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Genetic divergence and character association studies in indegenous ridge gourd (*Luffa Acutangula* (L.) Roxb.) Genotypes

Anjali Gautam, SK Maurya, Hirdesh Yadav and Pooja

Abstract
Forty two genotypes of ridge gourdgrown during summer season, 2013 were evaluated for genetic divergence using principal component analysis (PCA) and Nonhierarchical cluster analysis. PCA yielded a total of sixteen principal components (PC) out of which, first ten PC accounted 94.27 % of total variation. Seed width, number of node of first female flower, days to first fruit harvesting contributed most positively while, fruit length, average fruit weight, number of primary branches contributed most negatively in first PC accounted 35.17 % of total variation. The first ten PC score were used for clustering purpose which grouped the genotypes into three cluster accommodating 5, 22, and 15 genotypes in cluster I, II, and III, respectively. The Intra-cluster distances ranged from 2.724 (cluster I) to 3.550 (cluster II). The inter-cluster distances were found maximum (5.984) between cluster I and II, and minimum (3.419) between cluster II and III suggesting scope for exploiting heterosis upon hybridization between genotypes of these groups of desired traits. Character association studies revealed that fruit yield had positive and significant correlation with average fruit weight (0.774), number of fruits per plant (0.945), vine length (0.547), number of primary branches (0.472), fruit length (0.390), seed length (0.240) whereas, fruit yield had negative and significant correlation with number of node of first female/hermaphrodite f flower (-0.458), days of first female/hermaphrodite flower anthesis (-0.314) and days of first fruit harvesting (-0.401). These results suggest the wide scope of varietal improvement in ridge gourd through hybridization and selection.

Keywords: ridge gourd, *luffa acutangula,* principal components analysis (pca), non-hierarchical cluster, character association, genetic divergence

Introduction
Ridge gourd [*Luffa acutangula* (Roxb.) L.], 2n=2x=26, is one of the important cucurbitaceous vegetable crop with old world origin in subtropical Asian region including particularly India (Kalloo 1993). This crop has a long history of cultivation in the tropical countries of Asia and Africa. *Luffa* has nine species out of which seven (*Luffa acutangula* (L.) Roxb, *L. cylindrica* M. Roem, *L. echinta* Roxb., *L. graveolens, L. tuberose* Roxb., *L.umbellata)* are found in India. The probable centre of origin and the primary gene centre of *Luffa* is India. *Luffa acutangula* (Ridge gourd) and *Luffa cylindrical* (Sponge gourd) are grown throughout India in tropical and subtropical climate. *Luffa acutangula* has three varieties: var. *acutangula* is grown in South East Asia and other tropical areas; var. *amara,* a wild form is confined to Peninsular India, while var. *forskallii* (Harms.) Heiser and Schilling, another wild form, is confined to Yemen, *Luffa echinata* grows in natural habitat in Western Himalayas, central India and Gangetic plains. *Luffa graveolens* is a wild species distributed in parts of North-Central India and *Luffa hermaphrodita (satputia),* that bears fruit in clusters, is cultivated in Eastern Uttar Pradesh and Bihar (Sirohi *et al*. 2005) [26]. Ridge gourd, is grown throughout India in tropical and subtropical climate, both as spring-summer and rainy season crop known as ribbed gourd or angled gourd or silky gourd or angled loofah or vegetable gourd. Fruits of *Luffa* spp are very nutritious and good source of vitamin A, calcium, phosphorus, ascorbic acid and iron (Aykroyd 1963) [1]. Genetic divergence is the process in which two or more populations of an ancestral species accumulate independent genetic changes (mutations) through time, often after the populations have become reproductively is olated for some period of time. Genetic diversity is a prerequisite for an effective plant breeding programme. It is a useful and essential tool for parent's choice in hybridization to develop high yield potential cultivars and to meet the diversified goals of plant breeding Gaur *et al*. 1978 [5]; Shekhawat 2001 [23] and Haydar *et al*. 2007 [6]. Principal components analysis (PCA) helps in identifying the most relevant characters that can be used as descriptors by explaining as much of total variation in the origin

set of variables as possible with as few components as possible and reducing the dimension of the problem (Kumar *et al*. 2011) [12]. Non-hierarchical Euclidean cluster analysis is one of the potent techniques for measuring genetic divergence at both intra and inter cluster levels and thus provides a basis for selection of genetically divergent parents in hybridization programme. In ridge gourd, crop improvement through successful selection programme is only achieved using valid information about the correlation and genetic variability of traits of interest knowing full well that improvement in any crop is dependent on the amount of genetic variability in the population. Thus, the determination of correlation among the characters is important in selection. Correlation studies among yield and other traits of the crop will be of interest to breeders in planning hybridization programmes and evaluating the individual plants in the segregating populations. Thus the present study aimed to determine patterns of genotypic variation and to identify and classify groups of genotypes with different genetic diversity. The information on nature and degree of genetic divergence present in genotypes could help to select elite ones for direct use or further improvement through hybridization.

Material and Methods

The present experiment was conducted during the summer season, 2013 at Vegetable Research Centre (VRC) of Govind Ballabh Pant University of Agriculture and Technology, Pantnagar, Udham Singh Nagar, Uttarakhand, India. Geographically, Pantnagar is situated at 29.5° N latitude, 79.3° E longitude and at an altitude of 243.84 meters above the mean sea level in sub-mountainous region of Shivalik hills, known as *tarai*, which have a humid and subtropical climate. The climate of the region is broadly humid subtropical with cool winter and hot dry summer. During hot summer, maximum temperature exceeds 40°C. The monsoon generally starts from the third week of June and recedes by the end of September. The mean relative humidity remains almost 80-90 per cent from mid-June to end of February and then it steadily decreases to 50 per cent by the first week of May and remains so till mid-June. The soil at Pantnagar comes under mollisols and that of experimental field was sandy-loam with adequate drainage and optimum water holding capacity. The experimental materials comprised of forty two genotypes (36 monoecious and 6 hermaphrodite genotypes) of ridge gourd including two checks (Pant-Torai-1 and Satputia) which were collected from different parts of India and maintained at PCPGR, Pantnagar. The genotypes for the study were selected on the basis of genetic as well as eco-geographical diversity and evaluated for horticultural traits (Table 1). The experiment was laid out in augmented block design II. Five blocks were made and each block consists of eight genotypes and two checks. The spacing was kept 2 m x 0.75 m. All the analyses were carried out with mean observations of all the characters, and cluster analysis according to (Beale 1969) [2].

Results and Discussion

The principal component analysis of 42 ridge gourd genotypes based on correlation matrix of yield contributing traits yielded the 16 Eigen roots (Eigen values) and Eigen vectors. Eigen values and associated percentage of variation measure the importance and contribution of each component to total variance, whereas each coefficient of Eigen vectors indicates the degree of contribution of every original variable with which each principal component is associated. The eigen vector of the fifteen principal components has been scaled in such a way that the largest element in each vector as unity was interpreted as the relative weight given to the variable in each component (Kumar *et al* 2010) [13]. The higher the coefficients, regardless the sign, the more effective they will be in discriminating between genotypes thus they are important (Rojas 2003) [21]. These values and associated percentage of variation explained by Eigen root have been presented in Table 1 and Fig. 1. The Eigen root of first principal component was accounted approximately 35.13 per cent variation of total variation followed by second to sixteen components which accounted 14.28, 12.48, 8.78, 5.84, 5.49, 4.03, 3.42, 3.00, 2.15, 1.82, 1.45, 0.81, 0.63, 0.54 and 0.14 per cent of total variation presented among genotypes, respectively. Approximately 94.27 per cent variations were accounted by first 10 principal components however, principal components 11th, 12th, 13th, 14th, 15th and 16th contributed very small amount of per cent variation. The principal component analysis involves a mathematical procedure that transforms a number of (possibly) correlated variables into a (smaller) number of uncorrelated variables called principal components. The first principal component accounts for as much of the variability in the data as possible and each succeeding component accounts for as much of the remaining variability as possible. The first ten principal components contributed 94.27 per cent towards the total variance were included for summarization of original data of ridge gourd genotypes in reduced dimension meeting the criteria of (Rao 2003) [20] which follows of covering 90 per cent of total variance is more appropriate and being used by most of the workers now a days. The scales per corresponding eigen vector for principal component taking the largest element in each vector as unity has been presented in Table 1. (Jeffers 1967) [7] suggested that these elements may be interpreted as the relative weight given to the variable in each component and important variable all those which have high positive and negative weight. The variables seed width, number of node of first female flower, days to first fruit harvesting contributed most positively in first principal component accounted 35.13 % of total variation. Whereas, the most negative contribution comes from number of primary branches, average fruit weight, fruit length. In second principal component, fruit yield in combination with number of node of first female flower, days to first fruit harvesting contributed most positively while, seed length, seed width and 100 seed weight were the variables which contributed most negatively towards the variation. Similarly, principal component 3 and 4 gave high positive weights to 100 seed weight, and day to first fruit harvesting whereas high negative weights to seed width and vine length, respectively. The results are in agreement with the findings of Kundu *et al*. 2012 [14]; Singh *et al*. 2014 [25] and Yadav *et al*. 2016 [27]. Non hierarchical clustering patterns of forty two genotypes including checks (Pant Torai-1 and Satputia) could be resolved into three clusters indicating presence of considerable genetic divergence among the genotypes (Table 2). A perusal of data in the table revealed distribution of genotypes into different clusters were apparently random irrespective of their place of origin strengthening the fact of no sharp relationship between the clustering pattern of genotypes and their geographical sources. Thus, the tendency of cultivars occurring in the cluster cutting across geographical boundaries is possible due to genetic makeup of genotypes and subsequently natural selection during their development. Similar results were obtained by (Mathew *et al*.

2001) [15] in bottle gourd, Kumar *et al*. 2006 [11] in pumpkin; (Choudhary *et al*. 2011) [3] in ridge gourd. Contrary to this, these results are not supported by the findings of (Juned *et al*. 1988) [8] where a close relationship was noted between geographic and genetic diversity. The cluster I, II and III comprises 5, 22 and 15 genotypes, respectively. It is desirable to have high inter -cluster distance and low intra cluster distance. The magnitude of intra-cluster distances measured the extent of genetic diversity between ridge gourd genotypes of same cluster. Intra- cluster distances range from 2.724 to 3.550 in cluster I and cluster II, respectively (Fig 2). The presence of relatively lower values of intra-cluster distance suggests the presence of narrower genetic variation within a cluster. Genetic distance between two cluster is measured through inter cluster distance which was found maximum (5.984) between cluster I and II, and minimum (3.419) between cluster II and III. The grouping of genotypes in clusters reflects the relative divergence of clusters and allows a convenient selection group of genotypes with their overall phenotypic similarity for hybridization programme facilitating better exploitation of germ plasm. Generally crosses involving parents belonging to most divergent clusters are expected to give maximum heterosis and create wide variability in genetic architecture. Thus, hybridization between genotypes of Clusters I and II and also between genotypes of Clusters I and III would exhibit high heterosis and is also likely to produce new recombinants with desired traits. Therefore, more emphasis should be given on cluster I and II and also genotypes of Clusters I and III in selecting in breds for crossing in ridge gourd hybridization programmes. The results are in conformity with the findings of Kale *et al*. 2002 [9]; Quamruzzaman *et al*. 2008 [16] and Singh *et al*. 2008 [24]. Promising genotypes with desirable characters can be identified on the basis of mean values of characters which could be utilized in hybridization programme for the development of desirable genotypes. The cluster means (Table 3) of forty two genotypes revealed that lowest mean value for days to first female/hermaphrodite flower anthesis (41.97) followed by number of node of first female/hermaphrodite flower (4.16), and days of first fruit harvesting (48.34) were found in genotypes of cluster I. Highest mean value for fruit length (18.68 cm), fruit diameter (4.03 cm), average fruit weight (13.36 g), fruit yield (118.00 q/ha), number of primary branches (8.03) in genotypes of cluster I while, highest mean value for average fruit weight (15.45 g), fruit flesh thickness (0.26 cm) was recorded in genotypes of cluster III. Availability of sufficient variability and association among different characters are the pre-requisite for executing an effective selection programme for crop improvement. Yield, being a complex quantitative trait, is dependent on a number of component characters. Therefore, knowledge of association of different components together with their relative contributions has immense value in selection. The estimation of correlation coefficients among different economic traits has been presented in Table 4. The perusal of data revealed that fruit yield had positive and significant correlation with average fruit weight (0.774), number of fruits per plant (0.945), vine length (0.547) number of primary branches (0.472), fruit length (0.390), seed length (0.240) whereas, fruit yield had negative and significant correlation with number of node of first female/hermaphrodite f flower (-0.458), days of first female/hermaphrodite flower an thesis (-0.314) and days of first fruit harvesting (-0.401). Average fruit weight was found positive and significantly associated with fruit diameter (0.159), vine length (0.384), seed length (0.326), node number to first female/hermaphrodite flower (0.422), number of fruits per plant (0.444), fruit length (0.504) and fruit yield (0.774). However, average fruit weight was found negatively correlation with days of first female/hermaphrodite flower anthesis (-0.245), days to first fruit harvesting (-0.296). Fruit length had positive and significant correlation with fruit flesh thickness (0.589), average fruit weight (0.504), vine length (0.498), number of primary branches (0.437), yield (0.390), seed length (0.060), seed width (0.262), number of seeds per plant (0.037). Whereas, fruit diameter (0.047), number of fruits per plant (0.225), 100 seed weight (0.117) and negatively correlation with days of first female/hermaphrodite flower anthesis (-0.017), number of node of female/hermaphrodite flower (-0.104) and days to first fruit harvesting (-0.183).Days to first fruit harvesting was significantly correlated in positive direction with days to first female flower/hermaphrodite flower (0.639) and node number to first female/hermaphrodite flower (0.805) and number of seed per fruit (0.427). 100 seed weight was significantly correlated in positive direction with vine length (0.0.326), number of seeds of fruit (0.368), However, it was negatively correlation with (-0.179) and days of first fruit harvesting (-0.322). The identification of important components and information about their association with yield and other traits are very useful for developing efficient breeding strategy for evolving high yielding varieties in ridge gourd. In present investigation, fruit yield perceived positive correlation with fruit length, number of fruits per plant and average fruit weight. This indicates that selection for these traits would be effective to improve fruit yield in ridge gourd. Positive correlation of fruit yield has been reported with fruit length, number of fruits per plant and fruit weight Rao *et al*. 2000 [20]; Ram *et al*. 2006 [18]; Samadia 2011 [22]; Rabbani *et al*. 2012 [17] and Dubey *et al*. 2013 [4] in ridge gourd.

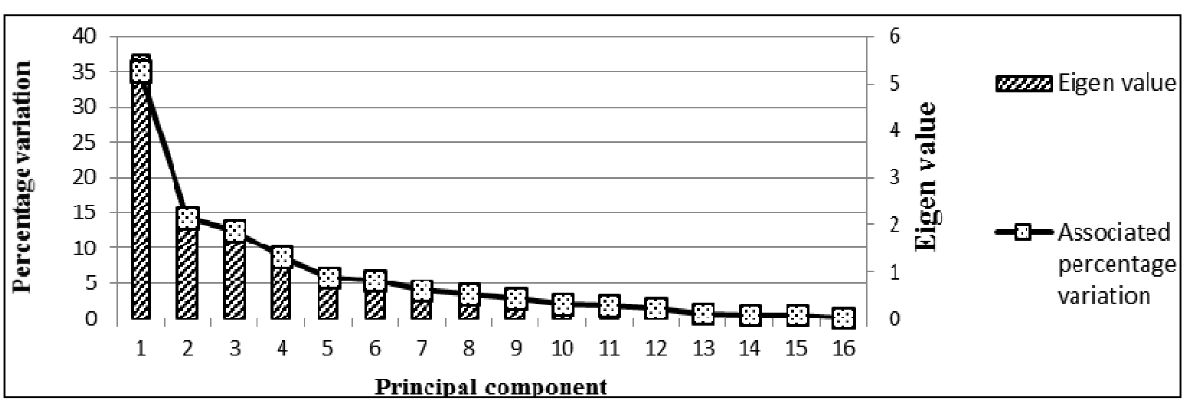

Fig 1: Cattel scree graph for variation explained by principal components based on yield attributing traits in ridge gourd genotypes

Table 1: Eigen vector, Eigen root and associated variation for principal components in ridge gourd for various yield attributing characters

Sl. No.	Characters	Eigen vector															
		1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	**15**	**16**
1.	Days to first female/hermaphrodite flower anthesis	0.19	0.28	0.28	-0.20	-0.08	0.01	-0.28	-0.33	-0.34	-0.37	-0.33	-0.30	-0.13	0.001	-0.21	-0.17
2.	Number of node of first female flower	0.35	0.21	0.24	-0.15	-0.07	0.19	0.15	0.05	0.06	0.09	-0.03	-0.09	0.48	0.51	0.37	0.09
3.	Days to first fruit harvesting	0.32	0.35	0.29	0.46	0.51	0.22	0.04	0.12	0.13	0.07	-0.08	0.11	-0.14	-0.13	-0.16	-0.15
4.	Fruit length (cm)	-0.18	-0.03	0.13	-0.19	-0.17	0.26	0.43	0.02	0.38	0.29	-0.31	-0.31	-0.18	-0.05	-0.17	-0.35
5.	Fruit diameter (cm)	0.20	0.001	0.15	0.17	-0.09	-0.82	0.10	0.15	0.07	0.06	-0.01	-0.21	0.05	-0.07	0.13	-0.31
6.	Fruit flesh thickness (cm)	0.07	0.16	0.27	0.03	-0.36	0.06	-0.17	0.33	0.03	0.16	-0.05	-0.18	-0.24	-0.37	0.18	0.55
7.	Average fruit weight (g)	-0.31	-0.19	0.12	0.06	0.21	0.16	-0.35	0.37	-0.14	-0.05	-0.15	-0.11	-0.17	0.15	0.50	-0.35
8.	Number of primary branches	-0.46	0.03	0.46	0.22	-0.16	-0.003	0.31	0.13	-0.31	-0.20	-0.09	0.26	0.35	-0.10	-0.14	0.02
9.	Vine length (m)	0.14	-0.16	0.20	-0.59	0.28	-0.12	-0.20	0.28	0.10	0.12	-0.21	0.35	0.21	-0.22	-0.20	-0.008
10.	Number of fruit per plant	0.17	0.11	0.08	-0.18	-0.49	0.12	-0.04	0.12	-0.06	-0.01	0.46	0.40	-0.23	0.01	0.02	-0.43
11.	Fruit yield (q/ha)	-0.15	0.20	0.15	-0.32	0.28	-0.08	0.32	-0.38	0.01	-0.09	0.16	0.09	-0.17	-0.32	0.53	0.04
12.	Seed length (cm)	0.18	-0.44	0.29	0.28	-0.17	0.02	-0.13	-0.46	0.21	0.08	-0.30	0.37	-0.10	0.02	0.18	0.02
13.	Seed width (cm)	0.37	-0.35	-0.03	-0.06	0.09	0.02	0.49	0.22	-0.47	-0.09	-0.12	0.03	-0.36	0.13	-0.002	0.14
14.	Number of seeds per fruit	-0.07	0.05	0.04	0.004	0.05	-0.01	-0.09	-0.22	-0.53	0.79	0.05	-0.03	0.04	-0.01	-0.03	-0.06
15.	100 seed weight (g)	-0.06	-0.42	0.48	-0.09	0.13	0.01	-0.07	-0.09	0.07	-0.04	0.57	-0.35	-0.03	0.14	-0.21	0.11
Eigen root		5.62	2.28	1.99	1.40	0.93	0.87	0.64	0.54	0.48	0.34	0.29	0.23	0.12	0.10	0.08	0.02
Percent variation		35.13	14.28	12.48	8.78	5.84	5.49	4.03	3.42	3.00	2.15	1.82	1.45	0.81	0.63	0.54	0.14

Table 2: Cluster classification of 42 ridge gourd genotypes based on principal component analysis

Genotype with place of origin		
Cluster	**Genotype**	**Place of origin**
Cluster I	PCPGR-7243	Lucknow, U.P.
	PCPGR-5560	Gorakhpur, U.P.
	PCPGR-7279	Rishikesh, Haridwar, Uttarakhand
	PCPGR-7450	Kumarganj, Fahzabad, U.P.
	PCPGR-3701	Sahiadpur, Ambedakar nagar, U.P.
Cluster II	PCPGR-5564	Sirodgaown, Almora Uttarakhand
	PCPGR-3768	Babugarh, Dehradun, Uttarakhand
	PCPGR-7260	Kashipur, U.S.Nagar, Uttarakhand
	PCPGR-5558	Baritorava, Gorakhpur, U.P.
	PCPGR-7272	Haridwar, Uttarakhand
	PCPGR-7269	Bazpur, U.S.Nagar, Uttarakhand
	PCPGR-7660	Akhand nagar, Sultanpur,U.P.
	PCPGR-3731	Kishanpur, Nainital, Uttarakhand
	PCPGR-7500	Lucknow, U.P.
	PCPGR-7449	Kumarganj, Fahzabad, U.P.
	PCPGR-7170	Ratanpur, Raibearaly, U.P.
	PCPGR-3712	Sahjadpur, Ambedakar nagar, U.P.
	PCPGR-3703	
	PCPGR-7495	
	PCPGR-7470	Varanasi, U.P.
	Pant Torai-1(C)	VRC, Pantnagar, Uttarakhand
	PRG-45	Ranichauri, Tehari, Uttarakhand
	PRG-48	
	PRG-44	
	PRG-43	
	PRG-46	
	PCPGR-7284	
Cluster III	PCPGR-4493	Samastipur, Bihar
	Satputia	RAU, Samastipur, Bihar
	PCPGR-5559	Mahiidiya, Gorakhpur, U.P.
	PCPGR-7273	Haridwar, Uttarakhand
	PCPGR-3113	Shivpur, Baharaich, U.P.
	PCPGR-7244	Lucknow, U.P.
	PCPGR-7643	Pauri, Uttarakhand
	PCPGR-7483	Mau, U.P.
	PCPGR-3756	Maihera, Nainital, Uttarakhand
	PCPGR-5743	Nandganj, Ghazipur, U.P.
	PCPGR-7268	Bazpur, U.S.Nagar, Uttarakhand
	PRG-47	Ranichuri, Tehari, Uttarakhand
	PRG-53	
	PRG-42	
	PRG-49	

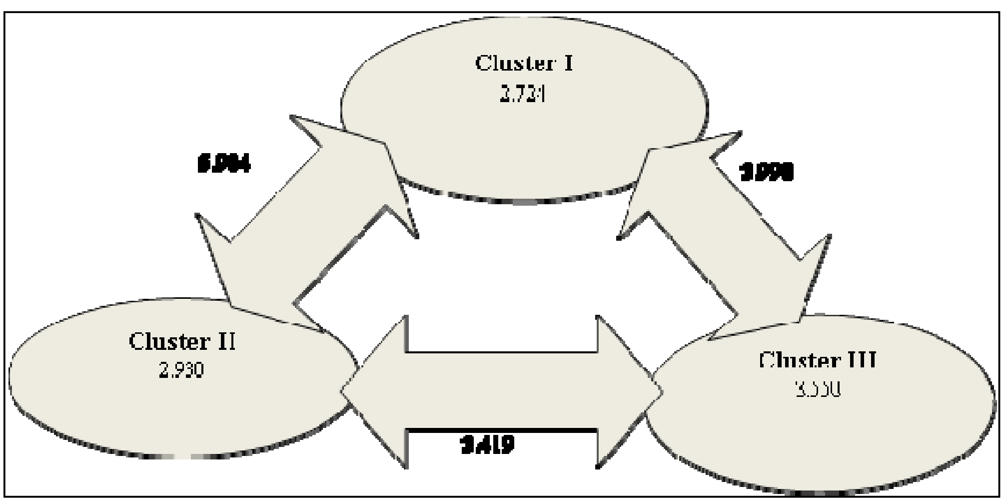

Fig 2: Cluster diagram showing the average intra- and inter-cluster distances of ridge gourd genotypes.
(The values along the arrows indicate inter-cluster distances and the values within the circle indicate intra-cluster distances.)

Table 3: Cluster mean and standard deviation for different economic traits in ridge gourd

Cluster		Days to first female/hermaphrodite flower anthesis	Number of node of first female flower	Days to first fruit harvesting	Fruit length (cm)	Fruit diameter (cm)	Fruit flesh thickness (cm)	Average fruit weight in (g)	Number of primary branches	Vine length (m)	Number of fruits / plant	Fruit yield (q/ha)	Seed length (cm)	Seed width (cm)	Number of seeds / fruit	100-seed weight (g)
I	Mean	41.97	4.16	48.34	18.68	4.03	0.13	13.36	8.03	12.69	13.34	118.00	1.21	0.72	12.95	92.30
	SD	1.27	0.64	1.93	1.92	0.35	0.04	2.65	0.74	1.63	2.17	30.68	0.11	0.02	2.65	53.58
II	Mean	44.52	7.09	54.42	13.92	3.61	0.24	9.70	4.51	7.32	7.93	50.55	1.11	0.73	11.25	60.50
	SD	1.89	1.40	2.03	3.20	0.58	0.06	2.69	0.79	1.45	2.92	16.79	0.08	0.05	1.67	25.36
III	Mean	42.70	5.82	52.90	14.19	3.42	0.26	15.45	5.11	8.71	11.27	113.49	1.13	0.71	12.47	70.54
	SD	2.35	1.08	1.67	2.92	0.78	0.06	1.50	1.00	1.44	2.17	20.17	0.18	0.08	3.11	40.08

Table 4: Phenotypic correlation between different pairs of characters of ridge gourd genotypes

Sl. No.	Characters	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1.	Days to first female/ hermaphrodite flower anthesis	1.000	0.710**	0.639**	-0.017	0.086	0.128	-0.245	-0.253	-0.314*	-0.201	-0.284	0.220	0.219	0.560**	-0.179
2.	Number of node of first female flower		1.000	0.805**	-0.104	0.097	0.226	0.422**	-0.342*	-0.458**	-0.420**	-0.399**	-0.159	0.154	0.409**	0.226
3.	Days to first fruit harvesting			1.000	-0.183	-0.012	0.200	-0.296	-0.286	-0.401*	-0.562**	-0.511**	-0.121	0.120	0.427**	-0.322
4.	Fruit length (cm)				1.000	0.047	0.589**	0.504**	0.225	0.390*	0.498**	0.437**	0.060*	0.262*	0.037*	0.117
5.	Fruit diameter (cm)					1.000	0.126	0.159*	0.085	0.122	0.192	0.323*	0.024*	-0.094	-0.075	0.141
6.	Fruit flesh thickness (cm)						1.000	0.097	-0.001	0.085	-0.078	-0.004	0.042*	0.133	-0.022	0.004
7.	Average fruit weight (g)							1.000	0.444**	0.774**	0.384*	0.292	0.326*	0.124	0.301	0.067
8.	Number of primary branches								1.000	0.472**	0.805**	0.413**	0.129	-0.018	0.225	0.307
9.	Vine length (m)									1.000	0.547**	0.805**	0.218	-0.050	-0.271	0.326*
10.	Number of fruits per plant										1.000	0.413**	0.174	0.015	0.303	0.180
11.	Fruit yield (q/ha)											1.000	0.240*	0.039	-0.166	0.304
12.	Seed length (cm)												1.000	0.555	-0.041	0.280
13.	Seed width (cm)													1.000	0.383*	0.044
14.	Number of seeds per fruit														1.000	0.368*
15.	100-seed weight (g)															1.000

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