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Research Article

VARIABILITY, HERITABILITY AND ASSOCIATION ANALYSIS IN SCENTED RICE

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DOI: 10.7897/2321–6328.01414

Article Received on: 01/10/13
Accepted on: 19/11/13

Abstract

The investigation conducted with fifty rice genotypes comprising both Basmati and aromatic short grain types revealed significant differences among the genotypes for the yield, its components and grain quality characteristics. High estimates of GCV were observed for productive tillers per plant, filled grains per panicle whereas, the estimates for panicle length, days to 50 percent flowering, kernel breadth and kernel elongation ratio were low. The yield components, *viz*., productive tillers per plant and filled grains per panicle which exhibited high heritability coupled with high genetic advance as percent of mean were under the influence of additive gene action. The remaining traits were mostly under the influence of non additive gene action as they recorded low to moderate estimates of genetic advance. The correlation analysis indicated that grain yield was significantly associated with harvest index, plant height, days to 50 percent flowering, panicle length, number of grains per panicle and filled grains per panicle. The characters, plant height, harvest index, number of grains per panicle at genotypic level exhibited moderate positive direct effects; whereas, days to 50 per cent flowering and 1000- grain weight had low positive direct effects. The study on correlations and path analysis indicated that emphasis should be given for selection of plants possessing higher number of grains per panicle with increased panicle length and optimum plant height so as to maintain higher harvest index to develop high yielding varieties for rainy (kharif) season.

Keywords: Rice, variability, heritability, genetic advance, correlations, path analysis

INTRODUCTION

Rice is the major food crop in India occupying nearly 44 m hectares with a production of 96 million tonnes and productivity of 2181 kg/ha. In Andhra Pradesh, India it is grown in an area of 40 lakh hectares with production of 122 lakh tonnes and productivity of 3050 kg/ha. Indian Sub-continent is well known for native wealth of aromatic rices. Despite their poor yield, they are endowed with aroma, excellent cooking quality traits with immense consumer preference. India is the leading exporter of the Basmati Rice to the global market. The country has exported 31,78,174.42 MT of Basmati Rice to the world for the worth of Rs. 15,449.61 crores during the year 2011-12 with major export destinations like United Arab Emirates, Saudi Arabia, Iran, Kuwait and Iraq[2]. In addition to these aromatic long grain varieties, India abounds with scores of indigenous aromatic short grain cultivars and land races and every state has its own set of aromatic rice's that are very popular in native areas. Chittimutyalu, Godavari isukalu, Jeeraga samba and Rajanalu are the popular aromatic land races of Andhra Pradesh, India. As the yield potential of aromatic varieties and land races is very low (2.5-3.0 t/ha) compared to non-basmati high yielding varieties, there is a need to raise the present productivity levels to 5.5-6.0 t/ ha, which is possible through development of high yielding semi- dwarf aromatic varieties with resistance to biotic and abiotic stresses. Plant breeders are constantly using various biometrical techniques to have a greater understanding of nature of gene action for various quantitative traits to plan an effective breeding programme for the improvement of grain yield. Before launching any breeding programme, a thorough knowledge of nature and magnitude of genetic variability, heritability, genetic advance, and also character association in a crop species is essential. Keeping in view the importance of the aforesaid aspects, the present investigation was carried out to estimate the genetic variability among genotypes for yield and quality traits and the extent of association between characters and the direct and indirect effects of the characters on yield were worked out.

MATERIAL AND METHODS

The present experiment was carried out during kharif, 2009 at Rice Section, Agricultural Research Institute, Rajendranagar, Hyderabad, India. The experimental material consisted of 50 aromatic rice genotypes. Source/ parentage of the genotypes are given in Table 1.

Each genotype was transplanted in four rows of 6 m length with a spacing of 20 cm between rows and 15 cm between plants in a randomized block design replicated thrice. Crop management practices and plant protection methods for raising a healthy nursery and main crop were followed as recommended by Acharya N.G. Ranga Agricultural University (ANGRAU) during the crop season. Ten competitive plants of each genotype in each replication were selected randomly from central two rows and the data on 15 characters viz; Days to 50 per cent flowering, Plant height (cm), Number of productive tillers per plant, Panicle length (cm), Number of grains per panicle, Number of filled grains per panicle, 1000-grain weight (g), Grain yield per plant (g), Harvest index (%), Kernel length (mm), Kernel breadth (mm), L/B ratio, Kernel length after cooking (mm), Kernel Elongation Ratio and Volume Expansion Ratio were collected. Analysis of variance was computed based on randomized block design as per standard statistical procedure[24]. The genotypic and phenotypic variances were calculated as per the formulae[3]. Genotypic and phenotypic coefficients of variation were calculated according to the formula given by Falconer[13]. Heritability in broad sense refers to the proportion of genotypic variance to the total observed variance in the total population which was calculated according to the formula given by Allard[1]. From the heritability estimates the genetic advance was estimated as per Burton[2]. Correlation coefficients were calculated at genotypic and phenotypic level using the formulae suggested by Falconer[12]. The direct and indirect effects both at genotypic and phenotypic level were estimated by taking seed yield as dependent variable, using path coefficient analysis suggested by Wright[38] and Dewey and Lu[11].

RESULTS AND DISCUSSION

Variability in the population is a prerequisite especially for characters where improvement is required. Success of plant breeding programmes largely depends on the amount of genetic variability present in a given crop species for the character under improvement. The genotypic coefficient of variation measures the range of variability available in the crop and also enables a breeder to compare the amount of variability present among different characters. The phenotypic expression of the character is the result of interaction between genotype and environment. Hence, the total variance should be partitioned into heritable and non-heritable components to assess the true breeding nature of the particular trait under study. A perusal of genetic parameters (Table 2) revealed that phenotypic and genotypic coefficient of variations were high in case of number of filled grains per panicle followed by number of productive tillers per plant, number of grains per panicle, grain yield per plant, L/B ratio, kernel length after cooking and 1000-grain weight in decreasing order of their magnitude. High estimates of PCV and GCV for seed yield /plant and for number of productive tillers per plant[20,23,26], L/B ratio[34] and for kernel length after cooking[30]. Moderate estimates of PCV and GCV were recorded for kernel length, plant height and kernel elongation ratio. These results are in conformity with the earlier findings[4,21,25,37]. Low estimates of PCV and GCV were recorded for days to 50 per cent flowering, kernel length, panicle length, harvest index and this finding was in accordance with earlier reports[10,16,28,29]. The difference between PCV and GCV was less for all traits under study. This suggested that the traits were less influenced by environment and hence, they could be improved by following phenotypic selection. Heritability estimates indicate the relative degree at which a character is transmitted from parents to off-spring. High heritability values indicated that the characters under study were less influenced by environment in their expression. The traits exhibiting high heritability could be improved by adopting simple selection methods. Further, the information on genetic variation, heritability and genetic advance helps to predict the genetic gain that could be obtained in later generations, if selection is made for improving the particular trait under study. High heritability coupled with high genetic advance as percent of mean (Table 2) was observed for number of productive tillers per plant, number of filled grains per panicle, number of grains per panicle, kernel length after cooking, 1000- grain weight, L/B ratio, kernel length, plant height, kernel elongation ratio, volume expansion ratio, which indicated that these traits were controlled by additive type of gene action. It was evident from the results obtained from the present study, that these traits were controlled by additive type of gene action. Therefore, response to selection could be anticipated in improving the yield. The results were in conformity with the earlier findings for number of productive tillers per plant[7,16], for number of filled grains per panicle[15,26], for kernel length after cooking[9,21], for kernel elongation ratio[6,9]. Further, High heritability coupled with moderate genetic advance as percentage of mean were observed for panicle length and harvest index suggesting the presence of both additive and non-additive gene actions, and simple selection offers best possibility of improvement of this trait. These results were in accordance with earlier findings[8,26,27]. The estimate of heritability was high with low genetic advance as percentage of mean for days to 50 percent flowering[16,36] and kernel breadth[21,35] which indicated that high heritability were due to non-additive gene effects and influence of environment. Hence, there was a limited scope for selection.

A thorough understanding of the association of plant characters among themselves and with yield is essential for successful crop improvement programme. It enables the breeders to manipulate the expression of these traits in crop improvement. The efficiency of selection for yield mainly depends on the direction and magnitude of association between yield and its components and among themselves. Correlation analysis provides information on the nature and magnitude of the association of different component characters with grain yield, which is regarded as a complex trait which the breeder is ultimately interested in. It also helps us to understand the nature of inter-relationship among the component traits themselves. Therefore this kind of analysis could be helpful to the breeder to design selection strategies to improve the grain yield. Genotypic correlations in general are high as compared to their phenotypic correlations and indicated strong inherent association between the characters which might be due to masking or modifying effects of environment. The correlation analysis (Table 3) indicated that grain yield was significantly associated with harvest index, plant height, days to 50 percent flowering, panicle length, number of grains per panicle and filled grains per panicle. Similar kind of association was revealed for number of grains per panicle, days to 50 percent flowering, panicle length[32], for plant height[18] by earlier reports. The grain yield per plant had non-significant positive association with number of productive tillers per plant[19] and significant negative association with 1000-grain weight[22] indicating lesser importance of these components in final yield. Grain yield can be increased whenever there is an increase in characters that showed positive and significant association with it and these characters only can be considered as criteria for selection for higher yield. Days to 50 per cent flowering had significant positive association with number of productive tillers per plant[31] at genotypic level. The association of number of productive tillers per plant with number of grains per panicle was significantly positive[14] at genotypic level whereas with harvest index it was significantly negative.

Table 1: Details of aromatic rice genotypes used in the study

S. No.	Genotype	Source/Pedigree
1	Jeerakasala	Land race from Kerala
2	Gandasala	Land race from Kerala
3	CR 2616- 3-3-3-1	Pusa 44/ Dubraj
4	RNR 2465	RNR –M 7/ RNR 19994
5	KJT-4-4-36-12-13-29	KJT 9-333/ Indrayani
6	JGL 15281	JGL 4870 / Godavari Isukalu
7	JGL 15336	JGL 384 / Godavari Isukalu
8	NDR 6235	Selection from Kalanamak Basti
9	NDR 6242	Selection from Kalanamak Birdpur
10	Ranbir Basmati	Selection from Basmati 370
11	Narendra lalmatti	Selection from Local lalmatti
12	NDR 8018	BKP 246 / Sabita // IR 40931-33-1-B-2
13	Pusa 1121	Pusa 614-1-2 / Pusa 614-2-4-3
14	Kasturi	Basmati 370 / CRR 88-17-1-5
15	NDR 9542	BKP 242 / NDR 30030 // Swarna
16	MahiSugandha	BK 79 / Basmati 370
17	Vasumati	PR 109 / Pak Basmati
18	Haryana Basmati	Sona / Basmati 370
19	Geetanjali	Mutant from Basmati 370
20	Sugandhamati	Pusa Basmati -1 / IET 12603
21	Pusa Basmati	Pusa 150/ Karnal local
22	Pusa Sugandh -3	Pusa 2504-1-3-1
23	NDR 8428-1-2	PSBRC 68 / Kalanamak
24	NDR 9539	BPT 5204 / Kalanamak
25	HUR-ASG-GR-32-87 S	Selection from Gr-32
26	ASH 4022	Material from ASG trial
27	HUR-ASG-KN-23 S	Selection from Kalanamak collected from Nawgarh
28	CR 2600	NDR 8015 / Dubraj
29	CR 2603	NDR 8095 / Dubraj
30	CR 2613 -1-1-1-5-1	KJ / RP
31	CR 2615 -1	KK Selection
32	CR 2613 -1-5-2-5-1	KJ / RP
33	Badshabhog	Local selection
34	Kalanamak	Local selection
35	AS – 100	Material from ASG trial
36	Pak Basmati	Local selection
37	Basmati 386	Selection from Pak Basmati
38	Basmati 370	Selection from Pak Basmati
39	ASG- 4013	Material from ASG trial
40	Yamini	Bhurarata 4-10 / Pak Basmati
41	Taroari Basmati	Pure line selection from HBC 19
42	Chitti mutyalu	Local land race of Andhra Pradesh
43	Godavari Isukalu	Local land race of Andhra Pradesh
44	Sumati	Chandan / Pak Basmati
45	RNR 19186	BPT 5204 / Tella hamsa
46	RNR 22629	Kavya / Pusa Basmati
47	RNR 2009312	RNR 5997 / Kasturi
48	RNR 16511	Chandan / Pak Basmati
49	RNR 17818	WGL 48684 / Pusa Basmati
50	Gahansal	Local land race of Maharastra

Table 2: Estimates of genetic parameters for yield components and quality traits

Character	Mean	PCV	GCV	Heritability (h^2) (%)	Genetic advance	Genetic advance As percent of mean
Days to 50 % flowering	102.09	5.99	5.45	82.80	10.44	10.23
Plant height (cm)	126.83	21.79	21.49	97.3	55.40	43.68
Number of productive tillers / plant	13.24	34.82	34.15	96.1	9.13	68.97
Panicle length (cm)	25.61	10.50	9.08	74.8	4.14	16.18
Number of grains per panicle	198.53	30.91	29.43	90.7	114.64	57.74
Number of filled grains per panicle	152.77	35.55	32.99	86.1	96.33	63.05
1000-grain weight (g)	18.34	24.85	24.03	93.5	8.78	47.87
Grain yield per plant (g)	20.51	28.11	26.56	89.3	10.60	51.70
Harvest index (%)	40.55	16.90	13.34	62.4	8.80	21.71
Kernel length (mm)	6.03	22.16	21.93	97.9	2.70	44.71
Kernel breadth (mm)	1.93	8.35	7.53	81.4	0.27	14.0
L/B Ratio	3.13	25.63	24.01	87.7	1.45	46.34
Kernel length after cooking (mm)	10.53	25.42	25.38	99.7	5.50	52.20
Kernel elongation ratio	1.77	19.07	18.75	96.7	0.67	37.99
Volume expansion ratio	4.27	16.44	16.14	96.3	1.39	32.62

Table 3: Estimation of phenotypic and genotypic correlation coefficients between yield and yield attributing characters

Character		Days to 50% flowering	Plant height (cm)	Number of productive tillers/plant	Panicle length (cm)	Number of grains per panicle	Number of filled grains per panicle	1000-grain weight (g)	Harvest index (%)	Grain yield per plant
Days to 50% flowering	G	**1.0000**	0.1084	0.1662*	-0.0709	0.1125	0.0589	-0.1097	0.1598	0.2847**
	P	**1.0000**	0.0969	0.1389	-0.0981	0.0939	0.0416	-0.1094	0.1064	0.2511**
Plant height(cm)	G		**1.0000**	0.1357	0.5827**	0.1126	0.4082**	-0.1008	0.1312	0.6469**
	P		**1.0000**	0.1311	0.5015**	0.1026	0.3607**	-0.0971	0.1061	0.6053**
Number of productive tillers per plant	G			**1.0000**	0.1568	0.1697*	0.0868	0.1429	-0.2285**	0.0085
	P			**1.0000**	0.1295	0.1549	0.0746	0.1240	-0.1868*	0.0074
Panicle length(cm)	G				**1.0000**	0.1773*	0.2612**	0.0179	0.1121	0.2647**
	P				**1.0000**	0.1759*	0.2689**	0.0158	0.0766	0.2248**
Number of grains per panicle	G					**1.0000**	0.8656**	-0.5620**	0.1513	0.2418**
	P					**1.0000**	0.8486**	0.5089**	0.0954	0.2130
Number of filled grains per panicle	G						**1.0000**	-0.6034**	0.2784**	0.4599**
	P						**1.0000**	-0.5413**	0.1623*	0.3961**
1000 grains weight(gm)	G							**1.0000**	-0.2999**	-0.2577**
	P							**1.0000**	-0.1937*	-0.2275**
Harvest index (%)	G								**1.0000**	0.5743**
	P								**1.0000**	0.5091**

*5 % level of significance **1 % level of significance

Table 4: Estimation of genotypic and phenotypic direct and indirect effects between yield and yield attributing characters

Character		Days to 50% flowering	Plant height (cm)	No of productive tillers / plant	Panicle length (cm)	No. of grains per panicle	No. of filled grains per panicle	1000- grain weight (g)	Harvest index (%)	Correlation with Grain yield / plant
Days to 50% flowering	G	**0.1068**	0.0734	0.0018	0.0146	0.0157	0.0003	-0.0057	0.0778	0.2847**
	P	**0.1401**	0.0520	0.0000	0.0106	-0.0032	0.0080	-0.0010	0.0446	0.2511**
Plant height (cm)	G	0.0116	**0.6772**	0.0015	-0.1198	0.0157	0.0021	-0.0052	0. 0639	0.6469**
	P	0.0136	**0.5368**	0.0000	-0.0544	-0.0035	0.0693	-0.0009	0.0445	0.6053**
No. of productive tillers / plant	G	0.0177	0.0919	**0.0109**	-0.0322	0.0236	0.0004	0.0074	-0.1113	0.0085
	P	0.0195	0.0704	**-0.0002**	-0.0141	-0.0053	0.0143	0.0012	-0.0783	0.0074
Panicle length (cm)	G	-0.0076	0.3946	0.0017	**-0.2056**	0.0247	0.0013	0.0009	0.0546	0.2647**
	P	-0.0137	0.2692	0.0000	**-0.1085**	-0.0060	0.0516	0.000	0.0321	0.2248**
No. of grains/panicle	G	0.0120	0.0763	0.0018	-0.0364	**0.1391**	0.0044	-0.0291	0.0737	0.2418**
	P	0.0132	0.0551	0.0000	-0.0191	**-0.0343**	0.1629	-0.0048	0.0400	0.2130*
No. of filled grains/panicle	G	0.0063	0.2764	0.0009	-0.0537	0.1204	**0.0051**	-0.0312	0.1356	0.4599**
	P	0.0058	0.1936	0.0000	-0.0292	-0.0291	**0.1920**	-0.0051	0.0681	0.3961**
1000 grain weight (gm)	G	-0.0117	-0.0683	0.0016	-0.0037	-0.0782	-0.0031	**0.0517**	-0.1461	-0.2577
	P	-0.0153	-0.0521	0.0000	-0.0017	0.0175	-0.1039	**0.0093**	-0.0812	-0.2275
Harvest index (%)	G	0.0171	0.0889	-0.0025	-0.0230	0.0210	0.0014	-0.0155	**0.4869**	0.5743**
	P	0.0149	0.0570	0.0000	-0.0083	-0.0033	0.0312	-0.0018	**0.4194**	0.5091**

*Significant at 5 % level   Bold values – Direct effect   Residual effect (Phenotypic): 0.6198
**Significant at 1 % level   Normal values – Indirect effect   Residual effect (Genotypic): 0.5325

Plant height registered significant positive association with panicle length and number of filled grains per panicle indicating that the increased panicle length and number of grains per panicle is possible when there is corresponding increase in plant height. Results in similar lines with earlier reports[17,22,33]. Panicle length had highly significant positive association with the number of filled grains per panicle and number of grains per panicle. Similar results were also reported earlier[33,39]. In this context, the correlation studies finally revealed that plant height, number of filled grains per panicle, days to 50 percent flowering, panicle length, number of grains per panicle and harvest index, showed positive and significant association with grain yield and among these components, grains per panicle played predominant role. Hence, selection of plants with more number of grains per panicle and increased panicle length duely balancing the plant height would be the correct approach for improving the grain yield. The association of different component characters among themselves and with yield is quite important for devising an efficient selection criterion for yield. The total correlation between yield and component characters may be some times misleading, as it might be an over-estimate or under-estimate because of its association with other characters. Hence, indirect selection by correlated response may not be some times fruitful. When many characters are affecting a given character, splitting the total correlation into direct and indirect effects of cause as devised by38 would give meaningful interpretation to the cause of association between the dependent variable like yield and independent variables like yield components. This kind of information will be helpful in formulating the selection criteria.

Path coefficient analysis was used to compute direct and indirect effects of eight characters on grain yield in the present study and presented in Table 4. The characters viz., plant height, harvest index, number of grains per panicle at genotypic level exhibited positive direct effects at moderate level on grain yield; whereas, days to 50 per cent flowering and 1000- grain weight had low positive direct effects. This indicated that among different components, plant height, grains per panicle and harvest index were major yield contributing characters in rice. These findings were in agreement with the earlier reports for plant height[17,32], for harvest index[4], and for number of grains per panicle[17,33]. Plant height showed positive indirect effect through plant height, harvest index, panicle length and number of grains per panicle at genotypic level, panicle length on grain yield. These results are in consonance with the previous findings[19,33]. Harvest index exhibited positive indirect effects through plant height, number of grains per panicle at genotypic level, days to 50 per cent flowering on grain yield. The Panicle length exhibited positive indirect effect through plant height and harvest index, which is in conformity with the previous results[18,33].

CONCLUSION

A critical analysis of correlation and direct and indirect effects indicated that emphasis should be diverted towards selection of parents having higher number of filled grains per panicle coupled with high harvest index. As the yield component grains per panicle is intern dependent on panicle length and plant height, attention should be paid towards increasing the panicle length, maintaining height at optimum level. Thus a plant with medium height, sturdy culm with increased panicle length and higher number of filled grains per panicle would be more desirable for kharif in case of scented varieties to realize higher grain yields.

REFERENCES

1. Allard RW. Principles of Plant Breeding. Publishers by John Wiley and Sons Inc. New York USA; 1960. p. 485.
2. APEDA, India Export Statistics - 2012. http://www.apeda.gov.in /apedawebsite/index.asp
3. Burton GW. Quantitative inheritance in grasses. Proceedings of 6th International Grassland Congress Journal 1952; 1: 277-283.
4. Burton GW and Devane EH. Estimating heritability in tall fescue (*Festuca arundinaceae*) from replicated clonal material. Agronomy Journal 1953; 45(10): 478-481. http://dx.doi.org/10.2134/agronj 1953.00021962004500100005x
5. Chaudhary M and Motiramani NK. Variability and association among yield attributes and grain quality in traditional aromatic rice accessions. Crop Improvement 2003; 30(1): 84-90.
6. Chikkalingaiah, Shridhara S, Lingaraju S and Radhakrishna RM. Genetic variability of plant and quality traits in promising genotypes of scented rice (*Oryza sativa* L.). Mysore Journal of Agricultural Sciences 1999; 33(4): 338-431.
7. Anbanandan V, Saravonan K and Sahesan T. Variability, heritability and genetic advance in rice. International Journal of Plant Sciences 2009; 4(1): 61-63.
8. Bhadru D, Tirumala RaoV, Chandra Mohan Y and Bharathi D. Genetic variability and diversity studies in yield and its component traits in Rice (*Oryza sativa* L.). Sabrao Journal of Breeding and Genetics 2012; 44(1): 129-137.
9. Bharadwaj C, Mishra Rajesh, Satyavathi CT, Rao SK and Kumar KS. Genetic variability, heritability and genetic advance in some new plant type based crosses of rice (*Oryza sativa* L.) Indian Journal of Agricultural Research 2007; 41(3): 189-194.
10. De RN and Suriya Rao AV. Genetic variability and correlation studies in rice under semi-deep waterlogged situation. *Oryza* 1988; 25: 360-364.
11. Dewey JR and Lu KH. Correlation and path coefficient analysis of components of crested wheat grass seed production. Agronomy Journal 1959; 51: 515-518. http://dx.doi.org/10.2134/agronj1959.0002196 2005100090002x
12. Falconer DS. Introduction to quantitative genetics. Longmann, London and New York; 1964. p. 294-300.
13. Falconer DS. Introduction to quantitative genetics. Oliver and Boyd, London; 1981. p. 340.
14. Janardhanam V, Nadarajan N and Jebaraj S. Correlation and path analysis in rice (*Oryza sativa* L.). Madras Agricultural Journal 2001; 88(10-12): 719-720.
15. Karim D, Sarkar U, Siddique MA, Khaleque Miah and Hasnat MZ. Variability and genetic parameter analysis in aromatic rice. International Journal Of Sustainable Crop production 2007; 2(5): 15-18.
16. Krishna L, Raju CHD and Raju CHS. Genetic variability and correlation in yield and grain quality characters of rice germplasm. The Andhra Agricultural Journal 2008; 55(3): 276-279.
17. Kishore NS, Babu VR, Ansari NA , Ravindra Babu V, Shobha Rani N, Subba Rao LV and Ravichandran. Correlation and path analysis in aromatic and non aromatic rice genotypes. Agricultural Science Digest 2007; 27(2): 122-124.
18. Madhavi Latha L. Studies on genetic divergence and isozyme analysis in rice (*Oryza sativa* L.). M.Sc. (Ag.) Thesis, Acharya N.G. Ranga Agricultural University, Hyderabad; 2002.
19. Madhavi Latha L, Sekhar MR, Suneetha Y and Srinivas T. Genetic variability, correlation and path analysis for yield and quality traits in rice (*Oryza sativa* L.). Research on Crops 2005; 6(3): 527-537.
20. Nayak AR, Chaudhary D and Reddy JN. Genetic variability, heritability and genetic advance in scented rice. Indian Agriculturist 2002; 46(1, 2): 45-47.
21. Nayak AR, Chaudhary D and Reddy JN. Genetic variability and correlation study among quality characters in scented rice. Agricultural Science Digest 2003a; 23(3): 175-178.
22. Nayak AR. Heritability and correlation in scented rice. Indian Agriculturist 2007; 50(1, 2): 9-12.
23. Nayudu KSR, Varline YA and Vennila S. Studies on variability, heritability and genetic advance for certain yield compounds in rice. Crop Improvement 2007; 34(2): 142-144.

24. Panse VG and Sukhatme PV. Statistical methods for Agricultural Workers. ICAR, New Delhi; 1978. p. 235-246.
25. Patil PV, Sarawgi AK and Shrivastava MN. Genetic analysis of yield and quality traits in traditional aromatic accessions of rice. Journal of Maharashtra Agricultural Universities 2003; 28(3): 255-258.
26. Patil PV and Sarawgi AK. Studies on Genetic variability, correlation and path analysis in traditional aromatic rice accessions. Annals of plant physiology 2005; 19(1): 92-95.
27. Patra BC, Pradhan KC, Nayak SK and Patnaik SSC. Genetic variability in long awned rice genotypes. Environmental and ecology 2006; 24S (special 1): 27-31.
28. Reddy JN and De RN. Genetic variability in low land rice. Madras Agricultural Journal 1996; 83(4): 269-270.
29. Sinha SK, Tripathi AK and Bisen UK. Study of genetic variability and correlation coefficient analysis in midland land races of rice. Annals of Agricultural Research 2004; 25(1): 1-3.
30. Sadhukhan RN and Chattopadhyay P. Variability and character association between yields attributes and grain quality in aromatic rice. Journal of Interacadamicia 2000; 4(4): 494- 497.
31. Sakthivel P. Genetic divergence and genetic analysis of yield attributes and certain quality traits in rice (*Oryza sativa* L.). M.Sc. (Ag) Thesis, Acharya NG Ranga Agricultural University, Hyderabad; 2001.
32. Sankar PD, Sheeba A and Anbumalarnaths J. Variability and character association studies in rice (*Oryza sativa* L.). Agricultural Science Digest 2006; 26(3): 182-184.
33. Satish Chandra B, Dayakar Reddy T, Ansari NA and Kumar Sudheer S. Correlation and path analysis for yield components in rice (*Oryza sativa* L.) Agricultural Science Digest 2009; 29(1): 45-47.
34. Saxena RR, Saxena RR, Motiramani NK, Nichal SS and Sahu RK. Studies on variability, heritability and genetic advance in scented rice germplasm accessions. Journal of Inter acadamicia 2005; 9(4): 487- 489.
35. Venkata Suresh A. Genetic analysis for certain quantitative and qualitative traits in F_2 populations of rice (*Oryza sativa* L.). M.Sc. (Ag) Thesis, Acharya NG Ranga Agricultural University, Hyderabad; 2001.
36. Vijayalakshmi B, Vijay D, Raju PRK and Satyanarayana PV. Genetic divergence of qualitative and quantitative characters in low land rice germplasm. Crop Research 2008; 36(1, 2, 3): 212-214.
37. Vivekanandan P and Giridharan S. Genetic variability and character association for kernel and cooking quality traits in rice. *Oryza* 1998; 35(3): 242-245.
38. Wright S. Correlation and causation. Journal of Agricultural Research 1921; 20(7): 557-585.
39. Yogameenakshi P, Nadarajan N and Anbumalarmathi J. Correlation and path analysis on yield and drought tolerant attributes in rice (*Oryza sativa* L.) under drought stress. *Oryza* 2004; 41(3, 4): 68-70.

Cite this article as:
S.Vanisree, K. Anjali, Ch. Damodar Raju, Ch. Surender Raju and M. Sreedhar. Variability, heritability and association analysis in scented rice. J Biol Sci Opin 2013; 1(4): 347-352 http://dx.doi.org/10.7897/2321-6328.01414

Source of support: Nil; Conflict of interest: None Declared