

Short Communication

Genetic diversity analysis in ridge gourd (*Luffa acutangula* L. Roxb)

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Ridge gourd (*Luffa acutangula* L. Roxb.), $2n=2x=26$, is an edible vegetable having medicinal properties with its old world origin in subtropical Asian region including India. It is generally monoecious in nature but hermaphrodite, andromonoecious, trimonoecious and gynodioecious flowering forms have also been reported. Execution of any breeding programme depends on the magnitude of genetic variability and the degree of transmission of the character from one generation to the next. The phenotype of the polygenic traits in principle is the joint product of genotype and environment. Hence, it is essential to partition the overall variability into heritable and non-heritable components, which will be the pre requisite for the breeding programme to enhance the yield. The information regarding the nature and magnitude of genetic distance among the genotypes will help the breeder in choosing the suitable diverse combinations. Selection of genetically divergent varieties is important in the exploitation of heterosis and in the development of transgressive segregants for an efficient breeding programme. Very little work has been done to estimate the amount of genetic variability in ridge gourd (*Luffa acutangula* Roxb.), a popular and commercial vegetable of India.

The present investigation was carried out at the Vegetable Research Centre of G.B.P.U.A & T, Pantnagar, U.S.Nagar (Uttarakhand) during *kharif* season of 2009. One hundred and ten ridge gourd genotypes having distinct diversity in terms of morphology and performance were taken for the study. The experiment was laid out in randomized complete block design with three replications. Each genotype was accommodated in one row of five meter length spaced at 3m apart. Plant to plant distance was 1m. There were five hills per genotype with one plant per hill. The recommended agronomical

and plant protection practices were adopted for raising a healthy crop. Data on ten quantitative traits were recorded on individual basis on all five plants per entry. The quantitative traits for which genotypes were evaluated were days to first male flower, number of nodes to first male flower, days to first female flower, number of nodes to first female flower, fruit length (cm), fruit diameter (cm), average fruit weight (g), days to first harvesting, days to final harvesting and fruit yield per plant (kg). Genotypic and phenotypic coefficients of variation were computed following the method suggested by Burton and De Vane (1953).

Heritability estimates were calculated by following the methods of Hansen *et al.* (1956). The genetic advance was worked out by the formula given by Johnson *et al.* (1955). The mean values were also used to estimate genetic diversity among genotypes using multivariate techniques of principal component (Hotelling 1933) based Euclidean clustering (Beal 1969).

Based on the mean square values, highly significant varietal differences were recorded for all the characters under study. Mean values for all the ten characters are presented in Table 1. Which indicate wide range of variation for the days to first male flower (29.00-53.00), number of nodes to first male flower (3.00-22.00), days to first female flower (29.00-55.00), number of nodes to first female flower (5.00-31.00), fruit length (4.40-26.00), fruit diameter (2.40-4.70), fruit weight (20.00-313.00), days to first harvesting (39.00-61.00), days to final harvesting (62.00-80.00) and total fruit yield (0.25-2.89). High range of variation reflects good scope for improvement of these characters through selection.

The magnitude of phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variation (GCV) for all the characters (Table 1). However, the values of PCV and GCV were recorded high for fruit weight followed by number of nodes to first male flower, fruit yield per plant, number of nodes to first female flower. The substantial magnitudes of GCV

revealed the existence of great extent of genetic variability in these characters, thereby, further suggesting all possibilities of improvement in these traits.

The magnitude of heritability in broad sense was quite high for all the characters (Table 1). High value of heritability suggests the major role of genetic constitution in the inheritance of the character and such traits are considered to be dependable from breeding point of view. However, for a breeding programme aimed at improving a particular trait through selection, only that section of heritable portion is desirable which is due to additive genetic effect. According to Panse (1957) if heritability is chiefly due to additive gene effects, a high genetic advance may be expected. Hence, high heritability in broad sense in conjunction with high genetic advance is considered more useful than the broad sense heritability estimate alone in predicting the resultant effect in the selection programme (Johnson *et al.* 1955). High genetic advance coupled with high heritability were found for characters viz; average fruit weight, number of nodes to first male flower, number of nodes to first female flower, fruit yield per plant and fruit length which indicate good scope of improvement of these traits through phenotypic selection.

The hundred and ten genotypes were grouped into seven diversified clusters based on their D values. The cluster VI was found to be the largest containing 22 genotypes followed by cluster I and II (20 genotypes each) Table 2. The estimates of cluster mean values of seven clusters for different characters indicated relatively superior expression of some characters in various clusters (Table-3). Perusal of Tables 3 revealed that the genotypes with minimum days to first female flower were grouped in cluster V, whereas those with maximum days to first female flower were grouped in cluster IV. Cluster V had genotypes with less number of nodes to first male and female flower, minimum days to first

female flower and days to first harvesting. Cluster IV contained genotypes with maximum fruit length and minimum fruit diameter. Cluster VII had genotypes with maximum fruit weight and fruit yield per plant. Cluster II had genotypes with maximum days to final harvesting.

The estimates of the intra and inter cluster distance D (Table 4) revealed that cluster I had minimum within cluster distance (1.633) while, maximum within cluster distance (2.515) was found in cluster VII. Inter cluster distance represents the extent of differentiation between a set of genotypes grouped in one cluster and another set of genotypes grouped in another cluster. Based on the inter cluster distance it was found that cluster IV had maximum divergence with that of cluster V (5.658) followed by II and VII (5.530) and cluster II and V (5.347). Besides, fairly high inter cluster distance were also observed between cluster IV and VII (4.927), cluster I and IV (4.881), cluster I and VII (3.999), cluster I and II (4.170), cluster III and VII (3.784), cluster VI and VII (3.638), cluster II and III (3.586) and cluster IV and VI (3.574). Which further indicate abroad-inherent genetic diversity among the material taken for the study. Selection of parents for hybridization from genetically distance clusters may provide broad spectrum of genetic recombination, thus provide desirable segregates for selections. Many earlier workers observed that more diverse the parents within its overall limit of fitness, the greater the chain of broad spectrum of variability in segregating generations (Shete and Kale 1988, Dikshit *et al.* 1999). The results of the present investigation also suggested that crossing of the genotypes having higher average yield and belonging to more diverse cluster may lead to broad spectrum of variability in segregating generations for selection of higher yielding genotypes. Hence, selection of divergent parents may be useful for heterosis breeding in ridge gourd.

Table 1. Mean, range and estimates of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense (%) and genetic advance as percent of mean for yield and yield attributing traits in ridge gourd

Sl.No.	Characters	Range	Mean	GCV	PCV	ECV	Heritability (%)	Genetic advance	Genetic advance as percentage of mean
1.	Days to 1 st male flower	29.00-53.00	38.47	11.61	12.21	3.77	90.46	8.75	22.74
2.	No. of nodes to 1 st male flower	3.00-22.00	8.63	41.43	42.77	10.61	93.83	7.14	82.73
3.	Days to 1 st female flower	29.00-55.00	40.99	12.96	13.42	3.50	93.18	10.56	25.76
4.	No. of nodes to 1 st female flower	5.00-31.00	13.57	40.71	41.42	7.64	96.58	11.18	82.38
5.	Fruit length (cm)	4.40-26.00	14.96	35.51	35.82	4.73	98.25	10.85	72.52
6.	Fruit diameter (cm)	2.40-4.70	3.41	14.05	15.19	5.76	85.58	0.91	26.68
7.	Fruit weight (g)	20.00-313.33	79.95	43.70	43.86	3.65	99.30	71.74	89.73
8.	Days to 1 st harvesting	39.00-61.00	50.47	12.39	12.73	2.94	94.64	12.53	24.82
9.	Days to final harvesting	62.00-80.00	72.34	5.72	6.36	2.79	80.76	7.66	10.58
10.	Fruit yield /plant (kg)	0.25-2.89	0.98	40.90	42.59	11.86	92.24	0.79	80.61

Table 2. Clustering pattern of 110 genotypes of ridge gourd

Cluster No.	No. of genotypes	Name of genotypes
I	20	PRG-107,PRG-105,PRG-106,PRG-114,PRG-117,PCPGR-7255,PCPGR-7275,PRG-46, PRG-84,PRG-69,PRG-69,PRG-45,PRG-89,PRG-58,PRG-41,PRG-87,PRG-37A,PRG-21,PRG-48,PRG-22,PRG-39
II	20	PRG-129, PRG-138, PRG-141, PRG-144, PRG-145, PRG-53, PRG-119, PRG-82, PRG-95, PRG-92, PRG-24, PRG-29, PRG-65, PRG-34, PRG-77, PRG-73, PRG-23, PRG-57A, PRG-96, PRG-49
III	14	PRG-118, PCPGR-7260,PCPGR-7267,PCPGR-7273, PRG-39, PRG-36, PCPGR-7254, PRG-79, PRG-56, PRG-25, PRG-86, PRG-26, PRG-67, PRG-78
IV	11	PRG-127, PRG-102, PCPGR-7274, PRG-40, PRG-170, PRG-44, PRG-PCPGR-7247, PRG-19, PRG-60, PRG-61
V	13	PRG-142, PRG-125, PRG-15, PRG-137, PRG-149, PRG-120, PRG-12, PRG-100, PRG-108 PRG-42, PRG-71, PRG-33, PRG-54
VI	22	PRG-130, PRG-136, PRG-143, PRG-121, PRG-103, PRG-62, PRG-80, PRG-57, PRG-88, PRG-50, PRG-43, PRG-83, PRG-94, PRG-90, PRG-55, PRG-20, PRG-53, PRG-85, PRG-27, PRG-6, PRG-81, PRG-63
VII	10	PRG-131, PRG-132, PRG-113, PRG-115, PRG-109, PRG-37, PRG-75, PRG-66, PRG-47, PRG-59

Table 3. Cluster means for ten characters in ridge gourd

Characters	Cluster Mean						
	I	II	III	IV	V	VI	VII
Days to 1 st male flower	35.80*	42.30	36.95	44.56**	33.38	38.68	37.80
No. of nodes to 1 st male flower	6.20	11.32	6.43	13.00**	5.85*	9.00	9.30
Days to 1 st female flower	38.03	46.35	40.86	47.79**	34.38*	41.50	36.40
No. of nodes to 1 st female flower	11.02	17.15	12.21	21.45**	8.92*	12.05	14.17
Fruit length (cm)	13.41	8.99*	20.73	20.83**	16.74	12.37	18.93
Fruit diameter (cm)	3.13	3.19	3.28	3.09*	3.86	3.56	4.12**
Fruit weight (g)	60.00	44.02*	101.79	95.91	106.15	66.36	139.50**
Days to 1 st harvesting	44.47	55.95	54.14	57.18**	42.38*	52.95	44.10
Days to final harvesting	68.65*	76.75**	74.86	75.64	69.31	71.14	70.40
Fruit yield /plant (kg)	0.88	0.77*	0.80	1.00	1.09	1.00	1.73**

*Lower value, ** Highest Vales

Table 4. Intra and Inter cluster distances (D values) in ridge gourd genotypes

Cluster No	I	II	III	IV	V	VI	VII
I	1.633	3.932	2.869	4.881	2.369	2.111	3.999
II		2.097	3.586	2.944	5.347	2.487	5.530
III			2.187	3.343	3.160	2.341	3.784
IV				2.371	5.658	3.574	4.927
V					1.911	3.074	2.601
VI						1.895	3.638
VII							2.515

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