Estimation of Genetic Diversity in Ridge Gourd Hybrid (*Luffa acutangula* L.)

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ABSTRACT: This study, conducted at Pandit Jawaharlal Nehru College of Agriculture and Research Institute, Karaikal, U.T. of Puducherry, during the rabi season of 2021–2022, aimed to assess the genetic divergence among 18 ridge gourd hybrids. Employing a randomized block design with two replications, 18 traits were evaluated to understand the genetic makeup of the hybrids. Clustering analysis revealed eight distinct clusters, with varying numbers of hybrids in each. Cluster II displayed the highest diversity with five hybrids, followed by cluster VI with three. The average intra-cluster distances ranged from 349.996 to 486.754, indicating varying degrees of diversity among clusters. Fruit yield per plant (91.50 percent) was the most influential trait contributing to genetic divergence, followed by total soluble solids (3.27 percent), number of fruits per vine (2.61 percent), individual fruit weight (1.96 percent), and vitamin C content (0.65 percent). Notably, hybrids Deepika from cluster VIII, SW 1212 from cluster VI, and Vinayak F$_1$ from cluster VI demonstrated superior characteristics, offering potential for future crop improvement endeavours. This research provides valuable insights into optimizing ridge gourd hybrids for enhanced agricultural outcomes.

Keywords: Clusters genetic divergence, ridge gourd, D^2 analysis, cluster analysis.

INTRODUCTION

Cucurbitaceous vegetables are fundamental components of our diets, with ridge gourd (*Luffa acutangula* (L.) Roxb.) holding a prominent place in the Cucurbitaceae family. This versatile vegetable, also known as angled gourd, Chinese okra, and ribbed gourd, thrives in diverse agro-ecosystems, including riverbed areas and cultivated lands. It belongs to the Cucurbitaceae family and is characterized by a chromosome count of 2n = 2x = 26. The plant's growth pattern can be climbing or trailing, and it is typically cultivated during the spring-summer and rainy seasons throughout India. The genus name, *Luffa*, originates from the widely used product 'loofah,' which serves as a material for bathing sponges, scrubber pads, and even doormats. Moreover, mature fruits of ridge gourd find natural application as cleaning sponges. Ridge gourd is further distinguished by the presence of 'luffein,' a gelatinous compound with medicinal significance. Rich in essential nutrients like Vitamin A, C, and iron, it is recommended for individuals enduring malaria and seasonal fevers due to its ease of digestibility and appealing taste (Yawalkar, 1985; Gautam *et al*., 2017).

For successful crop improvement programs, a precise assessment of genetic diversity within a population is imperative. Selection strategies based on genetic diversity have proven their effectiveness in a wide array of crop species (Ananda and Rawat 1984; Manoj *et al*., 2018). Cluster analysis emerges as a pivotal tool for gauging genetic diversity, enabling the visual representation of relative genetic distinctions among hybrid collections spanning diverse crop species. Despite the documented diversity in ridge gourd across India, its commercial exploitation in coastal ecosystems remains limited, primarily attributed to the dearth of suitable hybrids. Hence, this study sets out to categorize a selection of ridge gourd hybrids that are well-suited for cultivation in the coastal region of Karaikal. In summary, ridge gourd stands as a versatile and valuable member of the Cucurbitaceae family, finding application in various agro-ecosystems and industries. Its rich nutritional profile and ease of cultivation make it a valuable addition to dietary practices, especially in

regions prone to seasonal fevers. However, unlocking its full potential requires a deeper understanding of its genetic diversity, a gap that this study aims to address by categorizing suitable hybrids for coastal cultivation.

MATERIALS AND METHODS

The experimental materials consisted of 18 ridge gourd hybrids, with Ridge Gourd COH-1 serving as the designated commercial check hybrid (Table 1). These experimental materials were cultivated following a Randomized Block Design (RBD) with two replications. The experimental soil was identified as clay loam, exhibiting medium fertility, and slightly alkaline soil reaction (pH 8.01). Within each replication, a total of five plants were randomly selected and individually tagged for recording observations pertaining to growth, yield, and quality parameters. The seeds, procured from various sources, were sown with a spacing of 2 meters between rows and 2.0 meters between individual plants. Standard horticultural practices and uniform plant protection measures were consistently applied. Analysis of variance was conducted in accordance with the methodology proposed by Panse and Sukhatme (1967). Genetic divergence was assessed employing the D^2 statistics devised by Mahalanobis (1936), and genotypes were clustered using Tocher's method as outlined by Rao (1952). The percentage contribution of specific traits towards genetic divergence was computed following the guidelines set forth by Singh and Chaudhary (2005). For the purpose of analysis of variance and the estimation of D^2 values, as well as for cluster formation, the GENRES Statistical Software Package (GENRES, 2) was utilized.

RESULTS AND DISCUSSION

The analysis of variance uncovered significant differences among all the characters examined, underscoring the genetic diversity among the experimental materials. The D^2 values spanned a range from 0.00 to 236929.00, indicating a substantial degree of divergence among the ridge gourd hybrids. By considering the relative magnitude of these D^2 values, the 18 hybrids were grouped into eight clusters. This clustering approach was based on the assumption that hybrids within the same cluster would exhibit smaller differences in D^2 values among themselves compared to those hybrids belonging to different clusters.

Grouping of hybrids into different clusters (D^2 analysis): The process of grouping the hybrids into different clusters based on genetic distance, as determined through D^2 analysis, resulted in the formation of eight distinct clusters (Table 2). Cluster II emerged as the largest cluster, comprising a total of five hybrids, while cluster VI followed closely with three hybrids. Clusters I, III, IV, and V each contained two hybrids. Interestingly, both cluster VII and cluster VIII consisted of a single hybrid, indicating that these clusters encompass the most genetically diverse hybrids among the studied group.

Average intra and inter cluster distances: The calculation of average intra and inter-cluster distances among the eight clusters provided valuable insights into the genetic relationships within and between these clusters (Table 3). Notably, cluster VI exhibited the highest average intra-cluster distance (486.754), closely followed by cluster II (349.996). These findings suggest that clusters VI and II encompass hybrids with greater genetic diversity, indicating a wider range of genetic differences among the hybrids within these clusters. Conversely, clusters VII and VIII displayed the lowest intra-cluster D^2 values, signifying a closer genetic relationship among the genotypes within these clusters. This observation implies that hybrids within clusters VII and VIII share more genetic similarities. When examining inter-cluster distances, clusters III and V exhibited the lowest value (116.367), indicating a relatively close genetic relationship between the hybrids in these clusters.

This proximity suggests that these clusters may yield hybrids with limited genetic diversity during crop improvement efforts. In contrast, the greatest genetic divergence was observed between clusters VII and VIII, with a maximum inter-cluster distance of 814.644. Cluster VI and VII followed closely with a substantial inter-cluster distance of 807.418. These findings emphasize the substantial genetic differences between hybrids from clusters VII and VIII and, to a slightly lesser extent, between clusters VI and VII.

Cluster means of characters: The calculation of average intra and inter-cluster distances among the eight clusters provided valuable insights into the genetic relationships within and between these clusters (Table 3). Notably, cluster VI exhibited the highest average intra-cluster distance (486.754), closely followed by cluster II (349.996). These findings suggest that clusters VI and II encompass hybrids with greater genetic diversity, indicating a wider range of genetic differences among the hybrids within these clusters. Conversely, clusters VII and VIII displayed the lowest intra-cluster D^2 values, signifying a closer genetic relationship among the genotypes within these clusters. This observation implies that hybrids within clusters VII and VIII share more genetic similarities. When examining inter-cluster distances, clusters III and V exhibited the lowest value (116.367), indicating a relatively close genetic relationship between the hybrids in these clusters. This proximity suggests that these clusters may yield hybrids with limited genetic diversity during crop improvement efforts. In contrast, the greatest genetic divergence was observed between clusters VII and VIII, with a maximum inter-cluster distance of 814.644. Cluster VI and VII followed closely with a substantial inter-cluster distance of 807.418. These findings emphasize the substantial genetic differences between hybrids from clusters VII and VIII and, to a slightly lesser extent, between clusters VI and VII.

Relative contribution of different characters towards divergence: The analysis of the contribution of different traits to genetic divergence, as shown in

Table 5 and Fig. 2, highlighted some key findings. Notably, the traitfruit yield per plant made the most significant contribution to genetic divergence, accounting for a substantial 91.50 percent of the total divergence. Following closely were total soluble solids at 3.27 percent, number of fruits per vine at 2.61 percent, weight of individual fruit at 1.96 percent, and vitamin C at 0.65 percent. These findings underscore the pivotal role of fruit yield per plant in driving genetic diversity among the ridge gourd hybrids. Furthermore, the results suggest that hybrids from specific clusters exhibit traits that contribute significantly to genetic divergence. For instance, cluster V, characterized by higher values for total soluble solids, could be a valuable source for enhancing genetic diversity in this trait. Similarly, cluster VIII, known for a greater number of fruits per vine, and cluster VI, which demonstrates higher values for the weight of individual fruit, can be considered promising candidates for contributing to genetic diversity in these respective traits. It's worth noting that previous studies by Rabbani *et al*. (2012); Ramesh *et al*. (2018); Manoj *et al.* (2018) have also reported the presence of diversity in ridge gourd, further emphasizing the importance of understanding and utilizing this genetic diversity for crop improvement and development.
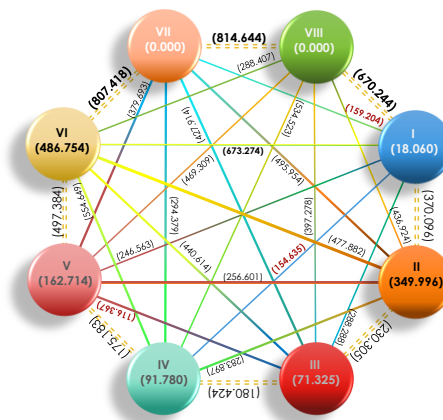

Fig. 1. Mean intra cluster and inter cluster distances (D values) in ridge gourd hybrids (not to scale)
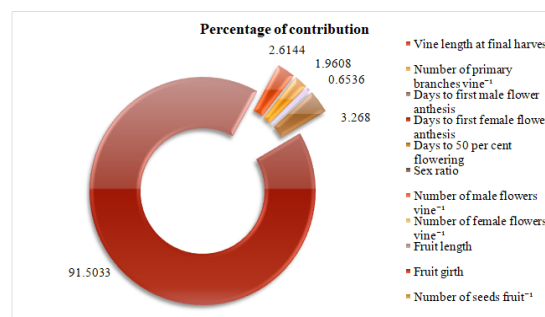

Fig. 2. Per cent contribution of different traits to the total divergence in 18 ridge gourd hybrids.

Table 1. Details of ridge gourd hybrids evaluated.

Sr. No.	Name of the Hybrids	Source
1.	Ridge Gourd COH-1	TNAU, Coimbatore
2.	KRH-1	KAU, COA, Vellayani, Kerala
3.	C-331	Clause Vegetable Seeds, Telangana
4.	Vinayak F_1	Clause Vegetable Seeds, Telangana
5.	Naavi F_1	East West Seed International, Aurangabad
6.	Naga F_1	East West Seed International, Aurangabad
7.	Kartik	Elite Seeds, Telangana
8.	KSP 1501 ANU	Kalash, Jalna
9.	Ratan	Know-You Seeds (India) Pvt. Ltd, Pune
10.	Mahy 7	Mahyco, Mumbai
11.	NS 3	Namdhari Seeds, Karnataka
12.	NS 474	Namdhari Seeds, Karnataka
13.	NBH-Raveena	Noble Seeds, Karnataka
14.	US6001	Nunhems, Telangana
15.	Durga	Saavi Seeds, Coimbatore
16.	Deepika	Sakata, Karnataka
17.	SW 1212	US Agriseeds, Telangana
18.	Rajni	VNR Seeds, Chhattisgarh

Table 2: Clustering pattern of ridge gourd hybrids.

Cluster number	Total number of hybrids	Hybrids	Source
I	2	NBH-Raveena (T$_{13}$)	Noble Seeds, Karnataka
		Rajni (T$_{18}$)	VNR Seeds, Chhattisgarh
II	5	Ridge Gourd COH-1 (T$_1$)	TNAU, Coimbatore
		KRH-1 (T$_2$)	KAU, COA, Vellayani, Kerala
		C-331 (T$_3$)	Clause Vegetable Seeds, Telangana
		Naavi F$_1$ (T$_5$)	East West Seed International, Aurangabad
		NS 3 (T$_{11}$)	Namdhari Seeds, Karnataka
III	2	KSP 1501 ANU (T$_8$)	Kalash, Jalna
		Mahy 7 (T$_{10}$)	Mahyco, Mumbai
IV	2	Kartik (T$_7$)	Elite Seeds, Telangana
		NS 474 (T$_{12}$)	Namdhari Seeds, Karnataka
V	2	Naga F$_1$ (T$_6$)	East West Seed International, Aurangabad
		Durga (T$_{15}$)	Saavi Seeds, Coimbatore
VI	3	Vinayak F$_1$ (T$_4$)	Clause Vegetable Seeds, Telangana
		US6001 (T$_{14}$)	Nunhems, Telangana
		SW 1212 (T$_{17}$)	US Agriseeds, Telangana
VII	1	Ratan (T$_9$)	Know-You Seeds (India) Pvt. Ltd, Pune
VIII	1	Deepika (T$_{16}$)	Sakata, Karnataka

Table 3: Mean intra cluster (diagonal) and inter cluster D^2 and D values.

	I	II	III	IV	V	VI	VII	VIII
I	**326.154 (18.060)**	136970.719 (370.096)	83109.930 (288.288)	23911.941 (154.635)	60793.250 (246.563)	453297.875 (673.274)	25345.854 (159.204)	15603.22 (670.244)
II		**122497.273 (349.996)**	53040.199 (230.305)	80597.539 (283.897)	65844.172 (256.601)	228370.844 (477.882)	245969.906 (495.954)	19061.98 (436.924)
III			**5087.266 (71.325)**	32552.820 (180.424)	13541.326 (116.367)	194140.391 (440.614)	183109.969 (427.914)	5713.75 (397.278)
IV				**8423.646 (91.780)**	30688.941 (175.183)	307635.875 (554.649)	86659.070 (294.379)	97318.56 (534.523)
V					**26475.729 (162.714)**	247391.203 (497.384)	144166.469 (379.693)	15230.12 (469.309)
VI						**236929.000 (486.754)**	651924.500 (807.418)	31761.67 (288.407)
VII							**0.000 (0.000)**	143.375 (814.644)
VIII								**0.00 (0.000)**

Values in parenthesis indicate 'D' values;　　　Bold diagonal values indicate intra cluster values

Table 4: Cluster mean for biometric characters of ridge gourd hybrids.

Sr. No.	Characters	I	II	III	IV	V	VI	VII	VIII
1.	Vine length at final harvest	395.000	418.000	412.500	472.000	412.000	508.000	290.000	**528.000**
2.	Number of primary branches vine^{-1}	4.975	5.230	6.075	6.100	5.225	5.867	5.000	**6.800**
3.	Days to first male flower anthesis	43.650	41.000	43.615	40.610	40.950	43.243	**46.510**	41.300
4.	Days to first female flower anthesis	43.250	43.940	44.950	41.700	40.388	42.225	**46.500**	39.300
5.	Days to 50 per cent flowering	43.500	43.900	43.750	41.750	41.750	41.500	**44.500**	39.000
6.	Sex ratio	14.990	21.981	8.290	17.823	10.405	17.870	4.040	15.895
7.	Number of male flowers vine^{-1}	227.100	283.830	141.400	286.000	220.200	361.667	135.000	357.800
8.	Number of female flowers vine^{-1}	15.300	17.656	17.500	18.175	15.050	25.152	10.000	**27.950**
9.	Fruit length	37.850	44.300	48.400	37.700	42.500	**54.933**	36.200	50.500
10.	Fruit girth	15.600	18.820	17.950	14.250	**19.800**	18.033	14.200	18.900
11.	Number of seeds fruit^{-1}	86.000	108.740	118.500	71.150	123.450	111.333	61.800	**135.900**
12.	100 seed weight	11.692	14.633	**16.700**	13.572	15.270	14.435	14.610	15.285
13.	Number of fruits vine^{-1}	11.700	12.190	12.150	9.663	8.050	14.300	4.900	**20.000**
14.	Weight of individual fruit	248.100	370.230	381.650	228.950	421.650	**449.700**	214.600	429.700
15.	Vitamin C	8.845	11.291	7.820	**11.923**	8.332	10.513	8.720	9.745
16.	Crude protein	0.690	1.096	0.935	0.645	0.720	0.723	**1.470**	0.630
17.	Total soluble solids	1.325	1.660	1.625	1.925	**2.000**	1.750	1.100	1.400
18.	Fruit yield vine^{-1}	3.275	4.818	4.667	2.507	3.858	6.993	1.455	**8.240**

Highest mean value = Bold; Lowest mean value – Underline

Table 5: Relative contribution of different characters to genetic diversity in ridge gourd hybrids.

Sr. No.	Characters	Number of first rank	Percentage of contribution
1.	Vine length at final harvest	0	0
2.	Number of primary branches vine^{-1}	0	0
3.	Days to first male flower anthesis	0	0
4.	Days to first female flower anthesis	0	0
5.	Days to 50 per cent flowering	0	0
6.	Sex ratio	0	0
7.	Number of male flowers vine^{-1}	0	0
8.	Number of female flowers vine^{-1}	0	0
9.	Fruit length	0	0
10.	Fruit girth	0	0
11.	Number of seeds fruit^{-1}	0	0
12.	100 seed weight	0	0
13.	Number of fruits vine^{-1}	4	2.6144
14.	Weight of individual fruit	3	1.9608
15.	Vitamin C	1	0.6536
16.	Crude protein	0	0
17.	Total soluble solids	5	3.268
18.	Fruit yield vine^{-1}	140	91.5033
	Total	**153**	**100**

CONCLUSIONS

The genetic divergence analysis conducted in this study unveiled a significant presence of genetic diversity among the 18 ridge gourd hybrids, resulting in their classification into eight distinct clusters. Cluster II emerged as the largest cluster, comprising five hybrids, followed by cluster VI, which encompassed three hybrids. Clusters I, III, IV, and V were composed of two hybrids each. Intriguingly, clusters VII and VIII were found to be mono-genotypic, indicating that they harbor the most diverse hybrids. Notably, the greatest diversity was observed between cluster VII and VIII, as reflected by the maximum inter-cluster distance. Cluster VIII exhibited higher cluster values for crucial parameters like fruit yield per vine, vine length at final harvest, number of primary branches per vine, number of female flowers per vine, number of seeds per fruit, and number of fruits per vine. Additionally, these hybrids displayed early traits, such as early female flower anthesis and fewer days to reach 50 percent flowering. Among the 18 traits investigated, fruit yield per vine demonstrated the highest contribution towards genetic diversity, followed by total soluble solids and number of fruits per vine. The application of hierarchical clustering through agglomerative cluster analysis effectively grouped the 18 hybrids into eight clusters. Notably, this analysis revealed no discernible correlation between geographical and genetic diversity within the population. Hybrids from different geographic locations were clustered together, emphasizing the need for genetic assessment beyond geographical parameters. Furthermore, the hybrids Deepika from cluster VIII, SW 1212, and Vinayak F_1 from cluster VI exhibited superior characteristics. These hybrids hold promising potential for future crop development programs, given their substantial contributions to genetic diversity and notable individual performance. This study provides invaluable insights into the genetic diversity of ridge gourd hybrids, offering a foundation for prospective endeavours in crop improvement.

FUTURE SCOPE

This study lays the foundation for further research in ridge gourd breeding programs, focusing on developing hybrids with enhanced yield and early flowering characteristics. Additionally, exploring the genetic basis of traits contributing to genetic diversity could lead to targeted breeding strategies.

Conflict of Interest. None.

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