



Deciphering Variability and Genetic Parameters in Traditional Scented Rice (*Oryza sativa* L.) Genotypes of Kerala, India

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Authors' contributions

This work was carried out in collaboration among all authors. Author AAR conducted the experiment, performed the statistical analysis and wrote the first draft of the manuscript. Author CRE designed the study and provided scientific advice. Author CB provided laboratory facilities for biochemical analysis. All authors read and approved the final manuscript.

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ABSTRACT

Gandhakasala and *Jeerakasala*, the most popular traditional scented rice cultivars of Wayanad district in Kerala were used to assess the nature and magnitude of variability and genetic parameters in this investigation. The study on twenty yield and associated quantitative, cooking and biochemical characters revealed significant differences among genotypes for each character except for leaf width indicating the presence of high genetic variability among the genotypes.

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Phenotypic and genotypic coefficient of variations showed high level of variability for grain yield (42.19%), number of spikelets panicle⁻¹ (31.36%) and test weight (26.23%) and moderate level of variability for leaf length, culm number, culm length, number of productive tillers, number of spikelets panicle⁻¹, panicle length, straw yield, grain length, grain width, amylose content and protein content. For most of the characters studied, the difference between GCV and PCV was narrow, indicating that environmental factors have little influence on these characters and are highly influenced by genetic factors. Heritability estimations ranged from low to high (17.86% to 99.90%). Characters like leaf length, culm number, number of spikelets panicle⁻¹ and straw yield showed high heritability along with high genetic advance reflecting that these characters were under additive gene action and these could be the desirable characters for effective selection for developing high yielding scented rice varieties. This study provides information about the genetic variability and heritability measures of the various yield and related characters which may help to establish the selection criteria for future improvement in short grain scented rice breeding programmes.

Keywords: Scented rice; Gandhakasala; Jeerakasala; variability; heritability; genetic advance.

1. INTRODUCTION

Rice (*Oryza sativa* L.) belonging to the family Poaceae is the second largest cereal crop in the world and a major staple source of calories for over half of the global population. Rice has adapted to various climatic conditions showcasing a wide range of genotypic and phenotypic diversity. Among the diverse group of rice genotypes, scented rice stands out as a small but unique and highly prized type due to its exceptional aroma and quality [1]. Non-Basmati traditional scented rice cultivars are generally small or medium grained [2]. Despite the low yield, these scented rice are endowed with aroma, taste, excellent cooking and eating quality attributes that make them more acceptable than Basmati with market being merger. All the major rice growing countries including India have their own traditional and evolved scented rice varieties. The genetic diversity of scented rice in India is largest in the world having more than 300 scented rice genotypes cultivated in different states. Traditional scented rice cultivars of Kerala include *Gandhakasala*, *Jeerakasala*, *Velumbala*, *Chomala*, *Kayama*, *Kothampalariikkayama*, *Pookkilathari*, *Mullanchanna*, *Poothadikayama*, *Kunjinellu Neycheera* and *Urunikazama* [3,4,5]. The scented rice cultivation is on the foothills of mountains and requires specific climatic conditions such as low temperature, soil quality and humidity, which are essential for developing and retaining high aroma [6]. Wayanad district which adorns the northern hills of Kerala, ranks first in the cultivation of traditional scented rice cultivars *Gandhakasala* and *Jeerakasala*, which are the registered Geographical Indications [7,8].

The research on these valuable genetic resources remains largely unexplored, despite their market potential leading to limited cultivation in certain pockets and a reduction in the diversity of these valuable genetic resources. It is crucial that non basmati scented rice genotypes have to be conserved and utilized for breeding programmes for genetic improvement. Traditional scented rice varieties are thermo-photosensitive, long duration and very low yielding due to their poor harvest index and tendency for lodging. Hence these rice genotypes need to be improved by combining the grain quality attributes with high yield potential. Yield being a complex trait, the knowledge about genetic parameters and the correlation between different yield attributing and quality characters is vital for an effective breeding program. Therefore, keeping the above in view, the current study aims to screen the scented rice genotypes to study the genetic variability and determine the genetic parameters among the selected genotypes. Biometric tools such as genotypic and phenotypic coefficients of variability, heritability and genetic advance are essential for measuring genetic divergence among genotypes and can be used to improve the scented rice genotypes through suitable breeding methods.

2. MATERIALS AND METHODS

The present investigation to study genetic variability, heritability and genetic gain was conducted at the Regional Agricultural Research Station, Kerala Agricultural University, Ambalavayal, Wayanad district, Kerala in a randomized block design (RBD) with three replications in a plot size of (3 X 2) m² with (20 x 10) cm² spacing with the recommended package

of practices of Kerala Agricultural University. The study consists of nine scented rice genotypes *Gandhakasala* types (GT 1 – GT 8), *Jeerakasala* type (JT 9) and a non-scented local check variety *Aiswarya* collected from different parts of Wayanad district in Kerala. Observations were recorded on twenty yield and associated quantitative, cooking and biochemical characters. The characters that were evaluated include seedling height (cm), leaf length (cm), leaf width (cm), culm number, culm length (cm), days to 50% flowering, number of productive tillers, panicle length (cm), number of spikelets panicle⁻¹, days to maturity, straw yield (kg/ha), grain yield (kg/ha), test weight (g), grain length (mm), grain width (mm), milling recovery (%), kernel elongation ratio, volume expansion ratio, total carbohydrate (%), amylose content (%) and protein content (%). Morphological observations were recorded at different stages of plant growth following the Standard Evaluation System of Rice [9] from ten randomly selected plants of each genotype in each replication and the mean was used for the statistical analysis. Grains were collected for biochemical and cooking quality analysis. Total carbohydrate, amylose content and protein content were estimated by the methods suggested by Sadasivam and Manickam [10].

Analysis of Variance was done using MSTAT package and treatments were compared using Duncan's Multiple Range Test (DMRT). The variance components were estimated using the method pioneered by Lush [11]. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were calculated by the formula suggested by Burton [12] and classified into low (<10%), moderate (10-20%) and high (>20%) as suggested by Sivasubramanian and Madhavamenon [13]. Heritability (h^2) in broad sense was estimated by the formula suggested by Lush and categorized into low (below 30%), medium (30- 60%) and high (above 60%) according to Allard [14]. The expected genetic advance (GA) under selection among the various characters were calculated according to the formula suggested by Johnson et al. [15].

3. RESULTS AND DISCUSSION

Significant difference has been revealed through ANOVA among the ten genotypes for all characters studied indicating significant inherent genetic differences (Table 1). These differences can be utilized for the genetic improvement of the

scented rice genotypes for yield and quality traits through selection. The mean sum of squares for the genotypes showed high significant differences for all the traits under study except for leaf width and similar results has been reported earlier [16].

3.1 Genetic Variability

In the present investigation, phenotypic coefficients of variation (PCV) were higher than genotypic coefficients of variation (GCV) for all the traits studied, indicating the impact of the environment on the appearance of these traits (Table 2). Similar findings were reported earlier [17,18]. The results of genetic variability indicated that, the highest GCV and PCV were for GY (40.42% and 42.19%) followed by NSP (28.08% and 31.36%) and TW (26.13% and 26.23%), suggesting that these traits were controlled mainly by genetic factors and were less affected by environment and hence these traits could be utilized for further improvement of scented rice genotypes through selection. The estimates were found to be in accordance with Hasib and Kole [19] for TW and GY; Dinkar et al. [20] for GY, NSP and TW, Nihad et al. for GY and NSP [21]. Moderate estimates of both GCV and PCV were exhibited by CL (17.32% and 17.88%), LL (17.29% and 17.97%), SY (17.02% and 19.59%), GW (12.81% and 14.83%), PC (12.70% and 12.71%), GL (12.64% and 12.89%), AC (12.51% and 12.51%), PL (12.25% and 13.98%), NPT (12.13% and 13.40%), CN (11.72% and 12.61%) and VER (10.96% and 11.28%). SH (5.27% and 8.07%), MR (6.09% and 6.10%), DF (8.75% and 8.77%), DM (8.87% and 8.88%) and TC (9.80% and 9.80%) had the lowest GCV and PCV exhibiting the influence of the environment and the narrow genetic base for these characters. The possibility of improving these characters were less through selection and could be made through combination breeding methods or induced mutagenesis to widen the genetic base followed by selection in advanced generations. The results were in conformity with the findings of Singh et al. [22] for DF, DM and MR; Lakshmi et al. for DF [23].

3.2 Heritability and Genetic Advance

h^2 determines the extent to which a trait is inherited or the value that is transferred from an individual to its progeny [24]. High estimates of h^2 were witnessed for LL (93.35%), CN (88.17%), CL (94.40%), CD (82.44%), DF (99.63%), NPT (84.13%), PL (78.77%), NSP (81.88%), DM

Table 1. Analysis of variance for grain yield and associated quantitative, cooking and biochemical characters in scented rice genotypes

Characters	Source of Variation (Mean Sum of Squares)		
	Genotype	Replication	Error
SH	8.6*	2.02	2.68
LL	170.74**	12.24	4.40
LW	0.012	0.02	0.01
CN	2.37**	0.11	0.12
CL	738.18**	22.79	15.91
DF	415.29**	0.63	0.56
NPT	2.51**	0.22	0.17
PL	28.99**	8.19	2.66
NSP	5986.60**	89.37	456.97
DM	725.43**	0.63	0.54
SY	1479466.24**	146855.00	141113.06
GY	1390348.34**	21169.67	40096.72
TW	50.13**	0.09	0.13
GL	2.11**	0.03	0.03
GW	0.23**	0.01	0.02
MR	49.49**	0.01	0.01
KER	0.16**	0.02	0.03
VER	1.04**	0.11*	0.02
TC	177.50**	0.06	0.02
AC	19.27**	0.002	0.001
PC	3.13**	0.00001	0.0001

* Significant at 5% level, ** Significant at 1% level of probability

SH: Seedling height; LL: Leaf length; LW: Leaf width; CN: Culm number; CL: Culm length; DF: Days to 50 per cent flowering; NPT: Number of productive tillers; PL: Panicle length; NSP: Number of spikelets panicle⁻¹ DM: Days to maturity; SY: Straw yield; GY: Grain yield; TW: test weight; GL: Grain length; GW: grain width; MR: Milling recovery %; KER: Kernel elongation ratio; VER: Volume expansion ratio; TC: Total carbohydrate; AC: Amylose content; PC: Protein content

Table 2. Estimates of variability parameters of different characters in scented rice genotypes

Characters	Range	Mean±S.E	Pcv%	Gcv%	H ² %	Ga %
SH	25.18 - 30.8	27.11 ± 1.34	8.01	5.27	46.92	7.59
LL	24.24 - 52.33	43.06 ± 1.71	17.97	17.29	93.35	34.46
LW	1.01 - 1.24	1.08 ± 0.09	11.26	4.14	17.86	4.07
CN	6.46 - 9.34	7.39 ± 0.28	12.61	11.72	88.17	22.59
CL	48.05 - 101.56	89.58 ± 3.26	17.88	17.32	94.40	34.71
DF	101 - 140.67	134.37 ± 0.61	8.77	8.75	99.63	17.99
NPT	6.34 - 9.27	7.28 ± 0.338	13.40	12.13	84.13	23.08
PL	16.38 - 27.1	24.19 ± 1.33	13.98	12.25	78.77	22.53
NSP	64.07 - 216.13	152.92 ± 17.45	31.36	28.08	81.88	52.54
DM	179.0 - 180.33	175.17 ± 0.61	8.88	8.87	99.79	18.26
SY	2923.98 - 5043.73	3910.83±306.72	19.59	17.08	78.02	31.24
GY	1077.87- 3055.33	1659.59±163.49	42.19	40.42	92.59	80.25
TW	12.74 - 25.81	15.63 ± 0.29	26.23	26.13	99.29	53.61
GL	5.48 - 8.47	6.58 ± 0.14	12.89	12.64	95.97	25.53
GW	1.69 - 2.39	2.05 ± 0.13	14.83	12.81	75.82	22.96
MR	61.81 - 72.12	66.65 ± 0.08	6.10	6.09	99.94	12.54
KER	1.71 - 2.49	2.12 ± 0.14	12.52	9.81	63.77	16.27
VER	5.21 - 6.07	5.54 ± 0.08	11.28	10.96	94.97	22.03
TC	64.89 - 87.09	78.48 ± 0.12	9.80	9.80	99.97	20.18
AC	17.82 - 26.36	20.25 ± 0.03	12.51	12.51	99.9	25.78
PC	6.38 - 9.70	8.04 ± 0.012	12.71	12.70	99.9	26.12

Mean±S.E: Means±Standard error; PCV %: Percent phenotypic coefficient of variation; GCV %: Percent genotypic coefficient of variation; h²: Broad sense heritability; GA%: Genetic Advance as percent of mean

(99.79%), GY (92.59%), SY (78.02%), TW (99.29%), GL (95.97%), GW (75.82%), MR (99.94%), KER (63.77%), VER (94.97%), TC (99.97%), AC (99.99%) and PC (99.99%). GA is a measure that explains the degree of gain that may be obtained in a trait under a particular selection pressure. Estimates of high heritability with high genetic advance are more reliable for selection [25]. The highest value of GA was observed for GY (80.25%) followed by TW (53.61%), NSP (52.545), CL (34.71%), LL (34.46%), SY (31.24%), PC (26.12%), AC (25.78%), GL (25.53%), NPT (23.08%), GW (22.96%), CN (22.59%), PL (22.53%), VER (22.03%) and TC (20.18%) which stated the presence of the additive gene action while moderate GA was detected for DM (18.26%), DF (17.99%), KER (16.27%) and MR (12.54%), which revealed non-additive gene action. LW had the lowest GA (4.07%) followed by SH (7.59%). High h^2 coupled with high genetic gain was observed for LL, CN, CL, NPT, PL, NSP, GY, SY, TW, GL, GW, VER, TC, AC and PC. High heritability coupled with high genetic gain indicates that the heritability of these characters was due to additive gene action and the negligible influence of environment in the expression of traits and hence selection based on these characters would be highly effective for the development of elite genotypes. These results conform with Pratap et al. [26], Gupta, et al. [27], Krishnan et al. [28], Basu et al. [29] and Borah et al [30]. Moderate GA with high h^2 was detected for DM, MR and KER, indicating the scope of individual plant selection for further improvement.

4. CONCLUSION

The scented rice genotypes differ significantly for different yield attributing and cooking quality characters under this study. *Jeerakasala* types recorded significantly higher yield (2735.22 kg/ha), grain length and test weight than *Gandhakasala* (1350.64 kg/ha) types. The scented rice genotypes had less milling recovery than check variety indicating the need for specially designed milling machines for maximum milling recovery. *Gandhakasala* types showed high kernel elongation ratio and low volume expansion ratio which gives finer appearance compared to *Jeerakasala* type and check variety. Total carbohydrate content was low for scented genotypes than the check variety and can be recommended for low carbohydrate diets. Based on genetic parameters, characters like grain yield, number of spikelets panicle⁻¹ and

test weight exhibited high GCV, PCV and high heritability coupled with high genetic advance indicating little influence of environment on the expression of these characters and responsiveness under selection to improve traits to increase the grain yield and quality parameters. Among scented genotypes, JT 9, GT 3 and GT 8 showed better performance based on the high grain yield, high straw yield, intermediate amylose content and moderate aroma which are the preferred qualities for specialty rice. These genotypes could be used for the development of high yielding scented rice varieties with better cooking and biochemical characters. Also, superior genotypes identified can be further evaluated and used for combination breeding. Hence, we suggest to conduct further studies on these genotypes to validate the results and use for varietal development.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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