



## Biometrical approaches for selection of parents in vegetable cowpea (*Vigna unguiculata*) breeding programme

HIRA LAL<sup>1</sup>, NAGENDRA RAI<sup>2</sup> and VISHWA NATH<sup>3</sup>

ICAR-Indian Institute of Vegetable Research, Varanasi, Uttar Pradesh 221 305

Received: 13 April 2016; Accepted: 21 February 2017

### ABSTRACT

Eighty nine genotypes of vegetable cowpea collected from different parts of India were evaluated for yield and yield-attributing traits for genetic variation, character association, cause-effect analysis and genetic diversity among the genotypes through  $D^2$  statistics. High values of genotypic and phenotypic coefficient of variations, broad sense heritability and genetic advance were estimated for plant height, pod yield/plant, number of peduncles and pods/plant, pod weight and pod length. Pod yield/plant showed strong positive correlation with pod weight, number of peduncles and pods/plant, pod length and number of seeds/pod, while negative correlation with days to 50% flowering at genotypic and phenotypic levels. The maximum direct positive effect on pod yield/plant was contributed by pod weight followed by number of pods/plant. Based on degree of divergence the genotypes were grouped into twelve clusters. The genotypes of cluster XII showed maximum genetic divergence with cluster X, hence, crossing between genotypes within these groups could produce good recombinants and desirable segregants. Cluster III was found to be the best performing for number of pods/plant, pod weight and pod yield/plant while the cluster IX flowered much earlier. Thus, crossing between genotypes within these groups could produce desirable transgressive segregants for earliness and high yielding genotypes. Plant height contributed highest towards divergence (29.37%) followed by number of peduncles/plant (26.30%), number of pods/plant (18.39%) and pod weight (16.42%) among vegetable cowpea genotypes.

**Key words:** Correlation, Genetic divergence, Genetic variability, Heritability, Path analysis, Vegetable cowpea

Vegetable cowpea (*Vigna unguiculata* (L.)  $2n = 2x = 22$ ) is grown for its immature pods in almost all the regions except high hilly areas of India, Bangladesh, Indonesia, Philippines and Sri Lanka (Pant *et al.* 1982 and Chakraborti 1986). In India, it is grown as an important summer and rainy season vegetable. It is strictly a self-pollinated crop due to its cleistogamous nature. Pod yield in vegetable cowpea is a highly variable, complex character and is associated with a number of component characters (Umaharan *et al.* 1997, Lal *et al.* 2007 and Huque *et al.* 2012a). So while selecting for yield one should take into account of the component characters. The knowledge of genetic variability, character association, i.e. genotypic and phenotypic correlation between yield and its component characters is an essential requirement for yield improvement (Fraser and Eaton 1983). Cause-effect analysis provides an effective means of partitioning the correlation coefficients into direct and indirect effects of the component characters of yield on the basis of which, crop improvement programme can be

logically devised (Rao *et al.* 1997).

Evaluation of genetic diversity is a useful tool in quantifying the degree of divergence in a biological population at genotypic level and to assess relative contribution of different components to the total divergence both at intra and inter-cluster levels (Jatasara and Paroda 1978). Cluster analysis is also carried out to detect divergent parents for hybridization purposes and to attain meaningful group constellations of a collection of genotypes. The progress of breeding is conditioned by the magnitude and nature of inter-relationship among the characters and variation of different characteristics. Better knowledge on genetic diversity or genetic similarity could help to get long term selection gain in plants (Chowdhury *et al.* 2002). Evaluation of genetic diversity is important to know the source of genes for a particular character within the available germplasm (Tomooka 1991).

Mahalanobis's  $D^2$  statistic as a tool for estimating genetic divergence in crop plants can be used to choose parents before initiation of any hybridization programme (Bhatt 1970), as it permits precise comparison among all possible pairs of population in any group before affecting actual crosses. In addition to aiding in the selection of divergent parents for hybridization, statistics measures

<sup>1</sup>Principal Scientist, Vegetable Science (e mail: hiralaliivr@gmail.com), <sup>3</sup> Senior Technical Officer (e mail: vishwanathbhargava@gmail.com), Division of Crop Improvement.

the degree of diversification and determines the relative contribution of each component character to the total divergence (Singh 1990). Therefore, an attempt was made to study the genetic variability, inter-relationship, cause-effect analysis between yield and its components and the nature and magnitude of genetic divergence to identify important selection indices influencing pod yield and selection of suitable genotypes that can profitably be utilized in a hybridization programme.

#### MATERIALS AND METHODS

The present investigation was carried out at the research farm of Indian Institute of Vegetable Research, Varanasi, Uttar Pradesh, India (25° 10' N latitude and 82° 52' E longitude at mean sea level of 128.93 m). Three hundred fifty nine cowpea genotypes including landraces, released varieties and advance breeding lines collected from different parts of India were sown during *khariif* season, 2013. Among 359 genotypes, 89 genotypes were found suitable for vegetable purpose based on pulpy and parchment free pods. The genotypes either belong to *Vigna unguiculata* cv-gr. *sesquipedalis* or *Vigna unguiculata* cv-gr. *unguiculata*. They were evaluated in a randomized complete block design (RCBD) with three replications during *khariif* season of 2014. The land was prepared into plots of 3.0 m × 2.7 m size and the seeds were directly dibbled 3 cm deep on ridges adopting a uniform spacing of 60 cm between the rows and 30 cm within the row. The crop was raised by following standard agronomic practices.

Data on nine horticultural traits, viz. days to 50% flowering, plant height (cm), number of primary branches/plant, number of peduncles/plant, number of pods/plant, pod length (cm), pod weight (g), number of seeds/pod and pod yield/plant (g) were collected from five randomly selected plants from each plot. Pod characters, viz. pod length (cm), pod weight (g) and number of seeds/pod were recorded from 12 days old immature pods. Data was subjected to analysis of variance by using MSTAT-C software (Russell and Eisensmith 1983). Genotypic and phenotypic coefficients of variations were estimated as per Burton (1952). Heritability

in broad sense was calculated by the formula given by Singh and Ceccarelli (1996). The expected genetic advance was estimated according to the formula suggested by Allard (1960) and genetic advance expressed as percentage of mean was estimated by Comstock and Robinson (1952). The phenotypic and genotypic correlation coefficients were calculated according to Kwon and Torrie (1964) and path coefficient analysis was done based on Dewey and Lu (1959) to partition the correlation coefficients of pod yield into direct and indirect effects. Mahalanobis D<sup>2</sup> statistics (1936) was used to determine the degree of genetic divergence among the 89 genotypes and the genotypes were grouped into clusters following Tocher's method (Rao 1952).

#### RESULTS AND DISCUSSION

##### Genetic variability

The analysis of variance revealed significant differences among the genotypes for all the characters studied (Table 1). The wide range especially for plant height, number of peduncles and pods/plant, pod yield/plant and pod characters indicated the diversity among the genotypes. The phenotypic coefficient of variation (PCV) was slightly higher than genotypic coefficient of variation (GCV) in all the cases for all the characters. The minimum magnitudinal differences in GCV and PCV for all the traits implied that the traits are mostly govern by genetic factors with little role of environment in the phenotypic expression of these characters. Thus, selection of these traits on basis of phenotypic value may be effective. Plant height recorded the highest values of genotypic and phenotypic coefficients of variation followed by pod yield/plant, number of peduncles/plant, pod weight, number of pods/plant and pod length. This suggests that these characters are amenable for selection. Similar results were earlier reported by several workers (Lal *et al.* 2007, Ullah *et al.* 2011 and Nwofia *et al.* 2013). Broad sense heritability estimates in this study were high (more than 73%) for all the characters. High values of broad sense heritability (more than 90%) in conjunction with high genetic advance as percentage of mean (more

Table 1 Estimates of genetic parameters for various yield contributing characters in different genotypes of vegetable cowpea

Character	MSS	Mean	Range	PCV (%)	GCV (%)	h <sup>2</sup> B (%)	GA (%)
Days to 50% flowering (DAS)	131.204**	49.11	32.0 - 63.7	14.67	12.82	76.37	23.08
Plant height (cm)	18096.607**	119.42	35.8 - 388.7	65.43	64.84	98.18	132.34
Primary branches/plant (No.)	0.913**	4.20	2.6 - 5.4	14.49	12.41	73.34	21.89
Peduncles/plant (No.)	169.850**	18.07	7.1 - 39.6	42.25	41.32	95.67	83.26
Pods/plant (No.)	120.776**	21.59	6.8 - 38.6	30.08	29.05	93.27	57.79
Pod length (cm)	193.172**	29.01	12.4 - 46.1	28.28	27.34	93.50	54.47
Pod weight (g)	28.973**	10.09	3.4 - 15.3	31.21	30.61	96.21	61.85
Seeds/pod (No.)	15.418**	12.35	8.0 - 18.2	19.07	17.98	88.92	34.93
Pod yield (g/plant)	24476.870**	214.25	52.3 - 438.2	42.93	41.77	94.66	83.72

MSS = mean sum of squares, PCV = phenotypic coefficient of variation, GCV = genotypic coefficient of variation, H<sup>2</sup>B (%) = broad sense heritability, GA (%) = genetic advance as % of mean.

than 54%) were obtained for plant height, pod yield/plant, number of peduncles/plant, pod weight, number of pods/plant and pod length and it is an indicative of additive gene action and selection based on these parameters would be more reliable. Previous workers (Nath *et al.* 2009, Huque *et al.* 2012a and Chattopadhyay *et al.* 2014) reported similar findings in vegetable cowpea.

#### Character association

Mutual association of traits is often expressed by phenotypic, genotypic and environmental correlations (Akinyele and Osekita 2006). Phenotypic correlation is directly proportional to genotypic and environmental correlations. On the other hand, a positive genetic correlation between two desirable traits makes selection easy for improving both the traits simultaneously while the reverse will be the case for negative correlation. In the present study, the genotypic correlation coefficients were in general higher than phenotypic correlation coefficients, indicating greater contribution of genotypic factor in the growth and development of these traits association (Table 2). Correlation of pod yield/plant with pod weight, number of pods/plant, number of peduncles/plant, pod length and number of seeds/pod was found to be highly significant and positive at genotypic and phenotypic levels which imply that selection for these characters would lead to simultaneous improvement of pod yield in vegetable cowpea. Conversely, significant negative correlation was exhibited for days to 50% flowering with pod yield/plant at genotypic and phenotypic levels. It could be implied that cowpea genotypes which flowered early would produce more pod yield. Similar kinds of results were reported by Huque *et al.* (2012a), Chattopadhyay *et al.* (2014) and Madhavi *et al.* (2014).

*al.* (2014) and Madhavi *et al.* (2014).

#### Cause-effect analysis

Path coefficient analysis performed to disclose the causes and effects of chain relationships of different yield contributing characters on yield. The correlation coefficients of vegetable pod yield/plant with the eight yield components were further partitioned into direct and indirect effects and the results are presented in Table 2. Among the eight yield component traits, pod weight followed by number of pods/plant showed highly positive direct effect on pod yield/plant at genotypic level. Pod weight also exerted maximum positive indirect effect through pod length and number of seeds/pod. Several studies identified pod weight as one of the major contributors to pod yield (Lal *et al.* 2007, Nath *et al.* 2009 and Chattopadhyay *et al.* 2014). The present study indicated that number of pods/plant and pod weight should be given due importance in selection programmes for yield improvement in vegetable cowpea. The residual effect of the present study was 0.168 at genotypic level indicating that the characters studied contributed 83.2% of the yield. It is suggested that maximum emphasis should be given on the above characters for selecting vegetable cowpea with higher yield.

#### Genetic diversity

The analysis was carried out for relative magnitude of D<sup>2</sup> values for all the characters. Based on D<sup>2</sup> values all the 89 genotypes were grouped into 12 clusters (Table 3). Among the clusters, the maximum number of genotypes (56) were included in cluster I followed by cluster VI (12 genotypes), cluster V (11 genotypes), cluster X (2 genotypes) and clusters II, III, IV, VII, VIII, IX, XI and XII (one genotype each). The clustering did not follow any geographical pattern of genotype source. Generally, the geographical diversity has been considered as a measure of genetic diversity. However, this is an inferential criterion, and it may not be so effective in quantifying different populations. The present pattern of grouping of genotypes indicated that the genetic diversity was not fully associated with geographical distribution. Similar observations were reported by Narayanankutty *et al.* (2005), Suganthi *et al.* (2007), Huque *et al.* (2012b) and Chattopadhyay *et al.* (2014). The findings indicate that forces other than geographical separation such as natural and artificial selection, exchange of genetic stock, genetic drift, spontaneous mutation etc. are responsible for genetic diversity in vegetable cowpea. Sulnathi *et al.* (2007) demonstrated that genetic drift and selection pressure under different environments would have caused greater divergence rather than geographical distance in cowpea. Therefore, choice of parents for hybridization should be decided on the basis of genetic diversity rather than geographical diversity.

The intra- and inter-cluster distance among 89 genotypes revealed that values of inter-cluster distances were larger than the intra-cluster distances suggesting wider genetic diversity among the genotypes of different groups (Table 4).

Table 2 Genotypic and phenotypic correlations and direct effects of different yield contributing characters on pod yield per plant in vegetable cowpea

Character	rg with pod yield per plant	rp with pod yield per plant	Effects of yield contributing traits on pod yield per plant at genotypic level	
			Direct	Indirect
Days to 50% flowering	-0.504**	-0.453**	-0.109	0.049
Plant height (cm)	-0.125	-0.116	0.037	0.028
Primary branches/plant (No.)	0.021	0.096	-0.027	-0.001
Peduncles/plant (No.)	0.591**	0.594**	0.079	-0.012
Pods/plant (No.)	0.679**	0.680**	0.551	-0.090
Pod length (cm)	0.523**	0.516**	-0.019	-0.033
Pod weight (g)	0.734**	0.734**	0.699	1.094
Seeds/pod (No.)	0.321**	0.337**	0.003	-0.006

\* and \*\* indicate the significant at 5% and 1% level of probability, respectively; rg = Genotypic correlation coefficient; rp = Phenotypic correlation coefficient; Residual effect, at genotypic level = 0.1679

Table 3 Group constellation of 89 vegetable cowpea genotypes in 12 different clusters

Cluster	No. of genotypes	Name of genotypes along with source of collection
I	56	VRCP-67-1, VRCP-72-5, VRCP-50-1, VRCP-51-2, VRCP-66-4, VRCP-71-2, VRCP-92-1, VRCP-98-4, VRCP-80-4, VRCP-84-1, VRCP-18-8, VRCP-81-4, VRCP-51-5, VRCP-54-1, VRCP-55-3, VRCP-52-3, VRCP-68-2, VRCP-77-2, VRCP-97-3, VRCP-8-3, VRC-422, VRC-427, VRC-433, VRC-426, VRC-432 VRC-439, VRC-411, VRC-435, VRC-438, VRC-431, VRC-421, Red Seeded (Varanasi); NDCP-8, NDCP-13 (Faizabad); Ujjain AC (Ujjain), Dehradun AC (Dehradun); IC-559397, IC-559394, 35-A, 40-A, 41-A, 47-A (New Delhi); Sweta, Vanita (Raipur); Swarn Harita (Ranchi); Ankur Gomati (Nagpur); KVCP-21, KVCP-12, KVCP-33 (Jalna); KPC-1, KPC-4, KPC-6, KPC-8, KPC-11 (Koraput); Arka Garima (Bengaluru); Vayjyanthi (Thrissur)
II	1	RGC-4 (Rayagada)
III	1	VRCP-62-5 (Varanasi)
IV	1	VRCP-65-8 (Varanasi)
V	11	Kashi Kanchan, Kashi Nidhi, Kashi Unnati, Kashi Gauri, Kashi Shyamal, VRCP-75-3, VRCP-9-4, VRCP-96-4, VRCP-82-7, VRCP-52-2 (Varanasi); 867/05 (New Delhi)
VI	12	KVCP-2, KVCP-5, KVCP-70 (Jalna); VRC-424, VRC-425, VRC-428 (Varanasi); Bengal AC (Nadia); CWP-11 (Thrissur); Sel-16 (Bengaluru); Indira Hari (Raipur); IC-536636, IC-536572 (New Delhi)
VII	1	VRCP-48-2 (Varanasi)
VIII	1	LC-03-2 (Jaunpur)
IX	1	VRCP-49-5 (Varanasi)
X	2	Kalimpong AC, Kashyong AC-1 (Darjeeling)
XI	1	IC-3803 (New Delhi)
XII	1	VRCP-20-15 (Varanasi)

The highest intra-cluster distance was present in cluster VI (10.34) composed of 12 genotypes followed by cluster I (9.42), cluster X (7.47) and cluster V (6.91). The high intra-cluster distance in cluster VI indicated the presence of wide genetic diversity among the genotypes in this cluster.

The nearest inter-cluster distance was observed between cluster III and IV (2.52) followed by cluster IV and V (5.67) and cluster III and V (6.35) indicating genetically close relationship among the genotypes included in these clusters (Table 4). The widest inter-cluster distance was found between cluster X and XII (26.49) followed by cluster II and XII (23.08) and cluster V and X (22.50).

Cluster XII showed maximum genetic divergence with cluster X and II. Based on these observations, the crosses may be attempted between the genotypes of cluster X, viz. Kalimpong AC and Kashyong AC-1 followed by cluster II, viz. RGC-4 and cluster XII, viz. VRCP-20-15 to obtain better recombinants. Kallo *et al.* (1980) suggested that the crosses between selected varieties from widely separated clusters were most likely to give desirable recombinants.

The contribution of an individual character to the divergence has been worked out in terms of number of times it appeared first (Table 5). This study helps in utilization of genetic material for the improvement of specific character.

Table 4 Average intra- (bold face) and inter-cluster distance ( $D^2$ ) for 89 vegetable cowpea genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	<b>9.42</b>	11.26	10.88	11.11	12.69	12.65	11.17	12.13	11.51	17.29	15.35	17.60
II		<b>0</b>	12.47	12.59	14.17	8.20	13.99	16.32	13.83	15.33	19.87	23.08
III			<b>0</b>	2.52	6.35	15.18	12.97	11.06	10.95	21.97	15.63	19.85
IV				<b>0</b>	5.67	15.13	13.82	11.61	11.95	22.33	14.87	20.13
V					<b>6.91</b>	16.47	14.40	13.33	14.96	22.50	14.04	21.94
VI						<b>10.34</b>	16.00	16.82	15.29	14.88	19.47	22.18
VII							<b>0</b>	16.89	15.59	17.47	17.06	21.97
VIII								<b>0</b>	8.30	22.19	14.65	10.78
IX									<b>0</b>	22.41	20.33	13.14
X										<b>7.47</b>	20.16	26.49
XI											<b>0</b>	19.55
XII												<b>0</b>

Table 5 Relative contribution of individual character (%) towards divergence

Source	Times ranked 1st	Contribution (%)
Days to 50% flowering (DAS)	4	0.10%
Plant height (cm)	1150	29.37 %
No. of primary branches/plant	16	0.41 %
No. of peduncles/plant	1030	26.30 %
No. of pods/plant	720	18.39 %
Pod length (cm)	181	4.62 %
Pod weight (g)	643	16.42 %
No. of seeds/pod	164	4.19 %
Pod yield/plant (g)	8	0.20 %

Among nine characters studied, the highest contribution to the divergence was through plant height (29.37%) followed by number of peduncles/plant (26.30%), number of pods/plant (18.39%) and pod weight (16.42%). These characters may be used in selecting the genetically diverse parents for hybridization programme to exploit either maximum heterosis or to execute efficient selection in the segregating generations. These observations were in accordance with the findings of Pandey (2007) and Vavilapalli *et al.* (2014).

It is evident that different clusters exhibit distinct mean values for almost all the nine characters (Table 6). A wide range of variation was observed among different clusters for all the characters means. The cluster II had highest mean value for pod weight (14.77 g). Cluster III had highest mean value for pod yield/plant (388.80 g), Cluster VI had highest mean value for pod length (38.63 cm) and number of seeds/pod (13.48). Cluster VII had highest mean value for number of primary branches/plant (5.43). Cluster IX had lowest mean value for days to 50% flowering (32.00). Cluster X had highest mean value for plant height (335.18

cm). Cluster XI had highest mean value for number of peduncles/plant (34.57). Cluster XII had highest mean value for number of pods/plant (34.97). It was observed that the genotype grouped under cluster III ranked first by having six characters, viz. days to 50% flowering, number of primary branches/plant, number of peduncles/plant and number of pods/plant, pod weight and pod yield/plant (1-3 scores) at desirable direction followed by genotypes under cluster V with three characters (2-3 scores), viz. number of peduncles/plant, pod length and pod yield/plant, and cluster IV with three characters (2-3 scores), viz. days to 50% flowering, number of seeds/pod and pod yield per plant. Genotypes belonging to these clusters could be regarded as useful sources of gene for improving pod yield of vegetable cowpea. Therefore, selection and hybridization among the genotypes belonging to these clusters would be useful to generate desirable genetic resource, viz. dwarf plant and higher pod yield with early maturity that can be fitted well in multiple cropping systems.

High estimates of genotypic coefficient of variation, heritability and genetic advance for the characters, viz. pod yield/plant, number of peduncles/plant, number of pods/plant, pod weight and pod length indicate that improvement of these characters can be achieved through selection. Correlation and path coefficient studies suggests that pod weight and number of pods/plant were the most important characters as they exhibited high direct effects on pod yield/plant along with significant positive correlation at genotypic and phenotypic levels. It is concluded that these characters should be given due importance in selection programme for yield improvement of vegetable cowpea. The genetically divergent genotypes from Cluster XII and cluster X can be used for future hybridization programmes intended to create wider genetic variability. Crossing between the genotypes of cluster III, IV and V may be used to produce desirable transgressive segregants for

Table 6 Cluster mean values for various quantitative characters in vegetable cowpea

Cluster	Days to 50% flowering (DAS)	Plant height (cm)	No. of primary branches/plant	No. of peduncles/plant	No. of pods/plant	Pod length (cm)	Pod weight (g)	No. of seeds/pod	Pod yield/plant (g)	Total score	Rank
I	50.15 (8)	106.21 (5)	4.14 (7)	15.94 (7)	20.26 (8)	27.72 (6)	9.55 (8)	12.27 (7)	191.29 (8)	64	VIII
II	49.33 (7)	190.93 (3)	4.00 (10)	14.60 (8)	18.47 (9)	38.57 (2)	14.77 (1)	12.80 (4)	263.40 (5)	49	IV
III	36.00 (2)	53.20 (9)	4.67 (3)	29.13 (3)	30.93 (3)	28.67 (5)	12.80 (2)	12.40 (6)	388.80 (1)	34	I
IV	39.00 (3)	57.67 (8)	3.90 (11)	28.43 (4)	28.70 (6)	29.40 (4)	12.13 (4)	12.90 (3)	358.90 (2)	45	III
V	41.21 (4)	61.13 (7)	4.29 (5)	32.72 (2)	29.97 (4)	29.73 (3)	11.67 (5)	12.18 (8)	333.63 (3)	41	II
VI	53.14 (10)	224.71 (2)	4.12 (8)	13.69 (10)	18.42 (10)	38.63 (1)	12.26 (3)	13.48 (1)	223.64 (6)	51	V
VII	47.67 (6)	44.70 (12)	5.43 (1)	16.20 (6)	15.50 (11)	26.10 (8)	10.90 (6)	12.60 (5)	163.90 (9)	64	VIII
VIII	44.67 (5)	62.13 (6)	4.23 (6)	22.40 (5)	33.63 (2)	18.37 (10)	6.33 (10)	8.03 (11)	204.70 (7)	62	VI
IX	32.00 (1)	49.30 (10)	4.07 (9)	12.20 (11)	27.00 (7)	27.30 (7)	10.47 (7)	10.53 (10)	282.60 (4)	66	IX
X	53.33 (11)	335.18 (1)	4.92 (2)	9.88 (12)	8.65 (12)	20.83 (9)	6.65 (9)	10.72 (9)	62.37 (12)	77	XI
XI	63.67 (12)	136.03 (4)	4.50 (4)	34.57 (1)	29.47 (5)	13.73 (12)	3.37 (12)	13.00 (2)	97.40 (11)	63	VII
XII	52.33 (9)	47.80 (11)	4.50 (4)	14.43 (9)	34.97 (1)	15.73 (11)	3.57 (11)	12.80 (4)	117.80 (10)	70	X

more than one economic character.

#### ACKNOWLEDGEMENT

The authors are thankful to the Director, Indian Institute of Vegetable Research, Varanasi, for providing necessary facilities for this investigation.

#### REFERENCES

- Akinyele B O and Osekita O S. 2006. Correlation and path coefficient analyses of seed yield attributes in okra (*Abelmoschus esculentus* (L.) Monech). *African Journal of Biotechnology* **5** (14): 1330–6.
- Allard R W. 1960. *Principles of Plant Breeding*, p 485. John Wiley and Sons Inc., New York.
- Bhatt G M. 1970. Multivariate analysis approach to selection of parents for hybridization aiming at yield improvement in self-pollinated crops. *Australian Journal of Agricultural Research* **21**: 1–7.
- Burton G W. 1952. Quantitative inheritance in grasses. Proc. Endings of 6<sup>th</sup> International Grassland Congress **1**, pp 277–83.
- Chakraborti A K. 1986. Cowpea. (In) *Vegetable Crops*, pp 603–11. Bose T K, Som M G and Kabir J (Eds). Naya Prakash, Kolkata.
- Chattopadhyay A, Rana N P, Seth T, Das S, Chatterjee S and Dutta S. 2014. Identification of selection indices and choosing of parents for vegetable cowpea (*Vigna unguiculata* CV-GR. *sesquipedalis*) breeding programme. *Legume Research* **37**(1): 19–25.
- Chowdhury M A, Vandenberg V and Warkentin T. 2002. Cultivar identification and genetic relationship among selected breeding lines and cultivars in chickpea (*Cicer arietinum* L.). *Euphytica* **127**(3): 317–25.
- Comstock R E and Robinson H E. 1952. Genetic parameters, their estimation and significance. Proc endings of 6<sup>th</sup> International Grassland Congress **1**, pp 284–91.
- Dewey D R and Lu K H. 1959. A correlation and path coefficient analysis of components of crested wheatgrass seed production. *Agronomy Journal* **51**: 515–8.
- Fraser J and Eaton G W. 1983. Application of yield component analysis to crop research. *Field Crop Abstracts* **36**: 787–97.
- Huque A K M M, Hossain M K, Alam N, Hasanuzzaman M and Biswas B K. 2012b. Genetic divergence in yardlong bean (*Vigna unguiculata* ssp. *sesquipedalis* (L. Verdc.)). *Bangladesh Journal of Botany* **41**(1): 61–9.
- Huque A K M M, Hossain M K, Alam N, Hasanuzzaman M, Biswas B K and Arifuzzaman M. 2012a. Genetic variability, correlation and path analysis for yield and its component characters in string bean (*Vigna unguiculata* ssp. *sesquipedalis* (L. Verdc.)). *Jahangirnagar University Journal of Biological Sciences* **1**(1): 1–10.
- Jatasara D S and Paroda R S. 1978. Genetic divergence in wheat under different environmental conditions. *Cereal Research Communication* **6**: 307–17.
- Kallo G, Singh V P, Dudi B S and Pratap P S. 1980. Analysis of variation and genetic diversity in garden pea (*Pisum sativum* L.). *Haryana Agricultural University Journal of Research* **10**: 540–6.
- Kwon S H and Torrie J H. 1964. Heritability and interrelationship among traits of two soybean population. *Crop Science* **4**: 196–8.
- Lal H, Rai M, Shiv Karan, Verma A and Ram D. 2007. Multivariate hierarchical clustering of cowpea germplasm [*Vigna unguiculata* (L.) Walp.]. *Acta Horticulturae* **752**: 413–6.
- Madhavi K, Sivaji T and Amrutha N. 2014. Correlation studies for pod yield in vegetable cowpea [*Vigna unguiculata* (L.) Walp.]. *Trends in Biosciences* **7**(6): 465–7.
- Mahalanobis P C. 1936. On the generalized distance in statistics. *Proceedings National Institute Science India* **2**: 49–55.
- Narayanankutty C, Mili R and Jaikumaran U. 2003. Variability and genetic divergence in vegetable cowpea. *Journal of Maharashtra Agricultural University* **28**: 26–9.
- Nath Vishwa, Lal H, Rai M, Rai N and Ram D. 2009. Hierarchical clustering and character association studies in cowpea [*Vigna unguiculata* (L.) Walp.]. *Indian Journal Plant Genetic Resources* **22**: 22–5.
- Nwofia G E, Ogbonna N D and Agbo C U. 2013. Path analysis and heritability estimates of yield and yield components in vegetable cowpea as influenced by planting season. *American-Eurasian Journal of Agricultural and Environmental Sciences* **13** (9): 1283–9.
- Pandey I. 2007. Genetic diversity in grain cowpea (*Vigna unguiculata* (L.) Walp.). *Legume Research* **30**(2): 92–7.
- Pant K C, Chandel K P S and Joshi B S. 1982. Analysis of diversity in Indian cowpea genetic resources. *SABRAO Journal of Breeding and Genetics* **14**: 103–11.
- Rao A, Khan M A, McNeilly T and Khan A A. 1997. Cause and effect relations of yield and yield components in rice (*Oryza sativa* L.). *Journal of Genetics and Breeding* **51**: 1–5.
- Rao C R 1952. *Advanced Statistical Methods in Biometrical Research*. John Wiley and Sons Inc., New York.
- Russell D F and Eisensmith S P. 1983. MSTAT-C. Crop Soil Science Department, Michigan State University, USA.
- Singh B D. 1990. *Principles and Methods of Plant Breeding*, 4th edition. Kalyani Publishers, New Delhi.
- Singh M and Ceccarelli S. 1996. Estimation of heritability of crop traits from variety trial data. Technical Manual No. 21, International Centre for Agricultural Research in Dry Areas, Aleppo, Syria, p 21.
- Suganthi S, Murugan S and Venkatesan M. 2007. D<sup>2</sup> analysis in cowpea (*Vigna unguiculata* (L.) Walp.). *Legume Research* **30**(2): 145–7.
- Sulnathi G, Prasanthi L and Sekhar M R. 2007. Character contribution to diversity in cowpea. *Legume Research* **30**(1): 70–2.
- Tomooka N. 1991. Genetic diversity and landrace differentiation of mungbean (*Vigna radiata* L.) Wilczek and evaluation of its wild relatives (The subgenus *Ceratotropis*) as breeding materials. *Technical Bulletin Tropical Research* **28**: 1–4.
- Ullah M Z, Hasan M J, Rahman A H M A and Saki A I. 2011. Genetic variability, character association and path analysis in yard long bean. *SAARC Journal of Agriculture* **9**(2): 9–16.
- Umaharan P, Ariyanayagam R P and Haque S Q. 1997. Genetic analysis of yield and its components in vegetable cowpea [*Vigna unguiculata* (L.) Walp.]. *Euphytica* **96**(2): 207–13.
- Vavilapalli S K, Celine V A and Sreelathakumai I. 2014. Genetic divergence analysis in vegetable cowpea (*Vigna unguiculata* subsp. *unguiculata* [L.]) genotypes. *Legume Genomics and Genetics* **5**(2): 4–6.