Genetic variability studies in F_2 *populations of ridge gourd [Luffa acutangula L. (Roxb.)] for growth, yield and quality traits*

ABSTRACT

An experiment was conducted to study genetic variability in ridge gourd during mention season 2024 at ~~college~~ College of ~~horticulture~~ Horticulture Bagalkot. The observations were recorded on various growth, yield and quality contributing characters *viz*., population-I (Arka Prasan x Sirsi Local-2) and population- II (Jaipur Long x KLR-5). The analysis of variance indicated the prevalence of sufficient genetic variation among the genotypes from all the characters studied. The high phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were observed for node at first male flower appears, node at first female appears, TSS and crude fibre in population-I. Whereas, the traits like vine length, number of primary branches per vine, average fruit weight, fruit yield per vine and crude fibre in population-II. High heritability coupled with high genetic advance were observed for node at first male flower appears, node at first female flower appears, fruit length, fruit diameter, average fruit weight, fruit yield per vine, number of fruits per vine, number of seeds per fruit, fruit tenderness, TSS, crude fibre and vitamin C in the both F_2 populations indicating these characters are governed by additive gene action. Hence, direct selection may be followed for the improvement of ridge gourd for these characters.

Keywords: Ridge gourd, variability, heritability and genetic advance

1. INTRODUCTION

Ridge gourd *Luffa acutangula* L. (Roxb.)~~-~~, with a diploid chromosome number of 2n=2x=26, belongs to the Cucurbitaceae family and is an important vegetable crop cultivated in tropical and subtropical regions worldwide (Bose and Som, 1986) [4]. Various genotypes and cultivars of ridge gourd are grown across different areas of the country, each exhibiting diverse characteristics. This variability among genotypes can result from geographical differences or natural cross-pollination. A thorough understanding of the existing genetic variability in a crop is crucial before initiating any breeding program mention suitable reference. The phenotypic traits of plants are primarily influenced by their genetic makeup and the environmental conditions they encounter, as well as the interaction between genotypes and the environment. Plant genotype is determined by both heritable and non-heritable factors, making it essential to differentiate observed phenotypic variability into heritable and non-heritable components. In crop improvement, the genetic variation is important as this component is transmitted from one generation to another generation. The effectiveness of selection for any trait depends not only on the amount of phenotypic and genotypic variability, but also on the magnitude of heritability. The magnitude of heritability indicates the effectiveness with which selection of genotypes can be made based on phenotypic performance (Johnson *et al*., 1955) [10].

2. MATERIAL AND METHODS

The experiment was carried out at College of Horticulture, University of Horticultural Sciences, Bagalkot, Karnataka, during rabi season (months) of 2024 in augmented design by using F_2 generation of two crosses *viz*., population-I (Arka Prasan x Sirsi Local-2), population-II (Jaipur Long x KLR-5) and parents. Mention geographical location of experimental farm The crop received timely management practices as per recommended package of practices (Anon, 2022) [2]. The crop was maintained properly till last harvest and observations on growth as well as yield contributing characters was noted on F_2 progenies along with parents. From each cross 200 plants were studied and taken data from all the plants. Genotypic and phenotypic coefficient of variation were calculated as per the formula suggested by Burton and vane (1953) [5]. Heritability and expected genetic advance were calculated as per formula given by Johnson *et al*., 1955 [10].

The observations on vine length at harvest time (m), the number of primary branches at 45 DAP, days to first male flowering, days to first female flowering, the node of first female flowering, the node of first male flowering, sex ratio (male to female), days to first harvest and days to last harvest, number of fruits per vine, fruit length (cm), fruit weight (g), fruit diameter (mm), fruit yield per vine (kg), number of seeds per fruit, fruit tenderness (N), TSS (^{0}Brix), crude fibre(%) and vitamin C (mg/ 100 g) were recorded in both populations on individual plant.

Write procedure to record fruit tenderness and its unit

3. RESULTS AND DISCUSSION

Also mention the mean data of Parents and F1 for all the 21 traits in Tabular form

The results in the current study showed that the phenotypic coefficient of variation (PCV) values are higher than the genotypic coefficient of variation (GCV), suggesting that environmental factors have a significant impact on the performance of the F_2 population. The findings related to genetic variability, heritability and genetic advance for various traits are discussed in this study are presented in Table 1 and Table 2. Higher estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for node at first male flower appearance, node at first female appearance, TSS and crude fibre were found in population-I. Whereas, the traits like vine length, number of primary branches per vine, average fruit weight, fruit yield per vine and crude fibre were observed in population-II. The existence of a broad genetic base within the population is shown by high GCV and PCV values with small differences. This suggests consistent genotype expression for these traits, allowing for the potential for these qualities to be improved through simple selection. The similar results were also observed by Choudhary and Kumar (2011) [6], Saklesh (2016) [17], Bhargava *et al.* (2017) [3] in ridge gourd.

Moderate amount of GCV and PCV were observed for the traits like vine length, fruit length, fruit diameter, average fruit weight, number of fruits per vine, number of seeds per fruit, fruit tenderness and vitamin C in population-I. In population -II it was observed for traits like node at first female flower appearance, node at first male flower appearance, fruit diameter, number of fruits per plant, number of seeds per plant, fruit tenderness and vitamin C. As this character had moderate PCV and GCV representing that the trait is controlled by both additive and non-additive gene actions. Hence, recurrent selection can be practiced for improvement. These observations are in line with the findings of Varalakshmi *et al.* (2015) [23], Singh *et al.* (2020) [18] and Panda *et al*. (2022) [16] in ridge gourd.

Moderate GCV coupled with high PCV was observed for number of primary branches per vine and fruit yield per vine in population-I and for the traits like fruit length and TSS it was observed in population-II. Hence, the presence of moderate GCV and high PCV for a trait in a genetic study could indicate diverse underlying genetic factors like polygenic inheritance, epistasis, presence of genetic mutations or allelic variations, *etc*. contributing to the observed variability. These results are in accordance with Dubey *et al.* (2013) [7] and Tiwari *et al.* (2018) [22], Choudhary *et al*. (2011) [6], Koppad *et al*. (2015) [12] and Panda *et al*. (2022) [16].

Lower GCV and moderate PCV was observed for number of male flowers, number of female flowers and sex ratio in population-I and for the traits like number of male flowers and number of female flowers it was observed in population-II, which indicates the presence of moderate amount of variability for these traits and little influence of environment on these traits. These observations are in line with the findings of Manoj *et al.* (2018) [14], Harshitha *et al*. (2019) [9] and Thulasiram *et al.* (2022) [21].

Low magnitude of GCV and PCV were recorded for days to first male flower, days to first female flower, days to first fruit harvest and days to last fruit harvest in population-I. In population-II it was observed for days to first male flower, days to first female flower, days to first fruit harvest, days to last fruit harvest and sex ratio. In accordance with Choudhary *et al.* (2011) [6], Koppad *et al.* (2015) [12], Singh *et al*. (2017) [19], Manoj *et al.* (2018) [14], Methela *et al.* (2019) [15], Harshitha *et al.* (2019) [9], Kannan *et al*. (2019) [11], Akhila and Singh (2020) [1], Sravani *et al.* (2021) [20], Durga *et al.* (2021) [8] and Thulasiram *et al.* (2022) [21]. This indicates the low variability for these parameters in the germplasm and preponderance of non-additive gene action. This offers very limited opportunity for improving these traits by selection. This suggests the narrow genetic base and hence the variability has to be generated for these characters through hybridization to recover transgressive segregants or through mutation breeding.

High estimates of heritability coupled with high values of GAM were observed for the characters *viz*., number of primary branches, node at first male flower appearance, node at first female flower appearance, fruit length, fruit diameter, average fruit weight, number of fruits per vine, fruit yield per vine, number of seeds per fruit, TSS, crude fibre, fruit tenderness and vitamin C in population-I. Whereas, the traits like vein length, number of primary branches, node at first male flower, node at first female flower appearance, fruit length, fruit diameter, average fruit weight, fruit yield per vine, number of fruits per vine, number of seeds per fruit, fruit tenderness, TSS, crude fibre and vitamin C in population-II. This indicates predominance of additive components for these traits and hence direct selection would be more effective in improving these traits. These results are accordance with matching conclusions were confirmed by Singh *et al*. (2017) [19], Choudhary *et al*. (2011) [6], Dubey *et al*. (2013) [7], Varalakshmi *et al*. (2015) [23], Harshitha *et al*. (2019) [9] and Thulasiram *et al*. (2022) [21].

High heritability coupled with moderate GAM were observed for the traits *viz*., vine length, days to first male flower, days to first female flower, days to last harvest and number of male flowers in population-I. Whereas, in population-II it was observed for days to first female flower appearance, days to first male flower appearance, number of male flowers, number of female flowers and sex ratio. This indicates predominance of additive components

Table 1. Genetic variability estimates for various traits in the F_2 generation of population-I (Arka Prasan x Sirsi Local-2)

Sl. No	Traits	Mean	Range	PCV (%)	GCV (%)	h^2bs (%)	GAM (%)
1	Vine length at harvest time (m)	3.48	1.82- 4.59	14.29	11.10	60.36	17.79
2	Number of primary branches per vine (45DAS)	3.01	1.00-5.00	22.01	18.63	71.68	32.50
3	Days to first female flower	39.40	36.00-49.00	6.66	5.81	76.03	10.45
4	Days to first male flower	35.66	32.00-46.00	7.77	7.28	87.70	14.06
5	Node at first male flower appearance	5.19	3.00-14.00	38.90	36.16	86.42	69.34
6	Node at first female flower appearance	9.20	5.00-19.00	25.08	23.49	87.72	45.39
7	Number of male flowers	523.38	346.00-656.00	11.51	9.96	74.88	17.77
8	Number of female flowers	21.97	14.00-28.00	11.38	7.49	43.30	10.17
9	Sex ratio (M: F)	23.96	18.78-34.63	11.05	8.24	55.69	12.69
10	Days to first fruit harvest	46.19	44.00-53.00	3.98	3.23	65.83	5.41
11	Days to last fruit harvest	105.81	78.00-125.00	8.25	6.83	68.56	11.67
12	Fruit length (cm)	27.76	15.00- 41.50	14.55	12.70	76.20	22.88
13	Fruit diameter (mm)	35.64	20.90-49.20	12.19	10.98	81.07	20.39
14	Average fruit weight (g)	163.84	78.00-250.70	18.72	16.87	81.23	31.37
15	Fruit yield per vine(kg)	2.31	0.96-3.40	22.73	19.72	75.21	35.27
16	Number of fruits per vine	14.13	6.00-20.00	16.09	13.39	69.22	22.98
17	Number of seeds per fruit	119.92	72.00-180.00	16.61	13.08	62.04	21.26
18	Fruit tenderness (N)	6.28	3.68-8.54	19.98	18.49	72.66	33.56
19	TSS (˚ B)	3.29	2.10-8.21	24.12	22.04	83.50	41.54
20	Crude fibre (%)	0.62	0.22-1.61	30.89	29.30	89.99	57.34
21	Vitamin- C (mg/100g)	10.65	0.28-13.74	12.01	11.47	91.21	22.60

GCV- Genotypic coefficient of variation
PCV- Phenotypic coefficient of variation
h^2bs- Heritability (Broad sense)
GAM- Genetic advance over mean
S. Em- Standard Error deviation from mean

Table 2. Genetic variability estimates for various traits in the F_2 generation of population-II (Jaipur Long x KLR-5)

Sl. No	Traits	Mean	Range	PCV (%)	GCV (%)	h^2bs (%)	GAM (%)
1	Vine length at harvest (m)	3.03	1.62- 4.33	22.83	21.38	87.69	41.30
2	Number of primary branches per vine (45DAS)	2.75	1.00- 5.00	37.64	36.39	93.42	72.55
3	Days to first female flower	40.01	37.00- 51.00	8.83	6.45	81.42	11.43
4	Days to first male flower	36.14	34.00-39.00	6.53	4.73	60.72	10.35
5	Node at first male flower appearance	5.78	4.00-9.00	19.12	17.48	77.17	32.79
6	Node at first female flower appearance	10.43	5.00-14.00	14.63	11.86	71.63	21.13
7	Number of male flowers	520.18	346.00-675.00	11.35	9.42	68.93	16.14
8	Number of female flowers	21.17	14.00-28.00	11.23	9.38	69.74	16.15
9	Sex ratio	24.70	19.23-31.00	9.99	8.90	79.46	16.38
10	Days to first fruit harvest	46.99	44.00-51.00	5.64	3.80	46.56	5.53
11	Days to last fruit harvest	106.97	85.00-120.00	9.35	7.27	51.34	10.79
12	Fruit length (cm)	25.24	12.78-38.90	20.11	19.47	93.76	38.90
13	Fruit diameter (cm)	36.56	21.29-55.30	17.70	17.19	94.24	34.42
14	Average fruit weight (g)	129.42	59.40-226.00	23.49	21.71	85.44	41.40
15	Fruit yield per vine(kg)	1.79	0.66-2.71	26.08	22.95	77.41	41.65
16	Number of fruits per vine	13.85	9.00-22.00	15.94	13.58	72.50	23.85
17	Number of seeds per fruit	105.49	61.00-186.00	17.40	13.44	60.66	21.42
18	Fruit tenderness (N)	6.12	3.45-9.20	15.70	12.79	66.37	21.50
19	TSS (˚ B)	3.21	1.90-5.40	20.59	16.75	66.18	28.11
20	Crude fibre (%)	0.48	0.09-1.23	38.40	36.87	92.18	33.03
21	Vitamin- C (mg/100g)	10.55	7.17-13.70	10.47	10.15	93.93	20.29

GCV- Genotypic coefficient of variation
PCV- Phenotypic coefficient of variation
h^2bs- Heritability (Broad sense)
GAM- Genetic advance over mean
S. Em- Standard Error deviation from mean

for these traits and hence direct selection would be more effective in improving these traits. These results are accordance with findings of Manoj *et al*. (2018) [14], Kannan *et al*. (2019) [11], Akhila and Singh (2020) [1] and Thulasiram *et al*. (2022) [21].

Moderate heritability and GAM were observed for number of female flowers and sex ratio in population-I. Whereas, the trait days to last harvest in population-II, which indicated limited scope for improvement of these characters through direct selection. These results are accordance with Harshitha *et al*. (2019) [9], Singh *et al*. (2017) [19] and Panda *et al*. (2022) [16]. High heritability coupled with low GAM were observed for days to first fruit harvest in population-I and population-II, which indicated the effect of the environment on the expression of particular traits. A high heritability with low genetic advance may also indicate non-additive gene action and selection for such trait not be effective. These results are accordance with Kumari *et al.* (2018) [13], Akhila and Singh (2020) [1] and Thulasiram *et al*. (2022) [21].

4. CONCLUSION

The analysis of F_2 data in both populations indicate the presence of good amount of genetic variation for most of characters. High GCV and PCV were observed for node at first male flower appears, node at first female appears, TSS and crude fibre in population-I. Whereas, the traits like vine length, number of primary branches per vine, average fruit weight, fruit yield per vine and crude fibre in population-II. High heritability coupled with high genetic advance as per cent over mean were observed for node at first male flower appears, node at first female flower appears, fruit length, fruit diameter, average fruit weight, fruit yield per vine, number of fruits per vine, number of seeds per fruit, fruit tenderness, TSS, crude fibre and vitamin C in the both F_2 populations. Additive inheritance is predominant in these characters. Thus there is ample scope for improvement of these characters through simple selection.

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