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Variability and association analysis on traditional rice grain parameters for better plant selection

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Abstract
Thirty eight rice germplasm lines with three check varieties were evaluated for twelve grain traits to estimate the genetic variability, heritability, genetic advance and character association for grain yield with yield attributing traits. The analysis of variance revealed highly significant difference among the germplasm accessions for the traits studied indicating that a large amount of variability was present in a set of genotypes. The magnitude of phenotypic coefficient of variation was higher to corresponding genotypic coefficient of variation for all the traits. The genotypic correlation coefficient was found to be higher than phenotypic correlation coefficient indicating a strong inherent association for grain yield per plant, Grain length, width, Hulling percentage, Milling percentage, primary panicle, grain L/B, HRR, grain thickness, secondary panicle, number of grains per panicle and 100 seed weight Therefore, selection based on these traits will be effective in improving the grain yield.

Keywords: Variability, association, heritability, landraces

Introduction

Rice is perceived not only as a commodity of food but also as a life saving 'Aushadh' – the medicine in all ages. In the great literature of *Susruta Samhita* is a representative work of Ayurveda in India. Genetic variability studies provide basic information regarding the genetic properties of the population. Knowledge on nature and magnitude of genotypic and phenotypic variabilities present in any crop species play an important role in formulating successful breeding programme Association analysis measures the natural relationship between various plant characters and determines the components on which selection can be made for improvement. Knowledge of correlation that exists among important characters may facilitate proper interpretation of results and provide basis for planning more efficient breeding programmes and Ullah *et al.* (2011) [19] reported that grain yield was very strong positive genotypic correlation with number of grains per panicle, Grain L/B ratio, milling percentage and panicle length. Ukaoma *et al.* (2013) [18] reported that grain yield was also positively correlated with high positive significant correlation with grain yield. Rathore *et al.* (2014) [15] also reported that strong positive and significant association was found between panicle length,grain yield/ hill; between spikelets/panicle and grain yield/ hill; between grain yield/ hill and test weight. Kumar *et al.* (2014) [5] reported that the highest positive direct effect on grain yield per plant was observed for panicles weight per plant followed by number of spikelets per panicle, panicle index, number of leaves per plant, plant height, days to heading, hulling %, grain length, average panicle weight and flag leaf width, whereas the negative direct effect on grain yield per plant was observed for number of tillers per plant, milling %, head rice recovery %, grain Width and The number of productive tillers per plant had the maximum positive effect on grain yield followed by panicle length. These findings were also exhibited by Meenakshi *et al.* (1999) [8]. The days to heading and hulling % contributed positive direct effect on grain yield per plant was reported by Nandan *et al.* (2010) [11]. Selvaraj *et al.* (2011) [16] recorded negative direct effect of number of filled spikelets per panicle and panicle length per plant on grain yield per plant. The negative direct effect on grain yield were recorded by number of chaffy grains per panicle, number of filled grains per panicle, 100 grain weight, was reported by Ganesan *et al.* (1997) [3]. Keeping in this view, an attempt was made to characterize a set of untapped traditional land races to provide betterment parental selection for future crop improvement studies.

Research methodology
Research site
This investigation was carried out the rice bran oil content estimation of traditional rice

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germplasm at the Department of Rice (Paddy Breeding Station), Centre for Plant Breeding and Genetics (CPBG) and Department of forage crops (CPBG), Tamil Nadu Agricultural University (TNAU), Coimbatore. The station is located at N latitude and E longitude with an elevation of 426.72 m above the mean sea level.

Sample Collection
Investigation consists of 37 genotypes (Pic.1.) with medium and long duration traditional paddy varieties from Tamil Nadu, Kerala states of India and three improved varieties namely CR1009, IR20, CO (R) 50.
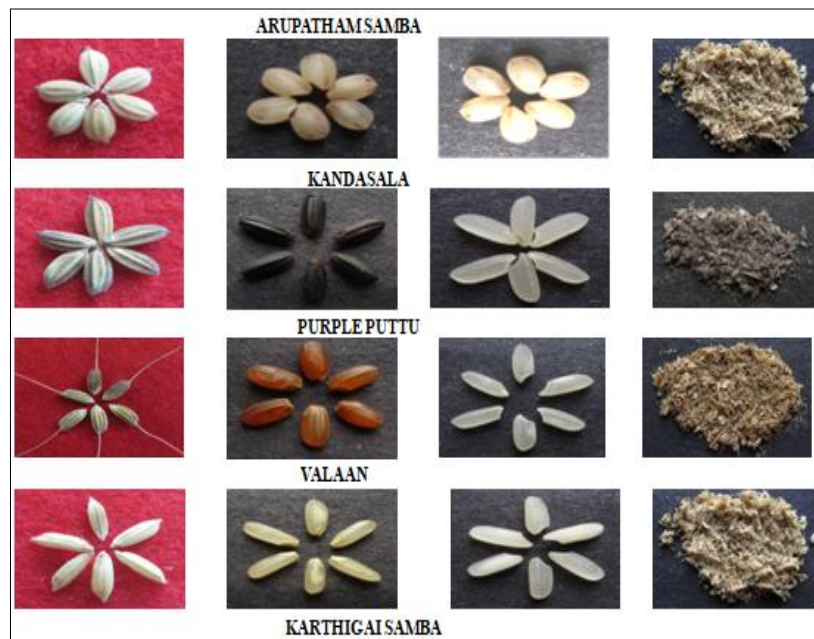
Pic 1: Grain diversity of different genotypes

These genotypes were selected based on the grain characters from different sources namely Paddy Breeding Station (Coimbatore), Hybrid Rice Evaluation Centre (Gudalore), Centre for Indian Knowledge System (CIKS) in Sirkali and Sharadashram, Ulunthurpet of Tamilnadu. recorded were converted into micronutrient concentration (Fe, Zn, Mn, and Cu) using standard curve.

Statistical analysis
Analysis of Variances: The analysis of variance of RBD and their significance for all the characters with two replications were worked out as suggested by Panse and Sukhatme (1961) [13]. The mean data collected from genotype were subjected to statistical analysis.

Phenotypic and genotypic variances
These were estimated according to the formulae given by Lush (1940) [6].

Genotypic variance$((\sigma^2 g) = M_1 - M_2 / r$

Phenotypic variance $(\sigma^2 p) = \sigma^2 g + \sigma^2 e$

Phenotypic and genotypic coefficients of variability (PCV and GCV)
For each character, phenotypic and genotypic coefficients of variability (PCV and GCV) were computed based on the method given by Burton (1952)

PCV (%) = $\sqrt{\sigma^2 p}$ / Grand mean X 100
GCV (%) = $\sqrt{\sigma^2 g}$ / Grand mean X 100

Heritability: Heritability (h^2) in a broad sense was calculated according to Lush (1940) [6].

h^2 (Broad sense) = $\sigma^2 g / \sigma^2 p$ X 100

Genetic advance: Genetic advance was derived according to the method given by Johnson *et al*., (1955)a for each character.

Genetic advance = $\sigma^2 g / \sigma p$ X K

Where,
$\sigma^2 g$ = genotypic variance
σp = phenotypic standard deviation
K = selection differential
Genetic advance was expressed as percentage of mean by using the formula suggested by Johnson *et al*. (1955) b [4].
r_{iy} = correlation coefficient between i and y

Association analysis: The correlation between yield and its component traits and among themselves as well as between quality characters were worked out as per the methods suggested by Johnson *et al*. (1955) [4].

Where,
r = correlation coefficients
Cov. xy = cov between the characters x and y,
The significance of the correlation estimates were tested by using the formula.

Where,
r = Correlation co-efficient
n = Number of paired observation
By comparing the 't' cal value with 't' table values at 5 per cent and 1 per cent levels at n-2 degrees of freedom, the significance was found.

Result and Discussion

The range for grain length was from 5.37mm (Rasakadam) to 8.93 mm (Purple puttu) with a grand mean of 7.40 mm. The phenotypic and genotypic variances were 0.77 and 0.69 respectively. The phenotypic coefficient of variation and genotypic coefficient of variation were 11.92 and 11.29 respectively. Heritability and genetic advance as per cent of mean 89.78 percent and 22.04 percent respectively. The grain width of the genotype ranged from1.78mm (CR 1009) to3.23 mm (Valaan) with the grand mean of 2.46mm The phenotypic and genotypic coefficients of variations were 17.42 to 15.55 respectively. It recorded the phenotypic variance of 0.18 and genotypic variance 0.14 of respectively (Fig.1.)
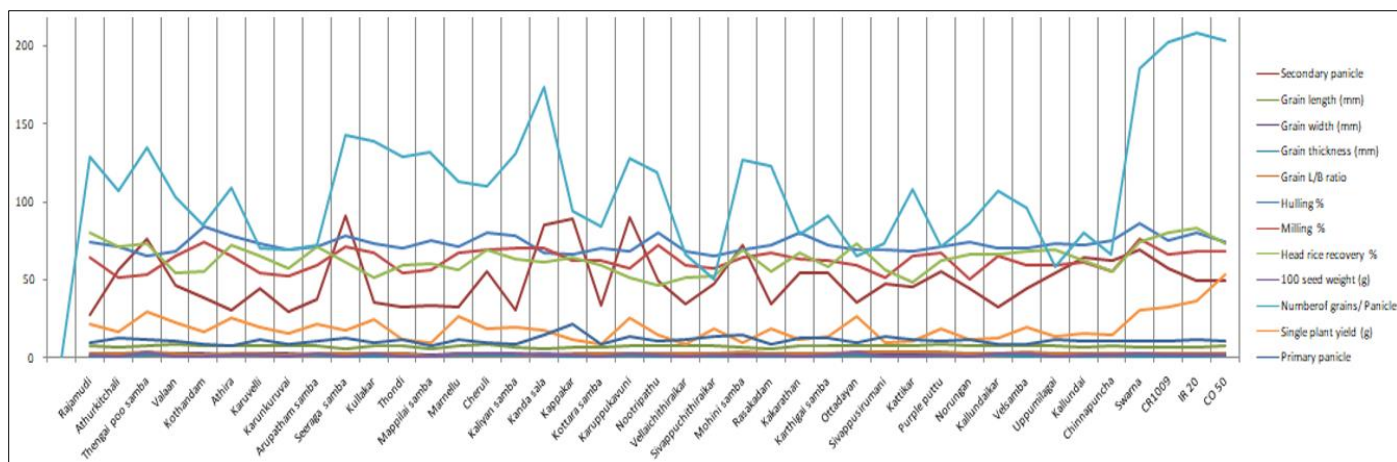

Fig 1: Mean performance of grain traits in rice land races

The estimate of heritability and genetic advance as per cent of mean were79.70 per cent and 28.60 per cent respectively. The grain thickness ranged from 1.27mm (Sivappu chithiraikar) to 2.13mm (Kallurandaikar) with the grand mean of 1.74mm. The phenotypic and genotypic coefficients of variations were 12.77 and 10.56 respectively. It recorded the phenotypic variance of and genotypic variance of 0.04 and 0.03 respectively. The estimate of heritability and genetic advance as per cent of mean were 68.47 per cent and 18.01 per cent respectively The grain L/B ratio showed variability range from 0.95mm (Mappilai Samba) to 4.10 mm (Sivappu sirumani) with the grand mean of 3.03 mm (Table 3). The phenotypic and genotypic variances were 0.32 and 0.28 respectively. This trait recorded phenotypic coefficient of variation of 18.74 and genotypic coefficient of variation of 17.47. It showed a high heritability of 86.89 per cent and 33.55percent as genetic advance. Hulling per centage of the genotypes showed a range variability between 65.30 (Thengaipoo samba) and 86.63 (Swarna) with the grand mean of 73.18. The estimates of phenotypic and genotypic variances were 30.32 and 22.52 with a moderate difference between them. The coefficient of variation due to phenotype and genotype were 7.52 and 6.49respectively. This trait was found to possess high heritability estimate of 74.29 percent along with the genetic advance of 11.52 as percent of mean Milling percentage of the genotypes showed a range variability between 50.22 (Norungan) and 76.22 (Swarna) with the grand mean of 62.47.The estimates of phenotypic and genotypic variance were 51.44 and 41.45 with a moderate difference between them. The coefficient of variation due to phenotype and genotype were 11.48 and 10.31respectively. This trait was found to possess high heritability estimate of 80.58 percent along with the genetic advance of 19.06 as per cent of mean. The head rice recovery ranged from 46.32 (Nootripathu) to 83.49 (IR 20) with a grand mean of 63.47. This trait recorded the phenotypic variance of 88.97 and genotypic variance of 82.81. The phenotypic and genotypic coefficients of variation were 14.86 and 14.34 respectively. The head rice recovery showed a heritability estimate of 93.08

per cent with the genetic advance of 28.50 percent of mean. Hundred grain weights of the genotypes showed range variability between 1.10g (Kothandam) and 3.47 g (Thengaipoo samba) with the grand mean of 1.85 g. The estimates of phenotypic and genotypic variances were 0.42 and 0.41 with a narrow difference between them. The coefficient of variations due to phenotype and genotype were 45.98 and 43.87 respectively. This trait was found to possess high heritability estimate of 91.03 per cent along with the genetic advance of 86.23 as per cent of mean. Number of grains per panicle the genotypes showed variability between 50.82 (Sivappu chithiraikar) to 207.92 (IR 20) with a grand mean of 113. The estimates of phenotypic and genotypic variances were 2731.62 and 2486.72 respectively. The coefficient of variation due to phenotype and genotype were 35.30 and 34.60. High heritability 96.06 per cent and high genetic advance 69.86 as per cent of mean were recorded for this trait. Number of primary panicles for the genotypes showed variability between 7.33 (Athira) to 21.67 (Kappakar) with a grand mean of 10.83. The estimates of phenotypic and genotypic variances were 10.15 and 4.55 respectively. The coefficient of variation due to phenotype and genotype were 29.29 and 19.62. High heritability 44.84 percent and high genetic advance 27.06 as percent of mean were recorded for this trait The number of secondary panicle the genotype showed variability between 27.67 (Rajamudi) to 91.00 (Seereaga samba) with a grand mean of 49.7. The estimates of phenotypic and genotypic variances were 387.63 and 290.06 respectively. The coefficient of variation due to phenotype and genotype were 39.61 and 34.26. High heritability 74.83 percent and high genetic advance 61.06 as percent of mean were recorded for this trait. Single plant yield for the genotype showed variability between9.10g (Kottara samba) to 53.18 g (CO 51) with a grand mean of 19.37 g. The estimates of phenotypic and genotypic variances were 57.13 and 52.02 respectively. The coefficient of variation due to phenotype and genotype were 64.50and 59.22. High heritability 82.2 per cent and high genetic advance 52.45 as per cent of mean were recorded for this trait. In the present investigation, the

phenotypic and genotypic coefficient of variations were highest for secondary panicles per plant, number of grains per panicle, 100 seed weight, single plant yield Singh *et al.* (2012), Mahalingam *et al.* (2013) [7] and Mohan Lal *et al.* (2011) [9]. Moderate GCV and PCV were recorded in the traits like grain length, grain width, stigma length, width were accorded with the findings of Rao *et al.* (2010) [14] and Paikhomba *et al.* (2014) [12]. High heritability was expressed by characters namely number of secondary panicles, grain length, grain width, grain thickness, grain L/B ratio, hulling per cent, milling per cent, head rice recovery, number of grains per panicle and hundred seed weight Similarly Akinwale *et al.* (2011) [1] estimated that there was a higher heritability present for the number of panicles per plant,

panicle length, panicle weight, number of grains per panicle, 100-grain weight and yield (t/ha) respectively. When there was a heritability of 1000 grain weight respectively, the heritability for yield (t/ha) was found to be 72.1 per cent. Seyoum *et al.* (2012) [17] estimated the heritability and reported for the traits *viz.*, panicle length, tillers per plant, panicles per plant, grains per panicle, spikelets per panicle, total spikelet fertility, 1000 grain weight and grain yield. Single plant yield showed positively and significant direct association with following traits like hulling percentage, milling percentage and number of grains per panicle likewise negative and significant association with number of primary panicles, grain length, grain width, grain thickness and 100 seed weight. (Table.1.)

Table 1: Association analysis of different grain traits in rice land races

Traits	PP	SP	GL	GW	GT	GL/B	HULL	MILL	HRR	100S	NP	SPY
PP	1											
SP	0.68792	1										
GL	-0.0053	-0.1921	1									
GW	-0.0627	-0.1393	0.51859	1								
GT	-0.0761	-0.0264	0.51442	0.73796	1							
G L/B	0.13904	0.05955	0.32254	-0.5735	-0.2529	1						
HULL	-0.3508	-0.0959	-0.1798	-0.0276	-0.0248	-0.1426	1					
MILL	-0.1069	0.10668	-0.2638	-0.1105	-0.1518	-0.0266	0.56842	1				
HRR	-0.0704	0.05566	-0.0997	-0.2805	0.03152	0.22175	0.23895	0.04588	1			
100S	-0.1038	0.11574	0.24161	-0.0547	0.00987	0.25954	-0.0808	0.11006	0.17075	1		
NP	-0.0112	0.24273	-0.543	-0.287	-0.191	-0.1176	0.31454	0.49912	0.40187	0.14462	1	
SPY	-0.1338	0.07142	-0.05	-0.0315	-0.0157	0.06422	0.19236	0.30084	0.48296	0.49562	0.62578	1

An attempt was made in the present study to estimate the correlation coefficient for twenty traits which indicated that Single plant yield positively significant direct association with following traits like days to fifty percent flowering, leaf length, leaf width, number of tillers, number of productive tillers, hulling percentage, milling percentage head rice recovery, head rice recovery, number of grains per panicle, likewise negatively significant with Pant height, culm length and primary panicle, grain length, grain width, grain thickness and 100 seed weight. These results were accordance with the findings of Ukaoma *et al.* (2013) [18] and Moukoumbi *et al.* (2011) [10]. Inter correlation among the yield component traits were also estimated and the study exhibited that the days to fifty per cent flowering showed significant positive correlation with number of grains per panicle. Plant height exhibited significant with positive association with intermodal length and leaf length positively correlate with important yield characters of number of grains/ panicle. Leaf width significant and positively correlate with number of tillers, number of productive tillers and head rice recovery. Total number of tillers shows significant and positive association with number of productive tillers. Grain width was significant positive correlation with grain thickness, grain L/B ratio. Hulling per cent had significant positive correlation with milling per cent and head rice recovery, same results were reported by *Moukoumbi et al.* (2011) [10]. The grain traits like hulling per cent, milling per cent, number of grains per panicles are significantly with positively associated to plant yield.

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