Research Article

ASSESSMENT OF GENETIC DIVERGENCE IN SEED PURPOSE WATERMELON / KALINGDA (*Citrullus lanatus*)

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Abstract: Kalingda [*Citrullus lanatus* (Thunb.) Matsum & Nakai] is an extremely valuable crop with medicinal properties. Despite of having its importance to the arid region, a very few genetic studies have been performed for describing the divergence in this crop. Therefore, the present experiment was executed with 12 genotypes, at two locations (ARS, Mandor and ARSS, Nagour) during *kharif* 2020. Significant differences were exhibited among genotypes for all the traits while environments were found significant for days to maturity, no. of fruits per plant and fruit yield (q/ha). G X E interaction was also reported significant for all traits except days to first fruit setting and 100 seed weight. Estimation of genetic divergence displayed a measure of diversity and grouped the genotypes into four clusters. Days to maturity, fruit yield (q/ha) and no. of fruits per plant contributed about three-fourth of total genetic divergence. Cluster III and IV were most divergent followed by cluster I and IV as they were having maximum inter cluster distance while maximum intra cluster distance was depicted by cluster I. Considering cluster distance and *per se* performance, six promising genotypes of kalingda have been recognized for tangible advancement in the seed yield and other ancillary traits.

Keywords: *Kalingda, Genetic Divergence, Genotypes*

Introduction

Seed purpose watermelon [*Citrullus lanatus* (Thunb) Matsum & Nakai] is an herbaceous creeping plant belonging to the family cucurbitaceae. It is famous as 'Mateera' in the western part of the Rajasthan while people of Gujarat traditionally called it 'Kalingda'. Sole cropping of this important crop is not in tradition; however, it is generally cultivated as a mixed crop with pearlmillet and clusterbean. To minimize the risk of crop failure under aberrant weather situations, farmers follow mixed/intercropping depending upon the rainfall and soil types in arid zone districts of western Rajasthan [1].

Mateera seed price varies from 5000-8000/q (sometimes crossed to 10000) in local market which is highest among rainfed *kharif* crops thus supporting the livelihoods of rural people of the arid zone in a big way [2]. The important part of this crop is seed, which contains 30-35% oil and 20-25% crude protein [3]. Its seed are largely used in confectionary and pharmaceuticals. Roasted seeds of kalingda are generally consumed as snacks. Watermelon seeds are supposed to regulate blood sugar levels, increase energy, maintain the nervous system and promote healthy skin [4].

Considering the above facts, it can be stated that kalingda is an immensely valuable crop with high market value and a number of healthy properties. It is playing crucial role in the subsistence of the farmers of arid region by providing them additional income. Despite of being such an important and versatile crop with higher returns and high market value, the crop has not gained enough attention due to unavailability of good varieties, poor marketing structure and lack of awareness. As we know that presence of ample amount of variability allows a breeder to choose from various traits and develop a superior variety in all possible aspects. Therefore, the knowledge of genetic diversity in such a good crop is pre requisite for establishing a successful breeding programme.

Similarly, choice of genetically divergent parents for hybridization under transgressive breeding programme is also dependent upon categorization of breeding materials on the basis of appropriate criteria [5]. Therefore, in the present investigation genetic diversity among twelve genotypes of kalingda was pursued for seed yield and related traits.

Materials and Methods

The study was laid out at two locations *i.e.*, ARS, Mandor and ARSS Nagour. Both the experimental sites are located in a typical arid type of climate with erratic rainfall and an average temperature of 20-35°C. A total of twelve improved genotypes (Obtained from CAZRI, Jodhpur) were evaluated in Randomized Block Design with 3 replications in the *kharif* season of 2020. These 12 genotypes were selected from initially evaluated 50 accessions, on the basis of *per se* performance. Data were recorded for days to first fruit setting, days to maturity, no. of fruit per plant, fruit diameter, 100 seed weight (g), fruit yield (q/ha) and seed yield (q/ha) by randomly selecting five plants from each genotype. Analysis of variance was computed as per standard statistical procedure given by Panse and Sukhatme [6] while the assessment of genetic divergence was carried out using Mahalanobis's D^2 statistic [7].

Result and Discussion

Pooled analysis of variance revealed significant differences among genotypes for all the traits under investigation and environments for days to maturity, no. of fruits per plant and fruit yield (q/ha) [Table-1]. The similar conclusion was also observed by Mahla *et. al.* [8] in seed purpose watermelon. The statistical differences between the genotypes for these traits are indicative of having sufficient variability among genotypes and environments.

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Table-1 *Means of the genotypes over the two locations*

Genotypes	Days to first fruit setting	Days to Maturity	No. of fruits per plant	Fruit Diameter (cm)	100 - Seed Weight (g)	Fruit Yield (q/ha)	Seed Yield (q/ha)
CAZJK 12	43	77	4	11.44	5.30	62.47	1.45
CAZJK 15	50	85	3	9.38	5.01	31.40	0.97
CAZJK 24	48	80	5	10.21	4.820	42.87	1.23
CAZJK 27	51	83	5	10.89	5.99	64.14	1.80
CAZJK 29	54	87	3	9.58	4.68	39.87	1.00
CAZJK 32	53	83	4	9.07	4.90	35.34	1.01
CAZJK 36	45	75	3	11.59	4.32	44.93	0.87
CAZJK 37	43	73	3	10.21	4.62	43.58	1.11
CAZJK 40	46	79	3	10.41	4.97	31.24	0.87
CAZJK 44	51	82	3	10.36	4.40	33.33	0.98
CAZJK 50	45	78	4	9.95	5.32	44.14	1.15
CAZJK 13-2	48	80	3	8.77	4.60	43.46	1.14
S.Em+	1.03	0.55	0.23	0.28	0.14	2.46	0.07
CD(5%)	2.93	1.58	0.64	0.81	0.39	7.00	0.20
CV	5.24	1.69	15.97	6.83	6.76	13.97	14.91
GM	48.07	80.00	3.47	10.16	4.91	43.06	1.13

Table-2 *Pooled Analysis of variance over the environments*

Source	d.f	Days to first fruit setting	Days to Maturity	No. of fruits per plant	Fruit Diameter (cm)	100 - Seed Weight (g)	Fruit Yield (q/ha)	Seed Yield (q/ha)
Env.	1	0.68	14.22**	6.47**	0.68	0.16	599.56**	0.1
Geno.	11	83.47**	96.48**	3.72**	4.59**	1.28**	690.76**	0.42**
Repl./Env.	4	9.39	0.32	0.31	0.24	0.19	16.22	0.01
Geno. x Env.	11	5.38	11.31**	1.21**	1.86**	0.19	140.51**	0.14**
Error	44	6.34	1.83	0.31	0.48	0.11	36.17	0.03

Table-3 *Intra (Diagonal) and inter cluster (Below diagonal) distance among Kalingda germplasm*

	Cluster 1	Cluster 2	Cluster 3	Cluster 4
Cluster 1	6			
Cluster 2	9.51	0		
Cluster 3	9.94	7.45	5.76	
Cluster 4	10.47	8.32	14.16	0

Table-4 *Cluster mean values of various quantitative traits in Kalingda genotypes*

	Days to first fruit setting	Days to Maturity	No. of fruits per plant	Fruit Diameter (cm)	100 - Seed Weight (g)	Fruit Yield (q/ha)	Seed Yield (q/ha)
Cluster 1	49.4	81.56	3.36	9.72	4.84	37.71	1.04
Cluster 2	43	76.67	3.83	11.44	5.3	62.47	1.45
Cluster 3	43.92	74.08	2.95	10.9	4.47	44.26	0.99
Cluster 4	50.83	82.67	4.97	10.89	5.99	64.14	1.8

Table-5 *Distribution of 12 kalingda genotypes into various clusters*

Cluster Number	Number of genotypes	Genotypes
Cluster I	8	CAZJK 15, CAZJK 24, CAZJK 29, CAZJK 32, CAZJK 40, CAZJK 44, CAZJK 50, CAZJK 13-2
Cluster II	1	CAZJK 12
Cluster III	2	CAZJK 36, CAZJK 37
Cluster IV	1	CAZJK 27

Table-6 *Contribution of various traits towards genetic divergence in kalingda genotypes*

Source	Times Ranked 1st	Contribution %
Days to first fruit setting	2	3.03%
Days to Maturity	27	40.91%
No. of fruits per plant	6	9.09%
Fruit Diameter (cm)	4	6.06%
100 - Seed Weight (g)	5	7.58%
Fruit Yield (q/ha)	19	28.79%
Seed Yield (q/ha)	3	4.55%

Table-7 *Promising genotypes identified for seed yield and related traits on the basis of cluster mean and distance*

Genotypes	Cluster	Seed Yield (q/ha)	100 seed weight (g)	Fruit Yield (q/ha)	No. of fruits per plant	Fruit Diameter (cm)	Days to first fruit setting	Days to maturity
CAZJK 27	IV	1.80	5.99	64.14	4.97	10.89	51.00	83.00
CAZJK 12	II	1.45	5.30	62.47	3.83	11.44	43.00	77.00
CAZJK 24	I	1.23	4.82	42.87	4.89	10.21	48.00	80.00
CAZJK 50	I	1.15	5.32	44.14	3.69	9.95	45.00	78.00
CAZJK 13-2	I	1.14	4.60	43.46	2.89	8.77	48.00	80.00
CAZJK 37	III	1.11	4.62	43.58	2.78	10.21	43.00	73.00

Significant mean squares of G×E interactions for all the traits except days to first fruit setting and 100 seed weight revealed the difference in performance of each genotype in different environments. These results are collaborative with the findings of Venugopalan and Pitchaimuthu [9] in watermelon.

Mahalnobis D^2 statistic is an important tool for identifying genetically diverse parents for taking advantage in hybridization program [10]. In the present investigation, 12 genotypes were grouped into four clusters based on D^2 values using Tocher's method [Table-3] and [Fig-1].
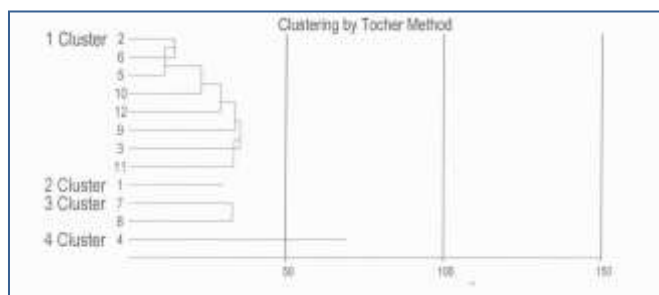
Fig-1 Dendrogram representing various clusters formed by Euclidean D^2 distance

Among the clusters, maximum number of genotypes *i.e.*, eight gathered in cluster I while two genotypes tumbled in to the cluster III. Cluster II and IV, each consisted only one genotype [Table-5] and [Fig-1]. Splitting of genotypes into various clusters illustrated the existence of genotypic and phenotypic variations. These finding are in line with the results of Yadav *et al.* [11] and Punitha *et al.*, [12]. Each cluster comprise distinct feature for different traits under study. Examination of cluster mean values [Table-4] for various traits across the clusters depicted that cluster IV had maximum mean values for no. of fruits per plant (4.97), 100 seed weight (5.99 g) and seed yield (1.80 q) while cluster II for fruit diameter (18.75). The minimum mean value for days to first fruit setting was also observed in cluster II (43 days) while for days to maturity in cluster III (74.08 days). Clusters I did not show higher or lower (as per desirability) mean values for any of the trait however it was consisting maximum number of genotypes. This cluster had 67 per cent of the total germplasm evaluated and genotypes represented in this cluster may not be rewarding for hybridization programme [13].

The highest inter cluster distance was recorded in cluster III and IV (14.16) followed by cluster I and IV while cluster I exhibited highest intra cluster distance (6.0) [Table-3] and [Fig-1]. Higher inter and intra- cluster distance specifies higher genetic variability among genotypes, between and within clusters, respectively. On the contrary, minimum inter and intra-cluster distance (cluster II & IV) illustrates proximity among the genotypes of two clusters and within the cluster also. The genotypes of those clusters *viz.* CAZJK 36, CAZJK 37, CAZJK 27 which depicted high inter cluster distance are advantageous for obtaining transgressive segregants in a breeding programme. Traits like Days to maturity and Fruit yield (q/ha) come up with highest no. of fruits per plant and 100 seed weight contributed highest moderately while days to first fruit setting, fruit diameter and seed yield (q/ha) contributed less towards genetic divergence [Table-6]. High genetic diversity for any of the trait always produces vast opportunities for making use of its economic and nutritional potentials.

Conclusion

The favorable outcome of any breeding programme largely depends on the degree of divergence among the parents selected and it contribute in expoiting highly heterotic hybrids and generating variability for efficient selection of advantageous recombinants. Therefore, the utilization of genotypes from dissimilar clusters for giving rise to transgressive segregants will manifest to be very beneficial for amelioration in seed yield of this crop. On the basis of cluster mean and distance, six promising genotypes were picked out [Table-7] that could be utilize in hybridization programme for improving seed yield in kalingda. Cluster I contributed three genotypes while rest of the three genotypes were advanced from different clusters possessing higher seed yield coupled with high 100 seed weight and hence can be used as a parent in breeding programme.

Application of research: The understanding of genetic diversity in crop like kalingda will necessarily empower a breeder to choose from various traits and genetically divergent parents which may throw advantageous transgressive segregants in upcoming generations.

Research Category: Crop Improvement

Abbreviations: g-Gram, cm-Centimetre, q-Quintal, ha-Hectare, q/ha-Quintal/hectare, G X E- Genotype X Environment, d.f.-Degree of Freedom

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Study area / Sample Collection: ARS, Mandor and ARSS Nagour

Cultivar / Variety / Breed name: Kalingda [*Citrullus lanatus* (Thunb.) Matsum & Nakai]

Conflict of Interest: None declared

Ethical approval: This article does not contain any studies with human participants or animals performed by any of the authors.
Ethical Committee Approval Number: Nil

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