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## Research Article

### Genetic variability studies in early generation prebreeding restorer germplasm of the cross CBSN 25 x WRM 93-20

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#### Abstract

The present investigation was carried out to understand the genetic variability, association, cause and effect relationships between yield and its attributing agronomic and physiological traits in 23 F<sub>3</sub> families of pre-breeding restorer germplasm in a hybrid rice program for six agronomic and three physiological characters. The variability and heritability parameters were grouped under the high category for the number of productive tillers per plant, leaf area per plant, dry matter production and single plant yield. The traits viz., the number of tillers per plant and panicle length, leaf area per plant and dry matter production showed a direct correlation with single plant yield and in cause and effect relationships. All traits had a direct influence on single plant yield except days to 50% flowering and chlorophyll index. At the intra-family level, six families namely 30, 35, 36, 46, 55 and 82 showed high variability and heritability values of all parameters for six traits. All nine traits exhibited normal distribution.

**Keywords:** Rice, pre-breeding, genetic variability, correlation and path analysis.

#### INTRODUCTION

Pre-breeding is an approach used to tap the desired genetic traits from un-adapted material such as crop wild relatives and utilize them into breeding lines that are more easily crossable with modern elite cultivars. It is crucial to exploit the genetic diversity derived from wild relatives and other unimproved materials for utilization. This forms the basis for the sustainable production of novel crop varieties for present and future challenges that arise due to various biotic and abiotic stresses.

The wild Rice MAGIC (WRM) lines developed by International Rice Research Institute, Philippines involving AA genome species viz., *O.rufipogon*, *O.longistaminata*, *O.nivara*, *O.barthii*, *O.meridonalis* and *O.glumaepatula* with two cultivated species, *O. sativa* and *O.glaberimma* were used for developing pre-breeding restorer germplasm

that can be tapped in hybrid rice program in future. Thus, the current research was aimed to determine the genetic variability, correlation of agronomic and physiological traits, their cause and effect relationship in F<sub>3</sub> families of Restorer x Wild Rice MAGIC lines for important yield and its contributing traits and physiological traits for their advancement to the F<sub>4</sub> generation.

#### MATERIALS AND METHODS

In the present study, the F<sub>3</sub> population comprising of 23 families of the cross CBSN 25 x WRM93-20 obtained from the Department of Rice, Tamil Nadu Agricultural University, Coimbatore was raised during Rabi 2021-22 season. Twenty eight days old seedlings of F<sub>3</sub> families along with their parents were transplanted by adopting a spacing of 15 × 10 cm in three rows of 2.9 m length/family.

Crop agronomy was taken care of throughout the cropping period. Observations were taken on five randomly tagged plants in parents and 15 tagged plants in each family for six agronomic traits viz., days to 50% flowering, plant height (cm), the number of total tillers and productive tillers per plant, panicle length (cm) and single plant yield (g) and three physiological traits namely leaf area/plant (cm<sup>2</sup>), chlorophyll Index and dry matter production (g). Data collected for each character was statistically analysed for genetic variability, correlation and path coefficients. Using the Burton and Devane (1953) formula, the phenotypic and genotypic coefficients of variation were determined. As suggested by Sivasubramanian and Madhavamenon (1973), the range of variation was divided into three categories namely high (>20%), moderate (10-20%) and low (10%). Heritability in the broad sense was calculated using the equations proposed by Allard (1960) and further classified using the scores proposed by Johnson *et al.* (1955) as high (> 60%), moderate (30-60%) and low (0-30%). Genetic advance as a percentage of mean (GAM) was calculated and classified as high (> 20%), moderate (10-20%) and low (< 10%) as given by Johnson *et al.* (1955). The correlation coefficients (Johnson *et al.*, 1955), path coefficient analysis (Dewey and Lu, 1959), the direct and indirect effects (Lenka and Misra, 1973) were computed.

## RESULTS AND DISCUSSION

Hybrid rice aims to exploit the heterosis of 15-20% over the inbred varieties. But, the low genetic diversity present in the cultivated *indica* restorer germplasm necessitates its diversification through the exploitation of tropical japonica types, wild species or pre-breeding materials. On these backgrounds, wild rice MAGIC lines offer scope for the development of pre-breeding lines by recombinant selection with the possibility to exploit greater heterosis in future. Fixing desirable recombinants from a segregating population should be based on scientific principles so

as to inherit the desired genotypes. The information on genetic diversity, gene action, heritability and the relative direct and indirect contributions of each component trait to grain yield forms the criteria for selection.

The base material was developed by the selection and advancement of those F<sub>2</sub> plants from the CBSN 25x WRM 93-20 population that exhibited amplification for the presence of the fertility restorer genes *Rf3* and *Rf4* through molecular screening (data unpublished).

The analysis of variance in F<sub>3</sub> families indicated highly significant variation among the genotypes for all the traits studied indicating the presence of variability. The data on heritability, genetic advance, genetic advance as percentage of mean, phenotypic and genotypic variability is represented in **Table 1**.

For all the characters except the number of days to 50% flowering, the estimates of GCV were lower than that of PCV. The traits namely single plant yield (41.46% and 50.0%) and the number of productive tillers per plant (21.84% and 35.04%) showed maximum GCV and PCV. These traits with a high degree of variability are amenable for direct selection for further advancement to the F<sub>4</sub> generation. Bharath *et al.* (2018) and Hema *et al.* (2019) also noticed high levels of phenotypic and genotypic coefficients of variation for productive tiller number and single plant yield in rice. The traits of plant height and panicle length had a moderate level of PCV and GCV, while days to 50% flowering exhibited lower values which demonstrated less variability for these traits and hence direct selection may not be effective. Hefena *et al.* (2016) and Abhilash *et al.* (2018) reported similar results.

According to Johnson *et al.* (1955), the estimates of variability alone do not provide sufficient information for selection. Estimation of heritability along with genetic

**Table 1. Genetic variability for yield and related traits in the F<sub>3</sub> population of CBSN 25 x WRM 93-20**

Traits	Mean	Range		Skewness	Kurtosis	Phenotypic coefficient of variation (%)	Genotypic coefficient of variation (%)	Heritability in broad sense (h <sup>2</sup> ) (%)	Genetic advance	Genetic advance as percentage of mean
		Maximum	Minimum							
Days to 50% flowering	99.74	112	93	0.66	-1.09	6.10	6.10	100	12.53	12.56
Plant height (cm)	120.23	167.5	78	0.40	-0.99	17.22	13.65	62.89	26.81	22.30
Number of tillers / plant	16.85	31	6	0.68	0.67	26.63	10.52	15.59	1.44	8.55
Number of productive tillers/plant	13.66	28	4	1.29	0.62	35.04	21.84	38.86	3.83	28.05
Panicle length(cm)	27.40	45.5	13	0.14	-1.04	23.47	14.75	39.51	5.23	19.10
Single plant yield (g)	18.76	46.51	4.18	0.66	0.64	50.00	41.46	68.77	13.29	70.83

**Table 2. Genetic variability for physiological traits and yield in the F<sub>3</sub> families of CBSN 25 x WRM 93-20**

Traits	Mean	Range		Skeweness	Kurtosis	Phenotypic coefficient of variation (%)	Genotypic coefficient of variation (%)	Heritability in broad sense (h <sup>2</sup> ) (%)	Genetic advance	Genetic advance as percentage of mean
		Maximum	Minimum							
Chlorophyll index	25.15	36.65	16.35	-0.362	0.917	13.78	4.89	12.60	0.90	3.58
Leaf area / plant (cm <sup>2</sup> )	683.93	1928.37	143.75	0.757	0.314	40.60	38.07	87.93	52.49	73.55
Dry matter production (g)	74.54	123.81	39.29	0.52	1.16	67.62	65.93	95.06	98.07	132.41
Single plant yield (g)	18.76	28.14	10.64	0.66	0.64	50.00	41.46	68.77	13.29	70.83

advance is more useful in predicting the resultant effect from the best individual. Hanson *et al.* (1956) suggested that broad sense heritability comprises of additive and non-additive components of gene effects. Single plant yield (68.77% and 70.83%) and plant height (62.89% and 22.30%) exhibited high heritability and high genetic advance as a percentage of mean which denotes the predominant role of additive gene action and hence, selection may be effective. Choudhary *et al.* (2018) also reported that plant height and productive tiller number had high heritability and high genetic advance as a percentage of mean in rice.

Hence, it could be deduced that the traits number of productive tillers per plant and single plant yield possessing high PCV, GCV, heritability values and high genetic advance as percentage of mean and panicle length with moderate GCV, heritability and genetic advance as percentage of mean are amenable for direct selection and advancement. All three physiological parameters studied had a higher phenotypic coefficient of variation (PCV) than genotypic coefficient of variation (GCV), informing the presence of environmental effect to some extent (Table 2).

The traits leaf area per plant (40.60%, 38.07%, 87.93% and 73.55%), dry matter production (67.62%, 65.93%, 95.06% and 132.41%) and single plant yield (50.00%, 41.46%, 68.77% and 70.83%) had high PCV and GCV with high heritability and high genetic advance as percentage of mean, whereas chlorophyll index (13.78%, 4.89%, 12.60% and 3.58%) had moderate PCV, low GCV, low heritability and genetic advance as percentage of mean. Iftekharruddaula *et al.* (2001) and Hasan *et al.* (2010) also reported that the leaf area per plant and dry matter production exhibited high values for PCV, GCV, heritability and genetic advance as a percentage of mean. Selection would be effective in elite genotypes with higher leaf area from segregating populations that would be transformed into dry matter and grain yield.

The component traits that can be chosen to improve grain yield genetically are determined by using correlation

analysis which provides information about the nature and degree of relationship among various traits. In the past, various researchers have examined the relationship between yield and its main attributing traits in segregating the population of rice. In this study, five traits were correlated with single plant yield (Table 3) among them the number of tillers per plant and panicle length expressed significant associations with grain yield. In inter- correlations, the number of productive tillers per plant was significantly positive correlated with the number of tillers per plant and panicle length. Plant height and total tillers per plant had a highly significant association.

It indicates that the number of tillers per plant and panicle length plays a crucial role in increasing the yield potential in the F<sub>3</sub> families of CBSN 25 x WRM 93-20. Suman *et al.* (2021) reported a positive significant association for the number of tillers per plant with single plant yield and Sudeepthi *et al.* (2020) reported a significant positive association for panicle length with single plant yield.

Path coefficient analysis examines the direct and indirect effects of correlation among and between the traits. The results are presented in Table 4. The trait panicle length (0.5902) exhibited a maximum positive direct effect on single plant yield followed by the number of productive tillers/plant (0.5368), the number of tillers per plant (0.3676) and days to 50% flowering (0.2496). A negative direct effect was exhibited by plant height (-0.4846). Similar results of a direct positive effect on the number of tillers per plant on single plant yield were reported by Vanisri *et al.* (2020). Sudeepthi *et al.* (2020) reported panicle length had a positive direct effect with grain yield. Sathish *et al.* (2020) reported a direct positive effect on the number of productive tillers per plant with a single plant yield.

In the analysis of agronomic traits, the residual effect is 0.432 indicating that the characters included in the present study contributed for almost 57% of variability influencing the dependent variable i.e., single plant yield. In F<sub>3</sub> families, the phenotypic correlation coefficients

**Table 3. Correlation among yield and yield associated traits in F<sub>3</sub> families of CBSN 25 x WRM 93-20**

Traits	Days to 50% flowering	Plant height	Number of tillers / plant	Number of productive tillers/ plant	Panicle length	Single plant yield
Days to 50% flowering	1.0000					
Plant height	0.0576	1.0000				
Number of tillers /plant	-0.1382	0.8998**	1.0000			
Number of productive tillers/plant	-0.2680	0.0793	0.8706*	1.0000		
Panicle length	-0.4275	0.0253	0.1955	0.8959*	1.0000	
Single plant yield	0.1165	-0.4609	0.6874**	0.5875	0.7816*	1.0000

\*Significant at 5%, \*\* Significant at 1%

**Table 4. Phenotypic path coefficient analysis representing the effects of direct and indirect on single plant yield by its attributed traits in F<sub>3</sub> population of CBSN 25 x WRM 93-20**

Traits	Days to 50% flowering	Plant height	Number of tillers /plant	Number of productive tillers/plant	Panicle length	Correlation coefficient for single plant yield
Days to 50% flowering	<b>0.2496</b>	-0.055	-0.0258	-0.038	0.0256	0.1165
Plant height	0.0144	<b>-0.4846</b>	-0.0367	0.0192	-0.0137	-0.4609
Number of tillers/plant	-0.0306	-0.0235	<b>0.3676</b>	-0.0104	0.0621	0.6574
Number of productive tillers/plant	-0.0744	-0.0187	0.2980	<b>0.5368</b>	0.048	0.5875
Panicle length	-0.1519	0.0123	0.1860	0.1812	<b>0.5902</b>	0.7986

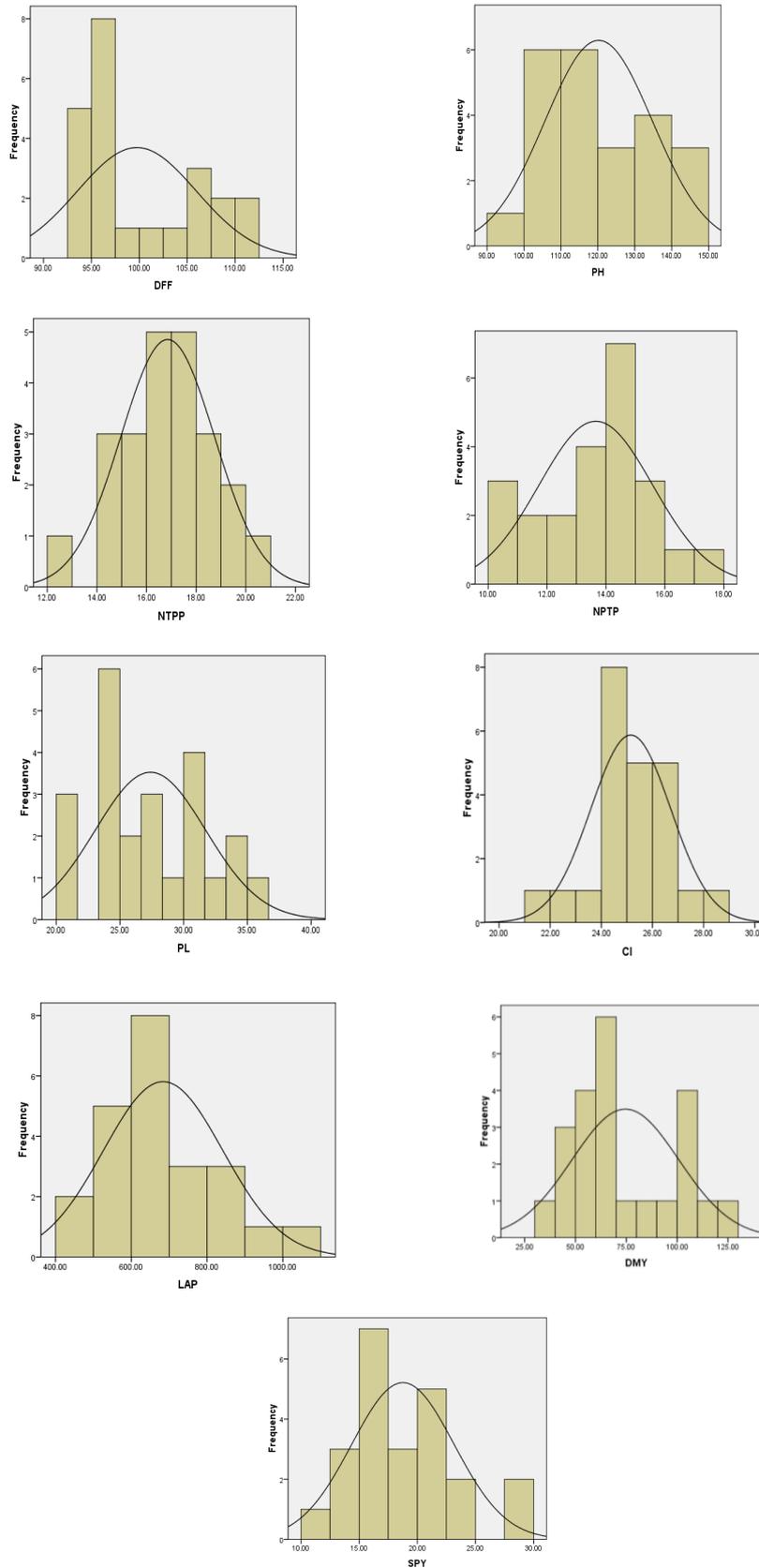
Residual effect = 0.432; The direct effects are bold values.

of chlorophyll index, leaf area per plant, dry matter production were related to single plant yield (**Table 5**). Single plant yield was significantly and positively associated with leaf area per plant and dry matter production because of high leaf area and accumulation of photosynthates, enhance high photosynthetic activity in grain which leads to increased grain yield and dry matter production (Sanghera *et al.*, 2012). The trait leaf area per plant showed a significantly positive correlation with chlorophyll index and dry matter production. Moosavi *et al.* (2015) published a positive significant association between dry matter production and grain yield. Akter *et al.* (2018) found a positive correlation of leaf area per plant with dry matter production and single plant yield.

The leaf number and size determine the plant's foliar surface which is important for solar radiation interception and photosynthetic activity in the plant. Lesser foliar surfaces do not fulfil sink demands during grain filling and carbon remobilization occurs from the stem to the grains (Bazargani *et al.*, 2012). Many authors have emphasized the importance of the third internode of rice plant as an important reserve source, which is mobilized and used

for grain growth. In general, dry matter of different plant parts diminished, mainly from the third internode as reported by Lopez *et al.* (2019), which suggested that grain filling was affected by photosynthate availability and it was necessary to mobilize reserves stored previously in different plant organs. In path analysis, both leaf area per plant (0.4796) and dry matter production (0.4593) exerted an equal but direct positive effect on single plant yield (**Table 6**), whereas chlorophyll index (-0.1345) showed a negative direct effect. In the present study, the residual effect for physiological traits is 0.4809 which contributed for 52 per cent variability.

The frequency distribution of individuals in the F<sub>3</sub> families for all nine characters is depicted in **Fig. 1 and Tables 1 & 2**. The non-significant 't' value for skewness indicates the symmetrical distribution of the curve for all traits studied and the negative non-significant kurtosis represents the mesokurtic curve. Hence, all nine traits showed normal distribution in the present material. Nikhitha *et al.* (2020) reported non-significant skewness and negative non-significant kurtosis for days to 50% flowering and panicle length.



**Fig. 1. Frequency distribution for different traits revealed different patterns of distribution in the F<sub>3</sub> population of CBSN 25 x WRM 93-20**

**Table 5. Correlation coefficient among physiological traits and yield in F<sub>3</sub> families of CBSN 25 x WRM 93-20**

Traits	Chlorophyll index	Leaf area /plant	Dry matter production	Single plant yield
Chlorophyll index	1.0000			
Leaf area /plant	0.9127*	1.0000		
Dry matter production	-0.0243	0.8999**	1.0000	
Single plant yield	-0.1396	0.7993*	0.7982*	1.0000

\*Significant at 5%, \*\* Significant at 1%

**Table 6. Phenotypic path coefficient analysis among physiological traits with yield in F<sub>3</sub> families of CBSN 25 x WRM 93-20**

Traits	Chlorophyll index	Leaf area /plant	Dry matter production	Correlation coefficient for single plant yield
Chlorophyll index	<b>-0.1345</b>	0.0061	-0.0112	-0.1396
Leaf area /plant	-0.0017	<b>0.4796</b>	0.3214	0.7993
Dry matter production	0.0033	0.3356	<b>0.4593</b>	<b>0.7982</b>

Residual effect = 0.4809; The direct effects are bold values

**Table 7. Genetic variability parameters in intra-families for agronomic and physiological traits of cross CBSN x WRM 93-20**

Traits	Families			
	High PCV	High GCV	High H <sup>2</sup>	High GAM
Number of tillers /plant	18, 20, 23, 30, 35, 36, 46, 55, 58, 63, 73, 76, 78 and 82 (14 families)			
Number of productive tillers/ plant	18, 20, 23, 24, 30, 35, 36,40, 46, 55, 58, 62, 63, 68, 73, 76, 78, 82 and 89 (19 families)			
Panicle length	18, 30, 32, 35, 36, 46, 55, 68, 76 and 82 (10 families)			
Leaf area per plant	5, 14, 18, 20, 23, 24, 30, 32, 35, 36, 40, 46, 55, 58, 62, 63, 68, 73, 76, 78 and 82 (21 families)			
Dry matter production	18, 30, 32, 35, 36, 40, 46, 55, 58, 62, 63, 68, 70, 73, 78, 82 and 89 (17 families)			
Single plant yield	5, 14, 18, 23, 24, 30, 35, 36, 40, 46, 55, 58, 62, 63, 68, 70, 73, 76, 78, 82 and 89 (21 families)			

The variability and heritability parameters were analyzed at intra-family level for each of the 23 families in **Table 7**. For the traits number of tillers per plant, the number of productive tillers per plant, panicle length, dry matter production and leaf area per plant, 14, 19, 10, 17 and 21 families, respectively expressed high values of PCV, GCV, heritability and genetic advance as percentage of mean. For single plant yield, 21 out of 23 families showed high values for all parameters. Among these, altogether six families 30, 35, 36, 46, 55 and 82 showed high values of all parameters for all the six traits. The families 76 and 18 showed moderate PCV for dry matter production and leaf area per plant, respectively, while for the rest of the parameters the values were high. For plant height, only two families viz., 76 and 40 had high PCV, heritability and GAM. Regarding the chlorophyll index, two families viz., 14 and 46 had fallen in the medium category for all the parameters and for leaf area per

plant two families viz., 70 and 36 had fallen in the low category for all parameters. It has been suggested by Huang *et al.* (2013) that further improvement in both sink and source can be brought out in the tropics if new rice cultivars are bred by selection for tillering (tiller number and size), high spikelet filling percentage and grain weight. Further, the focus should be given to growth traits during vegetative stages such as plant foliar surface and dry matter of the third internode (Lopez *et al.*, 2019) and on post-floral physiological processes to increase the potential yields of rice.

Thus, from the present study, it could be deduced that panicle length with medium heritability, productive tillers per plant, leaf area per plant and dry matter production with high heritability could be given emphasis in the selection and advancement of single plants in F<sub>3</sub> families of the cross CBSN 25x WRM 93-20 to next generation.

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