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Framing a pigeon pea improvement program through genetic analysis, character association and genetic diversity: A review

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Abstract

Pigeon pea [*Cajanus cajan* (L.) Millsp.], is the second most important pulse crop of India after chickpea. It is a rich source of protein, carbohydrate, vitamins, lipids and certain minerals. It has a wide range of genetic diversity which provides a tremendous scope for genetic improvement of economic traits. An improvement in yield and quality characters in pigeon pea crop is normally achieved by selecting the genotypes with desirable character combinations existing in nature or by hybridization. Hence, the information in a collection of some genotypes of pigeon pea in order to formulate a sound breeding plan for its improvement has been reviewed here.

Keywords: Pigeon pea, genetic improvement, variability, correlation, path analysis and genetic divergence

Introduction

Pigeon pea [*Cajanus cajan* (L.) Millsp.], is one of the most common tropical and subtropical legume cultivated for its edible seeds. There are several local names of *Cajanus cajan* in different parts of the world (Saxena, 2008) [32]. Among these "pigeon pea" is the globally popular name that was coined by (Plukenet, 1692) [24] in Barbados, where the crop was grown in barren lands for feeding its seeds to pigeons. In India it is popularly known as red gram, tur, or arhar is fast growing, hardy, widely adaptable, and drought resistant and a very old crop of this country. It is a diploid legume crop species (2n = 2x = 22) with genome size 1C = 858 Mbp, belongs to the sub-tribe Cajaninae of the agriculturally most important tribe Phaseoleae under sub-family Papilionoideae of the family Fabaceae (Leguminosae). The tribe Phaseoleae comprises many edible bean species (Phaseolus, Vigna, Cajanus, Lablab etc.). However, *C. cajan* is the only domesticated species under Cajaninae. Domesticated >3,500 years ago in India, Vavilov, 1951 [37]; De, 1974 [37]; Royes, 1976 [28].

Pigeon pea is consumed as a green vegetable as well as decorticated split peas, popularly called as 'dhal' with a rich source of protein, iron, iodine, carbohydrate, vitamins, lipids, certain minerals and important amino acids lysine, methionine and tryptophan. Dry pigeon pea seeds contain protein (20-22%), carbohydrate (67%), fat (1.9%), crude fibre (6.6%) calcium (120.8 mg $100g^{-1}$), magnesium (122 mg $100g^{-1}$), copper (1.3 mg $100g^{-1}$), iron (3.9 mg $100g^{-1}$) and zink (2.3 mg $100g^{-1}$). Saxena *et al.* (2010) [33].

In combination with cereals, pigeon pea makes a well-balanced human food. The pigeon pea crop has potential to reduce hunger and malnutrition while maintaining sustainable productivity of smallholder cropping systems. Because of its drought resistance it can be considered of utmost importance for food security in areas where rainfall is not consistent. The green leaves and tops of plants provide excellent fodder of outstanding value and are also utilized as a green manure. The dried stalks are used as fuel, for making baskets and thatching material. Roots of pigeon pea form a symbiotic association with Brady rhizobium spp. and perform biological nitrogen fixation to improve the fertility of soil.

The world area under cultivation and production of pigeon pea is continuously increasing day-by-day. India, occupies first rank in area as well as production at global level with an area of 5.38 million ha of pigeon pea and 4.87 million tonnes of production. Its average yield in India is about 904 kg per hectare. The world area under pigeon pea is about 7.02 million ha and production is 6.81 million tonnes. Its average yield in India is about 904 kg per hectare. [FAOSTAT: 2017] [1]

Botanical Description

Pigeon pea is an erect, short-lived perennial leguminous shrub that usually grows to a height of about 1-2 m, but can reach up to 2-5 m height. It quickly develops a deep (2 m depth) poisonous taproot. The branching pattern of stem may vary from bush type to compact upright type and is of determinate, semi-determinate, and non-determinate type based on the flowering pattern. The primary leaves are simple, opposite, and caduceus, while the latter ones are pinnately trifoliate with lanceolate to elliptical leaflets. Leaves and stems are pubescent. The flowers (5 to 10) are grouped in racemes at the apices or axils of the branches. The flowers are zygomorphic and papilionaceous borne on terminal or auxiliary racemes and are normally yellow in color with some variations. They can also be striated with purple streaks. It has ten stamens in diadelphous condition with light or dark yellow anthers. The ovary is superior with a long style attached to a thickened, incurved, and swollen stigma. Pigeon pea is an often cross-pollinated crop with an average of 20% cross-pollination. The fruit of pigeon pea is called pod, which is of various colors, with and without deep constrictions. Seeds (with 20–22% proteins and amino acids) can be round or lens shaped, in shades of white and brown color with yellow color cotyledon.

Compared to other food legumes breeding in pigeonpea has been more challenging due to its pollination behavior and sensitivity to biotic and abiotic stresses. Significant progress has been made over the last few decades through breeding for reducing crop duration, improving seed quality and overcoming the constraints of major diseases like wilt and sterility mosaic. Pigeonpea, being often cross pollinated has very high genetic variability but yield potential of this crop is very low. Seed yield is very complex character whose manifestation results from multiplicative interactions of several yield components and environmental factors.

Improvement in yield and success of any breeding programme primarily depends on the magnitude and the nature of genetic variability 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 a population. Mahalanobis (1936) [14] generalized distance has been used 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 seed 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 measure the magnitude of direct and indirect effects of characters on complex dependent characters like seed yield per plant and thus enable the breeders to judge best about the important component characters during selection.

Genetic variability and its parameters Studies

The basic information on the existence of genetic variability and diversity in a population and the relationship between different traits is essential for any successful plant breeding programme. Genetic improvement through conventional breeding approaches depends mainly on the availability of the diverse germplasm and presence of enormous genetic variability. The characterization and evaluation are the important pre-requisites for effective utilization of germplasm and also identify sources of useful genes. An insight into the nature and magnitude of genetic variability present in the gene pool is of immense value for starting any systematic breeding programme because the presence of considerable genetic variability in the base material ensures better chances of evolving desirable plant type.

Genetic variability studies provide basic information regarding the genetic properties of the population based on which breeding methods are formulated for further improvement of the crop. These studies are also helpful to know about the nature and the extent of variability that can be attributed to different causes, sensitivity of crop to environment, heritability of the character and genetic advance.

Burton (1952) [4] suggested the use of heritability estimates with genotypic coefficients of variation to give precise estimates of genetic advance.

Johnson *et al.* (1955) [9] have suggested that in selection programs heritability values as well as estimates of genetic advance are more useful than heritability alone.

According to Hanson *et al.* (1956) [8] heritability and genetic advance are the two complementary concepts. The heritability values may be used to estimates the expected genetic advance through selection. The high heritability enables the plant breeder to base his selection on phenotypic performance for improvement of characters.

Genetic variability, heritability and genetic advance in early maturing 100 genotypes of pigeon pea were studied by Birhan *et al.* (2013) [2]. The analysis of variance revealed highly significant difference ($p \leq 0.01$) for most traits. High phenotypic (PCV) and genotypic coefficient of variation (GCV) was recorded for harvest index and biomass yield per plant. High heritability coupled with high expected genetic advance as percent of mean was recorded for 100-seed weight, seed yield per plot, plant height, biomass yield per plant and harvest index indicating that these characters are controlled by additive gene effect and phenotypic selection of these characters would be effective for further breeding purpose.

Saroj *et al.* (2013) [29] conducted an experiment on genetic variability in 70 pigeon pea genotypes. The results of variance analysis showed all the traits exhibited highly significant difference among treatments which indicated adequate genetic variability among the cultivars. Genotypic coefficient of variation was the highest for secondary branches/plant followed by pods/plant and grain yield/plant, the lowest for days to maturity. The magnitude of the genotypic variance for all the yield components were however higher than the environmental variance. The low environmental influence observed compared to genetic factors suggests that the trait may be under genetic control rather than the environment, hence improvement can be achieved through selection

Singh *et al.* (2013) [34] studied genetic variability for seed yield and its component traits in 21 diverse genotypes of short duration pigeon pea. The results indicated that the genotypes showed significant variability for all the traits studied. The range of PCV was observed from 4.56 to 18.59 % and GCV ranged from 3.24% to 17.84% for the traits under study which provides a picture of the extent of phenotypic and genotypic variability in the population. Pods/plant, days to 50% flowering and seed yield/plant showed high magnitude of heritability in broad sense, suggesting that the highly heritable characters were least affected by environmental variation and selection for these characters based on phenotypic performance may be more effective for pigeon pea improvement.

Variability studies by Lakhote *et al.* (2015) [13] reveled that genotypic and phenotypic coefficient of variation were of high magnitude for most of the character studied. The analysis revealed significant differences among all genotypes for all the character's indicating presence of considerable amount genetic variability in the materials under study. GCV and PCV were of high magnitude for TSS (per cent) followed by 100 green seed weight, pod length, 100 green pod weight, number of primary branches and number of flower cluster. The estimate of high heritability (bs) accompanied with high-expected genetic advance for 100 green pod weight and days to 50 per cent flowering indicating the presence of additive gene action in the expression of these characters. This suggesting that such traits can be improved by direct selection.

During the study of genetic variability in 30 genotypes of pigeon pea, Kesha *et al.* (2016) [11] reported that all the traits exhibited highly significant difference among treatments, which indicated adequate genetic variability among the cultivars. Relatively higher value of genotypic variance was found for pods/plant. The genotypic coefficient of variation was the highest for secondary branches/plant followed by pods/plant and grain yield/plant, the lowest for days to maturity. The magnitude of the genotypic variance for all the yield components were however higher than the environmental variance. The low environmental influence observed compared to genetic factors suggests that the trait may be under genetic control rather than the environment, hence improvement can be achieved through selection.

Twenty-three pigeon pea genotypes were evaluated in a randomized block design during *Kharif* 2012-13 by Pandey *et al.* (2016) [20]. The analysis of variance revealed highly significant differences for all characters under study among the genotypes, indicating that the parents included in this investigation exhibit sufficient variability for all the character's studied. The presence of large amount of variability might be due to diverse source of materials taken as well as environmental influence affecting the phenotypes.

Patil *et al.* (2017) [23] have done the genetic analysis of 23 vegetable type pigeon pea genotypes. The ANOVA revealed significant differences among all the genotypes for the traits studied indicating the presence of large genetic variation amongst the genotypes selected for study. Genotypic and phenotypic coefficient of variation were of high magnitude for plant height, 100 green pod weight, 100 green seed weight, shelling percentage (%), TSS (%), days to 50% flowering, pod length, pod width and for number of primary branches per plant. The estimate of high heritability (bs) accompanied with high expected genetic advance for 100 green pod weight and days to 50% flowering indicate the presence of additive gene action in the expression of these characters.

Mallesh *et al.* (2017) [16] carried out an experiment for genetic variability, heritability and genetic advance of sixteen characters in twenty-eight genotypes including checks. Analysis of variance revealed significant difference among genotypes for all the sixteen characters studied. The magnitude of PCV and GCV was moderate to high for pods per plant, seed yield and primary branches per plant. High heritability combined with high genetic advance was recorded for number of pods per plant and seed yield per plant indicating that these characters are controlled by additive gene effect and phenotypic selection of these characters would be effective for further breeding purpose.

Kumar *et al.* (2018) [12] studied genetic variability, heritability and genetic advance for grain yield and component traits in 45 diverse genotypes of pigeon pea. The analysis of variance estimated that the significant differences among the genotypes for all the traits indicating presence of sufficient variability among the genotypes. GCV and PCV were high for grain yield per plant followed by number of pod per plant, 100-grain weight, number of primary branches per plant and number of secondary branches per plant. High heritability accompanied with high genetic advance as percent of the mean in case of grain yield per plant, 100-seed weight, pods per plant, number of secondary branches per plant, number of primary branches per plant and plant height indicate that these are simply inherited traits and most likely the heritability is due to additive gene effects and selection may be effective in early generations for these traits.

Genetic variability and correlation in pigeon pea genotypes were studied by Pushpavalli *et al.* (2018) [25]. Analysis of variance revealed that significant differences existed among the genotypes for the characters studied. Phenotypic coefficient of variation was relatively high compared to corresponding genotypic coefficient of variation for all the characters studied, indicating environmental influence on the expression of these traits. The range of PCV observed was 6.58 to 27.13% for the characters which indicates the extent of phenotypic variability in the population. Genotypic coefficient of variation which indicates the extent of genetic variability ranged from 4.55% to 22.07%. Maximum GCV was observed for number of pods/plant (22.07%), followed by days to 50% flowering (17.71%) providing an opportunity for genetic improvement.

Satyanarayana *et al.* (2018) [31] evaluated sixteen varieties of red gram for genetic variability, heritability and genetic advance. The ANOVA revealed significant difference among the genotypes for all the ten characters studied. The traits primary branches plant^{-1}, secondary branches plant^{-1}, pods plant^{-1}, 100 seed weight and seed yield showed high genotypic and phenotypic coefficient of variation suggesting that these characters are under the influence of genetic control. High heritability coupled with high genetic advance of mean was observed for all the characters indicate that these traits are simply inherited and most likely the heritability is due to additive gene effects and selection may be effective in early generation for these traits.

Correlations Studies

The first attempt to use the statistical method of correlation for measuring the resemblance between relatives with a view to study the heredity control of metric characters was made by Galton (1889) [7]. The theoretical basis of such correlations remained therefore obscure until Fisher (1918) [6] applied the Mendelian principles of inheritance in comprehensive manner. It was since established that the degree of resemblance between the relatives provides a powerful means of estimating the component of variance due to genetic effects. Correlation is an index of the proportion of the cause common in genesis of two variables to the total and not the causes themselves (Bowley, 1920) [3].

Before attempting to improve any character, it is necessary to understand degree and direction of association between different characters. Knowledge of the interrelationship among various characters helps in precise planning of the breeding programme. If several characters are related, improvement in one of them results in shaping the other characters. With this in view, both genotypic as well as phenotypic association among various characters have been studied by different workers.

Ten genotypes of pigeon pea were tested during three cropping season for their yield performance by Padi (2003) [19] observed that grain yield was found to be significantly and positively correlated with the number of days to 50% flowering, fodder yield, pods per plant, crop growth rate, pod growth rate and harvest index. It indicated that these attributes were more stimulating the yield in pigeon pea and they can serve as significant traits for enhancement of grain yield/plant.

Udensi and Ikpeme (2012) [36] studied correlation and path coefficient analyses of seed yield and its contributing traits in *Cajanus cajan* (L.) Millsp revealed that there were significant positive correlations between plant height and number of leaves plant^{-1}, leaf area plant^{-1} and number of seeds plant^{-1}. It also showed that the number of leaves plant^{-1} was positively correlated with the pod length and number of seeds plant^{-1}. Leaf area plant^{-1} had a positive significant association with the number of seeds plant^{-1}. Additionally, pod length plant^{-1} correlated positively with the number of seed plant^{-1} while number of nodules plant^{-1} correlated positively with 100-seed weight.

Fifty genotypes of pigeon pea were evaluated by Rao *et al.* (2013) [26] for genetic association. A significant and positive genotypic association among number of pods per plant, number of primary branches per plant, plant height, days to flowering and days to maturity and their positive association with seed yield indicated that these are major yield contributing traits in pigeon pea. Therefore, selection for any of these traits would offer the scope for simultaneous improvement of contributing characters in addition would be helpful in improving the yield potential in pigeon pea.

Saroj *et al.* (2013) [29] reported that genotypic correlations were higher in magnitude than the phenotypic correlation indicting strong inherent relationship among the characters except few which could be due to modifying effects in the environment. The days to 50% flowering had significant and strongly positive association with grain yield/plant, primary branch/plant, pods/plant, days to maturity, 100 seed weight and plant height in both genotypic and phenotypic level. It indicated that these characters are useful for taking them as the basis of selection for high grain yield in pigeon pea.

An experiment conducted by Singh *et al.* (2013) [34] revealed that the genotypic correlations had higher magnitude than corresponding phenotypic correlations for all the characters under study. This indicated that there was inherent association among the characters. Seed yield/plant was found to be significant positively associated with seeds/pod, pod length and plant height at genotypic level, indicating that these attributes are predominant and may contribute considerably towards higher seed yield of pigeon pea.

Lakhote *et al.* (2015) [13] studied the association among the different traits of pigeon pea for the 24 genotypes. The genotypic correlation of green pod yield plant^{-1} was found to be positively correlated with pod length, pod width, seed pod^{-1}, 100 green pod weight, 100 green seed weight, shellingpercentage, number of flower cluster and the days to 50 per cent flowering, numberof primary branches and TSS werenegatively correlated with green pod yield.

Thirty varieties of pigeon pea were evaluated by Kesha *et al.* (2016) [11] for genetic variability and correlation and found that grain yield/plant was found to be significantly and positively correlated with plant height, primary branches/ plant, pods/plant while, 100 seed weight had strong interrelationship with pods/plant. The character days to 50% flowering had significant and strongly positive association with grain yield/ plant, primary branch/plant, pods/plant, days to maturity, 100 seed weight and plant height in both genotypic and phenotypic level. It indicated that these attributes were more influencing the yield in pigeon pea and they can serve as important traits for improvement of grain yield/plant.

Pandey *et al.* (2016) [20] evaluated 23 pigeon pea genotypes in RBD design during *Kharif* 2012-13 and found that seed yield per plant was highly significantly and positively associated with biological yield per plant, pods per plant, 100-seed weight, secondary branches per plant and harvest index. Thus selection for higher yield on the basis of above characters would be reliable. Biological yield/plant showed significant positive correlation with pods/plant, 100-seed weight, plant height, secondary branches/plant and seeds/pod indicating that improvement in biological yield, if selection imparted may boost the per se performance of these characters.

Twenty-one genotypes of pigeon pea were used to investigate the nature and magnitude of association of seed yield with major agronomic characters by Narayanan *et al.* (2018) [18] revealed the positive and significant relationship of number of pods per plant, days to 50 per cent flowering, number of branches per plant with seed yield. Hence, these attributes were more influencing the yield in pigeon pea and they can serve as important traits for improvement of seed yield/plant.

Pushpavalli *et al.* (2018) [25] evaluated forty-nine pigeon pea genotypes at Agricultural Research Station Tandur during *kharif* 2015-16 and observed that seed yield was significantly and positively correlated with number of secondary branches/plant and number of pods/plant at the genotypic level, indicating that these traits contribute considerably towards seed yield in pigeon pea. Days to maturity was significantly correlated with days to 50% flowering. This indicated that genotypes flowered earlier matured earlier.

Satyanarayana *et al.* (2018) [31] reported that seed yield was found to be highly significant and positively correlated with the secondary branches plant^{-1} followed by plant height, pods plant^{-1}, days to 50% flowering and primary branches plant^{-1} suggesting that selection for these traits will improve the seed yield.

Path coefficient Studies

Path coefficient analysis is simply a standardized partial regression coefficient which splits the genotypic correlation coefficient into direct and indirect effect. Yield is a complex entity and is observed to be associated with a number of component characters. These characters are interrelated. Such interdependence of the contributory factors often affects their direct relationship with yield, thereby, making correlation coefficient less reliable in selection indices. The failure of correlation to explain cause and effect relationship between the characters concerned emphasized that the use of path coefficient analysis was inevitable.

Literature on the results of experiments conducted in context with path analysis is offered to view in the following paragraphs.

Padi (2003) [19] studied correlation and path coefficient analysis of yield and yield components in pigeon pea by testing ten genotype in three cropping season and revealed that crop growth rate, harvest index and number of pods per plant showed a large positive direct effect on grain yield as well as large positive indirect effect through each other on grain yield. Selection of these traits favors improvement in yield.

Path coefficient analyses of seed yield and its contributing traits in *Cajanus cajan* (L.) Millsp was studied by Udensi and Ikpeme (2012) [36] showed that different yield traits had varied magnitude of direct effects on yield. It was observed that 100-seed weight had the highest direct effect on yield, which was positive. This was followed by the pod length plant^{-1}, number of leaves and leaf area which directly contributed substantially towards seed yield, should be indices for selection in pigeon pea.

Rao *et al.* (2013) [26] revealed that number of pods per plant had the high positive direct effect on seed yield followed by harvest index, 100 seed weight, primary branches and days to maturity. Therefore, for obtaining higher seed yield in pigeon pea due emphasis should be given for higher number of pods per plant, more primary branches, more plant height and reasonable good test weight along with better harvest index, since all these characters had high positive direct and indirect influence on seed yield.

Saroj *et al.* (2013) [29] studied 70 pigeon pea genotypes using path coefficient analysis, the result indicated pods/plant, 100-seed weight, days to 50% flowering, primary branches and secondary branches had maximum direct effect resulted significantly positive correlation with grain yield/plant. These traits can be used to improve the grain yield of pigeon pea.

Lakhote *et al.* (2015) [13] evaluated 24 vegetable type genotypes of pigeon pea for path analysis and observed that green pod yield plant^{-1} had positive and significant direct effects with days to 50 per cent flowering, pod width, pod length, seed pod^{-1}, 100 green pod weight, 100 green seed weight, shelling percentage, number of flower cluster. Hence these traits should be given more consideration while deciding about selection criteria for vegetable type genotypes in pigeon pea.

An experiment with 21 diverse genotypes of short duration pigeon pea was carried out by Singh *et al.* (2013) [34] to study path analysis and observed that pod length exhibited the highest magnitude of direct effects on seed yield, followed by seeds/pod and primary branches/plant. These characters are considered the principal components of seed yield and may be helpful in increasing the seed yield of pigeon pea. The residual effect was found to be 0.594 in path analysis. This indicated that other attributing characters were also important and may play a critical role in pigeon pea improvement.

Path coefficient analysis for 30 genetically diverse genotypes of pigeon pea was done by Kesha *et al.* (2016) [11]. They observed that pods/plant, 100-seed weight, days to 50% flowering, primary branches and secondary branches had maximum direct effect resulted significantly positive correlation with grain yield/plant. These traits can be used to improve the grain yield of pigeon pea.

Kumar *et al.* (2018) [12] studied path coefficient analysis for grain yield and component traits in 45 diverse genotypes of pigeon pea. Path coefficient analysis of genotypic and phenotypic exhibited high positive and direct effect of number of pod per plant, days to maturity, 100-grain weight, number of seed per pod, number of chambers per pod and number of primary branches per plant towards grain yield. Thus any selection based on these characters will enhance performance and improvement in grain yield of pigeon pea.

Path coefficient analysis for seed yield and component traits in 21 diverse genotypes of pigeon pea were studied by Narayanan *et al.* (2018) [18]. Indicated that characters *viz*., plant height, number of pods per plant, days to 50 per cent flowering, and days to maturity should be considered as selection indices in seed yield improvement programme as they recorded high direct effects on seed yield per plant.

Pushpavalli *et al.* (2018) [25] carried out path coefficient analysis to estimate the direct and indirect contribution of various traits to seed yield and reported that days to maturity exhibited the highest magnitude of direct effects on seed yield followed by number of pods/plant. The direct effects of number of pods/plant on seed yield were mainly due to indirect effects via number of primary branches/plant and secondary branches/plant. Also number of pods/plant is positively and significantly correlated with seed yield. These characters are principal components of seed yield and can be considered as selection criteria for increasing the seed yield of pigeon pea.

Path coefficient analysis in red gram during *Kharif*, 2017 for seed yield and its contributing traits by Satyanarayana *et al.* (2018) [31] in Andhra Pradesh revealed importance of days to 50% flowering, 100 seed weight, secondary branches plant^{-1} and plant height for their contribution either directly or indirectly to seed yield and hence, during selection these traits should be given utmost attention for developing of high seed yielding red gram varieties.

Genetic divergence Studies

The development of new varieties is mainly governed by the magnitude of genetic variability in the base material and extent of variability for desired characters. Genetic variability and divergence is of greatest interest to the plant breeder as it plays a vital role in framing a successful breeding programme. The genetically diverse parents are likely to produce high heterotic effects and desirable segregants. The concept of D^2 analysis for measuring divergence between two populations was introduced by Mahalanobis (1936) [14]. It gave results based on the magnitude of divergence independent of size sample.

Mahalanobis *et al.* (1949) [15] applied the D^2 statistic in a detailed study of anthrapometric data of Uttar Pradesh, classifying it in twenty-three groups into three major clusters, i.e. Brahmin (B-cluster) at the top of Hindu social hierarchy, comprising nine groups, the Artisans (A-cluster) in the middle consisting of four groups, and the Tribal cluster (T-cluster) at the bottom comprising of ten groups.

Genetic divergence is a result of changes in the gene frequencies of different population due to evolutionary forces. While the frequency of given gene in turn is a function of its contribution in the total adaptation of individuals in natural populations. The individuals showing more fitness contribute more than those having less fitness to the population gene pool.

Murthy and Arunachalam (1966) [17] stated that the genetic drift and selection in different environments could cause greater diversity among genotypes than their geographical distance.

Joshi (1979) [10] stated that genetic diversity involving genetically diverse parents in crossing would be advantageous as it would provide an opportunity for bringing together gene constellations of divergent origin. Isolation in space and time results in locking up genes in different constellations these should be unshackled and brought together. Therefore, parents from different geographical groups should be brought together in hybridization.

Thirty pigeon pea genotypes studied for genetic divergence by Sreelakshmi *et al.* (2010) [35] using Mahalanobis D^2 statistic indicated wider genetic diversity. Among the 7 characters studied, seed yield contributed the most towards the divergence of genotypes followed by number of pods per plant, days to 50% flowering and plant height. The genotypes were grouped into 8 clusters, maximum inter cluster distance being observed between the clusters III and VII. Hence, crossing of parents from these clusters would be desirable for combining earliness, short plant height, more primary branches per plant with more pod number coupled with high seed yield.

Pandey *et al.* (2013) [21] studied the nature and extent of genetic diversity among 23 parents of pigeon pea hybrids employing Mahalanobis D^2 statistics. The genotypes were grouped into five different non-overlapping clusters. The highest contribution in manifestation of genetic divergence was exhibited by 100-seed weight followed by pods per plant, days to maturity, harvest index, biological yield per plant, days to 50% flowering and seed yield per plant. The maximum intra-cluster distance was observed for cluster III, followed by cluster IV, I and V. The highest inter-cluster distance was recorded between cluster II and IV followed by cluster I and IV and cluster V and II. The crossing between entries belonging to cluster pairs having large inter-cluster distance and possessing high cluster means for one or other characters to be improved may be recommended for isolating desirable recombinants in the segregating generations in pigeon pea.

Birhan *et al.* (2013) [2] assessed the genetic divergence using Mahalanobis D^2 statistics and the genotypes were grouped into six clusters. Distances between these clusters were significantly different for most of the cluster combinations. Therefore, the present study indicated that there is sufficient genetic diversity in pigeon pea germplasm that could be used as a base for improvement of the yield and other important attributes of this crop through direct selection and hybridization.

Quantitative assessment of genetic divergence in 47 pigeon pea genotypes with respect to seed yield and yield components by Reddy *et al.* (2015) [27] clustered them into 10 different groups. Among the ten clusters, cluster I was the largest comprising of 35 genotypes, representing collections from Andhra Pradesh, Karnataka and Bihar, while the clusters IV, V, VI, VII, VIII and X comprised of one genotype each. The distribution pattern of genotypes into different clusters revealed no parallelism between genetic and geographic diversity. An analysis of inter-cluster D^2 values revealed higher divergence between cluster VIII and cluster IX, followed by cluster IX and X indicated that hybridization between parents selected from these clusters may result in maximum heterosis.

D^2 analysis by Satankar *et al.* (2017) [30] grouped 30 genotypes into 5 clusters. The inter cluster D^2 values indicated that most diverse clusters were cluster II and V and seed yield per plant has maximum contribution in genetic divergence followed by seed yield per ha, number of pod per plant and number of primary branches per plant. The genotypes of cluster V (K.L.S. and Asha) showed highest cluster mean values for most of the yield contributing characters, and the genotype of cluster II (UPAS120) showed superior performance as early flowering and early maturity. Therefore, genotypes from cluster II and cluster V can be utilized as potential parents in crossing programme for improving more than one economic character such as high yield and early maturity.

Patel *et al.* (2018) [22] conducted an experiment to study the genetic diversity in pigeon pea using D^2 statistics method of Mahalanobis. The forty-five genotypes of pigeon pea were grouped into nine clusters which indicated the presence of diversity for different traits. The maximum number of diverse genotypes (35 genotypes) appeared in cluster I followed by cluster II (3 genotypes), cluster III, IV, V, VI, VII, VIII, IX with one genotypes. The maximum intra-cluster distance was recorded within cluster I (D=8.16) and the maximum inter cluster distance was observed between II and XI (D=34.47), indicating the existence of wide genetic variability. Based on mean performances, cluster III and cluster V found superior for yield and yield contributing characters. Therefore, genotypes selected for hybridization among the above said clusters would produce high heterosis and segregants for more than one economic character.

Forty-nine pigeon pea genotypes were grouped into six clusters based on Mahalonobis D^2 statistics by Pushpavalli *et al.* (2018) [25] to study the genetic divergence. Among the traits studied, days to maturity contributed to maximum genetic divergence followed by days to 50% flowering. Maximum inter cluster distance was observed between clusters II and VI and intra cluster distance in cluster I and II. Genotypes in cluster IV recorded lowest mean values for days to 50% flowering and days to maturity. While, genotypes in cluster V recorded highest mean values for no. of branches/plant, no. of pods per plant and seed yield. Thus genotypes in cluster IV and V can be utilized as parents for the development of early maturing and high seed yielding varieties.

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