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Research Article

Genetic studies to determine the selection criteria for advancing BC_1F_3 families of Azucena /CB 87R IN rice for restorer development

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Abstract

The aim of this study was to figure out genetic variability, correlation and path co-coefficients for seven traits in 42 F_3 families of the cross Azucena/CB 87R*[1] aimed for developing new restorer lines with *indica* tropical japonica background for their utilization in a hybrid program. The population exhibited high PCV and GCV for the traits *viz.,* the number of productive tillers per plant, panicle weight and single plant yield. For the same traits, high heritability combined with high GAM was also deduced. The traits panicle weight, the number of productive tillers per plant, panicle length, flag leaf length and flag leaf width showed positive and significant associations with single plant yield. Though the traits panicle weight and the number of productive tillers were negatively correlated, they both exerted a high direct effect on single plant yield.

Keywords: Rice, *indica*-tropical *japonica* restorers, Variability, Heritability, Correlation, Path analysis

INTRODUCTION

The current rice production and productivity trend will be insufficient to fulfil the future requirements of India, considering its rising population. Given the scarcity of resources, low productivity, and stagnant yields, increasing rice productivity through genetic mechanisms is the most viable option for the present and future demands. On these forefront, developing and growing hybrid rice with a yield benefit of at least 15–20% over pureline varieties is sustainable proposition (Virmani, 2003) and 138 commercial hybrids have been released so far in India (Annual Report 2021, AICRIP).

One of the bottle necks in hybrid rice is the realization of phenomenal heterosis that will motivate and bring a change in farmers' perception about hybrid cultivation. In our country, the hybrid rice technology has so far relied solely on *indica* germplasm. When compared to *japonicas*, parental lines of the *indica* origin show less hybrid vigour. Though hybridization of *indica* and *japonica* can enhance heterosis, the emergence of severe hybrid sterility makes this strategy impractical. Furthermore, the wild abortive male - sterility (WA-CMS) (Lin and Yuan, 1980), the most often utilised hybrid development method in *indica*, does not perform well in *japonica* parental lines. The tropical japonica (TRJ), an intermediate type, is, nonetheless, easily crossable to both subtypes. As a result, the utilization of TRJ lines may provide a means of bridging indica-japonica hybridization in rice hybrids (Khush, 1995), including "super" rice in China. On these backgrounds, Azucena, a Tropical *japonica* landrace from the Philippines was hybridized with CB 87R, the restorer parent of hybrid CORH 3 and the F_1 was used as a pollen parent and once backcrossed to CB 87R. The purpose of backcross is to realize more number of segregants with good spikelet fertility and to infuse the genome of Azucena for diversification. In BC_1F_2, 138 plants were phenotypically selected and screened with SSR markers for fertility restorer genes *Rf-3* & *Rf-4*. Finally 42 plants were selected that expressed amplification for markers targeted for both genes (data unpublished).

The 42 BC_1F_3 families thus forwarded formed the material of this study. It was aimed to assess the variance, phenotypic and genotypic co-efficients of variation, heritability, trait associations, cause and effect relationships prevailing in the population for seven traits to exercise selection and advancement to the next filial generation to develop restorer lines.

MATERIALS AND METHODS

The current study was conducted at the Tamil Nadu Agricultural University's Paddy Breeding Station in Coimbatore during *Rabi,* 2021. The current experimental material consisted of 42 BC_1F_3 families of the cross Azucena / CB 87R. Each family was raised in three rows of 3.5 m in length. Recommended crop agronomy practices were followed to maintain a healthy stand. In five randomly selected plants in parents and 15 tagged plants of each family, totalling to 630 plants, observations for seven biometrical traits *viz.,* plant height (cm), panicle length (cm), flag leaf length (cm), flag leaf width (cm), the number of productive tillers per plant (nos.), panicle weight (g) and single plant yield (g) were recorded. The data were subjected to statistical analysis to compute the phenotypic and genotypic coefficient of variation as per Burton (1953). As indicated by Sivasubramanian and Madhava Menon (1973), the variation was categorised as high (more than 20%), moderate (10-20%), and low (less than 10%). Allard's (1960) equations were used to calculate heritability and were further classified following Johnson *et al.* (1955) as high (more than 60%), moderate (30-60%) and low (less than 30%). Similarly, the genetic advance (GA) was calculated using Allard's formula and expressed in percentage as suggested by Johnson *et al.* (1955) as high (more than 20%), moderate (10-20%), and low (less than 10%). Correlation coefficients (Johnson *et al.,* 1955) and path analysis (Dewey and Lu, 1959) were computed.

RESULTS AND DISCUSSION

The capacity of the breeder to define and combine the needed variation and select for yield effectively through yield related and highly heritable traits is important in the progress of any crop improvement activities. The statistical information gained from breeding population being handled aids the breeder in predicting anticipated gains through selection. To assess the impact of the environment on certain attributes, estimation of PCV and GCV is required. The variances, PCV & GCV, heritability, genetic advance and GAM for seven quantitative traits are presented in **Table 1**. High PCV and GCV were observed for single plant yield (48.20 % and 43.18 %) followed by the number of productive tillers per plant (30.38 % and 25.12 %) and weight of panicle (27.36 % and 27.32 %). Similar results of high PCV and GCV for all these traits were observed by Bharath *et al.* (2018), Yaseen *et al.* (2020) and Bhargava *et al.* (2021). The traits flag leaf length (16.75 % and 9.58 %) panicle length (10.4 % and 8.27 %) and flag leaf width (10.37 % and 1.42 %) exhibited moderate PCV, while GCV was low, respectively. Such expression for panicle length is in line with the reports of Abhilash *et al.* (2018) and Bhargava *et al.* (2021). The narrow genetic base revealed by low values of PCV and GCV for plant height (9.41 % and 8.66 %) was also evidenced by Mallimar *et al.* (2015) and Muthuramu and Ragavan (2020). For all variables, the PCV values were greater than the GCV values. indicating a high degree of genotype-environment interaction (Saha *et al.,*2019).

Five out of seven traits namely panicle weight (99.72 %), plant height (84.58 %), single plant yield (64.49 %), the number of productive tillers (68.35 %) and panicle length (63.19%) showed high heritability. Of these, three traits

Table 1. Estimates of genetic variability parameters of 42 F_3 families of cross Azucena / CB 87R^{*1} in rice

Traits	Mean	σ^2p	σ^2e	σ^2g	PCV (%)	GCV (%)	h^2 (%)	GA	GAM
PH	105.65	98.93	15.26	83.68	9.41	8.66	84.58	17.33	16.40
PL	23.44	5.94	2.19	3.75	10.40	8.27	63.19	3.17	13.54
FLL	33.43	31.36	21.10	10.26	16.75	9.58	32.72	3.77	11.29
FLW	1.41	0.0214	0.0210	0.0004	10.37	1.42	1.86	0.01	0.40
NPT	18.08	30.17	9.55	20.62	30.38	25.12	68.35	7.73	42.78
PW	2.76	0.57	0.004	0.57	27.36	27.32	99.72	1.55	56.21
SPY	25.17	147.13	52.24	94.88	48.20	38.70	64.49	16.11	64.02

PH= Plant height; PL= Panicle length (cm) ; FLL= Flag leaf length (cm); FLW= Flag leaf width (cm); NPT= Number of productive tillers per plant; PW= Panicle weight (g); SPY= Single plant yield (g); σ^2p= Phenotypic variance; σ^2e= Environment variance; σ^2g= Genotypic variance; PCV= Phenotypic coefficient of variation; GCV= Genotypic coefficient of variation; h^2 = Heritability; GA= Genetic advance; GAM= Genetic advance as per cent of mean *viz.,* single plant yield (64.02 %), panicle weight (56.21 %) and the number of productive tillers (42.78 %) also possessed high GAM. Choudhary *et al.* (2018) and Balat (2018) reported for the traits plant height and productive tiller numbers. Yaseen *et al.*(2020) reported high GAM for single plant yield and the number of productive tillers. Harijan *et al.* (2021) reported high heritability for plant height. Moderate and low values were displayed by the traits flag leaf length (32.72 %) and flag leaf width (1.86 %) respectively. The GAM was moderate for plant height (16.40 %), panicle length (13.54 %) and flag leaf length (11.29 %), while it was low for flag leaf width (0.40 %).

High heritability combined with moderate GAM was also observed by Yaseen *et al.* (2020) for plant height and panicle length. Flag leaf length showed a moderate heritability and GAM which indicates that most likely it is due to additive gene action and selection may be effective. However, flag leaf width displayed low heritability and GAM implying a significant degree of environmental impact and poor selection.

Correlation analysis of different traits with single plant yield explains the existence and extent of interdependence among the component parameters and also the attributes that can be chosen to achieve high grain yield in the population genetically. In this study, the results of the analysis as correlation coefficients calculated using single plant yield as the dependent variable are depicted in **Fig. 1**. Five out of six traits namely panicle weight (0.6686**), number of productive tillers per plant (0.2257**), panicle length (0.1337**), flag leaf length (0.0897*) and flag leaf width (0.0992*)) showed positive and significant correlation with single plant yield. Bhargava *et al.*(2021) and Panigrahi *et al.* (2018) obtained similar results for productive tillers and panicle length; Kumar *et. al.* (2014) for panicle length; Rahman *et al.* (2014), Eswara reddy *et al.* (2013) for panicle length and Idris and Mohamed (2013) for the number of tillers per plant. Panicle weight showed a positive and highly significant association with panicle length (0.1302**) and flag leaf width (0.0903*), while it was negative and significant with the number of productive tillers and non-significant in the positive direction with plant height (0.0522).

The number of productive tillers per plant has shown a positive significant correlation with plant height (0.1190**) and flag leaf length (0.0876*) which was also observed by Bhargava *et al.*(2021), whereas, with panicle length (0.0779), the correlation was positive but non-significant. Flag leaf width had a positive and highly significant association with panicle length (0.2355**) and flag leaf length (0.0876*) but non-significantly positively correlated with plant height (0.0351). The length of the flag leaf had a positive and extremely significant relation with the length of the panicle (0.2710**) and plant height

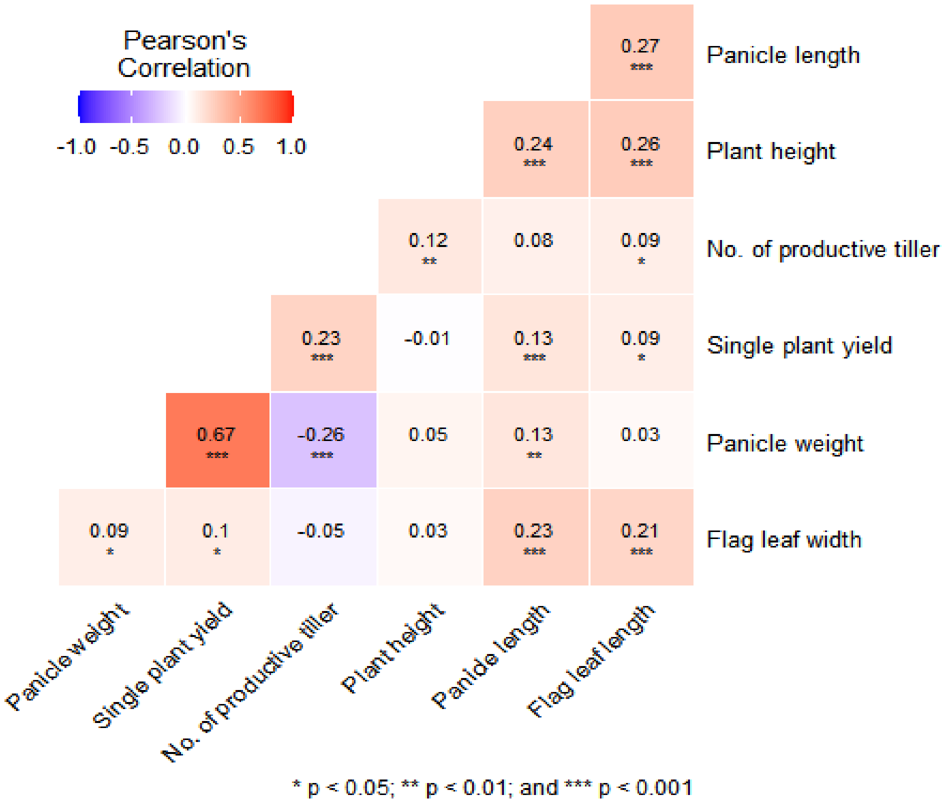

Fig. 1. Pearson's correlation coefficients between seven traits of rice in F_3 families of Azucena / CB 87R^{*1}

Table 2. Direct and indirect effects assessed through path analysis in F_3 families of the cross Azucena / CB 87R*[1] in rice

Traits	PH	PL	FLL	FLW	NPT	PW	Correlation for SPY
PH	**-0.1142**	0.0004	0.0124	0.0014	0.0525	0.0409	-0.0066
PL	-0.0278	**0.0017**	0.0127	0.0106	0.0343	0.102	0.1337**
FLL	-0.0302	0.0005	**0.047**	0.0098	0.0387	0.0241	0.0897*
FLW	-0.0034	0.0004	0.0101	**0.0455**	-0.0233	0.0687	0.0992*
NPT	-0.0136	0.0001	0.0041	-0.0024	**0.4415**	-0.2041	0.2257**
PW	-0.006	0.0002	0.0014	0.004	-0.1149	**0.7838**	0.6686**

RESIDUAL EFFECT= 0.6055 ; PH= Plant height; PL= Panicle length; FLL= Flag leaf length; FLW= Flag leaf width; NPT= Number of productive tillers per plant; PW= Panicle weight; SPY= Single plant yield

(0.2648**). The panicle length and plant height (0.2439**) had a positive and extremely significant relationship which was also noticed by Bhargava *et al.*(2021) and Swapnil *et al.* (2020).

Path coefficient analysis divides the correlations to explain the cause-and-effect relations and analyses the primary and indirect reasons of relation using other variables. The path coefficient analysis results for yield and its associated attributes are shown in **Table 2**. Panicle weight (0.7838) exerted the highest positive direct effect on single plant yield followed by the number of productive tillers per plant (0.4415), flag leaf length (0.047), flag leaf width (0.0455), panicle length (0.0017) implying that yield potential may be improved by selecting these characteristics. Similar results of a direct positive effect on plant yield were reported by Nandeshwar *et al.* (2010) and Bhargava *et al.* (2021) for the number of productive tillers and panicle length. A negative direct effect by plant height (-0.1142) on single plant yield per plant was also previously indicated by Saha *et al.* (2019) implying that tallness is due to higher photosynthate accumulation in vegetative portions and inefficient partitioning to sink. Panicle length exhibited a positive low indirect effect on panicle weight. Panicle weight showed a negative low indirect effect on the number of productive tillers per plant. The remaining attributes had a minor indirect influence on single plant yield and other characteristics. The residual impact was 0.6055 at the phenotypic level. In the present study, the variable panicle weight may be regarded as a key contributory factor to plant yield as it displayed the highest direct positive impact of all the yield influencing variables.

The present study highlighted the importance of the traits namely, the number of productive tillers per plant, the weight of the panicle and single plant yield as direct selection parameters for advancing to F_4 generation to bring genetic improvement in the population as PCV and GCV estimates, heritability and GAM were high. When the correlation and path coefficients were combined, it revealed that the number of productive tillers per plant and panicle weight though negatively correlated had direct significant effects on single plant yield. The single plants that will be selectively advanced to F_4 generation based on the above criteria will form the base material for the development of new restorer lines at F_6, combining the genome of both *indica* and Tropical *japonica* thus broadening the genetic base.

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