



Research Article

GENETIC VARIABILITY STUDIES AND MULTIVARIATE ANALYSIS IN F₂ SEGREGATING POPULATIONS INVOLVING MEDICINAL RICE (*Oryza sativa* L.) CULTIVAR KAVUNI

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Abstract- In order to evaluate the relationship between morphological characters in rice cultivars, two populations at F₂ generation were examined. Statistical analysis on fifteen biometrical or quantitative characters were studied for estimating descriptive statistics, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), genetic advance and heritability (Broad sense). Maximum standard deviation for total number of spikelets per panicle and total number of filled grains per panicle were recorded for both the crosses. Highest PCV and GCV was observed for panicle exertion, total number of filled grains per panicle in ASD 16 x *Kavuni* (Cross I) and productive tiller in *Swarna Sub 1* x *Kavuni* (Cross II). Difference between GCV and PCV was low in most of the characters studied. High estimates of heritability and genetic advance were observed for flag leaf width for both the crosses. Both positive and negative skewness was observed for different traits, while platykurtic distribution was observed for most of the traits in F₂ populations of two crosses.

Keywords- Rice, Descriptive statistics, Genetic variability, Heritability, Genetic advance, Skewness and Kurtosis.

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Introduction

Rice is the major cereal crop of South and South East Asia where ninety percent of the world's rice is produced and consumed [8]. Landraces provides a vast source of genetic variability for the present day rice improvement programme. Landraces possess several undesirable agronomic traits including tall plant stature, long crop duration, photosensitivity, and poor response to fertilizer and nutrient application resulting in very low yield. Though domesticated, un-adapted landraces are phenotypically less desirable, diverse plant types are valuable for creating new varieties and this forms the basic wealth on which plant breeders can operate for re-modelling the existing genotypes [20]. Segregating populations are more important for improving plant types by operating further selection improvement. The present study was formulated to analyze the descriptive statistics and quantify the extent of genetic variation available for grain yield and yield components in the segregating generations of rice and to assess the genetic gain that can be made by selection when landraces are involved in the hybridization. The nature and magnitude of genetic variation governing the inheritance of quantitative characters like yield and its components is essential for effective genetic improvement. A critical analysis of genetic variability is a prerequisite for initiating any crop improvement programme and for adopting of appropriate selection techniques. Keeping in view the above perspectives, the present investigation was designed primarily, to study the segregating populations (F₂) of two crosses for descriptive statistics, the gene action through skewness, kurtosis and genetic variability parameters to identify useful segregates with high yield coupled with desirable agronomic traits.

Materials and Methods

The research study was conducted in experimental fields of Paddy Breeding Station of Tamil Nadu Agricultural University, Coimbatore, India. The experimental

material consisted of 200 F₂ progenies each in crosses ASD 16 x *Kavuni* (Cross I) and *Swarna Sub 1* x *Kavuni* (Cross II) which were evaluated for morphogenetic traits in *Kharif* 2015 with row length of 3m and spacing of 20 x 20 cm, following need based plant protection measures and recommended agronomic management. ASD 16 and *Swarna Sub 1* are cultivated popular varieties and *Kavuni*, a traditional landrace from Tamil Nadu known for its medicinal properties. The biometrical readings were recorded as per Standard Evaluation system (SES) for rice (SES, 1996). Fifteen plant growth parameters viz., days to 50% flowering, plant height, total number of tillers, total number of productive tillers, flag leaf length, flag leaf width, panicle length, panicle exertion, total number of spikelets per panicle, total filled grains per panicle, hundred grain weight, kernel length, kernel breadth, kernel length by breadth ratio and single plant yield were recorded. Descriptive statistics such as mean, range and genetic variability parameters PCV, GCV and heritability [15] were estimated using MS Excel program. The third order statistics skewness and kurtosis were estimated as per Snedecor and Cochran [22].

Results and Discussion

Interrelationship between yield and its components plays a vital role in providing information to breeder in selection process of populations with potential yield and its contributing traits. Diversity and genetic relationships are essential information in crop improvement programs and success of plant breeding programs relies heavily on the existence of genetic variability for particular trait [5]. In the present study, the relationship between yield performance and fourteen agronomic characters were analyzed in two hundred F₂ genotypes each derived from two crosses. The descriptive statistics results and variability parameters were given in [Table-1] and [Table-2].

Among the characters under study, a varied range was observed for total number of spikelets per panicle, 102 to 390 with a mean value of 192 and total number of filled grains per panicle, 95 to 350 having 170 as mean value and showing maximum standard deviation of 48.21 and 47.11 respectively, followed by plant height of 109.37 cm mean value with range variation of 109 with standard deviation of 12.81 in Cross I. In the cross II, maximum standard deviation was

observed for total number of spikelets per panicle (40.23) and total number of filled grains per panicle (38.14) subsequently with range varying from (103 to 331) and (85 to 303) respectively. Selection of the yield contributing characters simultaneously will improve the grain yield in subsequent segregation population [7].

Table-1 Estimation of descriptive statistics and variability parameters of F₂ population derived from ASD 16 x Kavuni (Cross I)

Parameters	DFF	PH(cm)	TNT	TNPT	FLL(cm)	FLW(cm)	PL	PE(cm)	TNS/P	TFG	HGW(g)	KL(mm)	KB(mm)	KL/B	SPY(g)
Mean	104.54	109.37	14.69	12.89	32.71	1.32	28.89	3.00	196.22	169.95	1.98	5.45	2.68	2.04	32.33
Minimum	101.00	57.00	8.00	7.00	23.00	1.10	22.60	2.00	102.00	95.00	1.00	4.30	2.20	1.59	10.00
Maximum	110.00	136.00	25.00	20.00	39.40	1.60	36.00	4.60	390.00	350.00	2.50	6.20	3.00	2.61	52.50
Range	9.00	79.00	17.00	13.00	16.40	0.50	13.40	2.60	288.00	255.00	1.50	1.90	0.80	1.02	42.50
SD	1.68	12.81	3.01	2.58	3.42	0.12	2.40	0.56	48.21	47.11	0.20	0.42	0.16	0.18	6.93
PCV	1.76	10.44	21.35	23.93	10.57	9.85	9.12	38.12	36.17	39.82	8.21	7.21	6.18	8.17	22.70
GCV	1.11	10.34	21.14	23.34	10.52	9.00	8.83	37.94	36.01	39.77	8.12	7.11	5.93	7.99	22.60
Heritability	39.77	98.05	98.07	95.14	99.13	83.50	93.85	99.07	99.16	99.74	97.76	97.40	92.36	95.63	99.13
GA	1.42	26.91	6.14	5.12	7.12	0.22	4.71	1.16	99.17	97.16	0.43	0.85	0.31	0.36	14.49
GA(%)	1.50	21.93	43.56	47.44	21.97	17.65	17.92	77.79	74.40	82.13	17.48	14.71	12.01	16.32	47.43
Skewness	0.99	-0.48	0.52	0.42	-0.26	0.38	0.01	-0.36	0.97	0.79	-1.30	-1.15	-0.79	-0.23	0.30
Kurtosis	1.11	0.92	0.13	-0.04	-0.13	-0.75	-0.12	-0.29	1.35	0.73	5.94	1.30	0.72	0.58	0.80

Table-2 Estimation of descriptive statistics and variability parameters of F₂ population derived from Swarna Sub1 x Kavuni (Cross II)

Parameters	DFF	PH(cm)	TNT	TNPT	FLL(cm)	FLW(cm)	PL	PE(cm)	TNS/P	TFG	HGW(g)	KL(mm)	KB(mm)	KL/B	SPY(g)
Mean	119.24	154.20	15.90	15.09	31.93	1.34	27.97	1.19	189.85	166.08	2.13	5.39	2.46	2.21	25.64
Minimum	82.00	100.00	10.00	10.00	20.00	1.10	13.00	1.00	103.00	85.00	1.20	5.00	2.00	1.81	8.50
Maximum	163.00	200.00	29.00	28.00	47.00	1.80	40.40	1.50	331.00	303.00	3.03	5.90	3.10	2.80	77.09
Range	81.00	100.00	19.00	18.00	27.00	0.70	27.40	0.50	228.00	218.00	1.83	0.90	1.10	0.99	68.59
SD	11.87	18.55	5.22	5.26	5.58	0.15	3.92	0.09	40.23	38.14	0.35	0.22	0.24	0.22	10.28
PCV	10.08	15.15	32.83	34.84	17.37	10.98	14.96	5.56	25.77	27.74	14.61	3.93	9.88	9.11	33.29
GCV	9.88	14.96	31.94	34.37	17.23	9.84	14.47	2.79	25.61	27.60	14.60	3.85	9.55	8.90	32.82
Heritability	95.95	97.44	94.64	97.34	98.49	80.37	93.51	25.11	98.72	99.05	99.77	95.99	93.33	95.55	97.21
GA	21.83	36.49	10.18	10.54	11.20	0.21	7.41	0.24	80.94	77.52	0.71	0.41	0.46	0.41	20.31
GA(%)	18.31	23.67	64.00	69.85	35.08	15.61	26.48	20.14	42.63	46.68	33.29	7.57	18.80	18.59	79.20
Skewness	0.16	-0.78	0.83	0.89	-0.01	0.87	-0.05	-0.70	-0.25	-0.08	0.64	0.50	0.27	0.57	1.92
Kurtosis	0.86	0.76	-0.60	-0.59	-0.41	0.57	0.62	1.22	-0.06	0.11	-0.25	-0.11	0.11	-0.06	5.75

According to the results of the [Table-1] and [Table-2], the phenotypic coefficient of variations of various traits were slightly higher than the corresponding genotypic coefficient of variations estimates. The characters investigated in the present study exhibited low, moderate and high PCV and GCV values. In the cross I, among the yield characters, highest PCV and GCV values were recorded for number of filled grains, followed by panicle exertion and the lowest PCV and GCV values were recorded for days to 50% flowering. On the other side, moderate PCV and GCV values were recorded for single plant yield, total filled grains and low PCV and GCV for panicle exertion and kernel length in cross II. Similar results were observed by Kumar [6], Chaudhary [2], Pathak [11], Sarvanan [18], Rather [14], Satya [19], Shivani [21], Iftekarudduala [3] and Babu [1]. The studies indicated that the estimates of PCV were slightly higher than the corresponding GCV estimates for all the characters studied indicating that the traits were less influenced by the environment. Therefore, selection on the basis of phenotype alone can be effective for the improvement of these traits.

The estimates of heritability act as predictive measure in expressing the reliability of phenotypic value. Therefore, high heritability is useful in effective selection for a particular character. Heritability is classified as low (below 30%), medium (30-60%) and high (above 60%). The genetic advance is a helpful indicator of the progress that can be expected as result of exercising selection on the pertinent population. Heritability in conjunction with genetic advance would give a more reliable index of selection value [4]. Among both the crosses, all characters showed high heritability except for days to 50% flowering (40.78) in cross I. In cross I, high heritability and high genetic advance as per cent of mean was expressed for plant height, total number of tillers, total number of productive tillers, flag leaf length, panicle exertion, number of spikelets per panicle, number of filled grains per panicle and single plant yield indicating that the traits were controlled by additive gene action. High heritability and moderate genetic advance as per cent

of mean was recorded for flag leaf width, panicle length, hundred grain width, kernel length, kernel breadth, kernel length by breadth ratio which indicates the governance by non additive gene action. The characters studied in the present investigation of cross II high heritability and moderate genetic advance as per cent of mean for days to 50% flowering, flag leaf width, kernel breadth, kernel length by breadth ratio and high heritability and low genetic advance as per cent of mean for kernel length was recorded. High heritability indicates the scope of genetic improvement of these characters through selection. Similar results have been reported by Panwar [10], Sarawgi [17]. In general, the characters showing high heritability with high genetic advance are controlled by digenic gene action [9] and can be improved through simple or progeny selection methods. Knowledge on genetic variation, heritability and genetic advance helps to predict the genetic gain that could be obtained in further generations, if selection is made for improving the particular trait under study. Characters showing high heritability along with moderate or low genetic advance can be improved by intermating superior genotypes of segregating population developed from recombination breeding [16]. The study on distribution properties by third order statistics such as coefficients of skewness and kurtosis provides insight about the nature of gene action and number of genes controlling the traits respectively. They are more powerful than first and second degree statistics which reveal interaction genetic effects. The skewness and kurtosis values for quantitative traits were presented in [Table-1] and [Table-2]. It indicates that for plant height and flag leaf length, the distribution of frequency was negatively skewed and platykurtic in the two crosses. These results are in accordance with Raghavendra [13]. The kurtosis value is less than three for all traits except for hundred grain weight and single plant yield for crosses I and II respectively. Reported negatively skewed platykurtic distribution recorded that these traits were governed by large number of genes and majority of

them displaying dominant and dominant based duplicate epistasis. Hence, mild selection is expected to result in rapid genetic gain for those traits whereas, positively skewed platykurtic distribution indicated that these traits were governed by large number of genes and majority of them displaying dominant and dominant based complementary epistasis. Hence, intense selection is required for immense genetic gain in these traits [12].

Conclusion

According to the values of descriptive statistics of genotypes of F_2 populations of both the crosses and variability studies among the 15 traits. In the present investigation, it was found that there was presence of adequate genetic variability for various morpho-genetic traits. It was concluded that these traits were quantitatively governed by both additive and non-additive gene actions and were controlled by multiple genes showing gene interaction.

Conflict of Interest: None declared

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