desirable traits in genotypes (Kumar *et al.*, 2013, Balai *et al.*, 2014). Genetic diversity helps the breeders in deciding the most appropriate breeding method to increase the genetic potentialities as well as to surpass the yield barrier (Langade *et al.*, 2013). Use of genetically diverse parents in recombination breeding supposed to give maximum heterosis in F₁'s and also getting broad spectrum of variability for quantitative traits in segregating generations to select desirable recombinant. Therefore, genetic diversity is prerequisites for any successful breeding programme.

Keywords: Variability, okra, *Abelmoschus esculentus* L.

Introduction

Okra is one of the important vegetables of the tropical and subtropical regions of the world and is native to tropical Africa. Okra is highly nutritious and grown during summer and rainy seasons in all parts of the country. India is the largest producer of okra with area, production and productivity of 0.23 mha, 6.35 mt and 27.5 t/ha, (Anon. 2016). the young tender pods of okra are being used as fresh vegetable, canned, dehydrated and frozen products. When ripe, the black or white eyed seeds are sometimes roasted and used as a substitute for coffee in Turkey (Sharma and Prasad 2010). Okra is an annual and day neutral plant cultivated in all seasons for its delicious tender pods in one and other different parts of the country. Fresh okra fruit contains 35 calories, 89.6 g water, 6.4 g carbohydrate, 1.9 g protein, 0.2 g fat, 1.2 g fiber and minerals per 100 g of edible portion (Gopalan *et al.*, 2007).

The mucilaginous extract of okra is used for clarification of sugarcane juice while manufacturing brown sugar (Prasad and Nath 2002). Genetic diversity is one of the important tools to quantify genetic variability in both cross and self pollinated crops (Sharma and Prasad 2010). Numerous approaches are being used in estimation of genetic diversity among various genotypes. Principle component analysis (PCA) is a descriptive method which shows the pattern of covariation of characters among the individuals (Rhodes and Martins 1972). PCA produces Eigen vectors for each principle component axis and removes highly inter-correlated nature of prevalent variations. Thereby reduces the dimensions of multivariate data. The character loadings will be useful in determination of component scores and allows a multidimensional relationship to be plotted on two or three principle axes (Hayman 1967, Ariyo 1993, Nwangburuka *et al.* 2011). However, PCA alone is not sufficient to study the genetic diversity among the available germplasm unless it is accompanied with cluster analysis which classifies the genotypes into different divergent clusters.

Such a study permits the selection of genetically divergent parents to obtain highly heterotic hybrids (Moll *et al.* 1962) and desirable recombinants in the segregating generations (Sharma

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and Prasad 2010). Moreover, it allows confirming the role of geographic origin in diversity among the available germplasm. Hence, the Genetic diversity is an important factor for any heritable improvement. Divergence analysis generates valuable information on the nature and degree of genetic diversity, which is useful for selecting desirable lines from germplasm for successful breeding programme. The determination of genetic diversity of accessions for agro-economic traits is extremely important in breeding of crop plants for the development of successful varieties (Reddy *et al.*, 2014). In okra, pod yield is a complex quantitative trait as it is governed by a large number of genes and considerably affected by the environment. The traditional approach to germplasm evaluation is based on morphological features. Evaluation of germplasm is done to provide information on genetic diversity within crop. Selection of lines based on individual attribute may not be as advantageous as the one based on a number of important traits collectively.

Review of Literature

Genetic divergence in okra

According to Kiran Patro and Ravisankar (2004), cluster analysis in Okra revealed a considerable variation among the genotypes. Forty one genotypes were grouped into 8 clusters. They reported that among all the clusters, cluster IV had a maximum number (8) of genotypes, D2 values ranged from 205.03 to 32666.9. The cluster means revealed that plant height, yield per plant and germination percentage contributed towards divergence. In an evaluation of 50 genotypes of Okra Pradip *et al.* (2010), grouped it into 5 clusters. They observed that plant height had the highest contribution towards the total genetic divergence. Prakash and Pitchaimuthu (2010) studied 44 genotypes in okra. They reported that the characters namely days to 50% flowering (35.62%), 100 seed weight (28.44%), number of seeds per fruit (17.23%) and average fruit weight (8.14%) directly contributed towards maximum divergence and therefore, selection of divergent parents based on this character is recommended for getting good hybrids or segregants in okra. In a genetic divergence study in 44 Okra genotypes, Prakash Kerure (2010) grouped the genotypes into 12 clusters based on D2 analysis and reported that the characters like days to 50% flowering (35.62%), 100 seed weight (28.44%), number of seeds per fruit (17.23%) and average fruit weight (8.14%) were directly contributed towards maximum divergence.

Garg *et al.* (2011) evaluated 53 germplasm lines of okra to assess the genetic diversity. They reported that no parallelism between genetic and geographic divergence was observed. They also reported substantial variation in cluster mean. Saifullah and Rabbani (2013), conducted an experiment with 116 okra genotypes. They observed eight different electrophoretic zymotypes, all the zymotypes were polymorphic means presence of more than one band in each genotype. The genotypes were grouped in different polymorphic zymotypes, indicating considerable genetic diversity among the studied okra genotypes. Genetic divergence for seedling traits in tomato was studied by Rizvi *et al.* (2013). The scatter diagram partially indicated the clustering pattern and the clusters 3, 4 and 5 intermixed. Sub clustering of individual clusters revealed 5 sub clusters of cluster 1, three of cluster 2 and 5 in each case, six in cluster 3, 4 and 7 and cluster 6 and 8 had 4 each. The cluster 2, 3, 4 and 6 joined at higher genetic linkage with induction of single genotype in the cluster 2, 4 and 6, whereas in cluster 3, two main groups joined at higher distance including one group

comprising of the 41 genotypes and the second comprising 19 genotypes, which joined at 80% linkage distance. A Study carried out by Rathod *et al.* in 2015 revealed considerable genetic diversity among 43 genotypes of tomato for all the twenty characters which was pertaining to growth, earliness, yield and quality. Appreciable diversity within and between the clusters was observed. Seven clusters were fanned from the D2 analysis using Tocher's method. Cluster I topped with maximum number of genotypes among cluster fanned, while maximum intercluster distance was observed between cluster III and VI followed by cluster V and VI.

Morphological parameters

Pandey *et al.* (1994) reported that Pusa Sawani and Parbhani Kranti were at par in respect of growth and yields. Under closer spacing had poor growth. Gondane and Bhatia (1995) found that all the okra genotypes responded differently to the environments. Significant and marked variation was noted in the plant height. Gill *et al.* (1997) ^[12] developed a key for varietal identification on the basis of morphological characters, 10 varieties of okra (G-2, Parbhani Kranti, Pusa Makhmali, Punjab-7, Punjab Padmani, Pusa Sawani, IIHR-4, IIHR-10, HRB9-2 and EMS-B) were subjected to morphological characterization over 2 years. Considerable variation with respect to vegetative, floral and fruit characters and reaction to diseases and pests was recorded. A few distinguishing characters were identified in each variety. Hazra and Basu (2000) found that there was a wide range of variations for plant height (general mean=80.8 cm), leaves per plant (28.9), nodes per plant (14.9), days to first flower (49.9), fruit weight (15 g), number of fruits per plant (10), seeds per fruit (53.3), fruit yield per plant (155.7g), moderate variations for primary branches per plant (2.9) and fruit length (12.9 cm) and lesser variations for node at first flower (4.8), ridges per fruit (5.1) and dry weight of fruit (1.5 g). Primary branches per plant, which showed a moderate range of variation. Prakash *et al.* (2001) reported that Arka Abhay was best for high seed yield per plant (62.89g), fruit length (12.64cm), fruit weight (15.66g) and seed yield per fruit (3.71g).

Raji (2002) ^[22] studied on the growth, yield, and yield components of okra were conducted at Moor Plantation, Ibadan, Nigeria, in 1995 and 1996. Increase in plant height, leaf stalk, internode length, pod length, and pod diameter were largely determined by cultivar characteristics. Fruiting peduncle, leaf nodes, and edible fruit yield were significantly different among cultivars. Early flowering and long pods were indicators of low yield due to high negative correlation. However, late flowering, number of pods per plant, and length of fruiting peduncle were most highly positively correlated with yield, but highly negatively correlated with pod length. Bendale *et al.* (2003) ^[3] showed a wide range of genetic variability for yield and yield-contributing characters fruit length, weight, plant height, nodes per plant, internodal length, number of branches per plant, moisture content in fruit, fruiting period, seeds per fruit, 100seed weight, number of fruit per plant and yield per plant). The number of branches per plant. Duzyaman *et al.* (2003) recorded that the numerous okra genotypes of American, African, Indian, European and Turkish origin were examined for their pod properties and Hamed *et al.* (2003) reported that MNH 1999 had the highest number of branches per plant (12.59), number of early pods per plant (7.78) and total number of pods per plant (20.93). Kuwar *et al.* (2003) recorded that the cv. Parbhani Kranti had the highest leaf area per plant (18.92 dm²/m), plant height (18.22cm), dry matter per plant (60.62g), number of fruits per

plant (16.59), fruit diameter (1.47cm), fruit weight per plant (95.48g), the yield per plant (6.16kg), and yield/ha (38.04q). Arka Anamika and AKOV-97-16 had the highest fruit length (13.86cm) and number of branches per plant (4.28), respectively.

Sachan (2006) reported that the Arka Anamika recorded the highest plant height (90.62 cm), number of nodes per plant (17.35) and number of fruits per plant (14.08). Parbhani Kranti recorded the second highest plant height (89.79 cm), number of nodes per plant (17.00) and number of fruits per plant (13.16), Internode length was highest in Pusa Sawaney (8.11 cm). Chaudhary *et al.* (2006)^[7] found that the five okra hybrids were grown with the okra variety Antara as a check. The results indicated that the growth parameters differed within different hybrids and check variety. The differences in genetic makeup caused this difference. The vegetative characters *viz.*, plant height and internodal length showed positive effect on yield of okra. Nabi *et al.* (2010) evaluated the effect of fruit load on morphological characters and yield in okra. The results revealed that plant height and fruit yield were highest for the treatment where 12 fruits were retained and for other treatments *i. e.* fruit weight, fruit length and fruit diameter were highest where only six fruits were retained, respectively. Somashekhar and Salimath (2011) reported that the wider range of variation as evidenced for number of branches per plant, number of fruits per plant, average fruit weight (g), fruit length. Kumar *et al.* (2011)^[21] found that the analysis of variance (mean square) revealed significant differences among genotypes for all the characters under study. The results indicated considerable genetic variability among the genotypes for plant height, number of nodes per plant, number of fruits per plant. Nagre *et al.* (2011) reported that the highest genotypic coefficient of variation as well as phenotypic coefficient of variation was recorded for leaf area followed by number of nodes per plant, length of fruit, number of leaves per plant, yield per plant, Internodal length and chlorophyll content of leaves.

Phenological parameters

Sood (1999) reported that marketable fruit yield per plant varied from 154 to 467 g and yield was highest in okra genotypes IC-39135, IC-9856 and Punjab Padmini. IC-39135 also had the highest number of nodes per plant. LC-12 had the highest fruit weight (22.22g), followed by Perfect Long Green (21.60g), LC-26 (21.54g), LC-11 (20.86g) and LC-16 (20.79g). Days to 50% flowering varied from 44.33 to 71.00 days and IC -45791 was the earliest to flower among the genotypes. IC-14026 and IC-45796 had the highest duration of availability of edible pods (66 days). Prakash *et al.* (2001) reported that Parbhani Kranti registered as a superior parent for number of fruit per plant (16.60) and days to first flowers (44.90). Bendale *et al.* (2003)^[3] showed a wide range of genetic variability for yield and yield-contributing characters first flowering node, days to first harvest Hamed *et al.* (2003) reported that Balady green recorded the highest number of days to first flower (71.78) and number of nodes of first flower (11.31).

Alam *et al.* (2006) assessed the variabilities reported in Mymensingh, Bangladesh and reported wide range of variation was recorded for days to first flowering (40-52 days). Oppong-Sekyere *et al.* (2011) observed that the variation in petal colour, pubescence of the leaf and stem, fruit shape, anthocyanin pigmentation and variation in number of days to 50% flowering. Reddy *et al.* (2013) evaluated one hundred germplasm lines of okra (*Abelmoschus esculentus*

(L.) Moench) at the Vegetable Research Station, Rajendranagar, Hyderabad, Andhra Pradesh, India. Reported days to 50% flowering, first flowering node and first fruiting node had significant negative correlation with marketable yield per plant. Swamy *et al.* (2014) evaluated 14 different yield attributing traits in 32 advanced breeding lines of okra during summer season, 2012-13. Genotypic and phenotypic correlation coefficient studies revealed that days to 1st flowering and day to 50% flowering recorded significant negative correlation with pod yield per plant.

Variability and Heritability of Quantitative Traits

Selection of superior genotypes at one stage or the other is the most important aspect in any plant improvement programme and the effectiveness of the selection is dependent upon the existence of genetic variability within or among the population subjected to selection (Dixit *et al.*, 1971; Swamy Rao, 1972; Tikka *et al.*, 1974; Patnaik and Tak, 1974). Therefore, a quantitative measure of genetic variability would be extremely beneficial in breeding for improvement of quantitative traits. Most of the economically important characters in crop plants are quantitative in nature which are controlled by polygenes and also influenced by the environment (Hirachand *et al.*, 1975). The observable quantitative trait is only the phenotype which can be easily assessed but for purpose of selection, it is inadequate since plant is the resultant of the interaction of genotype and environment which creates difficult to ascertain whether variability is heritable or non-heritable (environmental).

Coefficient of Variation

Genotypic coefficient of variation is the genotypic standard deviation expressed as percentage of mean and phenotypic coefficient of variation is expressed as the phenotypic standard deviation expressed as the percentage of mean. A slight differences between phenotypic and genotypic standard deviation suggested negligible influence of environment on that character (Choudhary *et al.*, 1973). Coefficient of variation is defined as the measure of variation and is independent of unit of measurement which is used for comparing different populations. It is provided by the standard deviation expressed as percentage of mean (Panse and Sukhatme, 1954). Correlation studies carried out by Kiran Patro and Ravisankar (2004) in Okra, revealed that fruit yield per plant have significant positive correlation with germination percentage, number of branches per plant, number of ridges per fruit, fruit length, fruit weight and ascorbic acid content. They also revealed significant negative correlation of fruit yield per plant with plant height, number of days taken for first pod setting, fruit volume, shape index and longevity of tenderness.

Khan *et al.* (2005), conducted studies on correlation for ten quantitative characters on okra. They indicated that the yield was closely and positively correlated with its component characters like plant height, fruit length, node number and number of fruits per plant both at phenotypic and genotypic levels. According to Singh *et al.* (2006), the fruit yield per plant of okra was positively and significantly correlated with fruit length, fruit diameter, fruit weight and number of fruits per plant. From a correlation study, Mehta *et al.* (2006), suggested that the fruit yield was significant and positively correlated with fruit length and average fruit weight. Alam and Hossain (2008), indicated that in okra, the yield of green pod had highly significant positive association with the number of nodes per plant. In a correlation study utilizing ten

genetically diverse okra genotypes of Okra, Kumar *et al.* (2011)^[21], observed that fruit yield was negatively correlated with fruit length (-0.792) and positively correlated with weight of fruits per plant (0.662), fruit length was positively correlated with weight of fruit per plant (0.703).

Guddadamath *et al.* (2011), reported that the genotypic coefficient of correlation showed more significant relationship between the pairs of characters such as average fruit weight (0.859), number of fruits per plant (0.929), 100 seed weight (0.871), and number of branches per plant (0.916), during selection process in segregating populations, as these characters exhibited positive significant association with fruit yield per plant. Adiger *et al.* (2011) have undertaken a study on 163 genotypes of okra to determine genetic variability and nature of association among different yield attributes. They found that the fruit yield has significant positive correlation with plant height, number of branches per plant, inter-nodal length, fruit length, fruit weight and number of fruits per plant at both genotypic and phenotypic level. Simon *et al.* (2013) observed that genotypic coefficient of correlation showed more significant relationship between the pair of characters, meaning that, these characters are more related genotypically in Okra. An investigation was conducted to find out the correlation and path coefficient effects in okra by Jagan *et al.* (2013). They reported that fruit yield per plant showed highly significant positive association with a number of branches per plant and number of fruits per plant at phenotypic and genotypic levels.

Heritability

Heritability is one of the major properties of a quantitative character. It should be noted that the heritability is a property not only of a character but also of a population and the environmental conditions to which the individuals are exposed. Further, variation in quantitative traits occurs due to their degree of heritability. If heritability is 100% the phenotypic performance would be a perfect indication of genotypic value. However, in this hypothetical situation, the heritability values in provide no indication of the amount of genetic progress that would result from selecting the best individuals. Therefore, the utility of heritability is increased when they are used in conjugation with selection differential and the genetic advance is completely predicted as the product of heritability ratio and selection differential (Johnson *et al.*, 1955). Randhawa *et al.*, (1975) suggested that if the heritability of a character is high, better will be the opportunity for selecting a genetically good individual. Low value of heritability indicates high degree of nonheritable variability (Sharma *et al.*, 1966). Further, difference in heritability values also differ greatly depending on the methods used to estimate the parameter (Robinson, 1963) the units for which the variance is considered (Johnson *et al.*, 1955) and also the amount of genetic variation in population and environmental condition under which the population is evaluated (Allard, 1960).

Therefore the most important use of heritability lies in its predictive role, expressing the reliability of the phenotypic value as a guide to the breeding value. It also serves as a useful parameter in predicting genetic advance or response to selection. Dhankhar and Dhankhar (2002) evaluated 62 inbred lines of Okra at Hissar and found broader range of variation and high mean values in rainy season for number of fruits per plant, days to 50% flowering and number of branches per plant and in spring-summer season for fruit yield and plant height. They also reported high genetic variability for number

of branches per plant, fruit yield, number of fruits per plant and plant height in both the seasons. The magnitude of PCV was almost similar to the corresponding GCV in both seasons for fruit yield and plant height. Adeniji and Kehinde (2003) evaluated 7 accessions of West African Okra for heritability, genetic advance and genetic variability.

The dominant gene effects were low in magnitude, unidirectional (positive increasing alleles) for hundred seed weight, pod length and seed per pod and ambi-directional (positive increasing and negative decreasing alleles) for ridges per pod, seeds per ridge, pod width and seed weight. Khan *et al.* (2005) reported high phenotypic and genotypic variances in okra for characters like fruit yield, seed number, fruit number and node number and high phenotypic and genotypic coefficient of variation for number of fruits per plant, number of seeds per fruit, node number and yield per plant. They also recorded high heritability and genetic advance as percent of mean for number of nodes, number of seeds, fruit number, plant height and yield. While studying genetic variability, heritability and genetic advance on okra genotypes, Singh *et al.* (2006) observed high phenotypic coefficient of variation and genotypic coefficient of variation for internodal length, number of branches/plant, number of fruits/plant, number of seeds/pod and fruit yield/plant. They also observed high heritability along with high genetic advance for characters like number of seeds/pod, internodal length, number of branches/plant, fruit yield/plant, number of fruits/plant, plant height and 100 seed weight.

Genetic Advance

The heritability alone conveys no indication of the amount of genetic progress that will result from selecting the best individual. But when they are used together with the selection differential, the utility is increased (Tikka *et al.*, 1974). Heritability in narrow sense is the most important tool to estimate expected improvement due to selection or response to selection of genetic advance. Robinson (1963) and Johnson *et al.*, (1955) suggested that heritability estimates along with genetic advance were more valuable than the heritability value alone in predicting the response to selection. High heritability does not necessarily mean that the character will show high genetic advance. But the case where the above association exists, additive genes comes into prominence. It is because no genetic advance was due to non-additive genes, whereas additive genes are responsible for high genetic advance.

Path Analysis

Yield is a complex trait resulting from direct and indirect effects of several traits operating either in combination or individually. Selection for a trait in one direction may influence another trait by a direct or indirect effect via a third variable. The study of correlation gives only the extent of association among various characters taken in pairs. This extent of association does not imply the cause and effect relationship. Therefore the path coefficient analysis is used to determine the direct and indirect effects of various plant characters on crop yield. According to Wright (1921), path coefficient analysis provides a better knowledge of direct and indirect causes of associations and it permits a critical examination of the specific forces acting to produce a given correlation and measures the relative importance of each causal factor. This method was first used by Dewey and Lu (1959) in their analysis of seed yield in crested wheat grass. Since then several workers have applied this method for

analysis of character association in various crops. From a path analysis study Alam and Hossain (2008), observed that number of nodes per plant directly contribute towards the yield of green pod.

Adiger *et al.* (2011) undertaken association studies on 163 genotypes of Okra and observed that path analysis for fruit weight had maximum direct contribution (0.884) towards fruit yield followed by number of fruits per plant (0.852), plant height (0.024) and number of branches per plant (0.020). They also reported that days to 50% flowering exhibited highest negative direct effect (-0.013) followed by test weight (-0.009) and fruit diameter (-0.003). While studying the correlation and path analysis of quantitative characters in Okra Reddy *et al.* (2013) observed that fruit weight, total number of fruits per plant and number of marketable fruits per plant had positively direct effect on marketable pod yield per plant. They also observed that the fruit weight, total number of fruits per plant and number of marketable fruits per plant not only had positively significant association with marketable pod yield per plant, but also had positively high direct effect on marketable pod yield per plant and are regarded as the main determinants of marketable pod yield per plant.

Simon *et al.* (2013) suggested that the seed size has high positive direct effect on seed yield (0.703). They also suggested that the number of seeds per pod had the highest significant correlation effect on seed yield (0.846**) as well as highest negative direct effect with seed yield (-1.00) indicating that selection of number of seeds per pod will increase seed yield. Path analysis study in Okra conducted by Yonas *et al.* (2014), at genotypic level revealed that internodes number had highly positive direct effect on fruit yield ($p = 6.90$) followed by average fruit weight ($p = 6.89$) which had positively genotypic correlation with yield.

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