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Genetic variability studies in F1 rice (*Oryza sativa* L.) hybrids for yield and quality traits

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ABSTRACT

Analysis of variance among lines, significant differences was observed for plant height, number of productive tillers per plant, panicle length, number of filled grains per panicle, single plant yield and 1000 grain weight while days to 50 per cent flowering, plant height, panicle length, single plant yield, 1000 grain weight, milling per cent, head rice recovery, grain length, L/B ratio, kernel length after cooking, kernel breadth after cooking, breadth wise elongation ratio and amylose content exhibited significant differences among testers besides in L x T interaction, all characters along with yield. The magnitude of difference between genotypic coefficient of variation (GCV) and phenotypic coefficient of variation was less for the traits indicating slight influence of environment. A wide range of PCV (4.09 – 43.43 %) and GCV (6.58 – 43.39 %) was resulted for 19 traits. The presence of higher GCV and PCV observed in number of filled grains per panicle followed by single plant yield, Alkali spreading value, gel consistency and amylose content, which signifies the additive genetic control in inheritance of that trait. The presence of high scale of GCV and PCV for observed traits suggested having better possibility for the enhancement through simple selection procedure.

Keywords: Genetic advance, Heritability, Quality Traits, Rice, Variance, Variability.

INTRODUCTION

Rice (*Oryza sativa* L.) is a monocotyledonous angiosperm belongs to the family *Graminae*, sub-family Bamboosoideae and tribe *Oryzeae.* Rice contains minerals such as calcium, magnesium and phosphorus are present in addition to some traces of iron, copper, zinc and manganese. Rapid increasing of population globally, results in huge demand for rice will remain to rise in near upcoming years; hence, rice breeders across worldwide concentrate to increase the grain yield in rice [1]. Grain yield is a complex polygenic quantitative trait, controlled by several genes and combination of selected grain quality traits considered as most important objective following to increase in yield, which is influenced by environment factors highly [2]. Grain size, grain shape, uniformity and over-all appearance, grain shape and Length to Breadth (L/B) ratio are significant characters used for evaluating grain quality [3]. The assessment of gelatinization temperature (GT), amylose content (AC) and gel consistency (GC) are additional set of qualities, deciding cooking and eating quality. To develop new varieties with enhanced economically significant traits a better understanding of the association between grain yield and quality traits becomes essential for making an effective selection [4].

An extensive range of genetic variability for grain yield and quality traits has been reported previously, but presence of available variability in germplasm plays most important in choice of potential parents, in hybridization programme to achieve maximum heterosis and superior recombinants for yield and quality traits. To predict degree of variability existing in available germplasm and crossed F_1's, Genetic parameters such as genotypic coefficient of variation and phenotypic coefficient of variation are valuable and predicting heritability along with high genetic advance aids in determining the impact of environment, expression also reliability of grain yield and quality traits in F_1's and their genotypes [5].

In view of above perceptions, the current work was conducted with the objective of assessing the genetic variability for yield and quality traits, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h2), genetic advance over mean and genetic advance (GA) would support in selection addition of more development of rice genotypes to develop varieties with high yielding and good quality traits. The information of genetic variability and genetic parameter for grain yield and quality traits and their association with each other including grain yield is necessary to formulate appropriate breeding approaches for grain yield and quality enhancement [6].

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MATERIALS AND METHODS

The experimental materials for the present study comprised with fifteen genotypes of rice (*Oryza sativa* L.) which includes eight lines *viz,* BPT 5204, CR 1009, JGL 1798, JGL 3855, TPS 3, BRNS (WP) 5, CO 43 and ADT 39 and seven testers ASD 19, IR 20, IR 50, ADT 38, BRNS (WP) 22-2, CO 50 and Krishna Hemavathi (K.H). The parents used for the present study were collected from the germplasm bank maintained at the Department of Plant Breeding and Genetics, AC& RI, Killikulam.

Eight lines and seven testers were planted in a crossing block with a spacing of 20 x 15 cm then crossing programme is carried out in an eight x seven, Line x tester mating design to produce 56 hybrids during *kharif* and *rabi*, 2015-16 Wet cloth method of hybridization suggested by [7] was followed for crossing. The obtained 56 hybrids along with 8 lines and 7 testers were raised in a randomized block design with two replications at Agricultural College and Research Institute, Killikulam during *Rabi* 2016-17. Eighteen days aged seedlings were transplanted in the main field with a spacing of 20 x 20 cm with single seedling per hill. Five randomly selected plants selected from individual entry not including the border plants to reduce error and the following data were recorded: for important quantitative and quality traits such as days to fifty per cent flowering (DFF), plant height(cm), number of productive tillers per plant, panicle length(cm), thousand grain weight(g), single plant yield(g), number of filled grains per panicle, milling percentage(%), grain length(mm), grain breadth(mm), head rice recovery(%), L/B ratio, kernel length after cooking(mm), kernel breadth after cooking(mm), linear expansion ratio, alkali spreading value, gel consistency(mm) and amylose content(%).Collected data were subjected to statistical analysis using line × tester analysis by [8].

The milling percentage observations recorded using of SATAKE company make laboratory huller cum polisher. The milling characterizers were computed along with head rice recovery. grain length and grain width of 10 whole milled rice were measured by using of graph sheet and length/breadth ratio was computed as per [9]. Length and breadth of cooked grains and elongation ratio were recorded using graph sheet to quantify cooking traits. Alkali spreading value, gel consistency and amylose content estimated by following the standard methods. The treatment means for all the characters were subjected to analysis of variance techniques on the basis of model proposed by 10]. The genotypic and phenotype variances of 19 traits were calculated as per the formulae proposed by [11]. Heritability in broad sense (h^2broad sense) was calculated as per [12], as suggested by [13], heritability estimates, the genetic advance (GA) for 19 traits was calculated by the following formula given by [13].

RESULTS AND DISCUSSION

For selection of superior crosses over the existing genotypes, Genetic variability is prerequisite in rice crop. Among lines, significant differences was observed for plant height, number of productive tillers per plant, panicle length, number of filled grains per panicle, single plant yield and 1000 grain weight while days to 50 per cent flowering, plant height, panicle length, single plant yield, 1000 grain weight, milling per cent, head rice recovery, grain length, L/B ratio, kernel length after cooking, kernel breadth after cooking, breadth wise elongation ratio and amylose content exhibited significant differences among testers besides in L x T interaction, all characters along with yield. Therefore, there is an ample scope for selection of promising genotypes from the present gene pool for yield and its traits, these results were agreed by [14].

Table 1: Analysis of variance (mean squares) for 56 F₁'s, 8 lines and 7 testers, grain yield and quality traits in 55 genotypes rice (*Oryza sativa* L.)

S. No	Characters	Replication (d.f=1)	Genotypes (d.f=71)	Crosses (d.f=55)	Error (d.f=70)
1	Days to 50% flowering	0.253	295.692**	118.612**	1.61
2	Plant height	0.341	392.805**	267.563**	1.848
3	Number of productive tillers per plant	2.035	24.653**	27.666**	0.7066
4	Panicle length	1.171	11.038**	10.710**	0.314
5	Number of filled grains per panicle	19.781	3268.206**	3974.423**	3.524
6	1000 Grain weight	2.016	208.020**	150.329**	1.039
7	Single plant yield	0.025	22.204**	20.186**	0.432
8	Milling Percentage	1.713	56.566**	52.210**	0.3243
9	Head Rice Recovery	2.788	67.138**	49.396**	0.2
10	Grain length	0.262	0.534**	0.493**	0.003
11	Grain Breadth	0.101	0.041	0.038**	0.004
12	L/B ratio	0.029	0.151**	0.151**	0.007
13	Grain Length after Cooking	0.076	0.739**	0.693**	0.006
14	Grain Breadth after Cooking	0.051	0.070**	0.062**	0.003
15	Linear Elongation Ratio	0.007	0.025**	0.013**	0.001
16	Breadth wise expansion ratio	0.001	0.114**	0.106**	0.006
17	Gelatinization temperature	0.063	2.510**	2.377**	0.12
18	Gel consistency	7.256	676.054**	584.677**	0.647
19	Amylose content	2.083	60.391**	57.35**	0.033

*significance at 5% level   **significance at 1% level

Table 2: Estimation of genetic parameters of variability for yield associated traits and quality traits

| Characters	Mean	Range		GCV (%)	PCV (%)	Heritability (%)	Genetic Advance	Genetic Advance as % means
		Min.	Max.					
Days to 50% flowering	86.5	85.5	124.0	14.02	14.09	98.92	31.84	36.80
Plant height	83.3	82.75	114.7	16.78	16.86	99.06	28.67	34.40
Number of productive tillers per plant	18.5	15	19.5	18.75	19.29	94.43	6.93	37.53
Panicle length	21.2	16.35	24.2	10.94	11.25	94.47	4.64	21.90
Number of filled grains per panicle	93.1	28	103.5	43.39	43.43	99.78	83.14	89.28
1000 Grain weight	29.9	14.75	37.6	34.04	34.21	99.01	20.85	69.77
Single plant yield	23.2	16.7	24.1	14.23	14.51	96.18	6.67	28.75
Milling Percentage	72.5	62.9	76.2	7.32	7.36	98.86	10.86	14.99
Head Rice Recovery	68.5	53.65	69.8	8.44	8.47	99.41	11.88	17.34
Grain length	5.5	4.3	5.7	9.37	9.43	98.71	1.06	19.19
Grain Breadth	2.1	1.75	2.4	6.58	7.30	81.29	0.25	12.22
L/B ratio	2.7	2.1	2.8	10.05	10.56	90.66	0.53	19.72
Grain Length after Cooking	6.7	5.35	7.2	9.01	9.09	98.36	1.24	18.42
Grain Breadth after Cooking	2.6	2.2	2.8	7.09	7.49	89.45	0.35	13.80
Linear Elongation Ratio	1.2	1.04	1.4	9.14	9.30	96.77	0.23	18.53
Breadth wise expansion ratio	2.2	1.6	2.4	10.77	11.41	89.17	0.45	20.96
Gelatinization temperature	3.2	1	5.0	33.97	35.64	90.84	2.15	66.69
Gel consistency	81.7	28.5	100.5	22.51	22.53	99.81	37.82	46.32
Amylose content	27.0	14.75	29.5	20.33	20.34	99.89	11.31	41.86
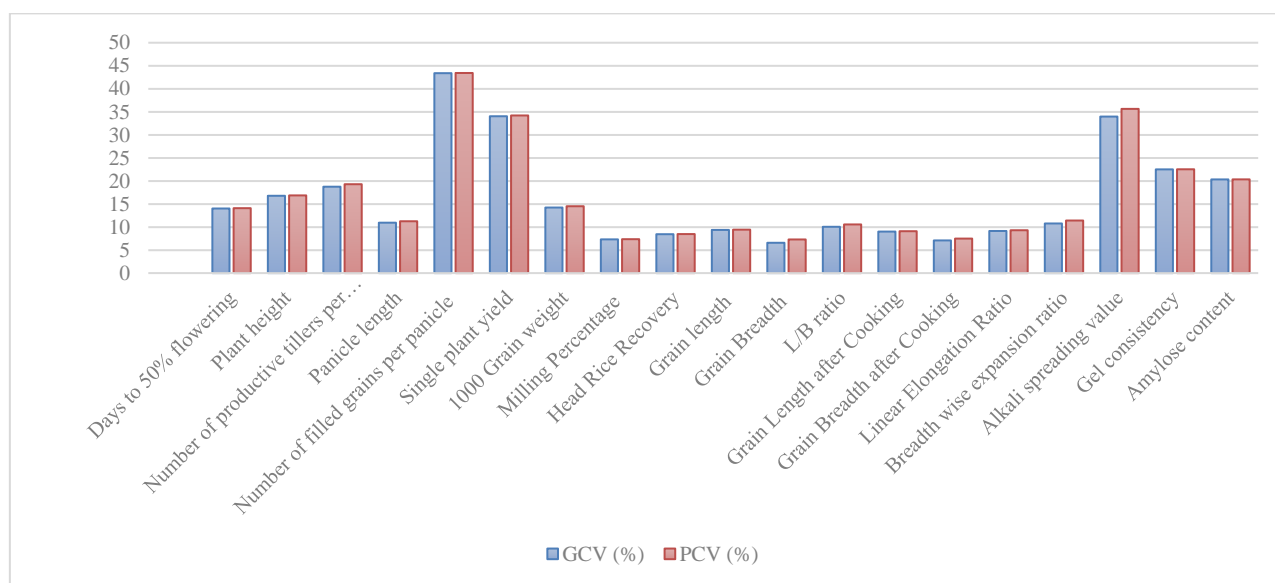
Fig 1: Phenotypic Coefficient of Variance (PCV) and Genotypic Coefficient of Variance (GCV) for 19 traits of Rice (*Oryza sativa* L.).
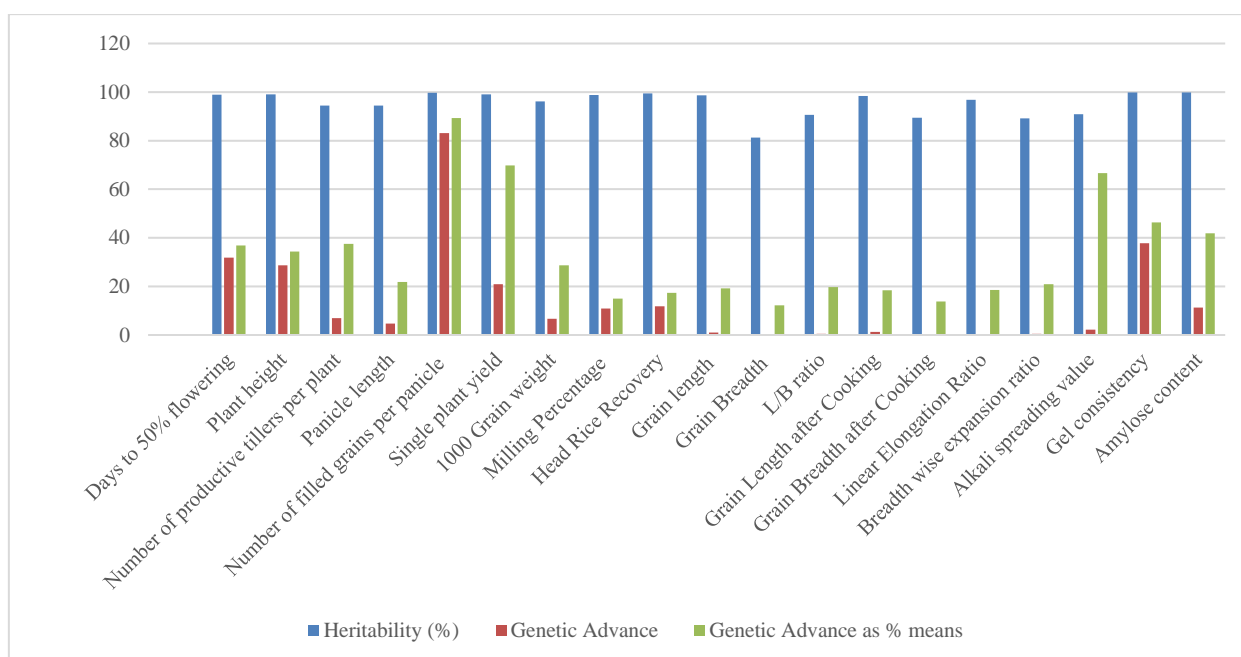
Fig 2: Genetic parameters (Heritability, Genetic Advance and Genetic Advance as % means) for 19 yield traits of Rice (*Oryza sativa* L.).

The superior achievement of rice breeding programme hinges on the selection of parents based on mean performance, a wide range of variation in56 F₁'s, 8 lines and 7 testers mean performance was observed for all the 19 traits in present study i.e. days to 50% flowering (85.5-124), plant height (82.75-114.65cm), number of productive tillers/plant (15-19.5), panicle length (16.35-24.15 cm), number of filled grains per panicle (28-103.85), 1000 grain weight (14.75-37.55), single plant yield (16.7-24.1g), milling percentage of rice (62.9-76.15%), head rice recovery (53.65-69.75 %), grain Length (4.3-5.7 mm), kernel Breadth (1.75-2.40 mm), L : B ratio (2.1-2.83), grain length length after cooking (5.35-7.2 mm), kernel breadth after cooking (2.2-2.75 mm), linear elongation ratio (1.04-1.35), breadth wise expansion ratio (1.6-2.35), alkali spreading value (1.0-5.0), gel consistency (28.50-100.50 mm) and amylose content (14.75-29.48). similar results were in agreement with the reports of [15] for 1000 grain weight and [16] for quality traits. The mean performance of F₁ hybrid rice, genotypes for 19 traits using critical differences revealed existence of very high level of variability in the lines, testers and crosses estimated in the present study.

Genetic improvement in crops depends on the magnitude of genetic variation and heritability of characters. A wide range of phenotypic coefficient of variation (4.09 – 43.43 %) and genotypic coefficient of variation (6.58 – 43.39 %) was recorded for 19 traits studied (Table 2). In the current investigation, estimation of genetic parameters revealed that the phenotypic co-efficient was slightly higher than the genotypic co-efficient of variability for 19 yield and quality traits studied, indicates all F₁'s and genotypes are interacted with environment. But, the slight variance between GCV and PCV, gives evidence of variability existing among the genotypes was mostly due to presence of genetic makeup. Similar observations for morphological traits were reported by [17, 18, 19]. In existing study, number of filled grains per panicle followed by single plant yield, Alkali spreading value, gel consistency and amylose content recorded high GCV and PCV it is conformity with the findings of [20, 21].

In case of quality traits phenotypic co-efficient (PCV) was slightly higher than the genotypic co-efficient (GCV) of variability for 19 yield and quality traits studied. In existing study, high GCV to PCV was observed for alkali spreading value and low GCV, PCV observed for grain breadth, Comparable findings were observed with [16, 22, 23, 24]. The presence of high scale of GCV and PCV for observed traits suggested better possibility for the enhancement through simple selection procedure.

Low GCV and PCV (< 10%) was recorded for the traits, milling percentage, head rice recovery, grain length, grain breadth, grain length after cooking, grain breadth after cooking and linear elongation ratio. Low GCV and PCV estimation of traits was noticed for milling per cent by [22, 23, 25]. Lower GCV and PCV results specifies narrow genetic base for these traits. hybridization or induced mutagenesis to widen genetic base followed by pedigree selection is followed to improve these characters.

Whereas moderate range of GCV and PCV (10 – 20 %) was observed for traits days to fifty percent flowering, plant height, number of productive tillers per plant, panicle length, 1000 grain weight, L/B ratio and breadth wise expansion ratio these results were consistent with the findings of [26,27] for L/B ratio. The moderate GCV and PCV specifies the presence of relatively moderate variability for these traits, which could be exploited for development by selection in advanced generations. The adjacent correspondence among the estimation of GCV and PCV for most of the traits indicated slighter environmental influence on the expression of traits and also reflected due to their high heritability values.

Presence of high heritability of a trait is an index of transmission of characters from parents to its progeny and estimation of heritability aids to plant breeder in selection of elite genotypes from diverse genetic population, hence a prerequisite prior knowledge is essential about the heritability of the traits for breeding programme [28]. Broad sense heritability defines both fixable (additive) and non-fixable (dominant and epistatic) variances which estimates the inheritance of a particular character [29].

In this context the existing study revealed heritability (broad sense) was high (> 60%) for all 19 yield and quality traits (Table 2), amylose content (99.89), gel consistency (99.81), number of filled grains per panicle (99.78), head rice recovery (99.41), plant height (99.06), single plant yield (99.01), days to 50% flowering (98.92), milling percentage (98.86), grain length (98.71), grain length after cooking (98.36), linear elongation ratio (96.77), 1000 grain weight (96.18), panicle length (94.47), Number of productive tillers per plant (94.43), alkali spreading value (90.84), L/B ratio (90.66), grain breadth after cooking (89.45), breadth wise expansion ratio (89.17) and grain breadth (81.29) similar high heritability estimates earlier reported by [24, 30, 31, 32].

Evaluation of high genetic advance (>20) was revealed for number of filled grains per panicle (83.14), gel consistency (37.82), days to fifty percent flowering (31.84), plant height (28.67), single plant yield (20.85), and gel consistency (20.03). Moderate genetic advance (10-20) for head rice recovery (11.88), amylose content (11.31) and milling percentage (11.86) and low genetic advance (0-10) for number of productive tillers (6.93), 1000 grain weight (6.67) panicle length (4.64), alkali spreading value (2.15), grain length after cooking (1.24), grain length (1.06), L/B ratio (0.53), breadth expansion ratio (0.45), grain breadth after cooking (0.35), grain breadth (0.25), linear elongation ratio (0.23), similar results was reported by [32, 33, 34].

Estimation of high genetic advance as percentage of mean results revealed that (>20) recorded for number of filled grains per panicle (89.28), single plant yield (69.77), alkali spreading value (66.69), gel consistency (46.32), amylose content (41.86), number of productive tillers (37.53), days to fifty percent flowering (36.8), plant height (34.40), 1000 grain weight (28.75), panicle length (21.90), breadth expansion ratio (20.96). Moderate genetic advance (%) of mean (10-20) observed for L/B ratio (19.72), grain length (19.19), linear elongation ratio (18.53), grain length after cooking (18.42), head rice recovery (17.34), milling percentage (14.99), grain breadth after cooking (13.8) and grain breadth (12.22), Similar results were also reported by [35, 23,33].

The knowledge only on estimates of heritability is not sufficient for an effective selection, along with heritability, genetic advance if studied might be more useful [21]. Selection of rice genotypes with high heritability along with high genetic advance as percentage of mean was recorded for amylose content, gel consistency, number of filled grains per panicle, plant height, single plant yield, days to 50 % flowering, 1000 grain weight, panicle length, number of productive tillers per plant, alkali spreading value, breadth wise expansion ratio, these results determines the predominance of additive gene action for high heritability and genetic advance traits and enables care of selection. These type of results with high genetic advance and high heritability were reported by [20, 21] for plant height, number of productive tillers per plant and number of filled grains per panicle 18] for plant height and number of filled grains per panicle, [22] for the traits L/B ratio, alkali spreading value and amylose content [16] for the traits grain length, L/B ratio, breadth after cooking, alkali spreading value and gel consistency [36, 6, 37] for single plant yield and number of filled grains per panicle.

The estimate of high heritability and moderate genetic advance as per cent of mean was observed for grain length, grain length after cooking, milling percentage, linear elongation ratio, L/B ratio, head rice recovery, grain breadth and grain breadth after cooking traits, specifies dominance and epistatic effects. The presence of dominance and epistatic effects important for inheritance of these traits and selection of such traits results less effective similar results reported by [28, 24].

CONCLUSION

Existence of genetic variability is the primary requirement in rice crop to improve economically important traits like yield and physico-chemical quality traits. From this study, we conclude that the lines, testers along with their F_1 crosses had adequate amounts of variability for yield associated traits and physico-chemical quality traits. Selection based on high heritability along with genetic advance was observed amylose content, gel consistency, number of filled grains per panicle, plant height, single plant yield, days to 50 % flowering, 1000 grain weight, panicle length, number of productive tillers per plant, alkali spreading value, breadth wise expansion ratio resulted that these traits are control of additive gene action in the inheritance of traits and selection pressure applying on these characters useful for the improvement of yield associated and quality traits.

Acknowledgement

Conflict of interest

None declared.

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