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Research Article

Genetic variability and frequency distribution studies in F$_2$ population involving traditional variety mappillai samba

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Abstract
An experiment was performed to analyse the variability parameters and frequency distribution properties in F$_2$ population of CBMAS 14065 x Mappillai Samba for grain yield and its associated parameters. The estimated genetic parameters showed, slightly higher PCV than GCV reflecting the influence of environment. High GCV, high PCV, high heritability along with high genetic advance as per cent of mean was observed in the number of filled grains per panicle suggests the additive gene action which is important for selection. The parameters like plant height, the number of productive tillers per plant, panicle length, the number of filled grains per panicle and thousand grain weight showed a significant positive correlation with single plant yield. Significant positive skewness were observed for the number of productive tillers and grain L:B ratio which helps in fixing the selection criterias and benefits the improvement of traits in F$_2$ generation.

Key word
Frequency distribution, Heritability, Rice, Skewness, Variability.

INTRODUCTION

Rice (*Oryza sativa* L.) is an edible cereal with high amount of starch. It is an annual monocot grown under submerged condition belonging to the family *gramineae*. More than 100 countries across the world consumes rice as their staple food. The peoples from East and South East Asia are fully depend on the rice to meet their daily nutritional requirements. The rice production in the world is about 759.6 million tonnes; while in India is about 172.58 million tonnes (FAOSTAT, 2018). The global human per capita of energy and protein which met by rice is about 21% and 15% (Ricepedia, 2018). A study was conducted at IRRI (IRRI, 2000) predicted that 800 million tonnes of rice is required to meet the demand by 2025. To meet such a demand, there is a need for improving the yield with respect to good nutritional quality and resistance to

various stresses. The inheritance pattern of yield and its associated parameters was necessary to increase the yield (Priyanka *et al.,* 2019).

The variability existing in the F$_2$ population is the key element to improve the trait of interest. The observable variations or the phenotypic variations were the result of genotypic and environmental components among the individuals of the population. By separating the genetic variation from the environmental variation the breeding potential of the genotype can be estimated accurately (Balat and Jignesh, 2018). Grain yield is determined by most of the interlinked polygenic characters (Panwar and Mathur, 2007). Greater level of genetic heterogeneity were observed in traditional landraces than improved

varieties (Khandappagol *et al.,* 2019). Based on this, the variance components such as phenotypic coefficient of variance (PCV), genotypic coefficient of variance (GCV), heritability and genetic advance as per cent of mean were studied. Knowledge of genetic variability parameters provides immense value in the selection of superior segregants for improving yield. The number of genes controlling for each trait and the nature of gene action can be well understood by the skeweness and kurtosis. The relationship between yield and other parameters can be analysed using the correlation studies. Yield component is always interrelated with its associated traits in both positive and negative ways (Lingaiah *et al.,* 2015). Hence, the current study was carried out to analyse the genetic variability, frequency distribution and correlation between yield and its associated traits to find out the superior segregants in F_2 population of CBMAS 14065 x Mappillai Samba.

MATERIALS AND METHODS
The current study was carried out at the Department of Rice, TNAU, Coimbatore. A total of 106 F_2 segregants which obtained from the hybridization between CBMAS 14065

The data on quantitative traits were collected in F_2 progenies and from randomly selected five plants in parents. The quantitative traits observed were days to first flowering (DFF), plant height (PH), the number of productive tillers (NPT), flag leaf length (FLL), panicle length (PL), the number of leaves in primary tiller (NLPP), the number of filled grains per panicle(NFG), single plant yield (SPY), grain L:B ratio and thousand grain weight (TGW). The mean values of F_2 population were used for analysis of coefficients of skewness and kurtosis using 'SPSS (16.0)' software program. Kurtosis point out the number of genes that controls the traits. Whereas, skewness points out the nature of gene action involved in inheritance of yield and yield contributing traits. GCV and PCV was calculated using the formula proposed by Johnson *et al.* (1955). The range of variation was categorized using Sivasubramanian and Madhavamenon (1973) method of estimation. Genetic advance was calculated by the method suggested by Johnson *et al.* (1955). Correlation and frequency distribution studies were carried out using SPSS 16.0 software (Verma, 2012).

RESULTS AND DISCUSSION
The estimation of genetic variability and its mean performances were of greater significance in crop improvement. Genetic variability, correlation studies and frequency distribution were carried out for ten biometrical traits recorded in F_2 segregating population and the results were presented in **Table 1, 2 and Fig 1**. In the present study, the estimates of GCV were slightly lower than the corresponding PCV estimates for most of the characters studied stating that the portion of PCV was more contributed by the genotypic component and less affected by the environment. Therefore, phenotypic

selection alone paves way for an effective improvement of traits. High PCV and GCV was observed in the number of filled grains per panicle indicates the high amount of variability. These results are in fullfilment with Seneega *et al.* (2019), Priyanka *et al.* (2019), Behara *et al.* (2018), Sheshaiah *et al.* (2018) and Badri *et al.* (2016). High PCV and high GCV for a trait may be due to an additive gene action which provides an extent for selection. Such traits could be improved through simple selection methods. Moderate PCV and GCV were observed in traits such as plant height, flag leaf length, the number of leaves in primary panicle and thousand grain weight indicating the existence of moderate variability. Such traits could be improved through selection in the advanced generations. These results are in accordance with Lingaiah *et al.* (2018) for plant height and thousand seed weight, kalaiselvan *et al.* (2019) and Behera *et al.* (2018) for flag leaf length. Low PCV and GCV were observed for days to first flowering, panicle length and grain L:B ratio. Lower GCV and PCV were due to the narrow genetic base. Such traits can be improved by widening the genetic base through hybridization or induced mutagenesis accompanying by pedigree selection in further generations. This results were similar with Divya *et al.* (2018) and Savithri *et al.* (2018) for days to first flowering and panicle length and Seneega *et al.* (2019) for grain L:B ratio. The PCV along with GCV is important in selection as certain genes are expressed under favourable environmental condition (Singh *et al.,* 1974).

Heritability is the measure of phenotypic variation due to the action of genes. Selection is practised for improving the character. The genetic variability transmitted from parents to offspring was reflected by the heritability. As heritability involve both additive and non additive gene action prediction of resultant effect based on heritability alone is not very much useful. Hence, it should be coupled with GAM for more reliable results.

High heritability coupled with high GAM was observed in DFF, PH, NPT, FLL, NFG and TGW. These traits were controlled by additive gene action and effortlessly fixed by selection. These results were in fulfillment with Sheshaiah *et al.* (2018), Hefeina *et al.* (2016) and Bharath *et al.* (2018) for days to first flowering, Seneega *et al.* (2019) for plant height, Divya *et al.* (2018), Bharat *et al.* (2018) and Savitri *et al.* (2018) for the number of productive tillers and thousand seed weight, Bharath *et al.* (2018) for flag leaf length. High heritability and moderate genetic advance as per cent of mean was observed in panicle length. This was in fulfilment with Singh *et al.* (2019) and Behera *et al.* (2018). High heritability and moderate GAM is the outcome of both additive and non additive gene action for the trait which can be improved by recurrent selection (Dhurai *et al.,* 2014). Low heritability and GAM was noted in grain L: B ratio and single plant yield. This result was in compliance with Behera *et al.* (2018) for grain L:B ratio

and Lingaiah *et al*. (2018) for single plant yield. Low heritability and genetic advance as per cent of mean were the result of non additive gene action and selection of such characters was not effective in plant breeding.

Table 1. Genetic Variability analysis for quantitative traits in F$_2$ generation

Traits	P$_1$	P$_2$	Mean	Min	Max	GCV	PCV	Heritability	GAM	Skewness	Kurtosis
DFF	111.00	120.50	111.66	89.00	140.00	10.12	10.19	98.56	20.69	0.11	-0.73
PH	97.42	146.80	137.52	87.00	170.20	12.84	13.02	97.36	26.11	-0.39	0.31
NPT/P	16.20	19.20	11.14	3.00	29.00	35.77	39.75	80.98	66.31	1.23**	2.62**
FLL	27.40	41.98	34.70	22.50	54.50	14.16	17.51	65.42	23.60	0.55	0.21
NLPT	3.00	3.20	2.97	2.00	4.00	11.28	14.95	56.92	17.53	-0.13	2.19**
PL	23.40	26.76	24.59	19.70	30.20	7.34	8.82	69.14	12.57	0.26	-0.48
NFG	328.40	180.00	182.26	58.00	396.00	25.85	28.55	82.03	48.23	0.52	1.95
LB ratio	3.78	2.99	3.22	2.59	4.28	6.08	10.08	36.38	7.56	0.90**	0.91**
TGW	13.30	29.34	19.52	13.30	26.00	12.48	13.03	91.75	24.62	-0.17	0.02
SPY	63.08	43.94	22.11	3.20	49.02	15.23	43.38	12.32	11.01	0.62	0.20

**. Significant at the 0.01 level. *. Significant at the 0.05 level.

DFF: Days to first flowering, PH: Plant height, NPT/P: Number of productive tillers per plant, , FLL: Flag leaf length, NLPT: Number of leaves in primary tiller, PL: Panicle length, NFG: Number of filled grains per plant, LB ratio: Grain Length and Breadth ratio, TGW: Thousand grain weight, SPY: Single Plant yield. PCV: Phenotypic coefficient of variation, GCV: Genotypic coefficient of variation, GAM: Genetic advance as per cent of mean
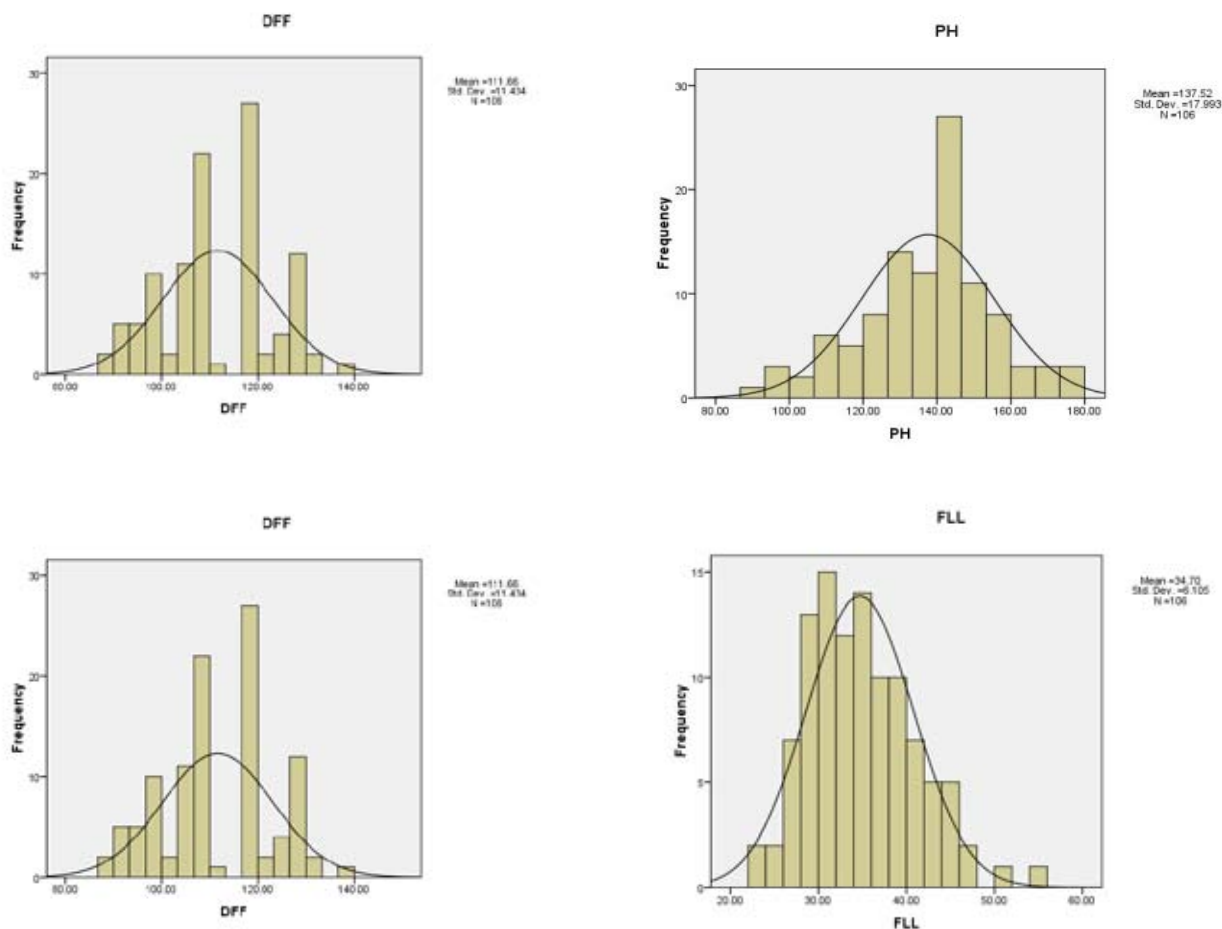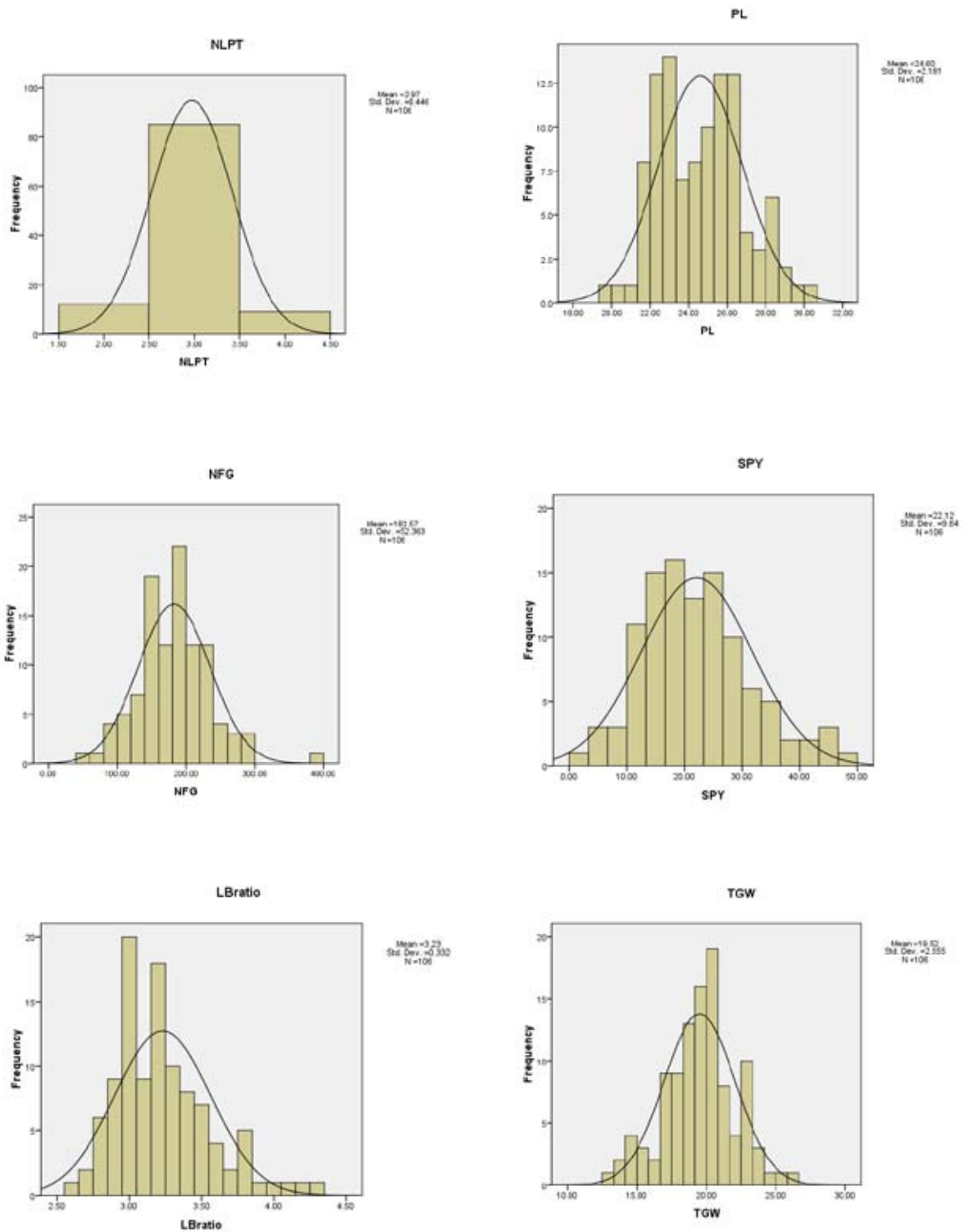
Fig. 1. Frequency distribution of quantitative traits in F_2 generation

Table 2. Genotypic correlation coefficient between the biometrical traits in F₂ generation

Character	DFF	PH	NPT	FLL	NLPT	PL	NFG	LB ratio	TGW	SPY
DFF	1	0.271**	0.060	0.093	0.190	0.057	-0.041	0.008	0.051	0.040
PH		1	0.011	0.194*	0.331**	0.344**	0.080	-0.148	0.286**	0.227*
NPT			1	-0.014	-0.089	-0.117	-0.055	0.112	-0.018	0.553**
FLL				1	0.079	0.398**	0.176	-0.098	0.007	0.108
NLPT					1	0.160	-0.031	-0.187	0.154	0.048
PL						1	0.342**	-0.066	0.057	0.289**
NFG							1	0.024	-0.008	0.354**
LBratio								1	-0.351**	-0.041
TGW									1	0.230*
SPY										1

**Correlation is significant at the 0.01 level.
* Correlation is significant at the 0.05 level.

Correlation studies provide breeder a wide knowledge about the association of characters, which aids in the selection of elite genotype. Grain yield is a complex trait largely affected by the contributing traits. Correlation studies between the grain yield and yield attributes provides a way for improving the yield. In the present study, plant height observed a significant positive correlation with panicle length and single plant yield. These results were in accordance with Hefeina *et al.* (2018). Number of productive tillers showed a significant positive correlation with single plant yield. These results were in conformity with Lilly *et al.* (2018) and Abhilash *et al.* (2018). Single plant yield was in significant positive correlation with panicle length, the number of filled grains per panicle and thousand grain weight. Phenotypic selection of these characters may be effective (Kahani and Hittalmani, 2015). Hence, the above traits could be considered as valuable yield improving traits and selection for this trait would ultimately improve the yield. These results were similar with results of Priyanka *et al.* (2019) for panicle length and for the number of filled grains per panicle, kalaiselvan *et al.* (2019) and Hefeina *et al.* (2016) observed similar results.

A significant positive skewness and leptokurtic nature of distribution was noticed for the number of productive tillers per plant which provides an opportunity for selecting superior segregant. These results were in fulfilment with sheshaiah *et al*. (2018) and priyanka *et al.* (2019). Significant positively skewed and platykurtic distribution was noticed in grain L:B ratio. These results were in fulfilment with Sheshaiah *et al.* (2018). Frequency distribution studies indicate a dominance based complementary epistasis gene action which was governed in the inheritance of these characters.

Knowledge about the genetic mechanism of segregating population is essential for the improvement of crop genetics to develop a superior variety. The trait with high GCV, PCV, heritability and GAM governed by additive gene action could be preferred for selection. In this study, the number of filled grains per panicle showed high PCV, high GCV, high heritability and GAM with positive skewness and leptokurtic nature of distribution. Correlation studies provide the relationship between traits. In this study, a significant positive correlation was noticed for single plant yield with panicle length, the number of filled grains per panicle and thousand grain weight. Frequency distribution studies provide a scope for selecting a superior trait. In this study, significant positive skewness was noticed for the number of productive tillers per plant and grain L:B ratio, this provides an opportunity for selecting the high yielding slender type grains simultaneously.

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