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Studies in F₂ generation for genetic variability, heritability, genetic advance in ridge gourd [*Luffa acutangula* (L.) Roxb]

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Abstract

The level of genetic diversity was assessed using various parameters such as the phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability, and the genetic advance as a percentage of the mean. This evaluation was conducted in the F_2 generation of two different crosses involving ridge gourd lines: IC-523886 × IC-523882, IC-523886 × IC-539714 during *rabi*, 2023 at the Horticultural Research Station located located in venkataramannagudem. Remarkable variability was detected in the high estimates of PCV and GCV across a range of attributes, such as the number of fruits per plant, fruit set percentage, fruit length, fruit weight, ascorbic acid content, the node number at which the first female flower appears, the node number at which the first male flower appears, fruit yield per vine, and fiber content. This indicates a substantial potential for selective breeding due to the wide variation observed in these characteristics. Furthermore, high heritability, along with a significant genetic advance as a percentage of the mean, was observed for all the traits except for internodal length, days to appearance of first male flower, days to first fruit harvest, fruit set percentage. This suggests the presence of additive gene action and indicates that selection for these traits can be effective, as they are less susceptible to environmental influences.

Keywords: Generation, heritability, genetic, GCV, Luffa acutangula

1. Introduction

Ridge gourd holds a significant status as a summer cucurbitaceous vegetable in India, with its primary centre of origin being subtropical Asia, particularly India. This plant is an annual creeper, typically displaying a climbing or trailing growth pattern. These plants are typically monoecious, but various other sex forms can also be found. The fruits of the ridge gourd feature ten to twelve distinct longitudinal ridges, which account for its common name, ridge gourd. Additionally, they possess anti-inflammatory and antibiotic properties, making them a recommended remedy for individuals suffering from malaria and other seasonal fevers. Luffaculin, a protein derived from ridge gourd seeds, demonstrates various biological activities, including abortifacient, antitumor, ribosome inactivating, and immunomodulatory effects.

Genetic diversity plays a crucial role in making meaningful selections. The cultivation of ridge gourd necessitates in-depth genetic research to bring about significant enhancements in both crop yield and quality. There exists a substantial potential for the development of superior varieties with specific attributes, including a high female-to-male flower ratio, early fruiting, desired consumer size, shape, colour, increased yield, and prolonged shelf life. To effectively harness this genetic potential within breeding programs, it is imperative to possess a prior understanding of how yield and quality traits are inherited. Consequently, in order to introduce these desirable traits, the F₂ progenies were subjected to assessments for variability (GCV, PCV), heritability, and genetic advancement to be utilized in crop improvement initiatives. While GCV and PCV provide insights into the overall variability within the population, they alone cannot indicate the heritability of these traits, which is elucidated through heritability studies. Genetic advancement offers valuable information regarding the genetic mechanisms at play. When combined with heritability, genetic advancement aids in predicting the genetic enhancements achievable through the process of selection.

2. Materials and Methods

The study was conducted during the rabi season of 2023 at the Horticultural Research Station in Venkataramannagudem, West Godavari District, Andhra Pradesh. Its primary objective was to evaluate the genetic variability within the F₂ generation of two ridge gourd crosses, specifically Cross-1 (IC-523886 \times IC-523882) and Cross-2 (IC-523886 \times IC-539714). The plants were grown with a spacing of 1.25 meters by 0.75 meters, and a total of 60 plants were examined for each cross. The experimental design employed was the Randomized Block Design (RBD) with three replications. Data were collected on a range of growth and quality traits, including vine length (in centimeters), internodal length (in centimeters), the node number at which the first male and female flowers appeared, the number of days to the first appearance of male and female flowers, number of days to first fruit harvest, number of fruits per plant, number of fruits per cluster, fruit set percentage, fruit length (in centimeters), fruit diameter (in centimeters), peduncle length (in centimeters), fruit weight (in grams), fruit yield per vine (in kilograms), and estimated yield per hectare (in tons per hectare). Additionally, biochemical parameters, including ascorbic acid content (in milligrams per 100 grams) and fiber content (in grams per 100 grams), were analyzed. For statistical analysis, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) following Burton and Devane's method from 1952 were calculated. Heritability, based on Lush's approach from 1943, and genetic advance as a percentage of the mean (GAM), as recommended by Comstock and Robinson in 1952, were also determined to gain insights into the genetic variation present in the study.

3. Results and Discussion

The analysis of variance pertaining to the two crosses of ridge gourd within the F₂ generation is succinctly presented in Tables 1 and 2. Across all the studied populations, it was evident that the estimates of Phenotypic Coefficient of Variation (PCV) consistently surpassed those of Genotypic Coefficient of Variation (GCV). Nevertheless, the disparity between these metrics remained minimal, implying that the influence of environmental factors was relatively limited. Notably, the higher GCV and PCV values were consistently observed in traits such as the number of fruits per plant (for both crosses), fruit length (for both crosses), fruit weight (for both crosses), the node number at which the first female flower appears (for both crosses), fruit set percentage (for cross-1), fruit yield per vine (for cross-2), and fibre content (for cross-2). In the case of ascorbic acid content, cross-1 exhibited elevated GCV and PCV values, whereas cross-2 displayed moderate GCV and high PCV values. This indicates the presence of substantial variability, underscoring the considerable potential for further selection and improvement in the aforementioned traits to enhance crop quality. These findings align with the research findings of Vaidya *et al.* (2020) ^[16], Gautham and Balamohan (2018) ^[4], and Sravani *et al.* (2021) ^[14].

Characteristics such as the time it takes for the first female flower to appear (cross-1 and 2), the node number where the first male flower appears (cross-2), fruit diameter (cross-2), peduncle length (cross-2), fibre content (cross-2), estimated yield per hectare (cross-2), fruit yield per vine (cross-2), vine length (cross-4), and fruit set percentage (cross-4) displayed moderate values of Genetic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV). This suggests that there is room for improvement to some extent in these traits, as validated by Kanal *et al.* (2019) ^[6], Kannan *et al.* (2019) ^[8, 9], and Ingole *et al.* (2021) ^[5].

On the other hand, traits like vine length (cross-1), internodal length (cross-1 and 2), node number where the female flower appears (cross-2), days until the appearance of the first male flower (cross-1 and 2), days to first harvest (cross-1), and fruit diameter (cross-2) exhibited a narrow range of GCV and PCV. Similar findings were reported by Vijaykumar *et al.* (2020) ^[17] and Pradhan *et al.* (2021) ^[13], suggesting that further selection in these characteristics may not lead to significant improvements, thus limiting genetic enhancement efforts.

This study also found high heritability and a significant genetic advance as a percentage of the mean for various traits. These traits include the node number where the first male flower appears (cross-1), fruit diameter (cross-1), number of fruits per plant (cross-2), fruit yield per plant (cross-1), node number where the first female flower appears (cross-1 and 2), fruit weight (cross-1), fibre content (cross-1), days until the appearance of the first female flower (cross-1), fruit length (cross-1 and cross-2), peduncle length (cross-1), estimated vield per hectare (cross-1 and cross-2), and vine length (cross-2), as well as ascorbic acid (cross-2). These findings suggest that these traits are influenced by additive gene action in their inheritance, consistent with previous studies by Koppad et al. (2015)^[11], Karthick *et al.* (2017)^[10], Gautham and Balamohan (2018)^[4], Kanimozhi et al. (2015)^[7], and Durga et al. (2021) [3]

Lastly, traits like fruit weight (cross-2), ascorbic acid (cross-1), vine length (cross-1), internodal length (cross-1), node number where the first male flower appears (cross-1), days until the appearance of the first male flower (cross-1), and fruit set percentage (cross-1) displayed a combination of high heritability and moderate genetic advance as a percentage of the mean. These findings align with results reported by Kanimozhi *et al.* (2015) ^[7] and Sravani *et al.* (2021) ^[14], possibly indicating the development of homozygosity as a contributing factor.

Table 1: Assessments of GCV, PCV, heritability and GAM in F2 generation of cross-1 (IC-523886 × IC-523882)

Parameter	General mean	Coefficient of variation (%)		Uaritability (0/.)	Constis advance	CAM @ 5%
		GCV	PCV	rieritability (76)	Genetic auvance	GANI @ 576
Length of the vine (cm)	264.53	7.06	8.38	71.13	32.48	12.28
Internodal length (cm)	13.23	5.81	6.19	88.27	1.49	11.26
Node number at which first male flower appear	7.28	17.07	18.18	88.21	2.40	33.04
Node number at which first female flower appear	14.64	20.68	23.05	89.71	3.11	21.26
Days to appearance of first male flower	29.44	7.99	8.08	95.48	4.78	16.10
Days to appearance of first female flower	35.91	10.19	10.63	91.91	7.40	20.14
Days to first fruit harvest	49.65	5.70	7.39	59.53	4.50	9.06

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Number of fruits per plant	19.50	36.60	36.79	98.95	17.98	75.00
Fruit set percentage (%)	61.95	25.57	28.75	88.93	6.89	11.12
Fruit length (cm)	22.78	24.39	24.89	95.99	11.21	49.23
Fruit diameter (cm)	3.76	13.81	14.61	89.35	1.02	26.89
Peduncle length (cm)	5.35	15.83	17.78	79.29	1.55	29.05
Fruit weight (g)	170.64	25.44	29.33	75.26	77.60	45.48
Fruit yield per plant (kg)	4.09	17.02	18.68	83.02	1.30	31.95
Estimated yield (t/ha)	23.49	16.33	18.05	80.99	7.11	30.28
Fiber content (g 100g ⁻¹)	0.90	14.11	16.27	75.16	0.51	25.20
Ascorbic acid (mg 100g ⁻¹)	7.52	20.55	28.52	72.04	0.64	18.33

Parameter	General mean	Coefficient of variation (%)		Howitchility (0/)	Constin advance	CAM @ 59/
		GCV	PCV	Heritability (%)	Genetic advance	GAM @ 5%
Length of the vine (cm)	315.15	13.10	13.28	97.38	83.96	26.64
Internodal length (cm)	12.90	5.96	6.30	89.30	1.49	11.60
Node number at which first male flower appear	5.97	23.47	34.81	67.42	0.66	11.06
Node number at which first female flower appear	13.92	7.22	7.64	89.32	1.95	24.07
Days to appearance of first male flower	26.95	4.81	5.25	83.81	2.44	9.07
Days to appearance of first female flower	34.33	12.72	19.49	65.26	1.49	4.36
Days to first fruit harvest	48.63	4.15	4.66	79.23	3.70	7.62
Number of fruits per plant	23.10	29.81	29.99	98.80	14.10	61.04
Fruit set percentage (%)	63.20	13.62	14.27	91.20	16.94	26.81
Fruit length (cm)	25.04	20.73	21.22	95.41	10.44	41.71
Fruit diameter (cm)	4.92	4.90	14.27	11.81	0.17	3.47
Peduncle length (cm)	5.98	8.05	11.16	52.09	0.71	11.97
Fruit weight (g)	201.63	29.39	38.83	75.68	35.55	16.79
Fruit yield per plant (kg)	25.54	7.64	12.62	36.68	2.43	19.53
Estimated yield (t/ha)	4.56	22.71	24.04	81.96	1.08	23.71
Fibre content (g 100g ⁻¹)	0.70	25.24	53.51	22.24	0.17	24.52
Ascorbic acid (mg 100g ⁻¹)	7.93	19.92	23.85	69.73	1.00	34.27

Low heritability along with low GAM values were for fruit diameter (cross-2) reveals the occurrence of additive gene action. The results were similar to the findings Kannan and Rajamanickam (2019)^[8, 9] in ridge gourd.

4. Conclusion

Traits such as the node number where the first male flower appears, the number of fruits per plant, fruit length, fruit weight, fruit yield per vine, and ascorbic acid content displayed significant genetic variation coefficients (GCV) and phenotypic variation coefficients (PCV). These elevated GCV and PCV values imply a substantial degree of diversity within these traits. Additionally, the high heritability and significant genetic advance as a percentage of the mean (GAM) suggest that these characteristics are less influenced by environmental factors and are more influenced by additive genetic effects. Consequently, selecting individuals based on these traits is likely to produce favourable outcomes in subsequent generations.

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