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Research Article

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Trait Association and Path Analysis Studies of Yield Attributing Traits in Rice (*Oryza sativa* L.) Germplasm

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Abstract

Forty-eight Rice germplasm were undertaken for estimating variability, heritability, genetic advance, correlation and path analysis for yield and yield attributing traits. The experiments were conducted in a randomized block design with three replications during two-season viz., July-Oct, 2017 and July-Oct, 2018 at the Agriculture Research Farm, Institute of Agricultural Sciences, Banaras Hindu University Varanasi. Analysis of variance revealed that genotypes contain significant differences for all the traits. High estimates of GCV and PCV were observed for traits like filled grains panicle^{-1} followed by total grains panicle^{-1}, grain yield plant^{-1} and number of effective tillers plant^{-1}. High heritability coupled with high genetic advance as % of mean was observed for the traits viz. plant height, days to 50% flowering and test weight. These characters exhibited less influence of environmental variance in their inheritance and hence could be improved by means of simple selection. Path analysis revealed that characters like filled grains panicle^{-1}, total grains panicle^{-1} and number of effective tillers plant^{-1} had prominent direct positive effects on grain yield plant^{-1}. Genotypes LC-53, LC-55 and LC-50 and LC-59 were found to be superior for yield and contributing traits during July-Oct, 2017 and July-Oct, 2018 respectively while LC-90 was found to be consistently overling under both seasons. Genotypes LC-54 and LC-56 were earliest in flowering and maturity suggesting that they can be used as a donor in hybridization programme for evolving early maturing rice variety.

Keywords: Rice, correlation, path coefficient, heritability, genetic advance

1. Introduction

Rice belongs to the genus *Oryza*, subtribe Oryzineae of the family Poaceae. It is one of the few crop species endowed with richest genetic diversity. The genus comprises of 24 recognized species, out of which only 2 are domesticated (*O. sativa* and *O. glaberrima*) and the rest 22 are wild representing 11 genomic groups, 6 are diploid (n=12: AA, BB, CC, EE, FF and GG) and 5 are polyploid (n=24: BBCC, CCDD, HHJJ, HHKK and KKLL). Rice found in Asia, America and Europe belongs to *Oryza sativa* and varieties grown in West Africa belong to *Oryza glaberrima*. The sativa rice species are commonly divided into three subspecies viz.; Indica, Japonica and Javanica. Globally rice is grown in an area of 167.24 Million hectares, with a production of 769.65 Million tonnes and a productivity of 46 q ha^{-1} (Anonymous, 2017). India is the second largest producer of rice after china, accounting 18% of the world rice production. In India

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rice is cultivated in an area of 43.78 Million hectares (20% cropped area), with a production of 168.5 million tonnes and productivity of 38.4 q ha^{-1} and contributes 25% to agricultural GDP (Anonymous, 2017). The world population is predicted to reach nine billion by the year 2050 and food insecurity could become a serious global problem (Alexandratos and Bruinsma, 2012). Therefore, it is crucial to augment the productivity of major cereal crops such as rice to satisfy ever increasing demand of a population.

Rice is a highly domesticated crop, and domestication processes are accompanied by genetic erosion, which in turn cause a reduction in genetic diversity among traditional varieties leading to gradual loss of landraces from the fields (Khare et al., 2014). Modern rice cultivars have been developed through the hybridization of elite lines and subsequent selection for yield and quality traits. The genetic potential and magnitude of heterogeneity are still present in local landraces that need to be characterize in available upland rice germplasm.

The base for any crop improvement programme relies on availability of amount and direction of genetic association of the traits, the base population (Girma et al., 2018), and adoption of appropriate selection techniques (Tiwari et al., 2011; Rani et al., 2016, Adhikari et al., 2018). Variability refers to the presence of differences among the individuals of plant population due to their genetic composition and the environment in which they are raised. The existence of variability is pre requisite for improvement of genetic material because effective selection utilises the genetic variability present among the individuals to be bred enabling the plant breeder to more rapidly produce new varieties or improve existing ones (Meena and Bahadur, 2014; Ranganatha et al., 2013; Yared and Misteru, 2016). The variability for yield in crop species will get exhausted sooner or later if not checked, which in turn limits the prospects of further improvements in the crop species. Thus, knowledge of genetic variability present in a crop species for the character under improvement is of paramount importance for the success of any crop breeding programme.

Yield as such is a complex entity and it is the resultant of different traits thus marking the importance of component traits (Hossain et al., 2015; Tiwari et al., 2019). Different traits are selected as per requirement and breeding programmes are carried out. Different genetic variability parameters, namely, Genotypic Coefficient of Variability (GCV), Phenotypic Coefficient of Variability (PCV), heritability and genetic advance for yield attributing traits are a major concern for any plant breeder and for crop improvement programs. The genetic improvement of quantitative traits expected in a crop species depends upon heritability pattern of the trait, nature and amount of variability present in the existing germplasm (Iraddi et al*.,* 2013; Rashmi et al*.,* 2017). Estimation of heritability along with genetic advance, conjointly, is helpful in predicting the gain under selection than heritability estimate alone (Moosavi et al., 2015). It is important that selection should be based on high heritability coupled with genetic advance. The correlation coefficient helps to identify characters that have little or no importance in the selection programme. The existence of correlation may be attributed to the presence of linkage or pleiotropic effect of genes or physiological and development relationship or environmental effect or in combination of all. Correlation study should aim in selecting traits showing positive association with grain yield. Correlation in grouping with path analysis would give a better insight into cause and effect relationship between different pairs of characters.

The spectrum of variability in germplasm for grain yield traits depends on the genetic diversity of the combining parents. Hence, estimation of genetic diversity for yield traits among accessions is important for planning the future crossing programmes. In view to the above facts continuous efforts are required to conserve the germplasm and exploiting their worth through analysing the yield potential and judging its component characters and therefore, the present investigation involves trait association and path analysis studies among forty eight upland rice germplasm.

2. Materials and Methods

The investigation was carried out during two crop seasons viz. July-Oct, 2017 and July-Oct, 2018 to study correlation and path coefficient in forty eight rice germplasm (Table 1).

The experiment was conducted at the Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi which is situated at 25^{0}18’ North latitude and 83^{0}03’ East longitude and at altitude of 123.23 m from sea level. The experimental unit had fertile alluvial-loam soil and is characterized as soil of Indo-Gangetic Plains. The germplasm were grown in a Randomized Block Design with three replications. Each plot consisted of three rows of 1.5 m length with spacing (15×20) cm^2. with recommended package of practices. Five random plants were tagged and the observations were recorded on 11 yield contributing traits viz*.,* days to 50% flowering, days to maturity, plant height, panicle length, effective tillers plant^{-1}, filled grains panicle^{-1}, unfilled grains panicle^{-1}, total grains panicle^{-1}, spikelet fertility %, test weight and grain yield plant^{-1}. ANOVA was done for partitioning the total variation into variation due to treatment and replication as per Panse and Sukhatme (1967). It is worked out to test the significance of ‘F’ and‘t’ test and further carried out according to the procedure of Randomised Block Design for analysis of each character as per methodology of Fisher and Yates (1938). Genetic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) were worked out as per Burton and De-Vane (1953) and classified as per categorisation suggested by Sivasubramanian and Menon (1973). Further Correlation analysis was performed. Path analysis was carried out following the method suggested by Dewey and Lu (1959).

Table 1: Forty eight upland rice germplasm evaluated during the two seasons

Sl. No.	Germplasm	Sl. No.	Germplasm	Sl. No.	Germplasm	Sl. No.	Germplasm	Sl. No.	Germplasm
1.	LC-50	11.	LC-60	21.	LC-70	31.	LC-81	41.	LC-91
2.	LC-51	12.	LC-61	22.	LC-71	32.	LC-82	42.	LC-92
3.	LC-52	13.	LC-62	23.	LC-73	33.	LC-83	43.	LC-93
4.	LC-53	14.	LC-63	24.	LC-74	34.	LC-84	44.	LC-94
5.	LC-54	15.	LC-64	25.	LC-75	35.	LC-85	45.	LC-95
6.	LC-55	16.	LC-65	26.	LC-76	36.	LC-86	46.	LC-96
7.	LC-56	17.	LC-66	27.	LC-77	37.	LC-87	47.	LC-97
8.	LC-57	18.	LC-67	28.	LC-78	38.	LC-88	48.	LC-98
9.	LC-58	19.	LC-68	29.	LC-79	39.	LC-89		
10.	LC-59	20.	LC-69	30.	LC-80	40.	LC-90		

3. Results and Discussion

Significant difference has been revealed through analysis of variance (ANOVA) of forty-eight genotypes for eleven traits representing the presence of inherent genetic difference (Table 2).

The mean sum of square due to treatment showed high significant differences for all the traits under study for both the season viz. July-Oct, 2017 and July-Oct, 2018 except panicle length. These findings are in accordance with Patra et al., 2006, Mustafa and Elsheikh (2007) and Rashmi et al., (2017).

Table 2: ANOVA for eleven traits in forty eight rice germplasm grown during July-Oct, 2017 and July-Oct, 2018

			Traits										
Years	Source	df	DF	DM	PH	PL	ET	FGP	UFGP	TGP	SF%	TW	GYP
2017	Genotype	47	128.15**	144.45**	1373.43**	25.26**	35.28**	4968.24**	1091.12**	6255.95**	389.44**	29.63**	272.77**
2018	Genotype	47	189.10**	207.14**	1008.05**	9.89**	33.21**	6049.43**	1209.26**	6748.55**	494.86**	28.37**	105.93**
2017	Replication	2	0.89	11.13	0.39	11.46	1.67	656.89	37.71	976.36	6.16	1.35	1.94
2018	Replication	2	1.59	11.63	25.00	2.64	4.88	27.89	302.02	332.31	94.93	1.47	17.06
2017	Error	94	1.43	1.85	3.89	2.00	1.17	150.25	61.44	284.91	18.54	0.27	6.20
2018	Error	94	1.11	1.67	50.55	2.11	3.11	123.26	82.45	193.10	21.41	0.35	10.82

Table 2: Continue...

**: significant at (p=0.01) level of significance

The study revealed genotypes LC-53 (54.99 g) followed by LC-55 (53.45 g) and LC-90 (50.16 g) while the genotype LC-50 (41.74 g) followed by LC-90 (36.52 g) and LC-59 (36.32 g) as the best for yield and yield contributing traits during July-Oct, 2017 and July-Oct, 2018 respectively (Table 3.1 and 3.2).

Therefore, these germplasm can be successfully utilized as parent (s) in future breeding programme. Genotype LC-56 was found to be earliest in flowering and maturity during July-Oct, 2017 while in July-Oct, 2018, genotype LC-54 and LC-56 were found to be earliest. These genotypes can be used as a donor parent (s) in hybridization programme for evolving early maturing rice variety.

3.1. *Genetic variability*

The estimates of Phenotypic Coefficient of variation (PCV) were found to be higher than Genotypic Coefficient of variation (GCV) for all the traits under consideration. The high estimates of PCV and GCV were observed for traits like filled grains panicle^{-1} followed by grain yield plant^{-1}, total number of grains panicle^{-1} and number of effective tillers during July-Oct, 2017 and 2018. (Table 4) suggesting that these traits were controlled mainly by genetic factors and is less affected by environment hence; they can be utilized for further improvement of crop. The estimates were found to be in accordance with Souroush et al., 2004.

3.2. *Heritability and genetic advance*

High heritability (h^2) coupled with high genetic advance

Table 3.1: Mean performance of forty eight upland rice germplasm for eleven traits for July-Oct, 2017

Genotypes	DF	DM	PH	PL	ET	FGP	UFGP	TGP	SF%	TW	GYP
LC-50	83.67	113	100.33	25	20.67	66.67	21.67	88.33	75.51	20.34	45.45
LC-51	96.33	127	113.67	28	7.33	99.67	36.33	136	73.26	21.74	28.8
LC-52	78.33	108	98	23.67	11.33	67	29	96	70.13	21.33	24.62
LC-53	85.33	111	154.33	27.67	8	147.67	31	178.67	82.2	26.12	54.99
LC-54	79.67	108	98.67	24	12	78.67	17.67	96.33	81.8	21.98	23.23
LC-55	90.33	119	158.67	29.67	9.67	168	21.67	189.67	88.74	27.42	53.45
LC-56	77	105	99.33	26.67	12	63	20	83	75.91	21.29	25.15
LC-57	78	106	97	23	10	65.67	14.67	80.33	81.71	21.8	20.79
LC-58	84.33	116	150.33	28.33	14.33	85.33	17	102.33	83.44	23.54	32.15
LC-59	91.33	119.67	156	29	10	172.67	23.67	196.33	87.92	19.72	30.05
LC-60	90.67	121	152.33	28.33	11.33	116	12.33	128.33	90.39	20.74	32.79
LC-61	92.33	122	156.33	25.67	6.33	92	12.33	104.33	88.67	19.91	16.84
LC-62	85.67	116	128	27.33	10.33	121.33	34	155.33	78.07	11.86	20.15
LC-63	85.67	116	130	29.67	12.67	128	42	170	76.27	12.61	29.32
LC-64	80	111	114	21.67	11.67	69.33	12.33	81.67	84.97	18.61	16.39
LC-65	90.67	121	164.33	30	7.33	171.33	24.33	195.67	87.61	22.81	35.96
LC-66	83.67	111.67	150.33	29.67	11.33	127.67	33	160.67	79.37	17.94	34.43
LC-67	83	113	131.67	24.67	13	79.67	24.67	104.33	76.74	16.61	23.7
LC-68	89.67	120	150.67	27.33	8.67	172.67	14.33	187	92.41	19.45	21.34
LC-69	91.33	124.67	148.33	23.67	17.67	48	12	60	80.21	21.05	35.21
LC-70	78	106.67	122.67	16.33	15	45.33	7.67	53	86.63	17.38	17.96
LC-71	88.67	118	159.33	25	9.33	168	12.33	180.33	93.09	17.86	20.45
LC-73	89.33	118	153	26	7.67	113.67	15.33	129	88.2	22.37	17.37
LC-74	82	110	144.67	26	12	119.67	23.67	143.33	83.63	22.44	21.03
LC-75	80	111	136.33	23.67	10.33	69.33	16	85.33	82.86	19.44	14.26
LC-76	86	116	150.67	21.67	16	78	9.33	87.33	89.36	23.02	27.17
LC-77	86.33	113.67	142	23.67	13.67	70	17.33	87.33	80.26	20.82	20.86
LC-78	82.33	111	117.33	26.33	15	67.67	44	111.67	60.85	22.91	19.61
LC-79	77.67	106	112.33	21.33	23.67	50.33	2.67	53	95.05	17.94	23.39
LC-80	101.33	128.33	118.67	29.33	9	84.67	53	137.67	61.45	17.96	26.59
LC-81	82.67	111	103.33	28.33	11	113.33	12	125.33	90.45	27.83	27.94
LC-82	85.33	113	143.33	27.33	6.33	147.67	17.67	165.33	89.36	22.75	27.34
LC-83	88.67	116	116.67	31.33	10	91.67	27.33	119	77.12	24.88	29.85
LC-84	82	111	137	26.33	10.67	85.67	18	103.67	82.81	23.86	32.75
LC-85	90	116	148.67	30.67	7.67	106.33	27.33	133.67	79.55	18.65	24.57
LC-86	86.67	115	97.33	26	12	124	77	201	62.02	18.65	32.28
LC-87	83.67	112	101.67	25.67	10.33	119.33	74	193.33	61.66	17.81	23.79
LC-88	90.67	117	116.67	30.67	8.33	77.67	40.67	118.33	65.58	24.64	20.89
LC-89	96.33	125	136.33	26.33	15	164	22.33	186.33	88.13	18.52	31.59
LC-90	101.67	132	128	27	12.67	219.67	41.67	261.33	84.04	18.5	50.16

Table 3.1: Continue...

Genotypes	DF	DM	PH	PL	ET	FGP	UFGP	TGP	SF%	TW	GYP
LC-91	94.33	123	117.67	27.67	11	130.67	28.33	159	82.47	21.96	20.66
LC-92	89	116	121.33	23.33	9.67	139	21	160	87.1	21.83	28.87
LC-93	94.67	126	115	26.33	10.67	136	47.33	183.33	74.43	19.88	28.79
LC-94	97.67	128	109.67	27	8	47.33	103.33	150.67	31.37	19.28	11.28
LC-95	98.33	127	106.67	26.33	13	91.67	45.67	137.33	66.74	19.54	18.47
LC-96	98.33	128	101.33	25.67	14	70	34.33	104.33	67.35	17.13	31.85
LC-97	84	110	104.33	30	13.67	89.67	25.67	115.33	77.49	21.81	12.61
LC-98	80.33	108	97.67	24.33	13.33	84.33	13.67	98	86.52	19.85	25.45

Table 3.2: Mean performance of forty eight upland rice germplasm for eleven traits for July-Oct, 2018

Genotypes	DF	DM	PH	PL	ET	FGP	UFGP	TGP	SF%	TW	GYP
LC-50	84	111	90.33	22.33	18.33	67.67	8.33	76	89	20.26	41.74
LC-51	95.33	122	101.33	25	10.67	101	50.33	151.33	66.97	21.7	24.35
LC-52	77.33	105	120.67	25.67	12.33	78	9	87	89.66	23.23	26.04
LC-53	89	116	135	25.33	7	185.67	15	200.67	92.48	26.13	31.78
LC-54	76.33	102	97.67	25	15.67	81.67	11	92.67	88.28	23.25	22.92
LC-55	90.33	118	138.67	26.67	8	160	18.33	178.33	89.93	28.48	27.52
LC-56	76.33	103	94.67	24.33	15.67	63.67	12	75.67	84.1	23.13	25.3
LC-57	77.67	107	94.67	23.33	12.67	72.33	11	83.33	86.81	22.45	23.98
LC-58	84	113	130	22.67	11.33	86	6	92	93.19	24.12	22.96
LC-59	88.33	116	143.67	25.67	9	153.67	13	166.67	92.13	21.53	36.32
LC-60	88.33	117	135.33	25.33	6.67	157	15.67	172.67	91	22.31	29.25
LC-61	90.33	119	146.33	27	7	156	8	164	95.22	23.8	24.95
LC-62	85	112	111.67	24	7.67	144	9	153	94.07	14.01	19.17
LC-63	84.33	111	106.33	28	8.33	168.67	20.33	189	89.26	14.26	23.86
LC-64	80	110	115	22.33	8.67	116.33	5.67	122	95.47	21.68	17.74
LC-65	92.33	124	147	27	5.67	248	18.67	266.67	93	23.25	25.73
LC-66	83.67	113.33	136	26.67	8	154	10.67	164.67	93.53	20.14	21.68
LC-67	83	114	131	24.33	9	116.33	5.67	122	95.36	19.93	19.96
LC-68	90	120	134.33	26	5	163.67	15.67	179.33	91.32	19.4	21.91
LC-69	88.67	118.67	128	23	15.67	77.33	6.67	84	92.36	24.19	25.86
LC-70	79.33	110	124.33	21.33	9.67	86	6.33	92.33	93.19	21.01	17.78
LC-71	88.67	116	136.33	24	4.67	166.33	16.67	183	91.05	18.56	14.95
LC-73	88.33	116	137.67	24.67	5.67	126	16.33	142.33	88.56	23.5	20.55
LC-74	85.33	116	129.33	25.67	6.33	121.67	11.67	133.33	91.29	22.47	15.57
LC-75	83	111	134	24.33	7.67	132.33	17.33	149.67	88.47	21.68	18.56
LC-76	86.67	116	119	21.33	11.33	80.67	8.67	89.33	90.29	25.83	22.1
LC-77	86.33	115	121.33	23.33	12.33	62.33	36.67	99	63.12	22.17	18.22
LC-78	90	118	95.33	25.33	9.67	64.67	13	77.67	83.42	26.56	17.96
LC-79	80.33	109	111.67	22	12.33	54.67	6.33	61	89.94	18.78	19.71
LC-80	107.67	136	113	29	7	144.33	72	216.33	66.76	19.24	20.06
LC-81	90	119	122.67	26.33	8.67	109.33	15.67	125	87.52	28.51	32.51

Table 3.2: Continue...

Genotypes	DF	DM	PH	PL	ET	FGP	UFGP	TGP	SF%	TW	GYP
LC-82	89.33	120	125.33	24.33	6.67	228.33	19.67	248	92.09	23.71	31.66
LC-83	92.67	122	100	26	13.33	109	27.33	136	79.96	24.23	26.24
LC-84	91	120	140	27	8.33	89	19	108	82.43	23.93	20.87
LC-85	96	135	133.67	29	8.67	104	41.67	145.67	72.74	19.24	21.91
LC-86	106	134	87.67	25.33	8.33	149	66.33	215.33	69.04	19.37	27.48
LC-87	91.67	121	92.67	23.67	9.67	72.33	62.67	135	55.9	16.55	14.59
LC-88	94.67	119.67	107.33	27.33	9	55.67	78	133.67	42.03	23.73	23.35
LC-89	104.67	130.33	119.33	26.33	8.67	168.67	23	191.67	88.13	17.91	27.41
LC-90	100.33	127.67	120	23.67	10.33	137	46.67	183.67	74.51	20.11	36.52
LC-91	100.33	131	93	24	7	128.67	34.33	163	78.94	21.77	17.65
LC-92	93.67	122	114.33	24.67	9.33	123.33	22.67	146	84.44	21.37	28.3
LC-93	101	130	102.33	24.67	10.67	120.33	69	189.33	63.73	19.19	26.7
LC-94	94.67	120.67	97.33	27.33	8	78	39.67	117.67	66.33	20.44	16.63
LC-95	101.67	132	86.33	24	9.67	104	49.67	153.67	67.57	19.32	20.61
LC-96	104.33	133	90.33	24.33	10	63	49	112	56.62	18.54	25.85
LC-97	92	120	95	26.67	10.66	66.33	39.67	106	63.23	24.78	17.66
LC-98	83.33	113	91	24.67	20.67	90	12	102	88.43	20.55	31.99

(GA) as % of mean was observed for plant height, number of effective tillers, number of filled grains panicle^{-1}, number of unfilled grains panicle^{-1}, total number of grains panicle^{-1}, spikelet fertility %, test weight and grain yield plant^{-1} for both the seasons viz. July-Oct, 2017 and July-Oct, 2018 (Table 4). This indicated the preponderance of additive gene action therefore simple selection would be effective for these traits. These results are in conformity with findings of Krishna et al*.*, 2010; Chouhan et al*.*, 2014 and Pratap et al*.*, 2018.

Table 4: Estimates of variability parameters for eleven traits in forty eight germplasm of rice grown during two seasons viz. July-Oct, 2017 and July-Oct, 2018

Traits	Year	Mean±S.E	Range	PCV %	GCV%	h^2 %	GA (k=2.06)	GA As % of mean
DF	Y_1	87.35±0.69	77-101.67	7.565	7.440	96.7	13.168	15.074
	Y_2	89.74±0.61	76.33-107.67	8.900	8.821	98.3	16.164	18.013
DM	Y_1	116.28±0.78	105-132	6.043	5.929	96.3	13.935	11.983
	Y_2	118.44±0.75	102-136	7.072	6.987	97.6	16.845	14.222
PH	Y_1	127.33±1.14	97-164.33	16.851	16.780	99.2	43.828	34.420
	Y_2	116.21±4.10	86.33-147	16.546	15.374	86.3	34.194	29.425
PL	Y_1	26.31±0.82	16.33-31.33	11.874	10.584	79.5	5.113	19.435
	Y_2	25±0.84	21.33-29	8.672	6.441	55.2	2.464	9.856
ET	Y_1	11.56±0.62	6.33-23.67	30.645	29.181	90.7	6.614	57.240
	Y_2	9.72±1.02	4.67-20.67	37.289	32.581	76.3	5.702	58.644
FGP	Y_1	105.10±7.08	45.33-219.67	39.873	38.129	91.4	78.944	75.110
	Y_2	116.38±6.41	54.67-248	39.365	38.191	94.1	88.828	76.329
UFGP	Y_1	27.76±4.53	2.67-103.33	72.455	66.728	84.8	35.148	126.595
	Y_2	24.81±5.24	5.67-78	86.256	78.108	82.0	36.152	145.702
TGP	Y_1	132.87±9.74	53-261.33	35.899	33.577	87.5	85.960	64.696
	Y_2	141.19±8.02	61-266.67	34.541	33.109	91.9	92.304	65.377

Table 4: Continue...

Traits	Year	Mean ± S.E	Range	PCV %	GCV%	h^2 %	GA (k=2.06)	GA As % of mean
SF%	Y_1	79.39±2.49	31.37-95.05	15.018	14.005	87.0	21.360	26.903
	Y_2	82.56±2.67	42.03-95.47	16.215	15.216	88.1	24.284	29.483
TW	Y_1	20.55±0.30	11.86-27.83	15.433	15.223	97.3	6.356	30.931
	Y_2	21.67±0.34	14.01-28.51	14.366	14.101	96.3	6.179	28.512
GYP	Y_1	26.93±1.44	11.28-54.99	36.205	35.003	93.5	18.774	69.713
	Y_2	24.01±1.90	14.59-41.74	27.161	23.452	74.6	10.015	41.714

DF: Days to 50% flowering; DM: Days to maturity; PH: Plant height (cm); PL: Panicle length (cm); ET: Number of effective tillers plant^{-1}; FGP: Number of filled grains panicle^{-1}; UFGP: Number of unfilled grains panicle^{-1}; TGP: Total number of grains panicle^{-1}, SF%: Spikelet fertility %; TW: Test weight (g); GYP: Grain yield plant^{-1} (g); h^2: Broad sense heritability; GA: Genetic Advance; GA As % of m: Genetic Advance as percent of mean; Y_1: First year (2017); Y_2: Second Year (2018); Mean±S.E: Means±Standard error; PCV %: Percent phenotypic coefficient of variation; GCV % : Percent genotypic coefficient of variation

3.3. Correlation between grain yield and other yield factors

During July-Oct, 2017 , significant positive correlation with grain yield was exhibited by filled grains panicle^{-1} (0.436) followed by total grains panicle^{-1} (0.369) and test weight (0.272) (Table 5.1). However, during July-Oct, 2018 , significant positive correlation with grain yield was manifested effective tillers plant^{-1} (0.336) followed by filled grains panicle^{-1} (0.229) and total grains panicle^{-1} (0.214) (Table 5.2). Similar findings were observed by Singh et al., 2015, Tuhina-Khatun et al., 2015, Anis et al., 2016.

3.4. Phenotypic path coefficient analysis

During July-Oct, 2017 , filled grains panicle^{-1} (0.557) exhibited maximum positive direct effect on grain yield plant^{-1} followed by number of effective tillers (0.436) and test weight (0.332), indicating as the major yield contributing traits in rice. Days to flowering (-0.082), unfilled grains panicle^{-1} (-0.247) and spikelet fertility % (-0.332) exhibited negative direct effect on grain yield plant^{-1} (Table 6.1). Similar results were observed by Ganesan (2001), Panwar et al., 2007; Haradari and Hittalmani (2017).

In July-Oct, 2018 , maximum positive direct effect on grain yield plant^{-1} was manifested by total grains panicle^{-1} (0.889) followed by effective tillers (0.771), days to flowering (0.697) and spikelet fertility % (0.335). Traits like days to maturity (-0.437), filled grains panicle^{-1} (-0.392) and unfilled grains panicle^{-1} (-0.080) exhibited negative direct effect (Table 6.2). These observations support the earlier finding by Nayak et al*.,* 2016.

3.5. Mutual association among different yield components

Days to 50% flowering exhibited highly significant positive correlation with days to maturity, panicle length, filled grains panicle^{-1}, unfilled grains panicle^{-1} and total grains panicle^{-1}. Days to maturity showed highly significant positive correlation with panicle length, filled grains panicle^{-1}, unfilled grains panicle^{-1} and total grains panicle^{-1}. Plant height observed highly significant positive correlation with panicle length, filled grains panicle^{-1}, total grains panicle^{-1} and spikelet fertility %.

Table 5.1: Estimates of phenotypic correlation between yield and its related traits in forty eight rice germplasm during July-Oct, 2017

	DF	DM	PH	PL	ET	FGP	UFGP	TGP	TW	SF%
DF	1.000	0.9527**	0.1903	0.394**	-0.2763**	0.3919**	0.3913**	0.5094**	-0.0914	-0.2486**
DM		1.000	0.2162**	0.329**	-0.219**	0.3585**	0.3585**	0.4587**	-0.1465	-0.2329**
PH			1.000	0.1977	-0.2698**	0.4522**	-0.3239**	0.2607**	0.1038	0.469**
PL				1.000	-0.4138**	0.3864**	0.2544**	0.4468**	0.192	-0.1446
ET					1.000	-0.3814**	-0.2119	-0.4245**	-0.1835	0.0919
FGP						1.000	0.0678	0.9072**	0.0233	0.341**
UFGP							1.000	0.4813**	-0.2114	-0.8733**
TGP								1.000	-0.0687	-0.0687
TW									1.000	0.1597
SF%										1.000
GYP	0.198	0.1873	0.2416	0.2399	0.0804	0.4369**	-0.0333	0.3698**	0.2722*	0.1815

**: significant at (p=0.01) level of significance

Table 5.2: Estimates of phenotypic correlation between yield and its related traits in forty eight rice germplasm during July-Oct, 2018

	DF	DM	PH	PL	ET	FGP	UFGP	TGP	TW	SF%
DF	1.000	0.953**	-0.1685*	0.3249**	-0.3099**	0.2233**	0.7053**	0.5193**	-0.1782	-0.5557**
DM		1.000	-0.1098	0.3148**	-0.3218**	0.2386**	0.6558**	0.5119**	-0.1766	-0.5017**
PH			1.000	0.202	-0.4729**	0.513**	-0.3788**	0.3156**	0.233**	0.4947**
PL				1.000	-0.2617**	0.2717**	0.2875**	0.3814**	0.0197	-0.1949
ET					1.000	-0.5623**	-0.1142	-0.5784**	0.0671	-0.0421
FGP						1.000	-0.091	0.8994**	-0.0872	0.3978**
UFGP							1.000	0.3534**	-0.2419**	-0.9125**
TGP								1.000	-0.1881	-0.0268
TW									1.000	0.1586
SF%										1.000
GYP	0.1303	0.0851	0.0268	0.1035	0.336**	0.2296**	-0.0035	0.2142	0.1613	0.1161

**: significant at (*p*=0.01) level of significance

Table 6.1: Estimates of phenotypic matrix of direct and indirect effects on grain yield plant^{-1} in forty eight rice germplasm during July-Oct, 2017

	DF	DM	PH	PL	ET	FGP	UFGP	TGP	TW	SF%
DF	-0.082	-0.0781	-0.0156	-0.0323	0.0227	-0.0321	-0.0321	-0.0418	0.0075	0.0204
DM	0.1319	0.1385	0.0299	0.0456	-0.0303	0.0485	0.0497	0.0635	-0.0203	-0.0323
PH	0.0182	0.0207	0.0956	0.0189	-0.0258	0.0432	-0.031	0.0249	0.0099	0.0448
PL	0.0344	0.0287	0.0172	0.0872	-0.0361	0.0337	0.0222	0.039	0.0167	-0.0126
ET	-0.1207	-0.0957	-0.1179	-0.1808	0.4369	-0.1666	-0.0926	-0.1854	-0.0802	0.0401
FGP	0.2185	0.1952	0.2522	0.2155	-0.2127	0.5576	0.0378	0.5059	0.013	0.1902
UFGP	-0.0967	-0.0886	0.08	-0.0628	0.0523	-0.0167	-0.247	-0.1189	0.0522	0.2157
TGP	0.0421	0.0379	0.0215	0.0369	-0.0351	0.0749	0.0398	0.0826	-0.0057	-0.0057
TW	-0.0303	-0.0486	0.0344	0.0637	-0.0609	0.0077	-0.0702	-0.0228	0.332	0.053
SF%	0.0826	0.0774	-0.1558	0.048	-0.0305	-0.1133	0.2901	0.0228	-0.053	-0.3322
GYP	0.198	0.1873	0.2416	0.2399	0.0804	0.4369	-0.0333	0.3698	0.2722	0.1815
Partial R²	-0.0162	0.0259	0.0231	0.0209	0.0351	0.2436	0.0082	0.0306	0.0904	-0.0603

R^2=0.4013; Residual effect: 0.7737

Table 6.2: Estimates of phenotypic matrix of direct and indirect effects on grain yield plant^{-1} in forty eight rice germplasm during July-Oct, 2018

	DF	DM	PH	PL	ET	FGP	UFGP	TGP	TW	SF%
DF	0.6973	0.6645	-0.1175	0.2265	-0.2161	0.1557	0.4918	0.3621	-0.1243	-0.3874
DM	-0.4167	-0.4373	0.048	-0.1376	0.1407	-0.1043	-0.2868	-0.2238	0.0772	0.2194
PH	-0.0225	-0.0147	0.1336	0.027	-0.0632	0.0685	-0.0506	0.0422	0.0311	0.0661
PL	0.0136	0.0132	0.0085	0.0419	-0.011	0.0114	0.0121	0.016	0.0008	-0.0082
ET	-0.2392	-0.2484	-0.3649	-0.2019	0.7717	-0.434	-0.0882	-0.4463	0.0518	-0.0325
FGP	-0.0876	-0.0935	-0.2012	-0.1065	0.2205	-0.3921	0.0357	-0.3527	0.0342	-0.156
UFGP	-0.0569	-0.0529	0.0305	-0.0232	0.0092	0.0073	-0.0806	-0.0285	0.0195	0.0736
TGP	0.4617	0.4551	0.2806	0.3391	-0.5142	0.7997	0.3142	0.8891	-0.1672	-0.0238

Table 6.2: Continue...

	DF	DM	PH	PL	ET	FGP	UFGP	TGP	TW	SF%
TW	-0.033	-0.0326	0.0431	0.0037	0.0124	-0.0161	-0.0447	-0.0348	0.1849	0.0293
SF%	-0.1865	-0.1684	0.166	-0.0654	-0.0141	0.1335	-0.3063	-0.009	0.0532	0.3356
GYP	0.1303	0.0851	0.0268	0.1035	0.336	0.2296	-0.0035	0.2142	0.1613	0.1161
Partial R²	0.0909	-0.0372	0.0036	0.0043	0.2593	-0.09	0.0003	0.1904	0.0298	0.039

R^2: 0.4903, Residual effect: 0.7139

Panicle length reported highly significant positive correlation with filled grains panicle^{-1}, unfilled grains panicle^{-1} and total grains panicle^{-1}. Filled grains panicle^{-1} observed highly significant positive correlation with total grains panicle^{-1} and spikelet fertility %. Unfilled grains panicle^{-1} observed highly significant positive correlation with total grains panicle^{-1}.

4. Conclusion

Filled grain panicle^{-1}, total grains panicle^{-1}, test weight and number of effective tillers plant^{-1} can be used as selection indices for improvement as it have direct positive effect on grain yield plant^{-1}. Genotypes LC-53, LC-55, LC-90 and LC-50 were found to be the propitious genotypes for yield and yield contributing traits during both seasons. Genotype LC-54 and LC-56 were earliest in flowering and maturity. Hence, these genotypes can be employed as parents in the hybridization programme to obtain potent transgressive segregants.

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