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Assessment of genetic variability, correlation and path coefficients in advanced breeding lines of rice (*Oryza sativa* L.) under irrigated conditions of command area

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Abstract

The experiment was conducted during *Kharif* 2019 across three locations *viz.*, ZAHRS, Shivamogga, AHRS, Honnavile and AHRS, Bavikere to evaluate 29 advanced breeding lines of rice including three checks in randomized complete block design with two replications for variability, correlation and path coefficients analysis for yield and its attributing traits. For all the characters examined, ANOVA reported significant differences among all the advanced breeding lines. For the traits *viz.*, number of spikelets *per* panicle, number of filled grains *per* panicle recorded high PCV and GCV values, while for plant height, test weight, L/B ratio and grain yield reported moderate PCV and GCV. High heritability coupled with high genetic advance recorded in traits *viz.*, number of filled grains *per* panicle, number of spikelets *per* panicle, test weight, L/B ratio and grain yield. The characters such as number of tillers *per* plant, number of productive tillers *per* plant, panicle length, and number of spikelets *per* panicle, number of filled grains *per* panicle, panicle fertility, test weight and L/B ratio had a positive significant correlation with grain yield. Six traits out of 12 traits had a positive and direct effect on grain yield *viz.*, days to 50 *per cent* flowering, number of tillers *per* plant, panicle length, number of spikelets *per* panicle, panicle fertility and L/B ratio.

Keywords: Pcv, gcv, heritability, genetic advance, correlation and path analysis.

Introduction

Rice (*Oryza sativa* L, 2n=24) is the most important food crop in the world (Asia, Latin America, parts of Africa and the Middle east), which accounts more than 21 *per cent* of the calorific needs of the world's population and up to 76 *per cent* of the calorific intake of the population of South East Asia (Melissa *et al*., 2009) [25].The estimates of different genetic parameters are important for a better understanding of the nature and magnitude of the genetic variability available in the base material. A broad spectrum of genetic variability among genotype with suitable selection criteria offers better scope for selection of appropriate genotypes over the seasons.

The information about the extent of several genetic parameters such as PCV, GCV, broad sense heritability and genetic gain on which the breeding methods are formulated for its further improvement is required for breeding for high yielding crops. Genetic variability is the basic factor to be considered while making selection. Heritability indicates transmissibility of a character in future generations (Satheeshkumar and Saravanan, 2012) [40]. High heritability coupled with high genetic advance is more helpful in forecasting genetic gain (Johnson *et al.,* 1955) [16]. Character association have been reported to vary with the environmental conditions. Hence, the study of character association under target environment helps the breeder in fixing proper selection criteria for grain yield in rice varieties understudy, such that the selection accomplished will possess the desired attributes under selection may limit genetic advance. Therefore, selection based on only yield is often unwise. So, it is necessary to know the association between yield and yield components which is determined by correlation analysis (Akhtar *et al.,* 2011) [3]. The level of contribution of each yield component trait on yield into direct and indirect effects is determined by path coefficient analysis (Ahmadizadeh *et al.,* 2011) [2].

Material and Methods

The experimental material for the current study comprises of 29 advanced breeding lines of F_6 generation with three checks JGL-1798, BPT-5204 and KKP-5 collected from Department of Genetics and Plant Breeding, College of Agriculture Shivamogga (Table 1). The research was carried out during *Kharif* 2019 at following three locations:

1. Zonal Agricultural and Horticultural Research Station, Shivamogga.
2. Agricultural and Horticultural Research Station, Honnavile.
3. Agricultural and Horticultural Research Station, Bavikere.

Seeds of rice advanced breeding lines were sown on 12th, 19th and 20thof July 2019 at Shivamogga, Honnavile and Bavikere, respectively, in raised beds of two m^2 each. Seedlings were transplanted after 21 days after sowing to the main field at the rate of one seedling *per* hill by following Randomized Complete

Table 1: List of advanced breeding lines of rice (F6) used under present investigation including checks

Cross combinations	Code	Advanced breeding lines	Grain shape	Grain color
JAYA × MYSORE MALLIGE	FABLE1	JAYA × MM 2-1-1-1	Medium slender	White
KPR 2 × IET SANNA	FABLE2	KPR2 × IS 9-2-2-2	Medium slender	White
BPT-5204 × MYSORE MALLIGE	FABLE3	BPT × MM 1-1-4	Medium slender	White
	FABLE4	BPT × MM 1-7-2	Medium slender	White
	FABLE5	BBT × MM 2-4-1	Medium slender	White
IET SANNA × HYDERABAD 3	FABLE6	IET SANNA × HYD3	Medium slender	White
	FABLE7	IS × HYD3 -3-2-1-2-2	Medium slender	White
MYSORE MALLIGE × KMLT4	FABLE8	KMLT × MM -4-2-2-5	Medium slender	White
	FABLE9	KMLT × MM -4-3-1-1	Medium slender	White
JGL-1798 X KPR2	FABLE10	JGL × KPR2 7-2-3-1-1-1	Medium slender	White
	FABLE11	JGL × KPR2 2-6-5-2	Medium slender	White
	FABLE12	JGL × KPR2 2-6-3-2	Medium slender	White
KPR2 × BASUMATI	FABLE 13	KPR2 × BASU 1-4-3-1	Medium slender	White
KMLT4 × KPR 2	FABLE 14	KMLT × KPR2 2-8-2-1 -1-2-3	Medium slender	White
JAYA × BILIYA	FABLE 15	J × B -FINE (WHITE)	Slender	White
	FABLE 16	J × B -FINE (RED)	Slender	Brown
JGL-1798 × KHP 2	FABLE 17	JGL × KHP2 2-6-3-3	Medium slender	White
CSR lines (Karnal lines)	FABLE 18	CSR-48	Medium bold	White
	FABLE 19	CSR-75	Medium slender	White
	FABLE 20	CSR-79	Medium bold	White
	FABLE 21	CSR-54	Medium bold	White
	FABLE 22	CSR-55	Bold	White
	FABLE 23	CSR-69	Medium slender	White
	FABLE 24	CSR-72	Medium bold	White
	FABLE 25	CSR-74	Short slender	White
	FABLE 26	CSR-76	Bold	White
	FABLE 27	CSR-80	Medium slender	White
	FABLE 28	CSR-81	Bold	White
	FABLE 29	CSR -82	Medium bold	White
JGL -1798	FABLE 30	Check	Medium slender	White
BPT-5204	FABLE 31	Check	Medium slender	White
KKP-5	FABLE 32	Check	Medium slender	White

Table 2: Estimation of mean, range, GCV, PCV, heritability and genetic advance *per cent* of mean for yield and yield attributing traits in 29 advanced breeding lines along with three checks of rice across three locations

Sl. No.	Character	Mean	Range		Coefficient of Variation		h^2_{bs} (%)	GAM (%)
			Min	Max	PCV (%)	GCV (%)		
1	Days to 50 per cent flowering	99.97	87.00	112.33	6.91	6.89	99.30	14.14
2	Days to maturity	130.84	118.00	142.33	5.26	5.24	99.30	10.76
3	Plant height (cm)	97.42	77.87	144.07	13.72	13.59	98.10	27.74
4	Number of tillers *per* plant	15.81	11.80	18.67	8.99	5.29	34.60	6.41
5	Number of productive tillers *per* plant	14.77	10.87	17.73	9.25	5.89	40.60	7.73
6	Panicle length (cm)	22.81	18.63	27.17	8.02	7.70	92.20	15.23
7	Number of filled grains per panicle	183.92	106.63	301.53	26.04	25.71	97.50	52.30
8	Number of spikelets per panicle	236.59	138.85	356.80	24.11	23.98	98.90	49.12
9	Panicle fertility (%)	77.56	67.20	84.84	5.02	4.66	85.90	8.89
10	Test weight (g)	21.52	16.07	31.96	19.56	19.39	98.30	39.59
11	Grain length and breadth ratio	3.85	2.92	5.15	15.72	15.70	99.70	32.30
12	Grain yield (Kg/ha)	5461.50	4080.00	6853.33	14.37	13.13	83.50	24.71

Block Design. The recommended packages of practice were followed to get a normal healthy crop. Five plants in all the advanced breeding lines were selected at random from each treatment for recording the observations *viz.*, days to 50 *per cent* flowering, days to maturity, plant height (cm), number of tillers *per* plant, number of productive tillers *per* plant, panicle length (cm), number of filled grains *per* panicle, number of spikelets *per* panicle, panicle fertility (%), test weight (g), L/B ratio and grain yield (kg/ha). Data on all the twelve characters from all the three locations were collected and pooled, then subjected to statistical analysis as phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was calculated by the formula given by Burton and Devane (1953) [8]. Heritability in broad sense (h^2b_s) and genetic advance as percent of mean were estimated by the formula as suggested by Hanson *et al*. (1956) [13] and Johnson *et al.* (1955) [16]. Correlation analysis was computed as per Karl Pearson (1932) [19] and path coefficient analysis was carried out as suggested by Wright (1921) [51].

Table 3: Estimation of phenotypic correlation for 12 yield and yield component traits in 29 advanced breeding lines along with three checks of rice

Traits	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}
X_1	1.000											
X_2	0.997**	1.000										
X_3	0.094	0.067	1.000									
X_4	-0.063	-0.059	-0.247*	1.000								
X_5	-0.051	-0.047	-0.274*	0.969**	1.000							
X_6	0.146	0.145	0.342**	0.009	-0.034	1.000						
X_7	0.521**	0.514**	0.426**	-0.023	-0.058	0.554**	1.000					
X_8	0.548**	0.542**	0.360**	-0.036	-0.074	0.588**	0.981**	1.000				
X_9	0.025	0.019	0.444**	0.067	0.071	-0.007	0.393**	0.208	1.000			
X_{10}	-0.661**	-0.668**	0.093	0.033	0.052	-0.207	-0.660**	-0.736**	0.149	1.000		
X_{11}	0.233	0.232	-0.528	0.308*	0.280*	0.321**	0.182*	0.301*	-0.472**	-0.405**	1.000	
X_{12}	0.240	0.233	0.094	0.496**	0.466**	0.320**	0.449**	0.427**	0.268*	-0.268*	0.343**	1.000

*& ** Significance at 5 % and 1 % levels respectively.

Where,

X_1 = Days to 50 *per cent* flowering X_2= Days to maturity X_3 = Plant height (cm) X_4 = No. of tillers *per* plant
X_5 = No. of productive tillers *per* plant X_6 = Panicle length (cm) X_7 = No. of filled grains *per* panicle X_8 = No. of spikelets *per* panicle
X_9 = Panicle fertility (%) X_{10} = Test weight (g) X_{11}= L/B ratio X_{12}=Grain yield (Kg / ha)

Table 4: Estimates of direct and indirect effects of yield components on yield at phenotypic level in 29 advanced breeding lines along with three checks of rice

Traits	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}
X_1	2.0799	2.0742	0.1958	-0.1302	-0.1064	0.3033	1.0836	1.1407	0.0511	-1.3752	0.4838
X_2	-1.9966	-2.0021	-0.1337	0.1182	0.0948	-0.2896	-1.0282	-1.0857	-0.0383	1.3385	-0.4647
X_3	-0.0148	-0.0105	-0.1575	0.0390	0.0432	-0.0539	-0.0671	-0.0567	-0.0699	-0.0146	0.0083
X_4	-0.0240	-0.0226	-0.0948	0.3834	0.3714	0.0035	-0.0090	-0.0138	0.0256	0.0127	0.1182
X_5	0.0011	0.0010	0.0059	-0.0207	-0.0214	0.0007	0.0012	0.0016	-0.0015	-0.0011	-0.0060
X_6	0.0283	0.0281	0.0664	0.0018	-0.0065	0.1940	0.1074	0.1141	-0.0014	-0.0402	0.0623
X_7	-1.4798	-1.4587	-1.2097	0.0665	0.1647	-1.5730	-2.8405	-2.7850	-1.1152	1.8758	-0.5178
X_8	1.5446	1.5273	1.0138	-0.1015	-0.2097	1.6558	2.7614	2.8164	0.5856	-2.0744	0.8477
X_9	0.0234	0.0183	0.4236	0.0638	0.0676	-0.0070	0.3746	0.1984	0.9542	0.1417	-0.4511
X_{10}	0.0200	0.0202	-0.0028	-0.0010	-0.0016	0.0063	0.0200	0.0223	-0.0045	-0.0302	0.0123
X_{11}	0.0581	0.0580	-0.0132	0.0770	0.0698	0.0802	0.0455	0.0751	-0.1180	-0.1013	0.2497
r Value	0.2401	0.2330	0.0936	0.4961	0.4659	0.3204	0.4490	0.4272	0.2675	-0.2684	0.3427

*& ** Significance at 5 % and 1 % levels respectively.

Where,

X_1 = Days to 50 *per cent* flowering X_2= Days to maturity X_3 = Plant height (cm) X_4 = No. of tillers *per* plant
X_5 = No. of productive tillers *per* plant X_6 = Panicle length (cm) X7 = No. of filled grains *per* panicle X8 = No. of spikelets *per* panicle
X_9 = Panicle fertility (%) X_{10} = Test weight (g) X_{11}= L/B ratio X_{12}=Grain yield (Kg / ha)

Result and discussion

Genetic variability

Availability of genetic variability in a population is major prerequisite for selection of superior genotypes. Analysis of variance revealed that all tested genotypes differed significantly for all the quantitative traits studied under the present investigation (Table 2, Figures 1-3). Genetic variability is significant in any crop for crop improvement and developmental programmes. The GCV and PCV also exhibited low value in the current analysis and the narrow difference between GCV and PCV that indicates a low environmental impact on the expression Of this feature in all three locations. In the present investigation, the coefficient of variation analysis indicates that estimates of the phenotypic coefficient of variation (PCV) for all traits were higher than the corresponding genotypic coefficient of variation (GCV), suggesting that to some degree they all interacted with the environment. The same result was also reported in rice by Bhadru *et al.* (2012) [6].

Coefficients of variability

In the present study observed low phenotypic and genotypic coefficients of variability for days to 50 *per cent* flowering, days to maturity, number of tillers *per* plant, number of productive tillers *per* plant, panicle length and panicle fertility, suggesting a

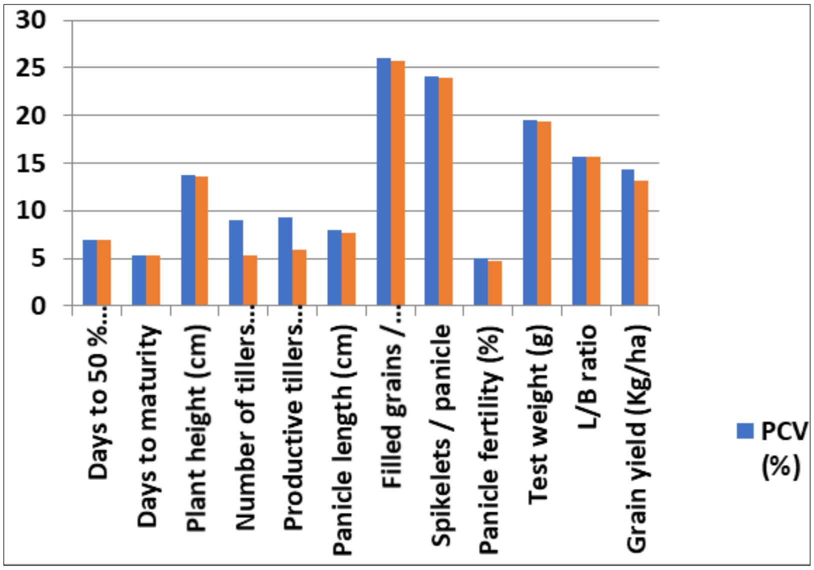

Fig 1: Histogram depicting estimates of GCV and PCV for 12 characters in rice.

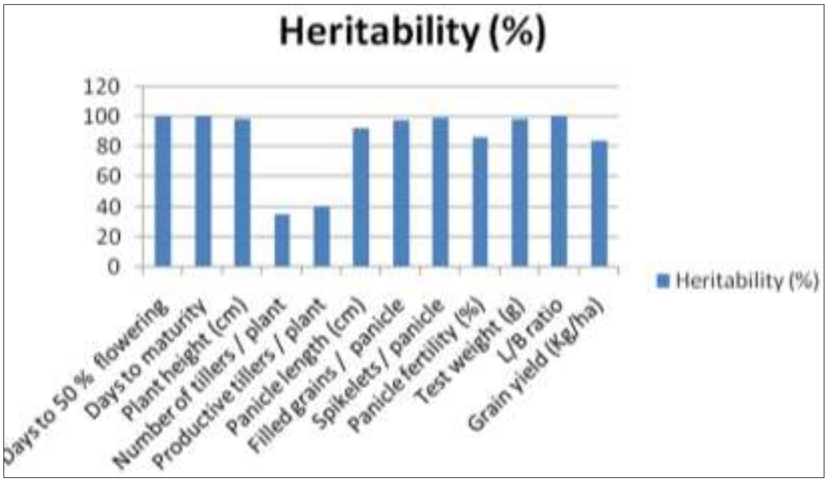

Fig 2: Histogram depicting estimates of Heritability for 12 characters in rice.

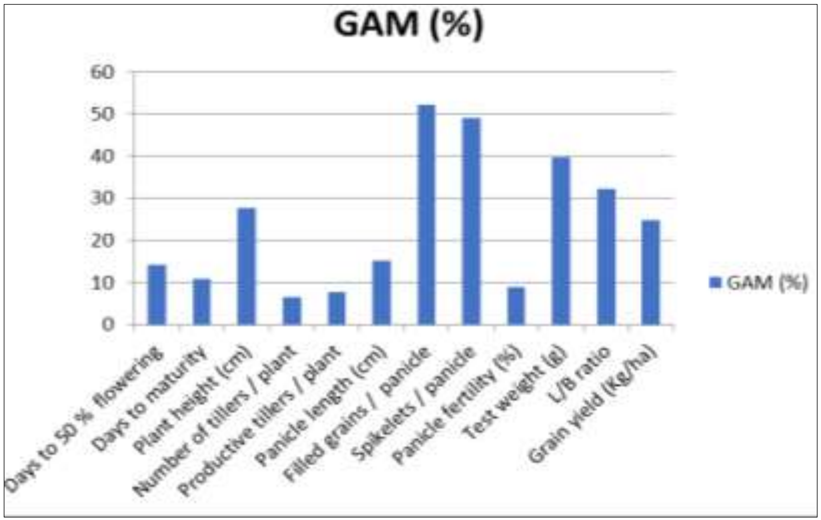

Fig 3: Histogram depicting estimates of Genetic advance mean (%) for 12 morphological characters in rice

Narrow genetic base for these traits. This result is similar with the findings of Kuchanur *et al.* (2009) [22]. Venkata Subbaiah *et al.* (2011) [48]. Ravindra Babu *et al.* (2012) [35]. Nirmaladevi *et al.* (2015) [30] and Rashid *et al.* (2017) [34].

Moderate phenotypic and genotypic coefficients of variability were observed for traits *viz.*, plant height, test weight, L/B ratio and grain yield, suggesting there is a narrow genetic base for these traits. This result is correspondence with earlier results of Sharma and Sharma (2007), Padmaja *et al.* (2008) [31]. Gangashetty *et al.* (2013) [12]. And Nirmaladevi *et al.* (2015) [30].

High phenotypic and genotypic coefficients of variability were observed for number of filled grains per panicle and number of spikelets per panicle, suggesting a high degree of variability and a better potential for development. This result is similar with the findings obtained by Karim *et al.* (2007) [18]. And Rita *et al.* (2009) [36].

Heritability and genetic advance

The high heritability coupled with high genetic advance observed for the traits *viz.*, plant height, number of filled grains per plant, number of spikelets per panicle, test weight, L/B ratio and grain yield. This result is similar with findings of Iftekharuddaula *et al.* (2001) [14]. Sangam *et al.* (2011) [38]. Ravindra Babu *et al.* (2012) [35]. Gangashetty *et al.* (2013) [12]. Kumar and Senapati (2013) [23]. In contrast high heritability coupled with low genetic advance recorded for panicle fertility and this result is similar with findings of Mina *et al.* (2011) [26].

The high heritability and moderate genetic advance observed for traits *viz.*, days to 50 per cent flowering, days to maturity and panicle length. This result is correspondence with the findings of Selvarj *et al.* (2011) [41]. Ashok *et al.* (2013) [4]. And Gangashetty *et al.* (2013) [12]. However, moderate heritability coupled with low genetic advance observed in number of tillers per plant and number of productive tillers per plant. This result is similar with the findings of Kuchanur *et al.* (2009) [22]. And Yadav *et al.* (2017) [52].

Correlation and Path Coefficient Studies

In most of the crop improvement programmes, crop yield improvement is the basic goal. As grain yield is a complex trait affected highly by other traits, selection based on simple correlation without taking into account of the component traits is not successful. Hence, correlation and path analysis are much importance in any plant breeding programme (Krishnaveni *et al*., 2006) [21]. Path analysis allows the splitting of the correlation coefficient into its components. One component being the path coefficient that estimates the direct effect of independent variables upon its dependent variables and the second component being the indirect effect(s) of independent variables on the dependent variables by another independent variables (Dewey and Lu, 1959) [10]. Keeping the stated concepts in mind, an effort was made among 29 advanced breeding lines, including three checks to know the correlation and path analysis of yield attributing traits (Table 3 and 4).

Correlation coefficient analysis

In the present investigation, grain yield had a positive phenotypic association with days to 50 *per cent* flowering, days to maturity, plant height, and number of tillers *per* plant, number of productive tillers *per* plant, number of spikelets *per* panicle, number of filled grains *per* panicle, panicle fertility and L/B ratio. Similar results were observed by Premkumar *et al*. (2015) [32] and Ramya Rathod *et al.* (2017) [33]. As a consequence, the enhancement of these traits by selection would certainly result in improved grain yield. A significant negative association was observed between test weight and grain yield. This result is in line with the observations of Minnie *et al*. (2013) [27].Days to 50 *per cent* flowering had a significant positive association with days to maturity and number of filled grains *per* panicle, this result is on par with the results of Kalyan *et al*. (2017) [17]. It had a significant negative association with test weight, which is comparable with the findings of Bekelebtal *et al.* (2013) [5] and Bhatia *et al.* (2013) [7]. Days to maturity had a significant positive association with days to 50 *per cent*, number of spikelets *per* panicle and number of filled grains *per* panicle, which are on par with Madhavilatha (2002) [24]. And Vinothini and Kumar (2008) [50]. Results.

Plant height had a significant and positive correlation with panicle length. Chakravorty *et al.* (2013) [9] reported similar results. There was a negative correlation with number of tillers *per* plant and number of productive tillers *per* plant. Such results are comparable with the observations of Karim *et al*. (2007) [18]. And Ratna *et al*. (2015). Number of tillers *per* plant had a significant positive association with number of productive tillers *per* plant. This is agreement with Khalid *et al.* (2012) [20]. Findings and it also had a positive significant correlation with L/B ratio. Number of productive tillers *per* plant had a significant positive association with number of tillers per plant, L/B ratio and grain yield, which is comparable with the results of Vijay Kumar (2015) [49]. While, it had a negative significant correlation with plant height. This result is comparable with the findings of Nagabhushan *et al.* (2003). Panicle length with plant height had a significant positive correlation and this result is on par with the findings of Ravindra *et al.* (2012) [35]. Number of spikelets *per* panicle with number of filled grains *per* panicle, panicle length and L/B ratio had a positive and significant association. This result is on par with the findings of Saravan *et al.* (2012) [39]. Whereas, it had a negative association with productive tillers *per* plant which, is similar to findings of Abdus *et al.* (2009) [1]. Number of filled grains *per* panicle showed a positive association with number of spikelets *per* panicle, panicle length, panicle fertility and L/B ratio. This was reported earlier by Yadhav *et al.* (2010) [53]. Number of filled grains *per* panicle exhibited a negative and significant association with test weight. This was reported earlier by Surek and Beser (2003) [45]. Panicle fertility had a significant positive correlation with number of filled grains *per* panicle. Similar results also recorded by Akhtar *et al.* (2011) [3]. Positive significant association recorded between panicle fertility (%) and number of filled grains *per* panicle. The findings are comparable with Akhtar *et al.* (2011) [3] findings. Test weight had a significant positive association with panicle fertility. Venkatalakshmi *et al.* (2014) [47]. Findings agree with this result. While, with grain yield it showed a negative significant association. This is in line with the observations of Minnie *et al.* (2013) [27]. L/B ratio showed a positive significant correlation with the number of productive tillers *per* plant, number of spikelets *per* panicle and number of filled grains *per* panicle. These findings agree with Chakravorty *et al.* (2013) [9]. Results. However, with test weight it showed a significant negative correlation. This result is comparable with findings of Veni and Rani (2006) [46]. Grain yield had a significant positive correlation with days to maturity and number of filled grains *per* panicle suggesting the importance of these traits as selection criteria in yield improvement programmes. This result is comparable with findings of Iftikharuddaula *et al.* (2001) [14]. And Nayak and Reddy (2005) [29].

Path Coefficient Studies

The path coefficient analysis was performed at the phenotypic level in the present study and these results are discussed below. Analysis of the phenotypic path coefficient on the yield related traits *viz.*, days to 50 *per cent* flowering, panicle length, number of spikelets *per* panicle and panicle fertility showed a positive direct effect on grain yield. Jayasudha and Sharma (2010) [15]. And Sharma *et al.* (2016) [43]. Have reported similar findings.

The negative direct effect was shown by plant height (Akhtar *et al.*, 2011 [3] and Ratna *et al.*, 2015) and test weight (Eidikohnaki *et al.*, 2013 [11] and Sudeepthi *et al.*, 2017) [44] on grain yield was also recorded. Days to 50 *per cent* flowering had an indirect positive effect on grain yield through panicle length. Similar findings are confirmed by Selvaraj *et al.* (2011) [41]. And Sala *et al.* (2015) [37]. This also had an indirect positive effect on days to maturity, panicle fertility, L/B ratio and number of tillers *per* plant.

Days to maturity had a positive indirect effect on grain yield *via* traits *viz.*, number of tillers *per* plant, number of productive tillers *per* plant and test weight. Plant height had a positive indirect effect *via* traits *viz.*, number of tillers *per* plant, number of productive tillers *per* plant and L/B ratio on grain yield. The number of tillers *per* plant had a positive indirect effect on grain yield through the traits *viz.*, number of productive tillers *per* plant, panicle length, panicle fertility, test weight and L/B ratio. Number of productive tillers *per* plant had a positive indirect effect *via* traits *viz.*, days to 50 *per cent* flowering, days to maturity, plant height, panicle length, number of filled grains *per* panicle and number of spikelets *per* panicle on grain yield. Positive indirect effect of panicle length on grain yield is recorded through the traits *viz.*, days to 50 *per cent* flowering, days to maturity, plant height, number of tillers *per* plant, number filled grains *per* panicle, number of spikelets *per* panicle, panicle fertility and L/B ratio. Number of spikelets *per* panicle had a positive indirect effect *via* traits *viz.*, days to 50 *per cent* flowering, days to maturity, plant height, panicle length, number of filled grains *per* panicle and panicle fertility on grain yield.

Number of filled grains *per* panicle on grain yield had a positive indirect effect *via* traits *viz.*, number of tillers *per* plant, number of productive tillers *per* plant and test weight. The positive indirect effect on grain yield was showed by panicle fertility through the traits *viz.*, days to 50 *per cent* flowering, days to maturity, plant height, number of tillers *per* plant, number of productive tillers *per* plant, number of filled grains *per* panicle, number of spikelets *per* panicle and test weight. The positive indirect effect on grain yield showed by test weight through the traits *viz.*, days to 50 *per cent* flowering, days to maturity, panicle length, number of filled grains *per* panicle, number of spikelets *per* panicle and L/B ratio. The positive indirect effect on grain yield showed by L/B ratio *via* traits like days to 50 *per cent* flowering, days to maturity, number of tillers *per* plant, number of productive tillers *per* plant, panicle length, number of filled grains *per* panicle, number of spikelets *per* panicle and panicle fertility. Taking into account that the nature and magnitude of traits relationship and their direct and indirect effects, it can be interpreted that in any selection program for selecting high yielding genotypes in rice, days to 50 *per cent* flowering, number of tillers *per* plant, number of filled grains *per* panicle, panicle length, number of spikelets *per* panicle and panicle fertility could serve as key traits.

Conclusion

Estimated high heritability coupled with high genetic advance *per cent* of mean for plant height, number of spikelets *per* panicle, number of filled grains *per* panicle, test weight, L/B ratio and grain yield. Thus, it indicated the predominance action of additive gene to control these characters. Those characters can therefore, be improved simply by selection in the future. From the analysis concluded that advanced breeding lines possessed adequate amounts of variability for yield and its associated traits. It can be seen from the correlation that those which are positively associated with each other and also with the yield of grain are equally economical to increase the yield of rice *per* hectare. It is therefore indicated that grain yield is increased whenever there is an increase in positively correlated traits (Minnie *et al.*, 2013) [27]. However, the negative correlation with other traits, as well as with the grain yield is also of equal importance during the improvement of the yield *per* hectare of rice production. In the present analysis, the residual effect is 0.6801, implying that the traits included in the experimental research had contributed about 32 *per cent* of the variability owing to the dependent variable *i.e.*, yield and also suggesting that characters examined in the present study were not adequate to explain the variability. This finding leaves the impression that other key characters other than those involved in this study may also contribute to the yield.

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