

## Studies on Biodiversity in Grain Cowpea [*Vigna unguiculata* (L.) Walp.]

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Sixty five genotypes of grain cowpea (Source: International Institute of Tropical Agriculture, Nigeria) were evaluated for thirteen metric characters to observe the genetic diversity existing among them by Mahalanobis  $D^2$  statistics. Out of sixty five, only sixty three genotypes responded towards flowering, on which further study was taken out. The analysis of variance revealed significant differences among the genotypes for each character under study. These sixty three genotypes were grouped into twenty four clusters and the maximum intra-cluster distance was observed in cluster VIII. The maximum inter cluster distance was recorded between cluster XVII and XXII. Based on the cluster means and cluster distances the genotypes EC 517122 (cluster X) and EC 517123 (cluster XXII) were found the most promising. Among the traits studied, days to first flowering and number of pods per plant contributed towards maximum divergence.

**Key words:** Cowpea, [*Vigna unguiculata* (L.) Walp.], Cluster,  $D^2$  statistics, Genotypes, Divergence

Among legumes, cowpea is being grown in almost all parts of India except high hills. It is a unique pulse crop with manifold uses such as pulse (dal), green vegetables, green fodder and as a cover crop for stopping soil erosion. But due to low yield we are unable to exploit the crop efficiently. Therefore crop improvement programme is necessary to increase the productivity. For any crop improvement programme variability is the first requirement. For proper utilization of variability in breeding programme an efficient screening, evaluation and documentation of germplasm lines for useful traits is essential so that the potential value of particular germplasm line may be assessed. In present research programme, genetic diversity in a set of sixty three cowpea genotypes was assessed by Mahalanobis  $D^2$  statistics for different traits.

### Materials and Methods

Sixty five genotypes of grain cowpea (Source IITA, Nigeria) were evaluated in Randomized Block Design (R.B.D) in the 'zaid' season of 2005. The genotypes were

sown in two meter rows with 3 replications at spacing of 45x15 cm. Out of sixty five genotypes, only sixty three genotypes responded towards flowering. Therefore, data were recorded on sixty three genotypes. Observations were taken on 5 randomly selected plants in each of these 63 genotypes from each replication for 13 quantitative characters i.e. days to 1<sup>st</sup> flowering, days to 50% flowering, days to 1<sup>st</sup> pod maturity, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, pod size, number of seeds per pod, 100 seed weight, seed yield per plant & green stover yield per plant. Analysis of variance was carried out for each trait & then multivariate analysis of Mahalanobis (1936). The genotypes were grouped into clusters by Tocher's method (Rao, 1952).

### Results and Discussion

The analysis of variance (ANOVA) showed significant differences among the genotypes for all the thirteen traits studied (Table 1). On the basis of  $D^2$  values, the different genotypes of grain cowpea were grouped into twenty

**Table 1.** Analysis of variance for 13 metric character in 63 cowpea genotypes

Source of variation	Degree of freedom	X <sub>1</sub>	X <sub>2</sub>	X <sub>3</sub>	X <sub>4</sub>	X <sub>5</sub>	X <sub>6</sub>	X <sub>7</sub>	X <sub>8</sub>	X <sub>9</sub>	X <sub>10</sub>	X <sub>11</sub>	X <sub>12</sub>	X <sub>13</sub>
Treatment	62	195.45 **	213.4 **	189.3 **	213.3 **	7822.90 **	4.501 **	164.0 **	658.768 **	9.544 **	13.69 **	27.58 **	1354 **	115120 **
Error	124	0.896	1.836	0.865	0.842	1.198	0.327	0.944	0.46507	0.220	0.289	0.142	0.12	8.45
G.M.		55.857	65.55	74.40	85.17	97.82	4.566	18.0	24.671	13.9	11.22	17.73	30.4	280.2
S.Em.		0.5465	0.782	0.537	0.529	0.632	0.330	0.560	0.39373	0.271	0.310	0.068	0.20	1.679
C.V.		1.6947	2.067	1.250	1.077	1.119	12.52	5.372	2.7641	3.356	4.794	0.673	1.14	1.037

X<sub>1</sub>= days to 1<sup>st</sup> flowering, X<sub>2</sub>= days to 50% flowering, X<sub>3</sub>= days to 1<sup>st</sup> pod maturity, X<sub>4</sub>= days to maturity, X<sub>5</sub>= plant height (cm), X<sub>6</sub>= number of primary branches/ plant, X<sub>7</sub>= number of secondary branches / plant, X<sub>8</sub>= number of pods / plant, X<sub>9</sub>= pod size (cm), X<sub>10</sub>= number of seeds / pod, X<sub>11</sub>= 100 seed weight (gm), X<sub>12</sub>= seed yield/ plant (gm), X<sub>13</sub>= Stover yield/plant (gm).

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four clusters. The cluster strength varied from single genotype (cluster IX-XXIV) to thirty genotypes (cluster I). The pattern of distribution of these germplasm lines into 24 clusters confirmed the existence of variability among the genotypes indicated by ANOVA. The average intra and inter cluster distances are given in Table 3. The intra-cluster distance ranged from 0.00 (cluster IX - XXIV) to 15.3 (cluster VIII). Maximum inter cluster distance (60.3) was recorded between cluster XVII & XXII showing maximum diversity followed by cluster XIX & XXI (59.9).

The average cluster mean for different characters (Table 4) exhibited that the cluster X had minimum days to 1<sup>st</sup> flowering & cluster XVII had minimum days to maturity. Cluster XXIII had maximum plant height whereas cluster IX had minimum plant height. Cluster V had maximum primary branches per plant and cluster

XVI had maximum secondary branches per plant. Cluster XXII had maximum number of pods per plant and cluster XVIII had maximum pod size. Cluster XVI had maximum number of seeds per pod. Cluster XXIV had maximum 100 seed weight. Cluster XXII had maximum seed yield per plant and green stover yield per plant.

As per earlier reports heterosis and better recombinants can be obtained by crossing between parents of clusters of high and low means (Usha Kumari *et al.*, 2000, Girish *et al.*, 2001). Therefore for getting better heterosis, the genotypes from cluster XXII and IX with high and low cluster means for majority of characters respectively can be used for hybridization programme for yield improvement in grain cowpea varieties.

In addition, the contribution of each character to genetic divergence was calculated. It was found that number of pods per plant contributed maximum towards

**Table 2. Composition of genotypes in clusters**

Cluster number	Number of genotypes included	Genotypes
Cluster I	30	EC-517112, EC-517114, EC-517115, EC-517117, EC-517120, EC-517124, EC-517128, EC-517133, EC-517134, EC-517138, EC-517139, EC-517141, EC-517144, EC-517149, EC-517150, EC-517151, EC-517152, EC-517153, EC-517154, Cowpea Black-2, EC-528689, EC-528694, EC-528695, EC-528696, EC-528697, EC-528698, EC-528699, EC-528700, EC-528701, EC-528703
Cluster II	3	EC-517130, EC-517136, EC-517146
Cluster III	2	EC-517125, Cowpea Black-1
Cluster IV	3	EC-517137, EC-528691, EC-528692
Cluster V	2	EC-517116, EC-517155
Cluster VI	3	EC-517147, EC-528602, EC-528693
Cluster VII	2	EC-517135, EC-517148
Cluster VIII	2	EC-517126, Com-1
Cluster IX	1	EC-517119
Cluster X	1	EC-517122
Cluster XI	1	EC-517129
Cluster XII	1	EC-517121
Cluster XIII	1	EC-517131
Cluster XIV	1	EC-517142
Cluster XV	1	EC-517113
Cluster XVI	1	EC-528690
Cluster XVII	1	EC-528687
Cluster XVIII	1	EC-517145
Cluster XIX	1	EC-517127
Cluster XX	1	EC-517132
Cluster XXI	1	EC-517118
Cluster XXII	1	EC-517123
Cluster XXIII	1	EC-517140
Cluster XXIV	1	EC-517143



Table 4. Cluster Means For 13 Characters of 63 Cowpea Genotypes

199	28.0	17.3	11.3	13.4	21.6	16.4	4.61	85.0	84.9	74.3	65.0	55.5	I
140	27.2	20.7	9.99	12.1	31.2	17.6	4.33	45.8	81.6	68.9	58.3	50.9	II
174	25.2	19.6	11.3	14.7	23.9	25.6	4.67	201	81.6	70.6	60.9	52.1	III
584	78.0	14.5	13.2	14.5	60.7	19.9	3.99	103	91.1	78.3	73.1	60.6	IV
187	26.6	20.4	7.16	12.2	19.6	22.6	8.99	44.8	77.8	68.4	59.3	50.3	V
207	14.4	13.2	5.67	10.3	34.1	15.3	4.21	63.1	80.5	70.2	61.0	51.1	VI
260	41.5	22.2	10.1	17.2	23.9	24.1	4.33	75.3	78.3	66.6	58.1	48.1	VII
377	25.0	17.8	12.4	15.2	41.3	9.9	3.33	76.9	89.9	81.3	71.1	60.8	VIII
56.3	11.3	17.6	11.3	12.6	13.6	24.3	4.67	39.6	77.3	62	57.6	50.3	IX
598	59.6	17.4	11.6	13.6	42.3	30.6	6.33	59.6	75.3	67.3	57	46.3	X
203	56.3	23.7	11.3	13.3	56.6	16.3	4.33	161	89.3	80.3	70.6	58.3	XI
97.6	15.6	18.2	12.6	13.6	13.6	10.3	4.67	84.6	75.3	69.2	51.6	51.6	XII
203	15.5	20	10.3	16.3	13.6	23.6	6.33	59.3	86.6	75.3	63	52	XIII
674	12.8	14.4	12	14.2	12.6	14.3	3.33	207	101	86.3	76	69.3	XIV
478	27.6	19.4	11.3	14.3	25.3	24.3	5.33	190	89.3	74	71	54.6	XV
200	31.7	13.7	15.3	19.3	26.3	40.6	4.33	90	80.6	70.6	61.3	53.3	XVI
449	11.6	12.8	13.6	11.6	9.67	15.3	3.67	214	72.6	62.6	53.3	46.6	XVII
275	11.4	15.9	13.6	17.6	6.67	11.7	3.33	149	93.6	86.6	77.3	68	XVIII
109	52.2	16.8	13.3	16.3	35	34.3	5.67	173	97.6	87.6	80.3	68.3	XIX
352	54.1	19.2	10	13.6	4.67	11.3	5.67	140	83.0	78.3	70.3	51.6	XX
98.3	28.9	22.2	11	11.5	16.6	8.3	3.33	110	74.3	67.6	60.3	56.6	XXI
779	121	16.6	13	16.7	70.3	19.7	6.67	160	97.3	88.6	79.6	70.3	XXII
178	16.7	13.9	13.3	14.1	17.3	22.6	5.67	223	104	84.6	78	71.6	XXIII
423	3.95	26.1	12.3	14.3	3.33	14.3	4.33	109	103	87.6	79	72.3	XXIV

X<sub>1</sub>= days to 1<sup>st</sup> flowering, X<sub>2</sub>= days to 50% flowering, X<sub>3</sub>= days to 1<sup>st</sup> pod maturity, X<sub>4</sub>= days to maturity, X<sub>5</sub> = plant height (cm), X<sub>6</sub> = number of primary branches/ plant, X<sub>7</sub>= number of secondary branches / plant, X<sub>8</sub>= number of pods / plant, X<sub>9</sub>= pod size (cm), X<sub>10</sub>= number of seeds / pod, X<sub>11</sub>= 100 seed weight (gm), X<sub>12</sub>= seed yield/ plant (gm), X<sub>13</sub>= Stover yield/plant (gm).

Table 5. Contribution of different characters to divergence

Character	%Contribution to Genetic Divergence
Days to 1 <sup>st</sup> flowering	9.626
Days to 50% flowering	6.451
Days to 1 <sup>st</sup> pod maturity	6.041
Days to maturity	7.680
Plant height	8.806
No. of primary branches/ plant	7.526
No. of secondary branches/ plant	8.038
Number of pods/ plant	9.573
Pod size	8.602
Number of seeds/ pod	6.195
100 seed weight	7.680
Seed yield/ plant	6.298
Stover yield/ plant	7.475

divergence followed by days to first flowering whereas days to first pod maturity contributed minimum towards divergence.

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