**Analysis of genetic divergence in vegetable cowpea [*Vigna unguiculata* (L.) Walp.]**

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**Abstract**

Analysis of genetic divergence of 60 genotypes for 12 characters in vegetable cowpea revealed wide range of (D = √D2) values ranging between 16.90 and 49.39 suggesting the presence of considerable amount of genetic diversity in the material studied. The 60 genotypes were grouped into ten clusters where, cluster II (20) was the largest followed by cluster I (16), cluster III (13) and cluster IV (5). No parallelism was observed between genetic diversity and geographical diversity. Maximum inter-cluster distance was recorded between clusters VIII and X followed by that between clusters VI and X, II and IX, IV and VIII representing wide divergence among the clusters. Based on the inter-cluster distance and cluster means, the genotypes from cluster X with cluster VIII and cluster VI; cluster IV with cluster VIII and cluster IX could be selected as parents in vegetable cowpea breeding.

***Key words:*** Genetic divergence, inter and intra-cluster distance, vegetable cowpea

**Introduction**

Vegetable cowpea is called as poor man’s meat or vegetable meat due to its high amount of protein in grain with better biological value on dry weight basis. Green tender pods form an excellent nutritious vegetable and have got a potential to solve the protein problem of human diet. Improvement of existing varieties is a continuous process in plant breeding. For an efficient breeding programme, selection of genetically divergent parents is important. Genetic divergence is used to measure genetic distance between different genotypes and to classify the genetic stocks into distinct groups. Inter-crossing between more divergent groups would increase the variability and range of frequency distribution. In a breeding programme, progenies derived from diverse crosses are expected to show a broad spectrum of genetic variability and provide a greater scope of isolating high yielding segregates in advanced generations (Arunachalam, 1981). Phenotypic diversity is usually considered as an indication of underlying genetic differences. Multivariate statistical methods and numerical taxonomy have been used extensively in summarizing and describing variation and its pattern in a population of crop genotypes. In addition, the Mahalanobis D2 statistic has been used to quantify the degree of divergence in different crops. The technique gives insight into the most genetically divergent parents that could be used for heterotic hybridization purpose. Mahalanobis’s D2 (1936) statistic is a powerful tool in quantifying the degree of divergence among the populations and has extensively been used to assess diversity. Ushakumari *et al.* (2000) have used the concept of generalized distance to isolate genetically diverse material in groundnut. Hence, present study was undertaken for comparing nature and extent of genetic diversity in vegetable cowpea.

**Materials and methods**

The experimental material for the present investigation comprised of 60 genotypes of vegetable cowpea. Genetically diverse genotypes of vegetable cowpea were collected from Vegetable Research Station, Junagadh Agricultural University, Junagadh; Main Vegetable Research Station, Anand Agricultural University, Anand; Indian Agricultural Research Institute, New Delhi and Research on Seed Spices, S.D.A.U., Jagudan. The genotypes were evaluated in a Randomized Block Design with three replications at the Vegetable Research Station, Junagadh Agricultural University, Junagadh during the year 2013. Each entry was accommodated in a single row of 3.0 m length with a spacing of 120 x 30cm. The observations were recorded on five randomly selected competitive plants from each genotype and replication for twelve characters *viz.,* days to 50% flowering, days to first green pod picking, pod length, number of primary branches per plant, pod width, hundred fresh seed weight, ten pod weight, number of pods per cluster, number of pods per plant and green pod yield per plant. The mean values were used for the analysis of variance for the experimental design as per Panse and Sukhatme (1985). The multivariate analysis was done as per Mahalanobis (1936) D2-statistic as described by Rao (1952). The genotypes were grouped into different clusters following Tocher’s method as described by Rao (1952).

**Results and discussion**

The analysis of variance showed significant differences among the genotypes for all the characters indicating presence of sufficient amount of genetic variability among the genotypes for the characters studied. D2-statistic estimated on sixty genotypes of vegetable cowpea for twelve characters showed that the generalized distance between two entries varied from 16.90 to 49.39, which was an indicator of availability of considerable diversity in the material evaluated. On the basis of D2-values, 10 clusters were formed from sixty genotypes (Table-1). The clustering pattern of genotypes showed that the genotypes of different origins were clubbed into one cluster whereas; the genotypes belonging to same state or origin were grouped into different clusters (Table-2). This suggests that there was no relation between genetic and geographic diversity and that the geographic distribution was not the sole criterion of genetic diversity. Murty *et al*. (1996) also stated that genetic drift and selection in different environments could cause greater diversity than geographic distance. Further, the free exchange of seed materials among the different regions consequently causes characters constellations because of the human interference and material may lose its individuality. The results obtained in the present study are in accordance to the findings of Hossain *et al*. (2012), who also reported that there was no parallelism between geographic distribution and genetic diversity. The cluster II contained 20 genotypes from different origins. On the other hand, the clusters V, VI, VII, VIII, IX and X possessed only one genotype in each cluster. In general, intra-cluster distance values were lower than the inter-cluster distances (Table 3). Thus, the genotypes included within a cluster tended to diverse less from each other. The lowest intra-cluster distance was observed in cluster I (D=18.40) revealing that the genotypes of this cluster resemble one another genetically and appeared to have evolved from common gene pool. The highest intra-cluster distance was in cluster IV (D=26.87) indicating substantial diversity within the cluster. The maximum inter-cluster distance (D=49.39) was found between clusters VIII and X followed by that between clusters VI and X (D=48.69), II and IX (D=48.49), IV and VIII (D=47.96), II and X (D=47.15), IV and IX (D=46.19), II and VIII (D=45.63) and III and VIII (D=39.97). The closest proximity was noticed between the clusters V and VII (D=16.90). The genotypes belonging to the clusters separated by high statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregates. In this context, the genotypes from cluster X (JCPL-07) with cluster VIII (JCPL-56) and cluster VI (JCPL-75); cluster IV (JCPL-16, JCPL-62, JCPL-04, JCPL-72, JCPL-89) with cluster VIII (JCPL-56) and cluster IX (JCPL-78) could be selected as parents in hybridization programme. A wide range of variation for several characters among single as well as multi-genotype clusters was observed. However, the differences were clearer for hundred seed weight followed by number of primary branches per plant, days to first picking and number of pods per cluster.The present findings are in conformity with those reported earlier in vegetable cowpea by (Ushakumari *et al*.; 2000 and Hossain *et al*.; 2012). The clustering pattern could be utilized in selecting the parents and deciding the cross combinations which may generate the highest possible variability for various traits. The genotypes with high mean values of any cluster can be used in hybridization programme for further selection and improvement. The mean values of each cluster for all the 12 characters are given in Table 4. It could be seen that the clusters differed with respect to mean performance of various characters, suggesting that the clusters formed are very distinct. The cluster VI differed from other clusters in respect to days to 50% flowering, pod width, number of pods per cluster and green pod yield per plant. For pod length, number of seeds per pod and hundred seed weight cluster X was the best. The cluster VIII had desirable value for number of primary branches per plant and plant height. The cluster II was the best for days to first picking. For ten pod weight cluster III was desirable.

Therefore, inter-crossing of genotypes involved in these clusters would be useful for inducing variability in the respective characters and their rationale improvement for increasing green pod yield in vegetable cowpea. The analysis of percent contribution of 12 characters towards total genetic divergence indicated that hundred seed weight (46.20%) followed by number of primary branches per plant (26.38%) contributed maximum towards total genetic divergence. These characters accounted for more than 72.58% of total divergence in the material studied. The contribution to the total divergence was the least by other characters ranging from 0.11% (days to 50% flowering) to 1.89% (ten pod weight). It has been well-established fact that more the genetically diverse parents used in hybridization programme, greater will be the chances of obtaining high heterotic hybrids and broad-spectrum variability in segregating generations (Arunachalam, 1981). It has also been observed that the most productive hybrids may come from high yielding parents with a high genetic diversity. Therefore, in the present investigation, based on high yielding genotypes and large inter-cluster distances, it is advisable to attempt crossing of the genotypes from cluster X with cluster VIII and cluster VI; cluster IV with cluster VIII and cluster IX which may lead to the generation of broad spectrum of favourable genetic variability for yield improvement in vegetable cowpea.

**Table 1. Grouping of 60 genotypes of vegetable cowpea in various clusters on the basis of D2-statistic**

|  |  |  |  |
| --- | --- | --- | --- |
| **Cluster** | **Number of genotypes** | **Name of the genotypes** | **Origin** |
| I | 16 | JCPL-17, JCPL-80, JCPL-35, JCPL-36, JCPL-20, JCPL-95, JCPL-82, JCPL-63, JCPL-10, JCPL-83, JCPL-43, JCPL-55, JCPL-49, JCPL-77 | Vegetable Research Station,  J.A.U., Junagadh |
| AVC-1 [C] | Vegetable Research Station,  A.A.U., Anand |
| JCPL-11-19 | Research on Seed Spices,  S.D.A.U., Jagudan |
| II | 20 | JCPL-92, JCPL-87, JCPL-97, JCPL-03, JCPL-93, JCPL-64, JCPL-74, JCPL-53, JCPL-05, JCPL-91, JCPL-12, JCPL-49, JCPL-11 | Vegetable Research Station,  J.A.U., Junagadh |
| JDNVC-39, JDNVC-41, JDNVC-58, JDNVC-62, JDNVC-74, JDNVC-75 | Research on Seed Spices,  S.D.A.U., Jagudan |
| Pusa Phalguni | I.A.R.I., New delhi |
| III | 13 | JCPL-06, JCPL-85, JCPL-81, JCPL-37, JCPL-44, JCPL-19, JCPL-86, JCPL-76, JCPL-15, JCPL-14, JCPL-69, JCPL-90 | Vegetable Research Station,  J.A.U., Junagadh |
| JCPL-11-17 | Research on Seed Spices,  S.D.A.U., Jagudan |
| IV | 5 | JCPL-16, JCPL-62, JCPL-04, JCPL-72, JCPL-89 | Vegetable Research Station,  J.A.U., Junagadh |
| V | 1 | JCPL-84 | Vegetable Research Station,  J.A.U., Junagadh |
| VI | 1 | JCPL-75 | Vegetable Research Station,  J.A.U., Junagadh |
| VII | 1 | JCPL-40 | Vegetable Research Station,  J.A.U., Junagadh |
| VIII | 1 | JCPL-56 | Vegetable Research Station,  J.A.U., Junagadh |
| IX | 1 | JCPL-78 | Vegetable Research Station,  J.A.U., Junagadh |
| X | 1 | JCPL-07 | Vegetable Research Station,  J.A.U., Junagadh |

**Table-2. Source and clustering pattern of 100 genotypes of vegetable cowpea**

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Source** | **I** | **II** | **III** | **IV** | **V** | **VI** | **VII** | **VIII** | **IX** | **X** | **Total number of genotypes** |
| **Vegetable Research Station, J.A.U., Junagadh** | 14 | 13 | 12 | 5 | 1 | 1 | 1 | 1 | 1 | 1 | 50 |
| **Vegetable Research Station, A.A.U., Anand** | 1 | - | - | - | - | - | - | - | - |  | 1 |
| **I.A.R.I.,**  **New Delhi** | - | 1 | - | - | - | - | - | - | - |  | 1 |
| **Research on Seed Spices, S.D.A.U.,**  **Jagudan** | 1 | 6 | 1 | - | - | - | - | - | - |  | 8 |

**Table 3. Average inter and intra-cluster (diagonal) distance [D= (D2)½] values in vegetable cowpea**

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Cluster** | **I** | **II** | **III** | **IV** | **V** | **VI** | **VII** | **VIII** | **IX** | **X** |
| **I** | 18.40 | 28.03 | 26.94 | 26.53 | 21.66 | 28.79 | 24.47 | 32.53 | 31.10 | 33.08 |
| **II** |  | 21.09 | 39.06 | 26.73 | 32.11 | 38.37 | 38.66 | 45.63 | 48.49 | 47.15 |
| **III** |  |  | 21.24 | 34.61 | 33.84 | 28.44 | 29.24 | 39.97 | 28.89 | 30.99 |
| **IV** |  |  |  | 26.87 | 32.81 | 39.34 | 38.33 | 47.96 | 46.19 | 38.14 |
| **V** |  |  |  |  | 0.00 | 22.97 | 16.90 | 23.55 | 29.36 | 43.72 |
| **VI** |  |  |  |  |  | 0.00 | 16.98 | 28.61 | 26.65 | 48.69 |
| **VII** |  |  |  |  |  |  | 0.00 | 17.92 | 19.19 | 42.32 |
| **VIII** |  |  |  |  |  |  |  | 0.00 | 20.62 | 49.39 |
| **XI** |  |  |  |  |  |  |  |  | 0.00 | 37.21 |
| **X** |  |  |  |  |  |  |  |  |  | 0.00 |

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Clusters** | **Days to 50% flowering** | **Days to first picking** | **No. of primary branches per plant** | **Plant height (cm)** | **Pod length (cm)** | **Pod width (cm)** | **No. of seeds per pod** | **No. of pods per cluster** | **Ten pod weight (g)** | **Hundred seed weight (g)** | **No. of pods per plant** | **Green pod yield per plant (g)** |
| **I** | 53.17 | 70.02 | 5.00 | 48.39 | 14.79 | 0.70 | 11.04 | 2.15 | 39.64 | 24.78 | 23.57 | 77.70 |
| **II** | 50.38 | 62.75 | 4.08 | 42.29 | 13.62 | 0.65 | 11.33 | 2.54 | 37.52 | 20.43 | 38.68 | 110.74 |
| **III** | 52.90 | 68.41 | 4.94 | 40.02 | 16.46 | 0.72 | 11.62 | 2.32 | 60.19 | 33.90 | 33.78 | 132.49 |
| **IV** | 52.60 | 68.93 | 3.66 | 36.58 | 16.67 | 0.73 | 10.46 | 2.42 | 33.20 | 24.39 | 31.02 | 130.35 |
| **V** | 56.00 | 71.67 | 5.95 | 60.85 | 13.10 | 0.74 | 10.60 | 2.97 | 31.20 | 20.01 | 15.00 | 43.50 |
| **VI** | 51.00 | 64.00 | 6.35 | 52.10 | 15.84 | 0.82 | 12.10 | 3.30 | 55.87 | 27.30 | 45.56 | 193.14 |
| **VII** | 52.33 | 72.00 | 6.90 | 52.20 | 15.33 | 0.66 | 11.25 | 2.65 | 49.17 | 23.35 | 41.87 | 171.23 |
| **VIII** | 55.00 | 69.33 | 7.85 | 74.50 | 14.42 | 0.62 | 11.35 | 2.08 | 37.06 | 20.35 | 20.08 | 51.65 |
| **IX** | 59.00 | 71.00 | 7.10 | 58.55 | 16.71 | 0.67 | 11.45 | 2.05 | 53.88 | 29.64 | 12.53 | 49.48 |
| **X** | 59.67 | 79.00 | 4.15 | 31.41 | 17.45 | 0.66 | 12.40 | 1.02 | 28.68 | 34.12 | 4.28 | 11.21 |
| **Mean** | 54.21 | 69.71 | 5.60 | 49.69 | 15.44 | 0.69 | 11.36 | 2.35 | 42.64 | 25.83 | 26.64 | 97.15 |
| **S. Em.**± | 0.57 | 0.42 | 0.060 | 1.52 | 0.52 | 0.016 | 0.32 | 0.05 | 1.93 | 0.34 | 2.39 | 11.05 |
| **C.V. %** | 1.88 | 1.08 | 2.21 | 5.96 | 5.99 | 4.13 | 4.85 | 3.91 | 7.75 | 2.31 | 13.20 | 18.08 |
| **Percentage contribution of characters towards total divergence** | | | | | | | | | | | | |
| **Number of times appearing first** | 2 | 213 | 467 | 14 | 3 | 31 | 4 | 134 | 32 | 818 | 16 | 36 |
| **% contribution** | 0.11 | 12.03 | 26.38 | 0.79 | 0.17 | 1.75 | 0.23 | 7.57 | 1.81 | 46.20 | 0.90 | 2.03 |

**Table 4: Cluster means for 12 different characters in 60 genotypes of cowpea**

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