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## Quantitative characterization on indigenous rice cultivars through Agro-Morphometric traits

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### Abstract

Genetic variation provides recombinant responses which are important for the development of new lines with different aspect of crop improvement studies. Keeping in this view, this work was carried out to evaluate genetic variability of different traditional land races in rice to create the relationships between their morphological and yield components. To target with two replications field trials were carried out on thirty seven rice genotypes with three check estimation to examine their multiple characters. Different traits with genotypic and phenotypic coefficients, variance components, expected genetic advance, heritability and Genetic advance were calculated. 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.

**Keywords:** Rice, quantitative trait, morphology, variability

### Introduction

Rice has widest germplasm collection than other cereal crops. It has to be made productive through several achievements in rice breeding programme. The germplasm provides immense scope for wide variability. Genetic divergence is an efficient tool for an effective choice of parents for hybridization programme. Ancient Tamil literary works and scriptures incorporate the remarkable medicinal qualities of different traditional rice varieties of those days. Estimation of genetic parameters *viz.*, coefficient of variation, heritability and genetic advance provide initial information about the amount of variability present in the germplasm and predicting the result and effect in selection of the best genotypes for yield and its attributing traits. The simple measures of variability partitions the variation into phenotypic, genotypic and environmental components.

Phenotypic coefficient of variation (PCV) is the measure of total variability resulting from the genotype, environment and interaction of both. Phenotypic and genotypic coefficients of variation provides the real picture of variability concealed in a population. Heritability coupled with gene action would give a more reliable index of selection value (Burton, 1952) <sup>[1]</sup>. Plant height is an important trait contributing yield. Prasad *et al.* (2013) <sup>[2]</sup> also reported that plant height has significant correlation with grain yield. Ullah *et al.* (2011) <sup>[3]</sup> reported that grain yield was very strong positive genotypic correlation with number of grains per panicle, total number of productive tillers per plant, harvest index, Ukaoma *et al.* (2013) <sup>[4]</sup> reported that grain yield was also positively correlated with all the characters except days to booting, days to.

### Research Methodology

#### Research methodology Research site

This investigation was carried out the rice bran oil content estimation of traditional rice 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 50% heading and unproductive tiller number. Rathore *et al.* (2014) <sup>[4]</sup> also reported that negative and significant association between days to 50% flowering and tillers/ hill, panicles/hill, biological yield, harvest index, spikelets/panicle, grain yield/hill and test weight and Kumar *et al.* (2014) <sup>[5]</sup> 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. These findings were also exhibited by Meenakshi *et al.* (1999) <sup>[6]</sup>, Nandan *et al.* (2010) <sup>[7]</sup>. Selvaraj *et al.* (2011) <sup>[8]</sup> There is future need to expand the genetic base of the rice crop by introgression genes from diverse sources. located at N latitude and E longitude with an elevation of 426.72 m above the mean sea level.



between 4.60 (Kaliyan samba) and 14.92 (Chinna puncha) with a grand mean of 8.68. The phenotypic and genotypic variances were 4.03 and 3.21 respectively. The phenotypic coefficient of variation was 23.18 and the genotypic coefficient of variation was 20.67. This trait recorded high heritability of 79.55 percent along with high genetic advance as a per cent of mean of 37.98. The inter node length range

from 13.61cm (Kothandam) to 35.23cm (Mappilai samba) with a grand mean of 23.17cm. The phenotypic and genotypic variances were 27.33 and 20.25 respectively. The phenotypic and genotypic coefficient of variations were 22.56 and 19.42 respectively. Heritability and genetic advance as per cent of mean were 74.1 per cent and 34.44 per cent respectively.

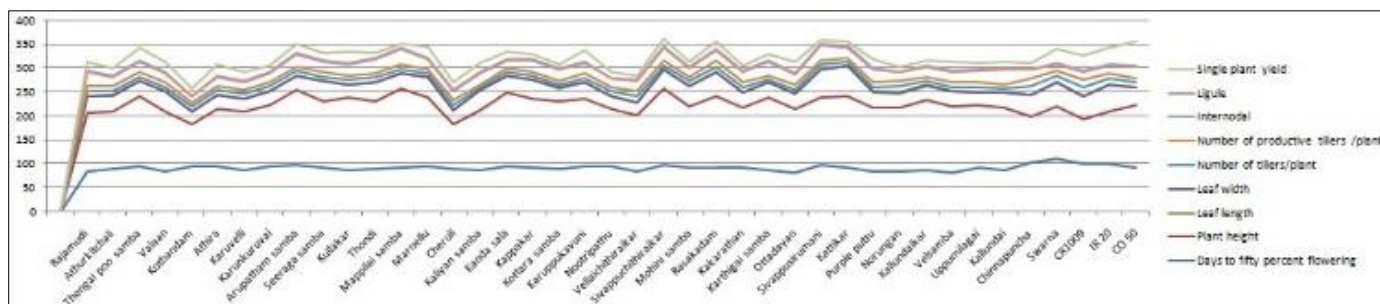


Fig 1: Mean performance of different biometrical traits in rice land races

The ligule length ranged from 0.2mm (Valaan) to 1.52 mm (Kattikar) with a grand mean of 0.62 mm (Fig.3). This trait recorded the phenotypic variance of 0.11 and genotypic variance of 0.09 the phenotypic and genotypic coefficients of variation were 53.35 and 49.85 respectively. The plant height showed a heritability estimate of 87.32 per cent with the genetic advance of 95.97. Number of grains per panicle the genotypes showed variability between 50.82 (Sivappu chithiraikar) to 207.92 (IR 20) with a grand mean of 113.67. 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 traits. Number of primary panicles for the genotypes showed variability between 7.33 (Athira) to 21.67 (Kappakar) with a grand mean of 10.83 These results were accorded with the findings of Rao *et al.* (2010) [18] and Paikhomba *et al.* (2014) [19] and Low GCV and PCV were recorded in days to fifty per cent flowering as stated by Paikhomba *et al.* (2014) [19]. These results were lined with Verma *et al.* (2010) [20] for tillering traits in rice.

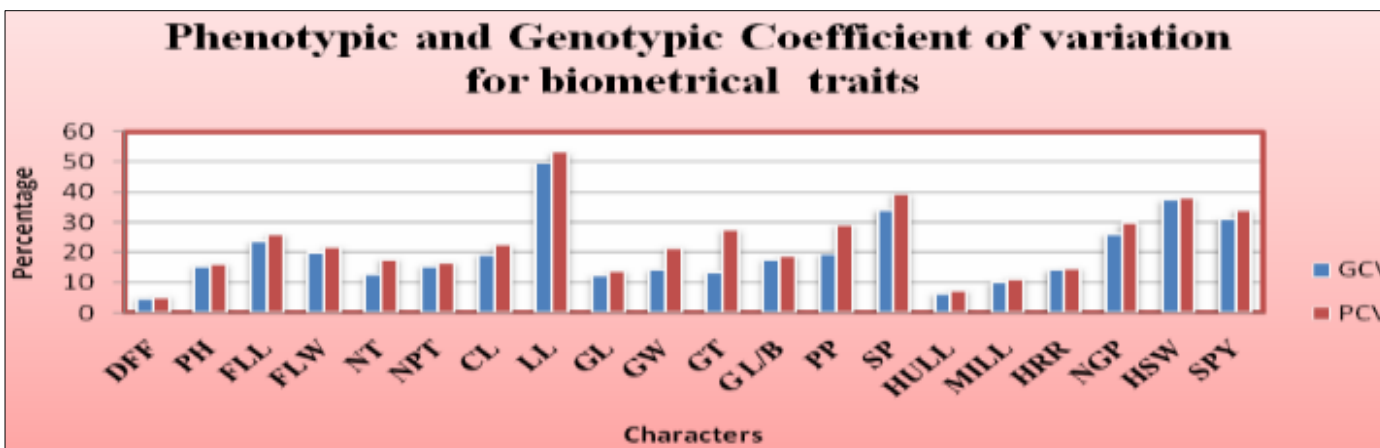


Fig 2: PCV and GCV for biochemical traits

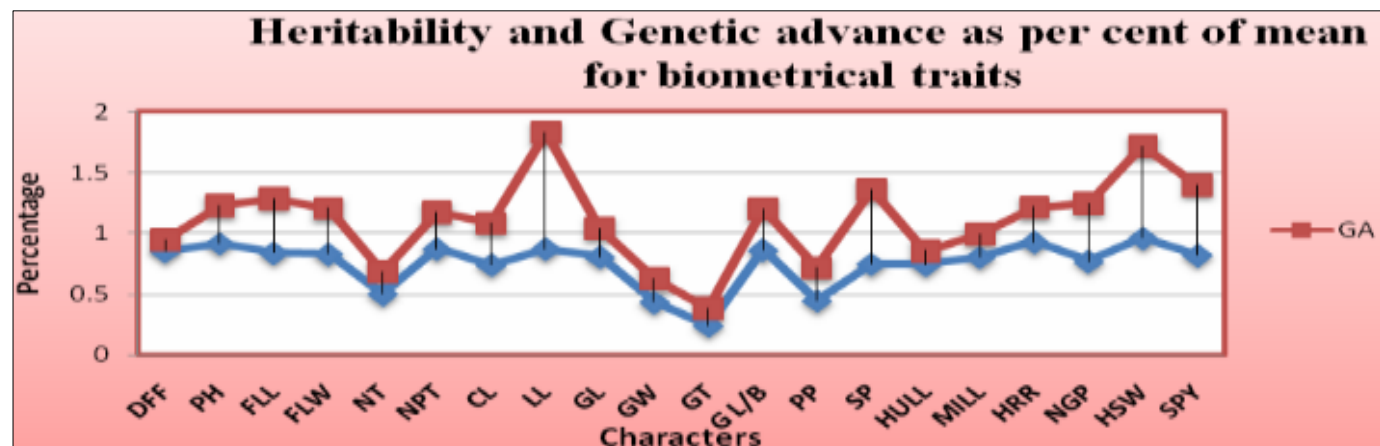


Fig 2: Heritability and Genetic advance for biochemical traits

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 between 9.10g (Kottara samba) to 53.18 g (CO 51) with a grand mean of 19.37g. The estimates of phenotypic and genotypic variances were 57.13 and 52.02 respectively. The coefficient of variation due to phenotype and genotype were 64.50 and 59.22. High heritability 82.2 per cent and high genetic advance 52.45 as per cent of mean were recorded for this trait. The similar results were observed Ukaoma *et al.* (2013) [4], Singh *et al.* (2013) [21] and Shejul *et al.* (2013). High heritability with moderate genetic advance observed for following characters like days to fifty per cent flowering, grain thickness, milling per cent, hulling per cent and also low heritability with low genetic advance observed in pasting temperature. The similar results were found by Rathi *et al.* (2010) [22] and Parikh. (2012) [23].

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