

## Spikelet Fertility Strongly Influences the Genetic Structure of F<sub>2</sub> Population of CB174R/Iguapecateto Cross in Rice (*Oryza sativa* L.)

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**ABSTRACT:** The next generation of hybrid rice is based on exploitation of inter subspecific heterosis for which, development of restorers in indica/tropical japonica background suitable for tropical countries like India assumes importance. The progenies of sub-specific crosses exhibit spikelet sterility of varying degrees that have an impact on genetic structure of the population and further selection. Hence, the present study was aimed to understand the F<sub>2</sub> population structure of an inter sub-specific cross CB174R/Iguapecateto in terms of mean, frequency of individuals, variability, heritability, correlation, direct and indirect influence of seven quantitative traits in whole and a subset of population for further selection. The population consisting of 781 plants was evaluated during June 2019 at Paddy Breeding Station, Department of Rice, CPBG, TNAU Coimbatore. Plants with 75% spikelet fertility were considered as highly fertile. Fifty five plants with above 75% spikelet fertility was formulated as a subset population. Majority of plants (70.87%) possessed 50.0-70.0% spikelet fertility in the whole population. A wide range noticed in the original population has been retained from 50-75% in subset population in different characters except spikelet fertility. The subset population had higher mean performance for most of the traits except 100-seed weight. Selection for spikelet fertility has influenced other traits like plant height, productive tillers, panicle length and single plant yield in frequency classes. Though PCV was higher than GCV for all the traits in both populations, differences were noticed for the traits spikelet fertility, hundred seed weight and single plant yield. Regarding heritability and genetic advance, spikelet fertility exhibited differences compared to whole population. High heritability coupled with high genetic advance as percent mean revealing additive action was noticed for the traits plant height, total tillers, productive tillers and single plant yield in both the populations and selection is effective in this generation. None of the traits expressed significant correlation with single plant yield in the original population, but values were in positive direction. In subset, spikelet fertility, number of total tillers, productive tillers and panicle length had a positive and significant influence on single plant yield of which, the influence of spikelet fertility was highly significant with high positive direct effect (0.5992). Total tillers showed moderate positive direct effect on the dependent variable. Selective advancement of highly fertile plants to F<sub>3</sub> and observation for further segregation will give us some conclusive evidences for fertility inheritance and stability of spikelet fertility in later generations.

**Keywords:** Rice, inter sub-specific cross, Spikelet fertility (%), Frequency distribution, Variability, Heritability, Correlations and Path.

### INTRODUCTION

The two subspecies of cultivated rice, *indica* and *japonica* (Kato *et al.*, 1928) are known to have distinct ecological preferences which have contributed to their geographic distribution and cultivation preferences (Chang, 1976; Khush, 1995). Hybrid rice is guaranteed technology for increasing the yield plateau after the

Piyari *et al.*,

revolution caused by semi-dwarf rice varieties globally. The degree of heterosis in different kinds of hybrid rice varieties has the following general trend: *indica/japonica* > *indica/javanica* > *japonica/javanica* > *indica/indica* > *japonica/japonica*. The *indica/japonica* hybrids possess the highest yield potential which may be theoretically 30% more than the

existing highest yield of inter-varietal hybrid varieties (Yuan, 1994). The strong heterosis of inter-sub-specific rice hybrids compared to intra sub-specific hybrids have been re-emphasized by Fu *et al.* (2014); Birchler (2015); Mi *et al.* (2019).

Inter varietal hybrid sterility of varying levels occurs in F<sub>1</sub>s between *indica* and *japonica* (Khush and Aquino 1994) which hinders the exploitation of heterosis (Cheng *et al.*, 2007; Zhang *et al.*, 2020). Out of about 50 loci that related to isolation of the genus *Oryza* so far identified (Guo *et al.*, 2016; Li *et al.*, 2020), only some of the loci are responsible for the hybrid sterility of *indica-japonica* crosses (Zhang, 2020). On the basis of morpho-agronomic studies, Oka (1958) concluded that *japonicas* and the so called *javanicas* from Indonesia are closely related. Experiments at IRRI have shown that tropical *japonica* when crossed with semi-dwarf *indica* exhibits stronger yield heterosis than *indica/indica* hybrids, provided either of the parental lines possess the wide compatible gene (Bharaj *et al.*, 1994).

Considerable variation exists for the traits amylose, gelatinization temperature, and grain types in the tropical *japonica* germplasm. Tropical *japonicas* are considered as the bridge for *indica-japonica* hybridization and a source for increasing genetic diversity in rice. They have fewer tillers, sturdy culm, and vigorous root architecture (Khush and Aquino 1994). Tropical *japonicas* cannot be used as such as a direct parent in hybrid rice because of their undesirable features like lower productivity, tallness, etc.

At IRRI, the tropical *japonicas* were crossed and new plant type (NPT) lines with less tillers, long panicles with more number of grains were developed. However, grain filling posed to be a major problem and subsequently solved by careful selection of parents with good grain filling. It was suggested that selecting parents with good grain filling traits, introduction of *indica* genes, and a refinement of original NPT design are expected to improve the performance of the NPT lines and yield enhancement can be obtained from inter sub-specific heterosis between *indica* and NPT lines (Peng *et al.*, 1999).

Shidenur *et al.* (2019) opined that the tropical *japonica* (TRJ) rice germplasm is an alternative source for scaling the heterosis level in rice. Singh *et al.* (2022) classified the 200 NPT genotypes into three sub populations with allelic variations and found great phenotypic variability related to new plant type (NPT) phenology. They suggested the exploitation of tropical *japonica* germplasm in parental line development, diversification, and hybrid breeding in rice.

In this study we are interested to know the population structure of an *indica/tropical japonica* cross in terms of frequency distribution of plants, variability, and heritability parameters in F<sub>2</sub> generation for seven quantitative traits of which, spikelet fertility is of foremost importance. Also, the influence of spikelet fertility on these measures of variation, changes in the association of traits and the traits that have direct influence on grain yield assume significance in the context of developing new breeding lines to be used as restorers in future, for hybrid rice program.

## MATERIAL AND METHODS

The F<sub>2</sub> generation of inter sub-specific cross namely CB174R/Iguapecateto consisting of 781 plants were evaluated individually along with parents and checks. The checks consisted of early, mid-early and medium duration released varieties namely CO 51, ADT 39 and CO 50 respectively. The experiment was conducted at Paddy Breeding Station, Department of Rice, Centre for Plant Breeding and Genetics during June 2019. The seedlings were space planted at 30cm × 20cm and all agronomic practices were followed to raise a healthy crop. Pre-harvest observations *viz.*, plant height (cm), total tillers (nos.), productive tillers (nos.), panicle length (cm) and three post-harvest observations *viz.*, spikelet fertility (%), hundred seed weight (g), single plant yield (grams) were recorded.

The data was analyzed using SPSS and TNAU STAT software. The measures of variability namely phenotypic, genotypic and environmental co-efficients (PCV, GCV, ECV) broad sense heritability (H<sup>2</sup>) as per Lush (1940), genetic advance (GA) and GA as mean of traits and correlation co-efficients (Pearson, 1905) were calculated and path analysis (Dewey and Lu, 1959) performed. The classification as high, moderate and low for PCV, GCV, heritability and GAM (Johnson *et al.*, 1955) was followed. The analysis was done as two aspects namely for whole population and subset population based on spikelet fertility.

## RESULTS AND DISCUSSION

The genetic structure of a population is defined as a community of individuals which share a common gene pool, determines its capacity to be improved or otherwise changed by selection which is of fundamental importance in deciding breeding and selection strategies especially in conventional plant breeding methods involving crossing and selection (Hayward and Breese, 1993). The long term goal of effecting this cross is to develop restorer lines which are derivatives of *indica-tropical japonica* to exploit the inter sub-specific heterosis in hybrid rice.

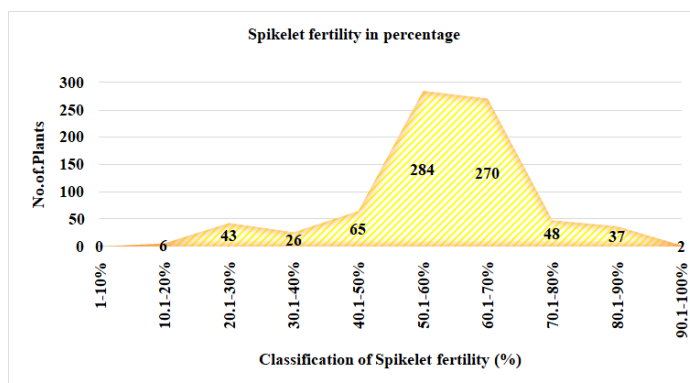
The parent CB 174R is the restorer for rice hybrid CO<sub>4</sub> released from Tamil Nadu Agricultural University. Regarding the other parent Iguapecateto, there are many reports regarding its origin - an upland cultivar originated at Brazil (Gupta and O'Toole 1986; Abamu *et al.*, 1992; Grain and Feed Annual report, USDA, 2018), pure-line traditional variety grown in West Africa (Alluri *et al.*, IITA, Abifarin, IITA, 1973, WARDA, 2000), pure-line land race introduced in West Africa in 1960 (Dalton and Guei 2003), *japonica* from Haiti (Yamagishi *et al.*, 2003, CGIAR and WARDA, 1999) and tropical *Japonica* from Haiti (Shreshta *et al.*, 2018), reported in the article table twice as originated from Haiti, South America and from Senegal, Africa (Cheng *et al.*, 2009), upland tropical *japonica* (Singh *et al.*, 2000).

The hybridization was effected in crop sown during December 2017 and the F<sub>1</sub> was evaluated during June 2018. The parents CB174R and Iguapecateto had spikelet fertility of 83.1 and 78.24% respectively. These two parents were diverse and fell in cluster III and V in D<sup>2</sup> analysis of 24 genotypes and in clusters IV and III in

molecular marker diversity studies using 69 SSR markers in an earlier study by Sangeetha *et al.* (2019). Since the program is aimed for restorer development, the presence of fertility restorer genes *Rf3* using markers RM10313, RM1, RM3233 DRRM-Rf3-10 and RM10318 and *Rf4* using markers RM6100, RM258, RM171, RM228 and RM25654 were scrutinized and both the lines were found positive for all the markers and thus carried both the genes of interest. The F<sub>1</sub> attained 50% flowering in 125 days and had mean values of 103.73cm plant height, 20 productive tillers, 72.70% spikelet fertility, 2.1g 100-seed weight and single plant yield of 21.93g. In crosses between 10 improved tropical *japonica* lines with indica tester IR36, Bharaj *et al.*

(1994) observed spikelet fertility ranging from 42.6 – 68.3%. Crossing of IR 58025B with the five *indica*, five *japonica*, and five tropical *japonica* testers produced F<sub>1</sub>s with pollen fertility that ranged from 75 to 85%, 35 to 93%, and 25 to 68% and spikelet fertility that ranged from 75 to 86%, 29 to 62%, and 51 to 70%, respectively (Priyadarshi *et al.*, 2018).

**Descriptive statistics of F<sub>2</sub> generation.** For spikelet fertility, the classification by Kumar and Chakrabarti (2000) was followed in which plants in parents, F<sub>1</sub>s and segregating progenies with a spikelet fertility percentage of 75% or above were classified as highly fertile, 50-75% as intermediate fertile and <50% as highly sterile.



**Fig. 1.** Frequency distribution of spikelet fertility classes in F<sub>2</sub> of CB174R/ Iguapecateto cross in rice.

A wide variation was observed for spikelet fertility among the 781 plants (Fig 1), hence fifty-five plants that showed above 75% spikelet fertility were selected as a

subset population and all comparisons were made for different analyses.

**Table 1: Mean and range for seven traits for the whole population and subset population of F<sub>2</sub> of the cross CB174R/Iguapecateto in rice.**

Sr. No.	Traits	Whole population			Subset population		
		Mean	Range		Mean	Range	
			Min	Max		Min	Max
1.	PH (cm)	107.37	41.0	184.0	114.91	63	169
2.	TT (no.)	17.47	8	35	18.54	9	33
3.	PT (no.)	15.40	1	32	17.52	9	27
4.	PL (cm)	25.80	17.0	36.5	26.71	20.4	33
5.	SF (%)	58.4	16	92	82.5	75	92
6.	HSW (g)	2.630	1.56	3.69	2.66	2.14	3.54
7.	SPY (g)	21.89	2.43	59.6	42.43	28.97	59.6

PH- Plant height  
SF-Spikelet fertility

TT- Total tillers  
HSW- Hundred seed weight

PT- productive tillers  
SPY- Single plant yield

PL- panicle length

The subset population of 55 plants had higher mean performance for most of the traits except 100-seed weight. In the whole population, the difference in the range of variation for different traits was 143cm for plant height, 27 and 31 nos. for total and productive tillers respectively, 19.5cm for panicle length, 76% for spikelet fertility, 2.13g for hundred- seed weight and 57.17g for single plant yield. In subset population, the range was 106cm for plant height, 24 and 18 nos. for total and productive tillers respectively, 12.6cm for panicle length, 1.4cm for hundred-seed weight and 30.63g for single plant yield. Thus, a wide range noticed in the original population has been retained from 50-75% in

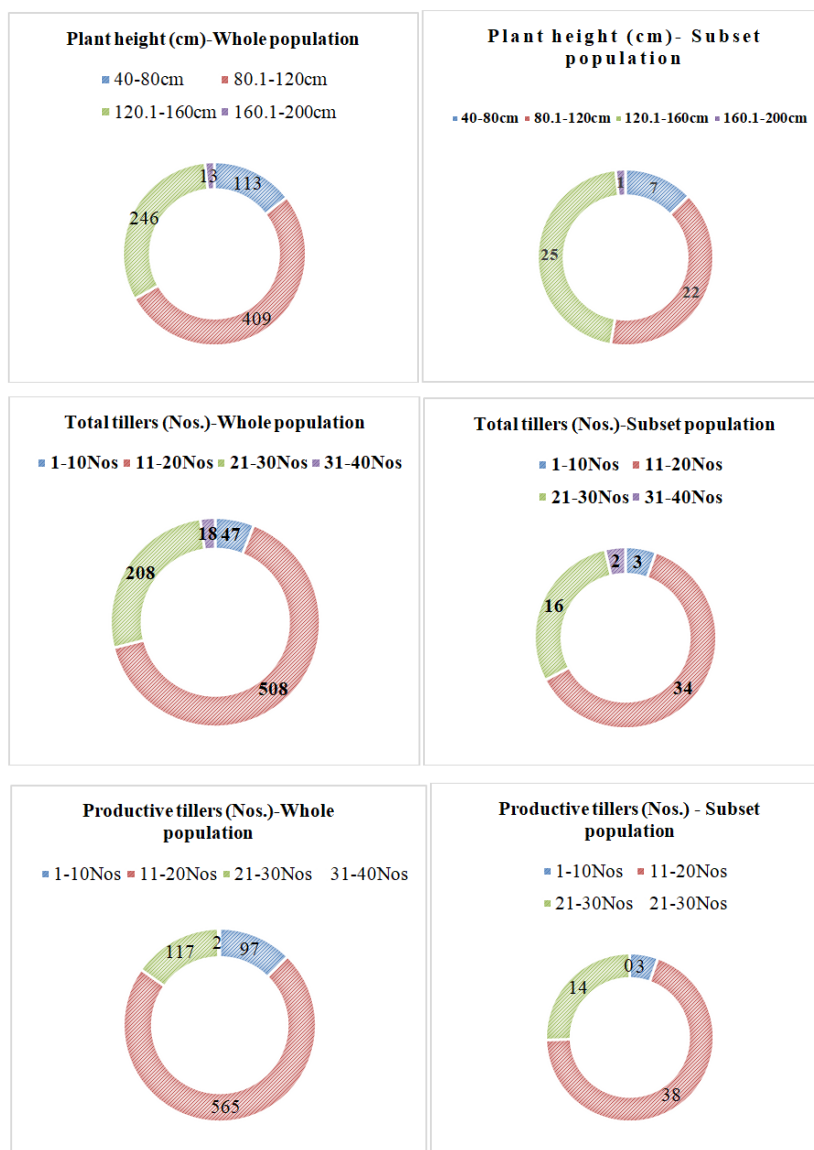
subset population in different characters except spikelet fertility for which thrust was given.

From the Fig. 2a, 2b, the frequency of plants in different categories can be deduced for different traits. Selection for spikelet fertility has notably influenced the frequency of plants falling under 81-120cm and 121-160cm plant height. In the first category, 52.36% was reduced to 40.0% and in the second category, 31.49% was increased to 45.4% in subset population which implies that less than half of the subset population consisted of tall plants with height ranging from 121-160cm. The extremes of <80.0cm and >160cm were not much influenced. The frequency of plants in four categories for the trait total tillers showed only marginal deviations in each category

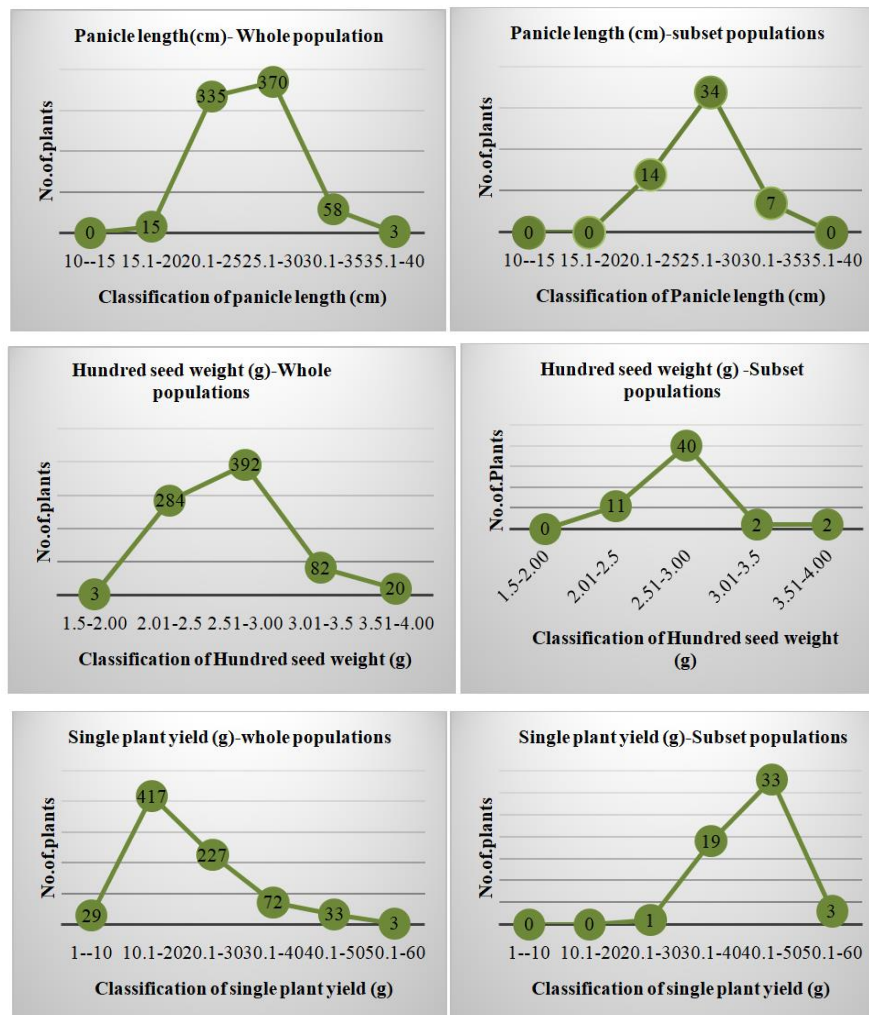
between the whole and subset population thus representing its diversity. The productive tillers showed an increase in the category of 21-30nos from 14.9% in original to 25.4% in subset population and a reduction in the category of 1-10 nos. from 12.4% to 5.4% in original and subset population respectively.

In panicle length, the short panicle category (15.1-20cm) and longest category (35.1-40cm) were eliminated in the subset population. The population consisted of exclusively intermediate and long category plants with the highest frequency of 61.8% plants possessing 25.1-30.0cm panicle length, followed by 25.4% of plants with

intermediate panicles and 12.7% plants with the range of 30.1-35.0cm. In hundred seed weight, the first category of fine grains (1.5-2.0g) was eliminated in subset population. The frequency of plants in very bold category (3.0-4.0g) had reduced a little over 50% (7.27%) from the original population (13.05%). A reduction was noticed in the category of 2.01-2.5g, which was 36.36% in original and 20.0% in subset population. Majority (72.7%) of the plants in subset population also fell between 2.51 -3.0g as like that of original (50.19%).



**Fig. 2a.** Frequency classes of plants for the traits plant height, total and productive tillers in F<sub>2</sub> of CB174R/Iguapecateto cross in rice.



**Fig. 2b.** Frequency classes of plants for the traits panicle length, hundred seed weight and single plant yield in F<sub>2</sub> of CB174R/Iguapecateto cross in rice.

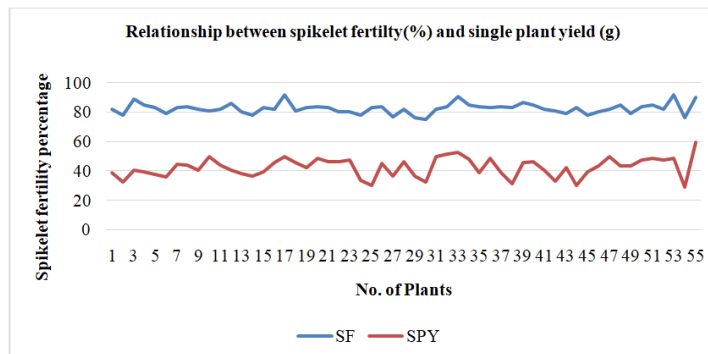
Regarding grain yield in the whole population, the highest frequency of 53.3% was observed in the class 10.1-20.0g followed by 20.1-30.0g (29.0%). Selection for spikelet fertility has a strong influence on grain yield witnessed by majority of plants (60%) falling under 40.1-50.0g followed by 34.5% of plants between 30.1-40.0g. Spikelet fertility is an important trait in inter sub-specific cross and the frequency distribution graph clearly shows plants in all classes at intervals of 10% except in 1-10%. The majority of plants (70.87%) possessed 50.0-70.0% spikelet fertility and were grouped as intermediate fertile. The relationship between spikelet fertility and single plant yield is depicted in Fig 3. Dan *et.al.*, (2014) worked out the relationships between the grain weight per plant and the seed setting rate. The found that inter sub-specific hybrids with a high seed setting rate could achieve a high grain yield value. At a seed setting rate value of approximately 85%, the grain weight per plant peaked at approximately 80 g/plant. Although the yield is a complex trait influenced by many agronomic traits, it was opined that the seed setting rate is a key element in determining the final output. Kumar and Chakrabarthy (2000) opined that the genetics of sterility in inter-sub-specific crosses is complicated and they obtained trigenic complementary ratio with one basic gene for WC trait in four crosses

studied. Moreover, the expression of *Wc* gene seemed to be highly cross specific due to the genetic differentiation for modifier genes between WCVs and normal variety (non-WCVs) and epistasis (non-allelic interaction). Long panicle lengths from 30.0-40.0cm are quite rare in *indica* genotypes. In the whole population, 61 plants fell in that range which constituted 7.81% of the population. Singh *et al.*, (2022) studied the genetic diversity of 200 TRJ lines and found that PC1 accounted for 36.0% variability followed by PC2 (21.2%) and PC3 (18.7%). Among the four traits that showed a larger contribution towards PC1, the contribution by panicle length (31.8%) was the highest. In PC2, grain yield (71.7%) was a major contributor while in PC3, the contribution of spikelet fertility (63.7%) was the highest, followed by tiller number (35.4%). They reported that agronomically, variations were evident for traits such as tiller number, panicle length and yield.

**Variability studies.** Analysis for whole population revealed that PCV was higher than GCV demonstrating the influence of environmental factors on the traits but as the difference is narrow, we can deduce that the traits except total tillers and productive tillers are principally governed by genetic factors as depicted in Table 1. The trait single plant yield expressed the highest co-efficients of genotypic and

phenotypic variation (38.05%, 39.05%) followed by number of total tillers, number of productive tillers, plant height and spikelet fertility (21.17%, 21.72%), all of which were categorized as high. The parameters were moderate for hundred seed weight. The GCV and PCV were low and moderate for panicle length respectively. In the subset population also, PCV was higher than GCV for all the traits. The scales were similar for plant height,

total tillers, productive tillers and panicle length as that of original population. Marked differences were noticed for the traits spikelet fertility, hundred seed weight and single plant yield. Both PCV and GCV was low for spikelet fertility, PCV was moderate but GCV was low for hundred seed weight and both parameters were moderate for single plant yield.



**Fig. 3.** Relationship between spikelet fertility(%) and single plant yield in subset population of F<sub>2</sub> of CB174R/Iguapecateto

**Table 2: Variability and heritability parameters in whole and subset F<sub>2</sub> population of the cross CB174R/Iguapecateto.**

Traits	Whole population					Subset population				
	GCV(%)	PCV(%)	H <sup>2</sup>	GA	GAM (%)	GCV(%)	PCV(%)	H <sup>2</sup>	GA	GAM (%)
PH	23.36	23.48	99.01	51.43	47.90	21.98	22.09	99.02	51.78	45.06
TT	27.28	30.58	79.61	8.76	50.15	24.10	27.39	77.44	8.10	43.00
PT	26.19	29.58	78.35	7.35	47.75	21.88	25.01	76.58	6.91	39.45
PL	8.69	11.45	57.63	3.50	13.59	7.01	10.01	49.04	2.722	10.11
SF	21.17	21.72	95.02	24.84	42.52	2.96	4.53	42.78	3.25	3.944
HSW	10.99	12.70	74.94	0.51	19.60	8.34	10.43	63.95	0.36	13.75
SPY	38.05	39.25	94.01	16.63	76.01	14.60	15.42	89.68	12.09	28.45

In F<sub>2</sub> segregating generations of *indica* × *indica* crosses, Nirubana *et al.* (2019); Priyanka *et al.* (2019); Balat *et al.* (2018); Savitha *et al.* (2015) obtained high GCV and PCV for plant height and single plant yield and Bassuony *et al.* (2022) for grain yield per plant alone in four populations. For the tillering traits, Yuvaraja *et al.* (2019); Nirubana *et al.* (2019) recorded similar high coefficients of variations. On the contrary, Muthuvijayaraghavan and Jebaraj (2022) recorded low values for productive tillers and hundred seed weight. Our results for the traits hundred seed weight are in line with that of Seneega *et al.* (2019); Singh *et al.* (2019); Savitha *et al.* (2015) and for panicle length with that of Ali *et al.* (2018). For panicle length, Asati and Yadav (2020); Muthuvijayaraghavan and Jebaraj (2022) obtained moderate and low scales of these parameters. The heritability in segregating generation aids to know the genetic variance of genotype-environment interaction and genetic component to be expected from selection in the next generation. According to Johnson *et al.* (1955), estimates of heritability along with genetic advance are more beneficial in selection programs. In this study, high heritability for all characters except panicle length in whole population and two traits namely panicle length and spikelet fertility in subset population

was noticed. These two traits had moderate heritability in respective populations. The genetic advance as percent mean was moderate for panicle length and hundred seed weight in the whole population. In subset population, it was low for spikelet fertility and moderate for two traits as that of whole population. All other traits exhibited high scales in both the populations. High heritability coupled with high genetic advance as percent mean indicates the predominance of additive gene action in this population and the selection may be effective for most of the traits except panicle length and hundred seed weight.

In intra-specific *indica* crosses, Yaseen *et al.* (2020) obtained high heritability for PH, NTPP, NPTP, and PL and high GAM for three traits namely number of tillers and productive tillers /plant and single plant yield. Priyanka *et al.* (2019) noticed high heritability for plant height, panicle length, grain yield per plant and high genetic advance as the percent of mean for plant height and single plant yield. High scales of heritability and GAM was noticed by Swapnil *et al.* (2020) for the traits such as plant height and number of tillers per plant. The results for plant height, number of total tillers, single plant yield and panicle length obtained in this study were also previously reported by Singh *et al.* (2022). Both

additive and non-additive components influencing hundred seed weight was also reported by Aliet al. (2018). Kalaiselvan et al. (2019) reported low PCV, GCV and GAM for spikelet fertility.

Asati et al. (2020) also encountered similar results as that of present study for spikelet fertility behavior in subset population. The high scale of parameters observed for the traits plant height, total and productive tillers and single plant yield in the whole population agreed with the results of Fathima et al. (2021). The results of our study for the traits hundred seed weight and single plant yield in whole population matched with that of Prajapati et al. (2022) in the F<sub>2</sub> of the cross NVSR2310/NVSR2115 for the former trait and in all six crosses for the latter trait.

**Correlation studies.** The degree and direction of association of related traits to grain yield will help the breeder to focus on those particular traits during selection in segregating generations. The results of correlation in whole population is presented in Table 3, which revealed that all the six characters showed positive but non-significant association with single plant yield. Inter-correlation of traits revealed that plant height had highly significant correlation with total tillers, productive tillers, panicle length and hundred seed weight in positive direction. Panicle length and number of productive tillers were positively and strongly inter-correlated (0.833). Total tillers and spikelet fertility expressed significant association in the positive direction.

**Table 3: Phenotypic correlation coefficient for yield and yield contributing traits in F<sub>2</sub> generation of CB174R/Iguapecateto whole population.**

Character	PH	TT	PT	PL	SF	HSW	SPY
PH	1						
TT	0.108**	1					
PT	0.119**	0.039	1				
PL	0.173**	0.035	0.833**	1			
SF	-0.047	0.088*	0.016	0.035	1		
HSW	0.103**	0.027	0.008	0.021	0.008	1	
SPY	0.041	0.039	0.004	0.027	0.028	0.008	1

\*\* = 0.01 level of significance \* = 0.05 level of significance

In *indica* crosses, non-significant positive association has been observed in F<sub>2</sub> population with single plant yield for the traits hundred seed weight (Seneega et al., 2019; Ali et al., 2018), plant height, panicle length, and number of productive tillers/plant (Lily et al., 2018) and panicle length (Thorat et al., 2018). The inter-correlation of plant height with total tillers, productive tillers and panicle length as observed in the present study agreed upon with the findings of Vennela et al. (2021); Dhavaleshwar et al. (2019).

In the subset population, notable changes were observed for correlation among traits and also with yield when compared to the whole population. Three traits viz., number of total tillers, productive tillers and panicle

length had a positive and significant influence on single plant yield. Spikelet fertility exerted highly significant positive association (0.559) with grain yield. Plant height, which previously had shown indirect association with four traits, showed negative and significant association with spikelet fertility in the subset population. New trait correlations were noticed. The phenotypic correlation co-efficient was highest and positive (0.904) between total and productive tillers. Panicle length and productive tillers were related (0.308), as observed in the whole population also. In addition, panicle length had significant positive association with spikelet fertility.

**Table 4: Phenotypic correlation coefficient for yield and yield contributing traits in F<sub>2</sub> generation of CB174R/Iguapecateto subset population.**

Character	PH	TT	PT	PL	SF	HSW	SPY
PH	1						
TT	-0.159	1					
PT	-0.085	0.904**	1				
PL	-0.148	0.095	0.308*	1			
SF	-0.267*	0.074	0.082	0.262*	1		
HSW	-0.006	0.023	-0.067	-0.114	0.078	1	
SPY	-0.058	0.275*	0.264*	0.280*	0.559**	0.053	1

\*\* = 0.01 level of significance; \* = 0.05 level of significance

The positive significant association of total tillers, productive tillers and panicle length with single plant yield was earlier reported by Kahani and Hittalmani (2015) in crosses involving the parents Moroberekan, Gandhasala, IR-50, IM-90, IM-114 and OYC-145. The correlation of total tillers and panicle length with the dependent variable yield was published by Satish Kumar et al. (2020). The positive significant association of productive tillers and panicle length with grain yield has been emphasized by Muthuvijayaraghavan and Jebaraj

(2022); Parween et al. (2022); Bhargava et al. (2021); Seneega et al. (2019); Lily et al. (2018). The positive association of spikelet fertility, panicle length and productive tillers with yield was revealed in the studies of Ali et al. (2018). In line with our study, Swapnil et al. (2020) obtained positive association of number of total tillers and spikelet fertility on grain yield. In inter-correlation among traits, Vennela et al. (2021) reported that panicle length and number of productive tillers were significantly and positively correlated. Seneega et al.

(2019); Lily *et al.* (2018) reported the negative and non-significant association of hundred seed weight with plant height.

**Path-coefficient analysis.** The path analysis employed in the current study was to assess the inter-relationship between yield and yield-contributing traits, as correlation analysis may not accurately determine the relative significance of direct and indirect effects of each trait on yield. By calculating path coefficients, both the direct and indirect effects of individual yield contributing traits on grain yield were determined, providing a clear understanding of their importance. Among the six different traits, spikelet fertility percentage exerted a striking impact on single plant yield

through its high positive direct effect (0.5992). These results were in accordance with that of Lu *et al.* (2022) in intercross magic F<sub>2</sub> Populations and Muthuvijayaraghavan and Murugan (2017), in F<sub>2</sub> generations under submergence condition. The moderate positive direct effect of total tillers (0.2752) on the dependent variable was also observed by Lu *et al.* (2022). The traits panicle length and hundred seed weight exhibited low negative effect on yield in this population. The effect of other two traits namely plant height and productive tillers were negligible in positive and negative direction on single plant yield. The residual effect indicated additional traits might influence the yield.

**Table 5: Phenotypic path co-efficient analysis for yield and yield contributing traits in F<sub>2</sub> generation of CB174R/Iguapecateto in subset population.**

Trait	PH	TT	PT	PL	SF	HSW	SPY
PH	<b>0.0897</b>	-0.0440	0.00369	0.0272	-0.1378	0.00114	-0.0581
TT	-0.0143	<b>0.2752</b>	-0.036	-0.0181	0.04194	0.0022	0.276
PT	-0.00807	0.2477	<b>-0.0410</b>	0.0054	0.0479	0.0080	0.264
PL	-0.0134	0.0275	0.001231	<b>-0.1817</b>	0.0838	0.01258	0.280
SF	-0.0206	0.0192	-0.00328	-0.0254	<b>0.5992</b>	-0.00915	0.559
HSW	-0.0008	-0.0055	0.00287	0.0199	0.0479	<b>-0.11440</b>	<b>0.053</b>

Residue: 0.572

Presence of wide compatibility gene in parents needs to be explored for reasonable spikelet fertility in F<sub>1</sub> of this cross, but the reason for subsequent breakdown in F<sub>2</sub> which had only 7.04% highly fertile plants needs to be further investigated. Oka and Doida (1962) found that among many inter-varietal crosses, F<sub>1</sub> fertility and mean F<sub>2</sub> fertility were not correlated. They studied cross combinations, which showed a high fertility in F<sub>1</sub> hybrids and observed that fertility of F<sub>2</sub> segregated in a wide range. Partially sterile F<sub>2</sub> plants that breed true for sterility was established. Degeneration of part of male and female gametes after normal meiosis was established in cytogenetic studies. The number of hybrid sterility genes and the genetic distance between the two parents decided the fertility of F<sub>1</sub> plants (Zhang *et al.*, 1989). In crosses between subgroups of *O. sativa*, hybrid gene interactions, including both allelic interaction at the same locus and non-allelic interactions at the different loci, were responsible for varying degrees of hybrid sterility (Zhang and Lu 1993; Kubo *et al.*, 2008). The loci *S7*, *S8*, *S9* and *S35(t)* were responsible for female sterility in crosses between tropical *japonica* and *indica* (Wan *et al.*, 1993, 1996; Chen *et al.*, 2012), and also promoted the differentiation between tropical *japonica* and *indica*.

Further studies on identifying and characterizing genes for hybrid sterility and segregation distortion, molecular mechanism and arriving at a blueprint for intraspecific hybrid sterility loci derived from cross combinations among the subgroups will allow the utilization of heterosis (Zhang *et al.*, 2022). Introgression of wide compatible genes which carried *Scn* and *S5n* loci from different donors in *indica* variety HJX74 single segment substitution library resulted in the development of nine wide compatible *indica* lines (WCILs) which were compatible with both *indica* and *japonica* rice in pollen fertility and spikelet fertility (Guo *et al.*, 2022). These

lines provide a technique to develop intersub-specific *indica-japonica* hybrid rice.

To conclude, the *indica/tropical japonica* cross synthesized using diverse parents was aimed to develop inter sub specific derivatives for restorer development. Though the F<sub>1</sub> had 72.70% spikelet fertility, the F<sub>2</sub> generation showed a wide range from 16 to 92% fertility signifying its impact on the structure of the population which consisted of only 7.04% fertile plants. The cause behind this drastic reduction of fertility needs to be further explored. In the present breeding material, selection and advancement of highly fertile plants to F<sub>3</sub> and observation of these families for further segregation of spikelet fertility will give us some conclusive evidence for fertility inheritance and stability of spikelet fertility in later generations up to F<sub>6</sub> for restorer development.

## CONCLUSIONS

The *indica/tropical japonica* cross synthesized using diverse parents was aimed to develop inter sub specific derivatives for restorer development. Though the F<sub>1</sub> had 72.70% spikelet fertility, the F<sub>2</sub> generation showed a wide range from 16 to 92% fertility signifying its impact on the structure of the population, which consisted of only 7.04% fertile plants. The cause behind this drastic reduction of fertility needs to be further explored. In the present breeding material, selection, and advancement of highly fertile plants to F<sub>3</sub> and observation of these families for further segregation of spikelet fertility will give us some conclusive evidence for fertility inheritance and stability of spikelet fertility in later generations up to F<sub>6</sub> for restorer development.

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