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Research Article

Genetic variation among biparental progenies in okra [*Abelmoschus esculentus* L. (Moench)] using coefficient of racial likeness and Mahalanobis D^2 statistics

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Abstract
A study was carried out in Nigeria to determine the extent of genetic variation within a biparental population in okra. Sixteen crosses were made and evaluated with nine parents in a randomized complete block design with three replications. Observations were made on important agronomic traits including pod yield. Data collected were subjected to Coefficient of Racial Likeness (CRL) and Mahalanobis D^2 statistic and dendrogram was constructed. The maximum CRL distance (24.70) was between NGB00347 x NGB00350 and NGB00371 x NGB00326 while the largest Mahalanobis D^2 distance (216.34) was between NGB00302 and NGB00356. The twenty-five genotypes were grouped into six clusters based on CRL while Mahalanobis D^2 statistic identified four clusters. The NGB00297 x NGB00326 in cluster 6 had earliness to flowering, longest pod, heaviest pod, widest pods, the highest number of pod/plant and yield/plant. The genotype would be useful in the future development program in okra breeding.

Key words
Clusters, Okra, Pod yield

INTRODUCTION

Okra has a substantial land area under cultivation in Africa and Asia due to its contribution of fats, proteins, carbohydrates, minerals and vitamins to human diet. However, its productivity is very low in the West and Central African sub-region because of several factors such as lack of adapted genotypes, pest and disease constraints and narrow genetic base of existing cultivars (Ahiakpa *et al.,* 2013). The wealth of any germplasm collection depends not only upon the number of accessions but also on the extent of variation inherent in the collections (Ahiakpa *et al.,* 2013). There are many techniques available to estimate the extent of variation in a germplasm collection. The Coefficient of Racial Likeliness (CRL) proposed by Pearson (1926) and Mahalanobis' D^2 -Statistic proposed by Mahalanobis (1936) have been used to measure the genetic variation in plant populations.

Genetic variations among okra genotypes have been reported by several researchers using coefficient of racial likeness (CRL) and Mahalanobis D^2 statistics. Ariyo (1990) investigated genetic variation among 18 genotypes of okra using coefficient of racial likeness technique and reported that genetic variation existed among the genotypes for the ten evaluated characters. Priyanka *et al.* (2017) conducted an experiment on genetic variability on 29 inbred lines of okra using Mahalanobis D^2 statistics. They reported a wide range of variation for the yellow vein mosaic virus, fruit length and days to 50% flowering among the 29 genotypes. Khalid (2017) studied genetic variation among 28 genotypes using Mahalanobis D^2 statistics and established the relatedness among the genotypes based on the genetic distance. Ranpise *et al.* (2018) investigated the genetic variations among 35 okra genotypes using Mahalanobis D^2 statistics and observed that fruit width, fruit length, and plant height contributed more to the genetic variation among the evaluated genotypes.

For effective breeding programme there is a need for proper selection of desirable genotypes and this can be achieved by having an adequate information on the nature

and magnitude of variation existing among the genotypes. The objective of this study was to determine the extent of genetic variation within the biparental population for the various characters using coefficient of racial likeness and Mahalanobis D^2 statistics.

MATERIALS AND METHODS

The study was carried out at the Teaching and Research Farm, Federal University of Agriculture, Abeokuta, Nigeria (latitude 7°29'N and longitude 3°3'E) and Laboratory of the Department of Plant Breeding and Seed Technology, Federal University of Agriculture, Abeokuta, Nigeria.

Nine lines sourced from gene bank of National Centre for Genetic Resources and Biotechnology (NACGRAB) were used. Six lines, NGB00303 (P3), NGB00346 (P4), NGB00347 (P5), NGB00297 (P6), NGB00356 (P7), and NGB00371 (P9) while the remaining three lines (NGB00326 (P1), NGB00302 (P2), and NGB00350 (P8) were designated as females and males, respectively to produce eighteen biparental progenies. However, only sixteen biparental progenies were successful and thus formed the bi-parental population. The crosses were made between March and July, 2018 while the field evaluation of parents and biparental progenies was carried out between August and December, 2018.

The nine inbred lines were sown in single row plot of 4 m length and inter-row spacing of 0.6 m and 0.4 m as intra-row. Hybridization was carried out using hand emasculation and pollination.

Emasculation was done late in the evening after sunset using scalpel and a pair of scissor. Mature flower buds of the female parent, that would likely blossom the next day, were selected for emasculation because the receptivity of the stigma is highest on the day of anthesis. The floral whorls of the flower buds were removed to expose the stigma and the closed anthers. Care was taken to avoid injury to the delicate stigma and style while all the anthers were scrapped off using scalpel. Before and after emasculation, the scalpel and the pair of scissor were sterilized in ethanol. The emasculated flower buds were covered up immediately to prevent contamination. The hand-pollination was don e very early in the following morning by plucking dehisced anthers from the male parent and dusted the pollen on the stigma of female parent and thereafter covered up to prevent contamination from foreign pollen. Subsequently, tagging of crosses was done to indicate the parents that were involved. At maturity, pods from the crosses were harvested and oven-dried at 37- 40°C for 24 hours separately and seeds were extracted.

Field evaluation of parents and biparental population

The sixteen biparental progenies and the nine parents were sown at the rate of two seeds per hole in 4.5m-single-row plots layout in randomized complete block design (RCBD) with three replications but later thinned to one plant per stand. The inter-row spacing was 0.70 m while there was 0.45 m between plants on the row. All the standard agronomic practices were followed as required. Observations were made on the number of days to 50% flowering, plant height at flowering (cm), final plant height (cm), stem girth (cm), number of branches per plant, number of pods per plot, number of pods per plant, pod weight (g), pod length (cm), pod width (cm) and fresh pod yield per plot (kg)

The data collected were subjected to the Coefficient of Racial Likeness according to Pearson (1926) to determine the level of genetic distance among the genotypes.

$$CRL_{ij}^2 = \frac{1}{N}\sum_{k=1}^{N}\left(\frac{\bar{X}ik-\bar{X}jk}{2se_k}\right)^2$$

Where,
N = the number of characters
Se = the standard error associated with the variety means for the K^{th} character
Xij and xjk = the means of the K^{th} character for varieties i and j, respectively.

CRL is a standardised distance and should have a value of two for a pair of varieties which differ at the 5% level of significance on all the characters considered (Ariyo, 1990).

A dendrogram was drawn from the CRL-distance values to highlight the genetic relationship among the genotypes.

Mahalanobis D^2 statistic was also used to assess genetic variation among the genotypes as described by Mahalanobis (1936).

$$D^2 = \Sigma\Sigma W^{ij} (\mu^1_i - \mu^2_i) (\mu^1_j - \mu^2_j)$$

Where,
D^2 = Square of generalized distance
W^{ij} = The inverse of estimated variance and covariance
$(\mu^1_i - \mu^2_i)$ and $(\mu^1_j - \mu^2_j)$ = The difference in the means of two population.

A dendrogram was drawn from the D^2-distance values to also elucidate the genetic relatedness among the genotypes.

RESULTS AND DISCUSSION

The mean squares from analysis of variance of twelve characters for the twenty-five genotypes of okra showed that there were significant genotypic effects for days to 50% flowering, plant height at flowering, number of branches per plant, final plant height, pod length, pod width, number of pod per plot, number of pod per plant, fresh pod yield per plot and yield per plant (Table not shown). The mean performance for twenty-five okra genotypes evaluated for twelve characters are presented in **Table 1.** The longest days to 50% flowering was observed in NGB00350 (75.33)

while NGB00347 x NGB00350 had the shortest days to 50% flowering (54.67). The NGB00303 x NGB00326 was the tallest plant at flowering (114.67cm) while NGB00356 had the shortest plant height at flowering (36.83cm). NGB00350 had the largest number of branches per plant (9.77) while NGB00347 had the smallest number of branches per plant (4.57). NGB00303 had widest stem girth (1.81cm) while NGB00346 had the smallest stem girth (1.16cm). NGB00297 had the shortest final plant height (87.37cm) while NGB00371 x NGB00326 had the longest final plant height (194.80cm).

The NGB00347 had the longest pod (6.57cm) while NGB00302 had the shortest pod (4.33cm). NGB00302 had the widest pod (2.37cm) while NGB00356 x NGB00350 had the smallest pod width (1.83cm). NGB00297 had the heaviest pod (12.10g) while NGB00356 x NGB00350 had the lightest pod (8.17g).

Table 1. Mean performance for twenty-five genotypes of okra evaluated for twelve characters

Genotype	50%F	PtH	NoB	StG	FPtH	PdL	PdWdt	PdWgt	NPdPlot	NPdPt	YPlot	YPt
NGB00326 (P1)	68.33a-d	75.70b-f	6.87 a-f	1.46 a-d	143.43b-e	5.30e-i	1.93d-f	8.77bc	94.67b-g	20.23b-e	0.93 b-f	192.83 b-e
NGB00302 (P2)	70.00 a-d	107.93 ab	5.73d-f	1.45 a-d	136.87 b-e	4.33j	2.37a	11.17 a-c	46.00h	10.10f	0.52f	121.07e
NGB00303 (P3)	56.33 gh	53.87e-g	5.90c-f	1.22cd	129.07c-f	5.93 a-f	2.13b-d	12.07a	126.00 ab	25.47 a-d	1.33ab	267.77a-d
NGB00303 X NGB00326 (P3 x P1)	68.67 a-d	114.67 a	8.93 a-c	1.81a	183.30ab	4.97h-j	2.20 a-c	9.07 a-c	123.00 a-c	25.30 a-e	1.33ab	300.90 ab
NGB00303 X NGB00302 (P3 x P2)	72.00 a-c	98.27 a-c	7.10 a-f	1.53 a-d	151.60 b-e	5.00g-j	2.20 a-c	10.73 a-c	79.33d-h	19.37b-e	0.91 b-f	200.83b-e
NGB00346 (P4)	55.67 gh	43.83fg	6.87 a-f	1.16d	103.30ef	5.47c-i	2.27 ab	11.10 a-c	100.67 a-g	21.13b-e	1.02a-e	213.47 a-e
NGB00346 X NGB00326 (P4 x P1)	68.33 a-d	102.67 a-c	8.33 a-e	1.68 a-c	150.77a-e	5.20f-i	2.17 a-c	10.20 a-c	106.33 a-g	25.03 a-e	1.17 a-d	271.40 a-c
NGB00346 X NGB00302 (P4 x P2)	69.67 a-d	84.67 a-e	5.67d-f	1.76 ab	169.40a-d	5.20f-i	2.17 a-c	10.90 a-c	99.67 a-g	18.00c-f	1.15 a-e	220.33 a-e
NGB00347 (P5)	56.00 gh	54.43d-g	7.90 a-e	1.37 a-d	146.37 b-e	6.47 ab	1.90ef	10.60 a-c	118.00 a-e	25.63 a-d	1.11 a-e	203.43b-e
NGB00347 X NGB00326 (P5 x P1)	59.67 e-h	57.20d-g	7.00 a-f	1.56 a-d	138.47 b-e	6.27 a-d	2.00c-f	10.50 a-c	114.33 a-f	24.27 a-e	1.18 a-d	256.73 a-d
NGB00347 X NGB00302 (P5 x P2)	73.33 ab	93.00 a-d	8.00 a-e	1.56 a-d	144.67 b-e	5.40e-i	2.20 a-c	10.67 a-c	67.00gh	16.87d-f	0.86b-f	213.77 a-e
NGB00347 X NGB00350 (P5 x P8)	54.67 h	38.40fg	4.57f	1.38 a-d	121.93d-f	6.57a	1.87f	9.13 a-c	92.33b-g	23.00 a-e	0.79c-f	186.57b-e
NGB00297 (P6)	55.67gh	40.43fg	5.40ef	1.38 a-d	87.37f	5.50c-i	2.13b-d	9.77 a-c	113.33 a-f	26.10 a-c	1.12 a-e	264.23 a-d
NGB00297 X NGB00326 (P6 x P8)	58.67f-h	58.10d-g	8.23 a-e	1.57 a-d	139.10 b-e	5.83 a-g	2.23 ab	11.50 ab	138.67a	30.57a	1.50a	328.30a
NGB00297 X NGB00302 (P6 x P2)	69.00 a-d	99.00 a-c	6.23b-f	1.68 a-c	184.23ab	5.23e-i	2.27 ab	11.67 ab	99.00 a-g	20.30b-f	1.17 a-d	236.20 a-e
NGB00297 X NGB00350 (P6 x P8)	68.00 a-d	64.33c-g	7.43 a-f	1.60 a-d	170.57a-c	5.37e-i	2.17 a-c	10.77 a-c	98.33 a-g	22.17 a-e	1.05 a-e	247.77 a-d
NGB00356 (P7)	57.00f-h	36.83g	7.67 a-e	1.49 a-d	106.10ef	6.30 a-c	2.00c-f	11.40 ab	98.67 a-g	21.97 a-e	1.01 a-f	215.17 a-e
NGB00356 X NGB00326 (P7 x P1)	62.67d-h	77.10 a-f	7.67 a-e	1.76 ab	145.87 b-e	6.07 a-e	2.13b-d	11.17 a-c	121.00 a-d	27.13ab	1.24 a-c	270.07 a-c
NGB00356 X NGB00302 (P7 x P2)	60.00e-h	68.27c-g	8.10 a-e	1.47 a-d	140.73 b-e	5.67b-h	2.13b-d	10.97 a-c	115.33 a-f	24.13 a-e	1.23 a-c	243.37 a-d
NGB00356 X NGB00350 (P7 x P8)	64.33c-f	82.43 a-e	6.33b-f	1.32b-d	147.17 b-e	4.77ij	1.83f	8.17c	77.33e-h	16.97d-f	0.70d-f	148.27de
NGB00350 (P8)	75.33a	100.27 a-c	9.77a	1.58 a-d	136.67 b-e	5.23e-i	2.10b-e	9.13 a-c	74.67e-h	16.23ef	0.66ef	151.20c-e
NGB00371 (P9)	70.67 a-d	86.33 a-e	9.00ab	1.48 a-d	150.77a-e	5.10f-j	1.93d-f	8.67bc	81.67c-h	17.20c-f	0.79c-f	186.93b-e
NGB00371 X NGB00326 (P9 x P1)	67.00c-e	108.50 ab	7.50 a-f	1.63 a-d	194.80a	5.90 a-f	1.90ef	12.10a	73.00f-h	19.50b-e	0.90b-f	224.00 a-e
NGB00371 X NGB00302 (P9 x P2)	63.67d-g	56.53d-g	7.23 a-f	1.33 a-d	117.10ef	5.43d-i	2.00cd-f	8.77bc	82.00c-h	18.77 b-e	0.77 c-f	183.40b-e
NGB00371 X NGB00350 (P9 x P8)	70.33 a-d	72.70b-g	8.67 a-d	1.64 a-d	137.40 b-e	4.87h-j	2.23 ab	10.57 a-c	86.33b-h	19.37 b-e	0.98 b-f	213.07 a-e

Means with the same alphabets within the column are not significantly different at 5% probability level
50%F= days to 50%flowering; PtH= plant height (cm); NoB= number of branches per plant; StG= stem girth (cm); FPtH= final plant height (cm); PdL= pod length (cm); PdWdt= pod width (cm); PdWgt= pod weight (g); NPdPlot= number of pod per plot; NPdPt= number of pod per plant; Yplot= yield per plot (kg); YPt= yield per plant(g).

The NGB00297 x NGB00326 had the highest number of pod per plot (138.67), number of pod per plant (30.57) and yield per plant (328.30g) while NGB00302 had the lowest number of pod per plot (46.00), number of pod per plant (10.10) and yield per plant (121.07g). The observed variations among the biparental progenies for most of the characters studied indicated a high prospect for improvement through selection and hybridization. Olayiwola *et al.* (2015) and Khalid (2017) also found genetic variation among okra genotypes for various agronomic traits.

The Coefficients of Racial Likeness (CRL) and D^2 measured the extent of relatedness among the genotypes. CRL distances among twenty-five genotypes of okra are presented in **Table 2.** Based on the twelve characters evaluated most of the genotypes varied from each other as evidenced by the CRL values ranging from 0.10 to 24.70. Information on the genetic distance among the genotypes is useful for breeding purposes and also for cataloguing and conservation of germplasm (Torkpo *et al.,* 2006).The maximum CRL distance was observed between P_5 x P_8 and P_9 x P_1 (24.70) followed by P_6 and P_9 x P_1 (23.70), P_7 and P_9 x P_1 (21.15), P_3 x P_1 and P_5 x P_8 (19.37) and P_2 and P_5 x P_8 (16.15) while the minimum distance was observed between P_3 x P_2 and P_5 x P_2 (0.10) followed by P_4 x P_2 and P_6 x P_2 (0.11), P_4 x P_1 and P_6 x P_8 (0.16), P_6 x P_2 and P_6 x P_8 (0.17), P_3 and P_6 x P_1 (0.17), and P_5 x P_1 and P_7 x P_2 (0.18). The maximum CRL distance observed between P_5 x P_8 (NGB00347 x NGB00350) and P_9 x P_1 (NGB00371 x NGB00326) implied that a cross between the F_1 genotypes could lead to a high yielding double cross hybrid of okra.

Table 2. Coefficient of Racial Likeness (CRL) distances between genotypes of okra

	P1	P2	P3	P3 x P1	P3 x P2	P4	P4 x P1	P4 x P2	P5	P5 x P1	P5 x P2	P5 x P8	P6	P6 x P1	P6 x P2	P6 x P8	P7	P7 x P1	P7 x P2	P7 x P8	P8	P9	P9 x P1	P9 x P2	P9 x P8
P1		4.02	1.07	2.74	0.35	2.47	0.63	0.58	1.73	2.53	0.29	5.12	3.64	1.59	0.55	0.23	3.87	0.85	1.70	0.27	1.01	1.18	7.42	0.30	0.71
P2			3.29	2.97	0.66	6.78	4.30	0.82	7.38	11.11	0.79	16.15	10.88	4.98	1.59	1.28	13.10	3.47	8.35	0.61	6.04	3.77	22.98	3.35	1.86
P3				7.48	2.21	0.48	4.47	1.22	0.54	0.77	1.37	1.30	0.81	0.17	2.92	2.01	0.80	0.37	1.97	1.42	7.39	5.55	13.62	0.84	2.51
P3 x P1					0.42	7.40	0.32	1.48	5.97	5.91	0.66	19.37	12.63	2.46	0.56	0.32	11.06	1.12	6.15	0.92	2.90	2.02	8.18	2.22	1.03
P3 x P2						4.93	0.57	0.39	4.21	4.52	0.10	12.03	8.16	2.84	0.29	0.33	7.95	1.17	4.20	0.35	0.92	1.22	7.98	1.31	0.42
P4							2.64	1.98	1.06	2.14	1.38	1.35	0.19	0.42	2.91	2.23	1.32	0.92	2.24	0.94	4.65	5.64	20.07	0.59	1.66
P4 x P1								1.02	3.95	3.61	0.30	13.81	8.54	1.69	0.36	0.16	7.67	0.63	3.47	0.68	1.54	1.05	5.53	1.18	0.61
P4 x P2									3.05	3.72	0.24	7.52	5.71	1.87	0.11	0.28	5.52	0.91	3.67	0.48	1.48	2.73	6.96	0.93	0.86
P5										0.43	1.60	1.69	1.82	0.93	4.23	2.16	0.59	0.51	0.99	2.30	12.70	3.45	13.92	1.92	3.34
P5 x P1											1.06	1.72	1.54	0.44	2.60	1.09	0.64	0.18	0.72	1.81	9.21	3.20	11.13	1.21	2.45
P5 x P2												10.76	7.08	2.40	0.51	0.54	6.01	0.82	3.82	0.68	0.51	0.59	4.72	0.98	0.45
P5 x P8													1.22	1.46	5.24	3.09	0.39	0.98	5.97	2.60	15.22	9.25	24.70	2.45	5.04
P6														0.44	3.19	2.52	1.21	0.74	4.03	1.14	6.01	7.93	23.70	0.62	2.49
P6 x P1															2.42	1.50	1.35	0.22	0.81	1.65	6.77	3.51	11.52	0.93	2.02
P6 x P2																0.17	7.38	0.86	4.25	0.66	2.00	2.49	4.65	1.49	0.91
P6 x P8																	2.92	0.50	1.05	0.64	1.73	1.60	8.35	0.53	0.49
P7																		0.49	2.54	2.09	10.13	5.25	21.15	1.43	2.85
P7 x P1																			0.51	1.64	6.79	1.71	5.18	1.08	1.80
P7 x P2																				0.95	3.70	1.78	7.58	0.39	1.01
P7 x P8																					2.92	1.93	13.72	1.03	1.20
P8																						0.68	8.00	1.34	0.65
P9																							8.20	0.78	0.46
P9 x P1																								1.87	1.93
P9 x P2																									0.90
P9 x P8																									

Table 3 shows Mahalanobis D^2 distance of twenty-five genotypes of okra. The D^2 distance for all possible pairs of twenty-five genotypes ranged from 2.17 to 216.34. Furthermore, D^2 had maximum genetic distance between genotypes P_2 (NGB00302) and P_7 (NGB00356) suggesting a cross between the two genotypes may lead

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Table 3. Mahalanobis D^2 distance value between genotypes of okra

Genotype	P1	P2	P3	P3 x P1	P3 x P2	P4	P4 x P1	P4 x P2	P5	P5 x P1	P5 x P2	P5 x P8	P6	P6 x P1	P6 x P2	P6 x P8	P7	P7 x P1	P7 x P2	P7 x P8	P8	P9	P9 x P1	P9 x P2	P9 x P8
P1																									
P2	38.51																								
P3	26.75	59.28																							
P3 x P1	37.62	106.20	49.78																						
P3 x P2	8.65	22.20	32.11	38.20																					
P4	48.93	131.40	19.86	42.90	65.22																				
P4 x P1	18.68	80.69	30.08	6.54	20.68	26.82																			
P4 x P2	33.12	3.34	50.60	88.72	18.36	119.42	69.31																		
P5	89.30	203.46	60.71	62.46	108.55	16.26	47.16	191.41																	
P5 x P1	26.39	93.33	11.09	30.10	37.16	5.17	13.44	82.64	24.44																
P5 x P2	19.18	68.03	40.37	24.85	13.90	43.01	8.30	62.01	62.96	23.13															
P5 x P8	35.94	41.99	19.64	107.33	47.98	67.75	76.72	38.64	129.84	49.97	82.10														
P6	26.98	59.88	14.31	74.12	45.60	42.58	53.06	50.66	103.57	33.62	68.33	11.19													
P6 x P1	81.39	187.57	52.83	33.66	93.79	13.26	31.16	167.86	13.30	21.84	54.11	129.65	89.85												
P6 x P2	34.86	10.42	41.61	67.03	14.37	101.97	53.25	4.87	163.84	68.40	49.37	46.67	55.72	137.93											
P6 x P8	18.47	72.67	23.66	10.69	17.34	25.77	2.17	59.69	50.84	11.70	7.67	67.72	47.52	32.64	44.11										
P7	95.48	216.34	69.28	79.15	118.56	18.71	57.32	205.86	4.36	29.86	67.39	136.98	107.54	20.16	182.45	60.06									
P7 x P1	31.87	97.54	18.56	20.50	34.92	9.69	7.96	86.20	23.63	3.23	16.26	69.01	50.64	16.69	66.08	6.69	31.81								
P7 x P2	60.21	158.82	41.84	30.31	72.85	8.50	21.02	145.06	6.67	11.81	36.81	108.40	77.95	4.22	119.61	23.90	12.69	8.38							
P7 x P8	6.99	35.19	34.01	60.40	21.72	68.99	40.76	32.13	119.10	44.56	47.21	25.65	22.08	113.94	40.18	42.17	128.77	56.35	89.20						
P8	81.71	196.44	113.52	54.01	90.08	65.85	40.72	188.84	45.30	58.13	36.03	189.85	155.77	50.79	165.86	49.73	44.18	45.69	35.49	125.90					
P9	47.37	155.50	75.97	29.98	63.61	40.61	19.81	145.40	34.71	32.67	25.20	135.98	101.98	35.11	128.90	28.67	36.76	27.48	21.21	78.03	8.78				
P9 x P1	23.71	54.31	27.33	33.78	15.27	44.51	16.37	50.83	62.24	21.72	12.42	61.14	63.33	62.95	35.12	15.30	76.26	16.68	41.98	41.58	64.71	46.94			
P9 x P2	15.83	94.24	25.38	31.74	34.90	15.19	13.22	85.75	35.91	7.83	20.51	56.73	34.39	35.08	79.53	15.43	36.49	13.56	20.56	31.85	45.72	19.18	31.10		
P9 x P8	48.34	146.39	62.86	22.92	56.47	29.75	13.63	134.19	29.69	24.67	18.26	129.69	94.53	21.44	113.48	17.99	31.36	16.47	13.13	84.31	10.95	5.01	41.18	19.41	

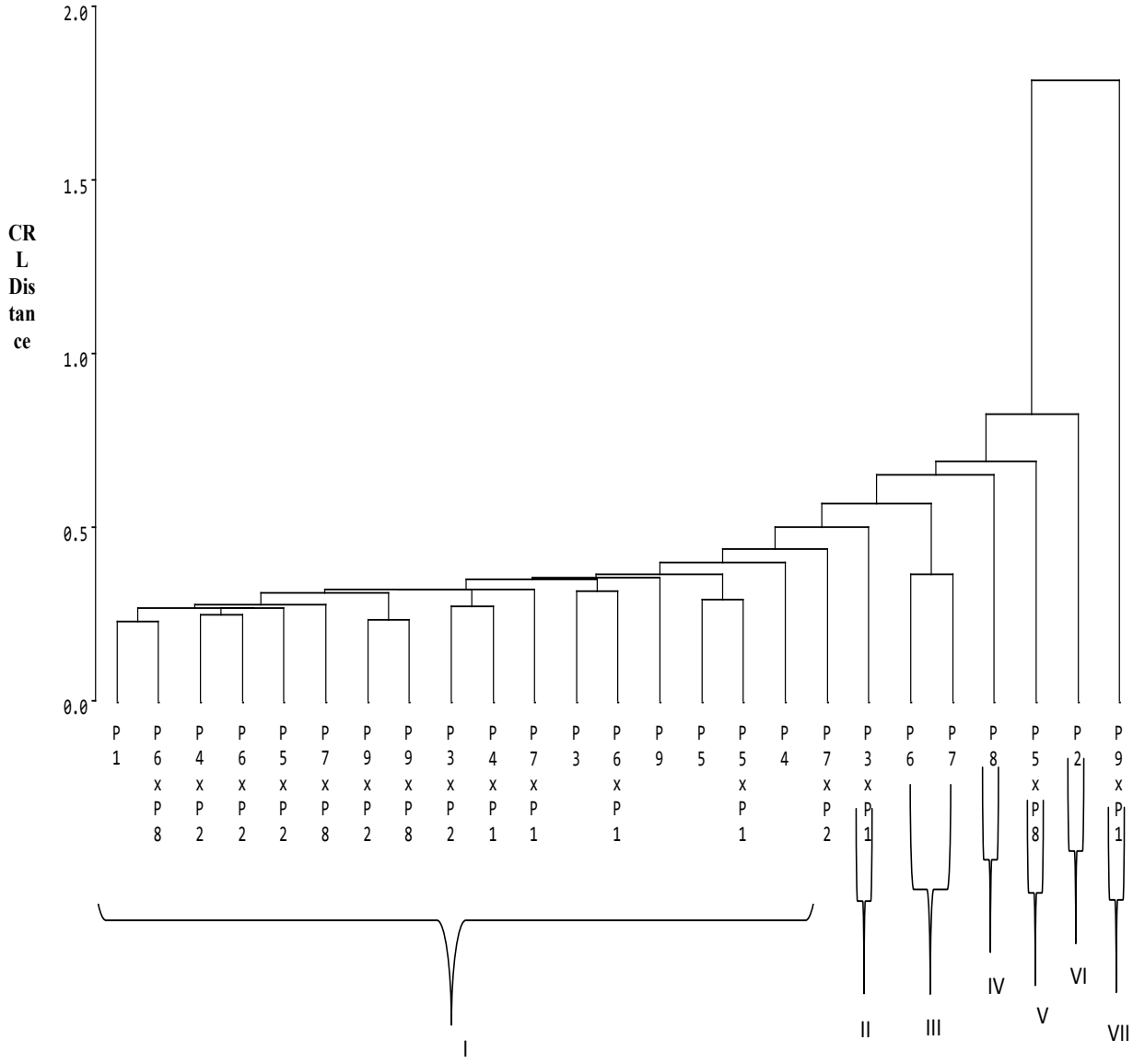

Fig. 1. Dendrogram showing genetic relationships among 25 genotypes of okra generated from CRL- distance value

to transgressive segregation therefore enhancing the chances of obtaining superior recombinants. P_7 and P_4 x P_2 (205.86), P_5 and P_2 (203.46), P_8 and P_2 (196.44), and P_8 and P_5 x P_8 (189.85) also had relatively high D^2 distance value while P_4 x P_2 and P_4, P_7 and P_3 x P_2, P_8 and P_3, and P_5 x P_8 and P_3 x P_1 had moderate D^2 distance value of 119.42, 118.56, 113.52, and 107.33, respectively. However, the smallest D^2 distance was between P_6 x P_8 and P_4 x P_1 (2.17) followed by P_7 x P_1 and P_5 x P_1 (3.23), P_4 x P_2 and P_2 (3.34), P_7 x P_2 and P_6 x P_1 (4.22), and P_7 and P_5 (4.36). Crosses between these genotypes may not be desirable because hybridization between parents that are not genetically diverse or with little genetic variation might not give higher heterotic value in F_1 and could show narrow range of variability in the segregating F_2 population.

Fig.1. is a Dendrogram showing genetic relationships among twenty-five genotypes of okra generated from CRL-distance values. At distance level of 0, all genotypes were separated from each other while at 1.8 distance level all the genotypes had formed a single cluster.

At a distance level of 0.2, first cluster was formed between P_9 xP_2 and P_9 xP_8. Seven clusters were formed at 0.5 distance level. Cluster 1 had nineteen genotypes which was the highest. Cluster 3 had two genotypes while cluster 2, 3, 4, 5, 6, and 7 had only one genotype.

Dendrogram showing genetic relationships among twenty-five genotypes of okra generated from D^2-distance matrix was presented in **Fig. 2.** At 0.6 distance level, all the genotypes had formed a single cluster while at

0.0 distance level no genotype was linked together. At distance level of 0.1, first linkage was formed between P_4 x P_1 and P_6 xP_8.

At 0.4 distance level, four groups were formed. Group 1 had the highest with twenty genotypes followed by group 3 with three genotypes while group 2 and 4 had only one genotype each.

The dendrogram summarized the genetic relationship among the twenty-five genotypes from 0.0 to 2.0 for CRL and from 0.0 to 0.6 for D^2 thereby giving credence to the existence of a wide range of variation among the evaluated genotypes of okra. However, genotypes in the same cluster may share common alleles at many loci and may not be appropriate for hybridization due to lack of complementary alleles that are required for heterosis. The dendrogram also showed that P_9 x P_1 (NGB00371 x NGB00326) was the most distinct genotypes for CRL but in D^2 statistics, P_8 (NGB00350) was the most distinct genotype. This indicates that crosses between NGB00371 x NGB00326 and NGB00350 could result into array of recombinant genotypes from which desirable characters may be selected (Shujaat *et al.* 2014).

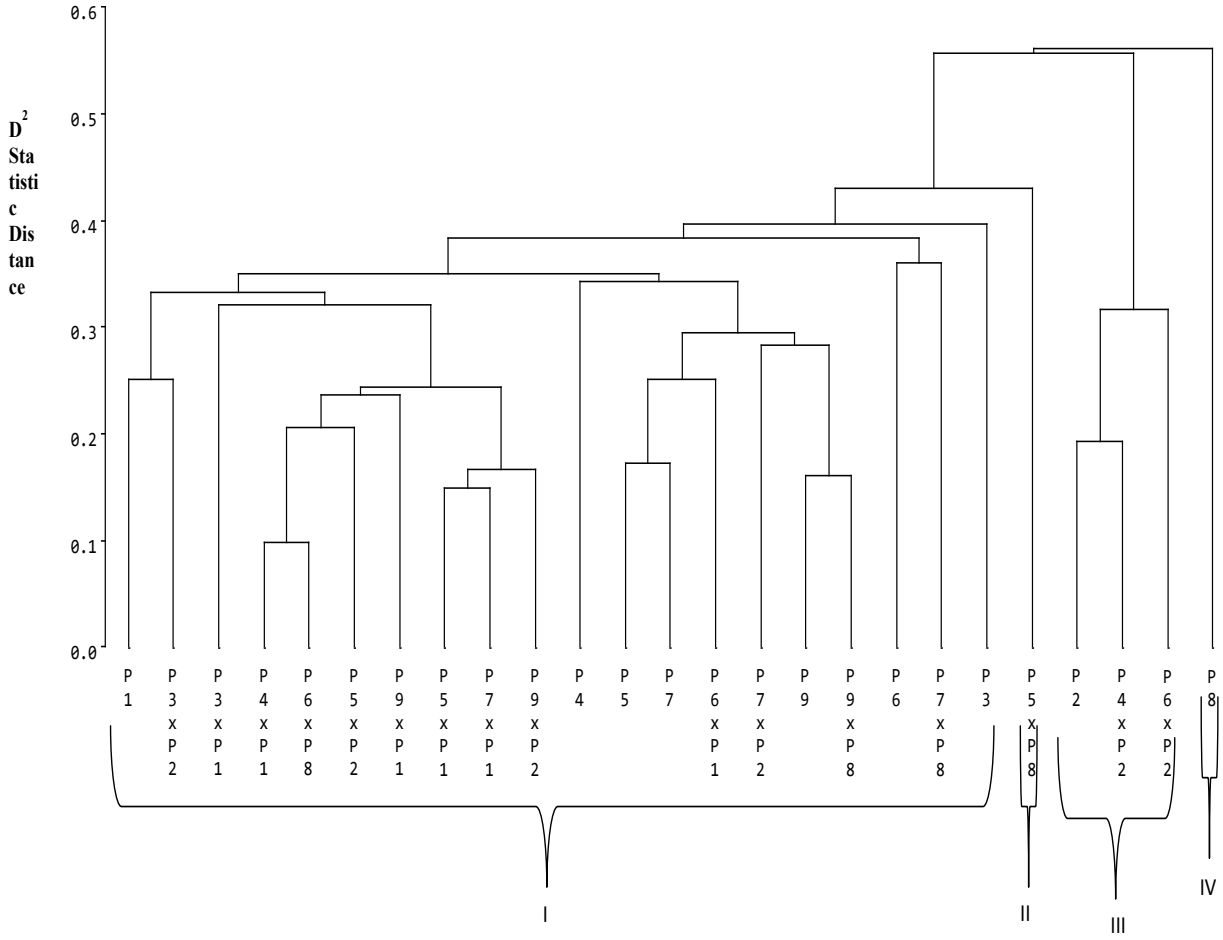

Fig. 2. Dendrogram showing genetic relationships among 25 genotypes of okra generated from D^2 distance value

Genotypes from more distant clusters could give better heterotic combinations as compared to those of closer clusters (Ranpise *et al.,* 2018). Genotypes in cluster 6 with high potential for early flowering, pod width, pod length, pod weight, number of pods per plot, number of pods per plant, yield per plot, and yield per plant could be used as parents in the development of early maturing and high yielding okra genotypes.

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