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Research Article

Genetic variability, frequency distribution and association analysis in ADT (R) 48 x Kavuni derived F_2 population of rice (*Oryza sativa* L.)

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Abstract
The current research was aimed for estimation of variability parameters, heritability, genetic advance, skewness, kurtosis, association and path coefficient analysis for twelve traits using F_2 population attained from the cross ADT (R) 48 x Kavuni. High GCV and PCV, higher range of heritability adjoined with eminent genetic advance as per cent of mean besides significant positive skewness for the characters namely; the number of tillers per plant, the number of productive tillers per plant, the number of grains per panicle, the number of filled grains per panicle and single plant yield was observed indicating the predominance of cumulative gene effect and an effective selection. High positive direct impact with strong positive correlation on single plant yield was observed in the traits, the number of tillers per plant and the number of filled grains per panicle perhaps to be considered as useful traits in yield improvement. The information obtained from the current study may be advantageous in the selection and for the advancement of yield in future rice breeding programs.

Key words: Rice, genetic variability, path analysis, skewness and kurtosis

INTRODUCTION

Rice, the primary source of nourishment for almost 70 per cent of people, is the livelihood source for nearly 120-150 million rural population. While global rice production is about 759.6 million tonnes, India contributes nearly 172.58 million tonnes (FAOSTAT, 2018). The average utilization of rice by an Indian is 103 kg/year/person. The estimated population boom by 2050 i.e., 1824 million, threatens the current production of rice suggesting that yield escalation from 37 million ha ought to be 137 million tons in 2050 implying that yield should be expanded by half in the next thirty years to maintain *food security in India*. Hence, guaranteeing food security in future is a big challenging task for rice breeders revealed from the plateauing trend observed in rice production and productivity. Rice varieties exhibiting elevated productivity and suitable agronomic features by breaking the yield barrier is the necessity of recent times. The foundation for all yield advancement programmes relies upon the genetic variability with the execution of suitable selection strategies (Allard, 1960).

Genotypic coefficient of variation computes, degree of genetic variability which mirrors the heritable part of variability. Heritability serves as a reliable indicator for the inheritance of traits to descendants from their parents (Falconer, 1981). Genetic advance remains as other valuable indexes for the attainment of a desirable outcome on traits concerned in a population pertaining to selection. Genetic advance as mean per cent gives further clear-cut outcome when compared with genetic advance. Kurtosis and skewness stipulate in understanding the means of

genetic effects besides the extent of genes associated with individual traits (Fisher,1932 and Robson,1956). Association analysis guides in the detection of traits connoting positive or negative association with yield such that those might be considered during breeding for idyllic plant stature. Correlation accompanying path analysis gives an enhanced vision in determining an association between different characters which would aid in deciding viable breeding techniques for the advancement of supreme plant kind. Considering the above viewpoints, the current analysis was directed for the determination of various genetic factors in the segregating population of the cross ADT (R) 48 x Kavuni.

MATERIALS AND METHODS

Genetically pure seeds of ADT (R) 48 and Kavuni was obtained and an experiment was conducted at the Department of Rice, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore. Parental seeds were raised and crossing work was done between ADT (R) 48 and Kavuni and the crossed seeds were used to raise F_1 generation. The F_1 plants were harvested individually and forwarded to the F_2 generation and a population of 200 segregants were planted with a spacing of 20 x 20 cm besides following a suitable package of practices. Twelve traits *viz.,* plant height (cm), the number of tillers per plant, the number of productive tillers per plant, panicle length (cm), the number of grains per panicle, the number of filled grains per panicle, spikelet fertility (%), hundred seed weight (g), grain length (mm), grain breadth (mm), length breadth ratio and single plant yield (g) was assessed in every individual F_2 plants.

Genotypic coefficient of variation and phenotypic coefficient of variation (GCV and PCV) were computed utilizing the method in recommendation with Burton (1952). An array of variations were classified accordingly in the range; low (< 10 %), moderate (10 - 20%), high (> 20%) (Sivasubramanian and Madhavamenon, 1973). Since segregants could not be assessed in replicated trials, the environmental variance was determined from parents raised in replicated trials. Broad sense heritability was worked out applying the formula stated by Lush (1940) and categorized as high (> 60%), moderate (30-60%) and low (0-30%). The genetic advance in mean per cent was assessed by embracing the technique provided by Johnson *et al.* (1955) wherein classification was done to the extent of low (< 10%), moderate (10-20%), high (> 20%). The association involving yield and its constituent attributes and further among characters were calculated applying formula given by Weber and Moorthy (1952) and path analysis with formula indicated by Dewey and Lu (1959) wherein analysis was enacted utilizing the software, TNAUSTAT (Manivannan, 2014). R software version 1.4.1717 was used for illustrating the association plot and SPSS16.0 software was used to depict frequency distribution in the form of a histogram for the traits studied.

RESULTS AND DISCUSSION

Analysis of segregating population revealed that the Phenotypic Coefficient of Variation (PCV) remained marginally greater when compared with the Genotypic Coefficient of Variation (GCV) for all characters considered which represents the environmental impact on the expression of the characters (**Table 1**). The traits *viz.,* the number of tillers per plant, the number of productive tillers per plant, the number of grains per panicle, the number of filled grains per panicle and single plant yield exposed high GCV in addition to high PCV in accordance with Rani *et al.* (2016), Khandappagol *et al.* (2019) and Seneega *et al.* (2019). Attributes namely, plant height, panicle length, spikelet fertility and hundred seed weight exhibited moderate range for both GCV along with PCV which were in agreement with reports of Kahani and Hittalmani (2015) for plant height and panicle length and Lingaiah (2018) reported akin for plant height and hundred seed weight. Low GCV and PCV were observed for grain length, grain breadth and low GCV accompanied with moderate PCV for length breadth ratio which agrees to outcomes witnessed by Sala *et al*. (2015), Rani *et al.* (2016), Seneega *et al*. (2019) and Swapnil *et al*. (2020) for grain length and grain breadth. All the characters under study had high heritability (**Table 1**). Similar findings were revealed by Savitha and Usha Kumari (2015), Rani *et al.* (2016) and Seneega *et al*. (2019). The higher range of heritability besides higher GAM in traits *viz.,* plant height, panicle length, the number of tillers per plant, the number of productive tillers per plant, spikelet fertility, the number of grains per panicle, the number of filled grains per panicle, hundred seed weight along with single plant yield recognized indicates the existence of cumulative gene effect signifying that advancement of those traits might be effectual by adopting clear-cut selection strategies. This stood in concordance with Rani *et al.* (2016) for plant height, the number of grains per panicle, the number of filled grains per panicle, the number of tillers per plant, the number of productive tillers per plant as well as single plant yield and Seneega *et al*. (2019) for panicle length, single plant yield, the number of productive tillers per plant, the number of grains per panicle and hundred seed weight. Moderate range of GAM was conveyed for length breadth ratio besides grain length wherein grain breadth exhibited GAM in the lower range which agreed with Savitha and Usha Kumari (2015). Heritability in the higher range with a low genetic advance in mean per cent reflects the occurrence of non-additive genetic action specifying that preference for those characters might not stand worthy.

Frequency distribution pattern of twelve quantitative traits based on skewness and kurtosis (**Fig. 1**) in segregants disclosed a significant positively skewed leptokurtic distribution for the number of tillers per plant, the number of productive tillers per plant and single plant yield in fulfilment with Sheshaiah *et al*. (2018) and Priyanka *et al*. (2019), Nikhitha *et al*. (2020) for the number
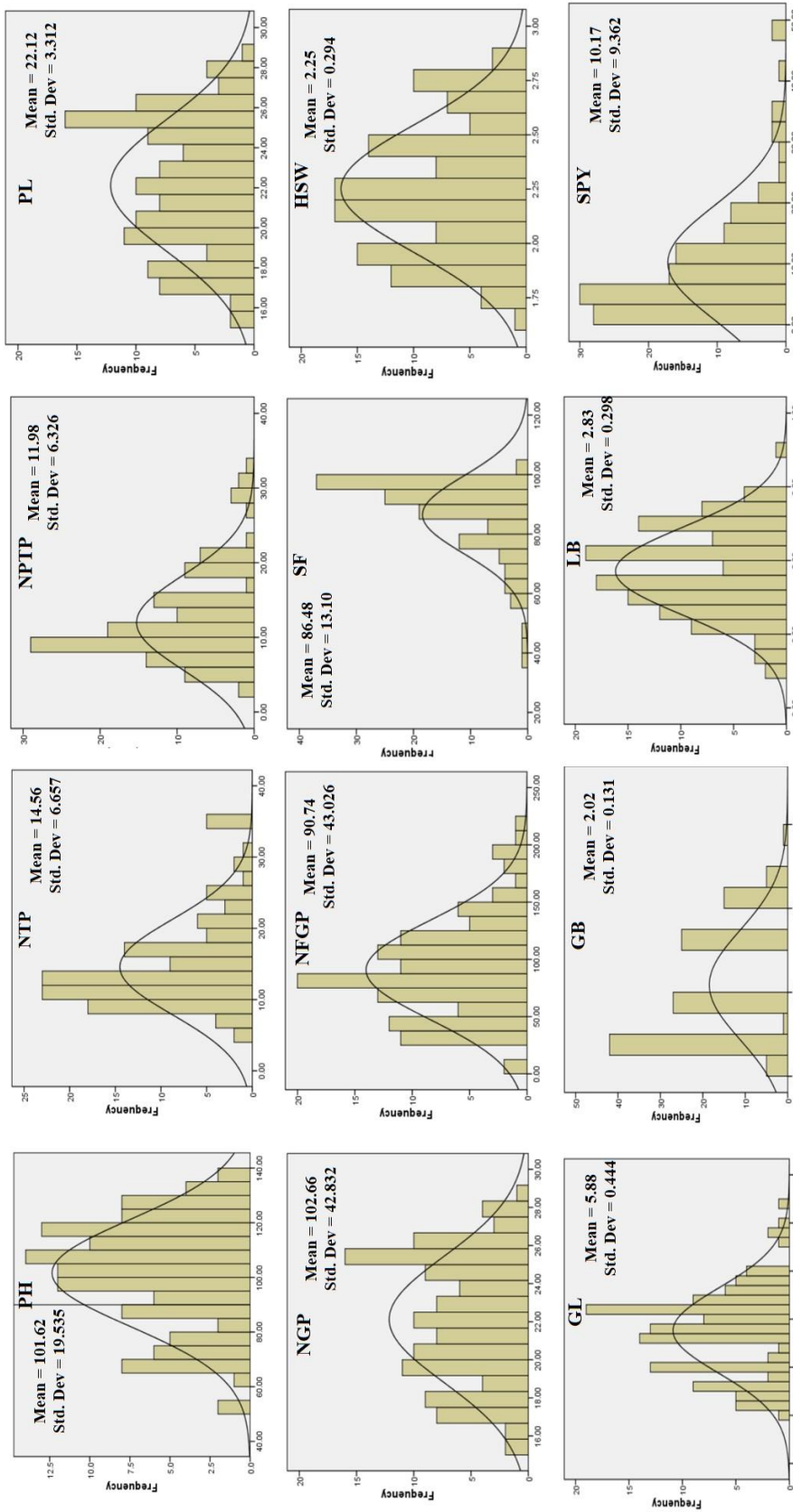
Fig.1. Frequency distribution for biometrical traits in F₂ generation of ADT (R) 48 x Kavuni cross

PH - Plant height, **NTP**- Number of tillers per plant, **NPTP** - Number of productive tillers per plant, **PL** - Panicle length, **NGP** - Number of grains per panicle, **NFGP**- Number of filled grains per panicle, **SF**- Spikelet fertility , **HSW** - Hundred seed weight, **GL**- Grain length, **GB**- Grain Breadth, **LB** - Length breadth ratio, **SPY** - Single plant yield.

Table 1. Genetic variability parameters of different biometrical traits in F$_2$ generation of ADT (R) 48 x Kavuni

Traits	Mean	Min.	Max.	PCV (%)	GCV (%)	h2 (%)	GAM (%)	Skewness	Kurtosis
PH (cm)	101.62	53	136.4	19.14	18.93	97.81	38.58	-0.46*	-0.53
NTP	14.56	5	35	45.52	44.12	93.93	88.09	1.37**	1.59**
NPTP	11.98	3	32	52.61	51.94	97.48	105.65	1.35**	1.58**
PL (cm)	22.12	15.5	28.7	14.91	14.67	96.78	29.74	-0.94**	2.00**
NGP	102.66	19	237	41.55	40.45	94.76	81.11	0.63**	0.20
NFGP	90.74	12	220	47.22	46.45	96.78	94.14	0.60**	0.26
SF (%)	86.48	37.5	100	15.08	14.28	89.56	27.83	-1.67**	2.97**
HSW (g)	2.25	1.68	2.82	12.98	12.70	95.67	25.58	-0.05	-0.74
GL (mm)	5.88	5	7.2	7.51	7.40	97.03	15.01	0.17	0.02
GB (mm)	2.02	1.8	2.4	6.45	5.31	67.72	9.00	0.58**	-0.36
L/B	2.93	2.26	3.79	10.13	9.21	82.59	17.24	0.02	-0.35
SPY (g)	10.17	1.5	49.81	91.77	91.03	98.68	186.55	2.09**	5.15**

*Significant at 5 % and ** Significant at 1 %level
PH - Plant height, NTP- Number of tillers per plant, NPTP - Number of productive tillers per plant, PL - Panicle length, NGP - Number of grains per panicle, NFGP- Number of filled grains per panicle, SF- Spikelet fertility , HSW - Hundred seed weight, GL- Grain length, GB- Grain Breadth, L/B - Length breadth ratio, SPY - Single plant yield. PCV- Phenotypic coefficient of variation, GCV- Genotypic coefficient of variation, h^2- Heritability, GAM- Genetic advance as per cent of mean.

of productive tillers per plant. Significant negatively skewed leptokurtic distribution was detected in traits, spikelet fertility and panicle length. Significant negative skewness and platykurtic distribution were witnessed for plant height indicating the chance of existence of dominance and dominance based duplicate epistasis specifying that more than one gene governs such trait. Transgressive segregants gained by the accumulation of favourable alleles for various traits studied to provide opportunity for the selection of segregants in either of the extremes. Eight segregants exhibit an extreme range of variation for plant height (**Fig. 2**).

Being an intricate quantitative attribute, yield enhancement should be carried out with aid of an indirect selection of traits contributing towards yield which could be achieved by means of association studies. Association analysis was performed to examine the nature of the relationship of various traits with yield and other allied traits. Since selection centred on one trait may directly or indirectly influence the performance of another trait particularly when concerned with complex attribute yield, in which direct selection was designated to be less effective. In this study, association analysis disclosed that single plant yield had a significant positive correlation with spikelet fertility, the number of grains per panicle, the number of productive tillers per plant, the number of tillers per plant, the number of filled grains per panicle and panicle length (**Fig. 3**). Similar outcomes were found out by Priyanka *et al*. (2019) and Swapnil *et al.* (2020) for panicle length and the number of filled grains per panicle and Abhilash *et al*. (2018), Seneega *et al.* (2019) and Bhargava *et al.* (2021) for the number of productive tillers per plant. A significant

and positive correlation of the number of tillers per plant was detected with panicle length, the number of grains per panicle, the number of filled grains per panicle, spikelet fertility, the number of productive tillers per plant similar to that of Swapnil *et al.* (2020) for the number of productive tillers per plant. Significant and positive association of the number of productive tillers per plant was witnessed with spikelet fertility, the number of filled grains per panicle, the number of grains per panicle and panicle length which was in accordance with Ali *et al.* (2018) for spikelet fertility, the number of filled grains per panicle and panicle length and Swapnil *et al*. (2020) for panicle length and spikelet fertility. Similarly, a significant and positive association of the number of filled grains per panicle was detected with spikelet fertility and grain length with length breadth ratio and plant height with panicle length, the number of grains per panicle and hundred seed weight. Panicle length displayed a positive and significant association with the number of grains per panicle, the number of filled grains per panicle and spikelet fertility in conformity with Kiani and Nematzadeh (2012) for the number of filled grains per panicle and Bhargava *et al.* (2021) for the number of grains per panicle. Grain width was found to be negatively associated with the length breadth ratio.

Determination of relationship amidst the attributes utilising correlation analysis might not convey an exact vision of the comparative significance of yield contributing characters. Hence, path analysis was utilized for the verdict of indirect and direct impacts to disclose the relationship among yield and its attributable traits. Outcomes of phenotypic path coefficient analysis uncovered indicating that amongst all the characters investigated, the number
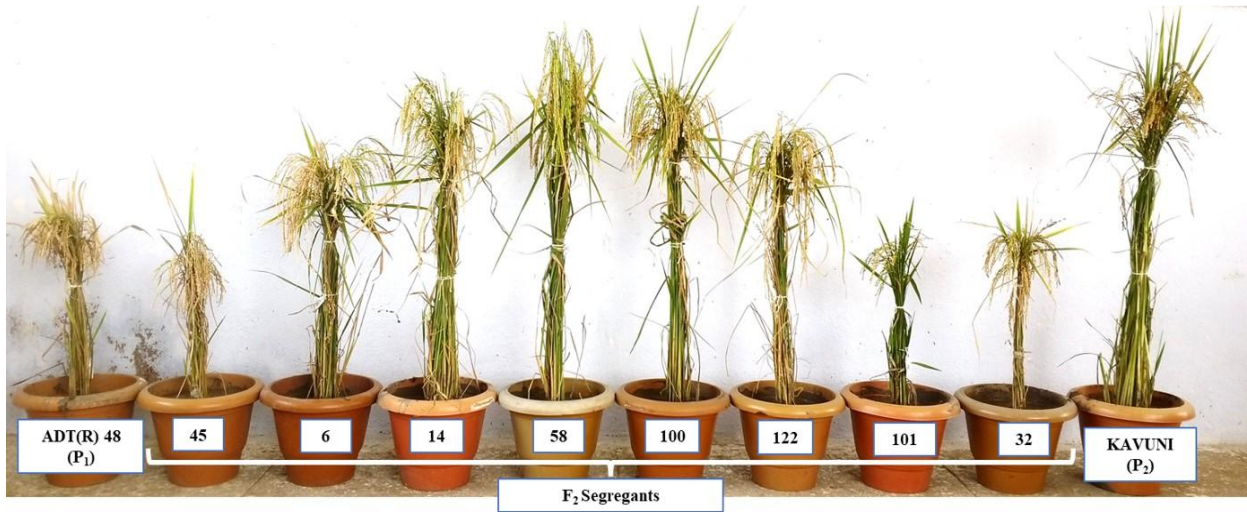
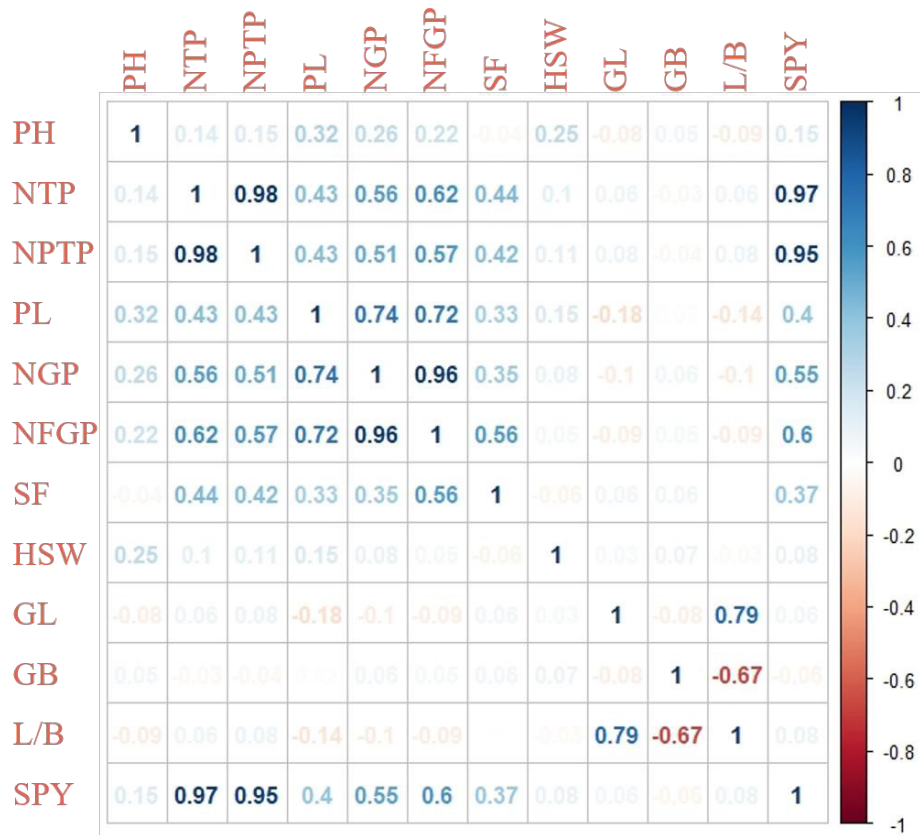**Fig. 2. Plant height variation observed in F2 generation of ADT(R) 48 x Kavuni cross**

Fig. 3. Heat map depicting phenotypic correlation among the biometrical traits in F_2 generation of ADT(R) 48 x Kavuni cross

Table 2. Direct and indirect effects of different biometrical traits as partitioned by path analysis for the cross ADT (R) 48 x Kavuni

Traits	PH	NTP	NPTP	PL	NGP	NFGP	SF	HSW	GL	GB	L/B	SPY
PH	0.0059	0.1068	0.0306	-0.014	-0.0485	0.065	0.0053	-0.0052	0.0159	0.0076	-0.024	0.1455
NTP	0.0008	0.7688	0.2029	-0.0189	-0.105	0.1834	-0.0617	-0.0021	-0.0116	-0.0046	0.0166	0.9687
NPTP	0.0009	0.7523	0.2073	-0.0189	-0.0961	0.1698	-0.0594	-0.0022	-0.0145	-0.0054	0.0201	0.9541
PL	0.0019	0.3283	0.0885	-0.0442	-0.1396	0.2134	-0.0466	-0.0031	0.0339	0.0022	-0.036	0.3988
NGP	0.0015	0.4274	0.1055	-0.0327	-0.1889	0.285	-0.0493	-0.0016	0.019	0.008	-0.0267	0.5473
NFGP	0.0013	0.4759	0.1189	-0.0318	-0.1817	0.2963	-0.0789	-0.001	0.0163	0.0069	-0.0234	0.5988
SF	-0.0002	0.3395	0.0881	-0.0147	-0.0666	0.1672	-0.1398	0.0012	-0.0107	0.0083	-0.0003	0.3718
HSW	0.0015	0.0789	0.0222	-0.0067	-0.0153	0.0145	0.0081	-0.0203	-0.0064	0.0105	-0.0066	0.0805
GL	-0.0005	0.0464	0.0157	0.0078	0.0188	-0.0252	-0.0078	-0.0007	-0.1916	-0.0115	0.2038	0.0552
GB	0.0003	-0.0253	-0.008	-0.0007	-0.0108	0.0145	-0.0083	-0.0015	0.0157	0.1402	-0.1742	-0.0581
L/B	-0.0006	0.0494	0.0161	0.0061	0.0195	-0.0268	0.0002	0.0005	-0.151	-0.0945	0.2585	0.0775

Residual effect = 0.2291; Diagonal and bold indicates the direct effects

of filled grains per panicle and the number of tillers per plant had a high positive direct impact on single plant yield and subsequently by the number of productive tillers per plant in addition to length breadth ratio (**Table 2**). Similar conclusions were derived by Kahani and Hittalmani (2015) for the number of tillers per plant, Shet *et al*. (2012), Hema *et al.* (2019), Kalaiselvan *et al.* (2019) and Bhargava *et al.* (2021) for the number of productive tillers per plant. A high positive direct effect of traits with single plant yield suggests the importance of such trait in yield enhancement. The characters such as the number of filled grains per panicle, the number of tillers per plant, the number of productive tillers per plant also displayed significant and positive association with single plant yield suggesting that yield enhancement could be attained by direct selection of these traits. Traits such as grain length, the number of grains per panicle and spikelet fertility exhibited low negative direct impact on single plant yield which are in accordance with Hema *et al.* (2019) conferring to grain length and Swapnil *et al*. (2020) with regard to the number of grains per panicle. Though the traits, the number of grains per panicle and spikelet fertility exhibited low negative direct impact on single plant yield they conveyed a high positive indirect effect on single plant yield *via* the number of tillers per plant. Similarly, the traits number of productive tillers per plant, the number of filled grains per panicle and panicle length exhibited a high positive indirect effect on single plant yield *via* the number of tillers per plant. Moderate positive indirect impact on single plant yield was observed in panicle length and number of grains per panicle *via* the number of filled grains per panicle and in grain length *via* length breadth ratio.

The outcomes of the current study indicate that high GCV, high PCV with the higher range of heritability in addition to higher genetic advance in mean per cent besides

significant positive skewness was exhibited for the characters namely the number of grains per panicle, the number of filled grains per panicle, the number of tillers per plant, the number of productive tillers per plant as well as single plant yield indicating the existence of cumulative gene action along with efficacious selection. Significant and positive correlation on single plant yield with spikelet fertility, the number of tillers per plant, the number of productive tillers per plant, the number of grains per panicle, the number of filled grains per panicle besides panicle length were recognised as traits in desirable direction to improve the yield.

Therefore, yield enhancement could be done indirectly by choosing F$_2$ plants exhibiting a high number of tillers per plant, the number of productive tillers per plant, the number of filled grains per panicle since these attributes revealed a higher range of heritability in addition to high genetic advance, significant positive skewness and retaining a strong positive direct impact besides a significant relationship for grain yield.

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