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AMELIORATING THE QUANTITATIVE TRAITS IN RICE THROUGH PHYSICAL MUTAGENESIS

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Abstract

The study was aimed at determining the genetic variability present in promising mutant rice lines at NIA and to investigate the relationship between yield and yield contributing traits through correlation and path analysis. Experiment was conducted in randomized complete block design. Analysis of variance showed significant ($p<0.05$) variation among genotypes. Seven mutant lines along with IR6 parent and two check varieties Shandar and NIA Mehran were evaluated for yield and yield attributing traits. The genotype OD-16B/2 was found to be the highest yielding mutant line. Correlation and path analysis revealed that yield contributing traits viz number of tillers per plant, thousand grain weight and fertile grains had positive direct effect on yield. Therefore selection for these traits could bring improvement in final grain yield.

Key words: Rice, Mutation, Correlation, Path analysis and yield.

Introduction

Rice is a self-pollinated crop having diploid chromosome number (2n=24) belonging to the genus *Oryza* of the family. Among the 25 recognized species of genus *Oryza*, only two *Oryza sativa* and *Oryza glaberrima* are cultivated and rest of the species are wild (Li *et al*., 2019). It is grown as annual crop in tropical and temperate regions of the world over a wide range of soil and climatic condition (Brar & Khush, 2003).

Rice is one of the staple cereals for more than half of the world's population. More than 90% of rice is grown in Asia (Ricepedia: online authority on rice). Production wise china stands at 1st position with production of 212 million tonnes of rice while Pakistan is at 10th position with the production of 10.8 million tonnes (Anon., 2018). The burgeoning human population across the globe and specifically in third world countries of Asia demands the high production of rice (Manomani & Khan, 2003). The arithmetic growth in productivity of rice does not meet the geometric growth of population. The expansion in arable land area is not a practical solution for increasing the rice production. Already cultivable land is under the pressure of urbanization and infrastructure development. The development of high yielding rice varieties is the prime solution of this emerging food security threat (Subbaiah *et al*., 2011). Therefore improving the rice yield is the major objective for rice breeders and growers. The prerequisite for high yield is the presence of genetic variability for selection of better performing genotypes (Ranganatha *et al*., 2013; Meena & Bahadur, 2013, 2014; Yared & Misteru, 2016). Selection of plants year after year for improving the traits causes narrowing of genetic base and restricting the genetic variability (Fentie *et al*., 2021).

Though hybridization program is mostly employed in rice breeding program for genetic improvement, however mutation breeding is one of the potential tools to create the genetic diversity among the rice crop (Aditya *et al*., 2011). Gamma rays of dosage between 100 to 300 gy are used for mutation purpose to create genetic diversity.

Mere genotypic potential is not enough for determining the yield of the plant because plant has to face many environmental factors which ultimately affect the yield (Agong *et al*., 2001). Rapid changing climatic patterns have affected the rice crop production. To understand the real potential of genotypes two year crop data was taken so that the environmental effects can be estimated more precisely if there any (Ketema *et al*., 2022). Many of the traits like thousand grain weight, fertile grains per panicle, number of tillers per plant etc. were studied which could help in final yield determination. The data was not significantly different in both the season which suggested that environmental changes did not affect the final yield estimation.

Material and Methods

The experiment was conducted during the Kharif season 2018–2019 and 2019-2020 at experimental farm of Nuclear Institute of Agriculture, Tando Jam, Pakistan to investigate the relationships between yield contributing traits and grain yield of rice. Seven advanced mutant lines along with two checks-NIA Mehran and Shandar and IR6 parent were selected for quantifying their yield attributing traits (Table 1). These genotypes were grown in randomized complete block design (RCBD) with three replications. The plant to plant (P×P) and row to row (R×R) distanced was maintained at 20 cm. The plot size was kept 15 m^2. The rice was sown on 12th of May 2018 and transplanted on 6th of June 2018. In next season the time of sowing and transplanting was the same. The management like irrigation, fertilizer application and weeding were carried according to recommended rice production technologies. The harvesting was carried in mid of November for both the seasons. The morphological data of yield associated traits of plant height (PH), number of tillers (NT), panicle length (PL), branches per panicle (B/P), fertile grains (FG), sterile grains (SG), 1000-grain weight (TGW), days to heading (DH), was recorded by following the standards of IRRI (Anon., 2002). Analysis of variance was performed to estimate genetic variability. The association of these agronomic traits with yield was determined through correlation analysis. Statistics 8.1 and MS Excel were used for statistical analysis of the data. Genotypic and phenotypic variances were estimated according to formula given by (Johnson *et al*., 1955).

Genotypic and phenotypic coefficients of variance were assessed according to (Burton 1952 & Singh *et al*., 1997). Path coefficient analysis was carried out to estimate the contribution of each yield contributing factor.

Seven mutant lines of coarse rice were evaluated in the present study. The names of these mutant lines along with parent and check genotypes are given in Table 1. The seed of parent varieties was exposed to different dosage of gamma rays for bringing out genetic change in the material (Table 1).

Results and Discussion

Analysis of variance: Analysis of variance is of great importance in breeding program for estimating the relationship between yield and yield contributing traits (Mary & Gopalan, 2006). Mean squares of various yield contributing traits were shown in Table 2. The results manifest the significant difference for primary yield contributing traits of number of tillers per plant, thousand grain weight and fertile grains. It indicated the inherent genetic difference present among the studied genotypes of rice. This suggests the selection of these traits for creating genetic variability and improvement of genetic architecture for high yielding. Similar results were also obtained by (Bekele *et al*., 2013). These characters showed stability across the years suggesting that environment had little influence in the final yield contributed by these characters.

Panicle length, plant height and days to flowering showed non-significance against the year factor as shown in (Table 2). It means the differences in these characters in studied genotypes do not exist significantly. These character need to be exposed to physical mutagens for creating further variations and selection for improvement of genetic architecture.

Least significant difference: The rice genotypes under study have the high variability for the morphological traits contributing to yield. The two consecutive seasons' data were also compared for these traits. In both years data did not vary suggesting the stability of the characters and less influence of the environment.

The data in the table 3 showed that the length of panicle ranged from 25.05 to 33.05 cm. The highest panicle length was recorded 33.05 cm for OD-10B/2 followed by 33.00 cm for NIA Mehran. The least panicle length was recorded 25.05 cm in Shandar. On the contrary branches per panicle did not show significant difference as the range of this morphological character was between 11.00 to 13.

The fertile grain is an important agronomical character which has the direct link with improving the grain yield of rice. The mean difference between the highest and the lowest genotypes was 77 grains per panicle. This significant difference can be exploited by keeping the high grain yielding genotype (IR6-2012A/1) in breeding program.

The minimum mean of unfilled grains was found in OD-16B/2 with 6.78 as shown in (Table 3). The highest number of unfilled grains was observed in IR6-2013A/3 (53.33). This character of unfilled grains in IR6-2013A/3 was 11 times more than that of OD-16B/2.

Thousand grain weights is prime factor in determining the yield. It has a direct link with the improvement of yield in rice. The check varieties of NIA Mehran and Shandar performed very well so far the 1000-grain weight was concerned and both had the values of 28g for 1000 grains. IR6-2012A/1also performed equally well and had the value of 27.67g. The least performing genotypes include the OD-10B/2and IR6-1013C/3.

Table 1. Genotypes of rice used for studies.

Sr. No.	Genotypes (Mutants)	Parent (Year of gamma radiation)	Dosage (Gy)
1.	IR6 (Parent)	IR6	--
2.	IR6-2013A/3	IR6 (2013)	100
3.	IR6-1014B/3	IR6 (2014)	200
4.	IR6-2012A/1	IR60 (2012)	200
5.	IR6-1013C/3	IR6 (2013)	150
6.	OD-19A/1	Sarshar (2015)	200
7.	OD-16B/2	Sarshar (2014)	250
8.	OD-10B/2	Sarshar (2015)	150
9.	Shandar	Shandar	--
10.	NIA Mehran	NIA Mehran	--

Table 2. Analysis of variance (ANOVA) of 10 rice genotypes for nine yield and yield attributing traits.

SOV	DF	PL	B/P	FG	SG	TGW	PH	NT	DH	Yield
Replications	2	21.21	0.65	462.2	146.86	0.73	11.82	11.85	5.72	0.66
Year* year	1	4.94^{ns}	2.16^{ns}	11116.6*	671.07*	3.47**	26.67^{ns}	17.06**	18.15^{ns}	0.50*
Genotypes	9	31.7*	4.69**	1432.9*	1700.72*	8.05**	377.230**	18.40**	364.55**	4.10*
Year* genotype	9	5.34^{ns}	1.47*	637.4^{ns}	285.50*	1.88*	10.18^{ns}	4.40**	7.22^{ns}	0.34*
Error	38	7.70	0.66	457.7	106.16	0.66	8.20	0.82	7.40	0.08

*=Significant at 5% probability level

SOV= Source of variation, **DF=** Degrees of freedom, **PL=** Panicle length (cm), **B/P=** Branches per panicle, **FG=** Fertile grains, **SG=** Sterile grains, **TGW=** Thousands grain weight (g), **PH=** Plant height (cm), **NT=** Number of tillers, **DH=** Days to heading

Table 3. Least significant difference of 10 rice genotypes for nine yield and yield attributing traits.

VAR	Year	PL	B/P	FG	SG	TGW	PH	NT	DH	Yield
1.	1	25.62 A	11.22 B	158.45 C	9.45 E	27.10 ABC	92.67 FGHI	13.00 BCDE	103.00 C	8.03 FGH
	2	25.55 A	11.44 B	197.44 ABC	11.00 DE	27.33 ABC	96.33 DEFGHI	13.33 BCDE	104.00 C	8.37 DEFG
2.	1	32.44 A	12.66 B	215.00 ABC	71.44 A	27.90 AB	87.67 I	11.33 EF	102.33 CD	9.51 ABC
	2	30.22 A	12.33 B	230.22 AB	30.22 BCDE	28.33 AB	90.67 GHI	14.33 ABCD	102.33 CD	9.85 AB
3.	1	29.55 A	11.00 B	200.67 ABC	12.67 DE	26.11 BCD	112.00 A	13.33 BCDE	101.00 CDE	8.92 CDE
	2	28.89 A	11.11 B	220.78 ABC	10.11 E	27.00 ABC	108.67 AB	16.67 A	102.00 CDE	8.92 CDE
4.	1	27.22 A	11.11 B	178.22 BC	23.890 BCDE	27.77 AB	100.33 BCDEF	13.00BCDEF	113.00 A	8.95 CDE
	2	27.72 A	11.33 B	255.67 A	10.00 E	28.44 AB	104.67 ABCD	15.33 AB	111.67 AB	9.99 A
5.	1	29.33 A	12.66 B	223.89 ABC	53.333 AB	24.92 CD	97.67 DEFGH	12.00 CDEF	90.00 F	7.05 I
	2	29.61 A	15.55 A	225.67 AB	45.000 ABC	26.33 BCD	98.33 CDEFG	14.33 ABCD	94.67 EF	7.05 I
6.	1	27.66 A	12.22 B	200.00 ABC	8.667 E	27.17 ABC	92.33 FGHI	13.00BCDEF	118.33 A	8.83 CDEF
	2	26.94 A	13.00 B	219.55 ABC	10.777 DE	27.00 ABC	95.33 EFGHI	13.67 BCDE	118.33 A	8.17 EFGH
7.	1	27.55 A	11.55 B	178.00 BC	6.780 E	26.333 BCD	104.00 ABCDE	15.00 AB	103.00 C	9.04 BCDE
	2	28.55 A	12.33 B	215.78 ABC	7.557 E	27.00 ABC	106.67 ABC	14.33 ABCD	103.00 C	9.04 BCD
8.	1	31.89 A	12.33 B	204.00 ABC	42.22 ABCD	24.33 D	112.33 A	14.00ABCDE	90.00 F	7.77 GHI
	2	33.05 A	11.89 B	221.56 ABC	29.67 BCDE	25.00 CD	109.67 A	12.00 CDEF	95.33 DEF	7.68 GHI
9.	1	25.05 A	12.55 B	174.22 BC	11.663 DE	24.23 CD	89.00 HI	10.33 F	103.67 C	7.46 HI
	2	26.39 A	12.00 B	195.56 ABC	16.00 CDE	27.00 ABC	89.33 HI	11.67 DEF	104.67 BC	8.23 DEFGH
10.	1	28.00 A	11.77B	193.00 ABC	12.00 DE	29.22 A	97.67 DEFGH	14.67 ABC	103.00 C	8.81 CDEF
	2	33.00 A	11.89 B	215.45 ABC	14.89 CDE	27.00 ABC	99.33 CDEFG	14.67 ABC	103.00 C	8.91 CDE

VAR= Varieties, **PL**= Panicle length (cm), **B/P**= Branches per panicle, **FG**= Fertile grains, **SG**= Sterile grains, **TGW**= Thousands grain weight (g), **PH**= Plant height (cm), **NT**= Number of tillers, **DH**= Days to heading

Table 4. Correlation coefficient of nine yield and yield contributing traits for 10 rice genotypes.

Traits	IFL	DH	PH	NT	B/P	SG	FG	TGW	Yield
IFL	1	0.88**	-0.33	0.09	-0.36	-0.61	-0.17	0.62	0.53
HUNFL	0.84**	1	-0.42	0.01	0.07	-0.35	0.06	0.41	0.33
PH	-0.32	-0.38	1	0.68*	-0.37	-0.15	0.26	-0.42	-0.01
NT	0.01	-0.02	0.57	1	-0.47	-0.34	0.26	0.36	0.47
PL	-0.43	-0.24	0.36	0.13	0.27	0.74*	0.84**	-0.24	0.09
BPP	-0.30	0.05	-0.34	-0.32	1	0.68	0.47**	-0.39	-0.62
SG	-0.55	-0.28	-0.14	-0.26	0.62	1	0.85**	-0.20	-0.24
FG	-0.14	0.03	0.18	0.26	0.36	0.44	1	0.01	0.15
TGW	0.55	0.36	-0.33	0.34	-0.35	-0.23	0.06	1	0.83**
Yield	0.47	0.31	0.01	0.48	-0.51	-0.18	0.133	0.75*	1

IFL= Initial flowering, **DH**= Days to heading **PH**= Plant height (cm), **NT**= Number of tillers, **B/P**= Branches per panicle, **SG**= Sterile gains, **FG**= Fertile grains, **TGW**= Thousands grain weight (g)

Number of tillers is an important agronomical feature which directly affect the grain yield. The number of tillers among the studied genotypes ranged between 10.33 to 16.67, IR6-1014B/3 had 16.67 tillers so it contributed in producing the highest yield of 8.916kg/plot.

Days to heading is also one of the important traits to develop early maturing rice genotypes. IR6-1013C/3 was found to have least number of days to heading which was a significant sign of less duration rice genotype. Therefore, this should be considered and exploited for further reducing the duration of currently cultivated rice genotypes.

Correlation coefficient analysis: Correlation coefficient analysis determines the association among characters in the final determination of grain yield. It also determines the traits on which selection can be made for genetic improvement in yield. On the basis of above mentioned fact the correlation coefficient analysis was taken to understand the association among yield and yield attributing traits. The genotypic and phenotypic correlation coefficients of yield contributing traits are exhibited in (Table 4). The research showed that in most of the cases, genotypic coefficients of correlation had higher values than their corresponding phenotypic coefficients of correlation leading to the conclusion that heritability of these characters was high and environment had little influence on the expression of these characters. Notwithstanding, in some of the cases the phenotypic correlation coefficients had higher values than their corresponding genotypic correlation coefficients indicating that environment had the influence in the final expression of grain yield.

Days to heading was positively correlated with the final grain yield. So was the case with number of tillers per plant, panicle length and TGW. Findings showed that final grain yield was least affected by plant height. The branches per panicle and unfilled grains were negatively correlated with the yield. The findings were supported by (Bala, 2001; Bidhan *et al.*, 2001; Monalisa *et al.*, 2006; Habib *et al.*, 2007; Kole *et al.*, 2008; Chandra *et al.*, 2009; and Ragvendra *et al.*, 2011; Singh *et al.*, 2013; and Joshi *et al.*, 2015).

Path coefficient analysis: Though correlation coefficients represents the relation of yield contributing factors with grain yield, it does not represent the accurate picture of character association with the final yield because of inter linkage of characters. For better understanding of the relation of yield contributing traits with final yield path analysis was carried out (Wright, 1921).

Path coefficients indicating the direct and indirect effect of yield contributing traits to final grain yield are shown in the (Table 5).

Hundred percent flowering had the highest positive direct effect (0.8219) on yield followed by fertile or filled grain (0.6555) and number of tillers (0.4776) as exhibited in table 5. The highest negative direct effect was shown by Branches per panicle (-1.3045) followed by plant height (-.5658).

The cumulative indirect effect of 1000 grain weight on grain yield was 0.8292 which was highly significant. The cumulative indirect effect of number of tiller to final grain yield is 0.4681 while the initial flowering had the value of 0.5322, suggesting that both these characters were positive and significantly related with grain yield. From the above findings it can be deduced that selection for high tillers per plant, days to initial and complete flowering, fertile grains per panicle and 1000 gain weight would lead to improve in final grain yield. The supportive findings were reported by (Gnanasekaran *et al*., 2008; Chandra *et al*., 2009; Bhandru *et al*., 2010; Fiyaz *et al*., 2011; Minnie *et al*., 2013).

Table 5. Estimation of path analysis of nine quantitative traits on grain yield of 10 rice genotypes.

Character	IFL	DH	PH	NT	PL	B/P	SG	FG	TGW	Yield
IFL	**-0.43**	0.73	0.19	0.46	-0.04	0.46	-0.40	-0.01	-0.01	0.53
HUNFL	-0.38	**0.83**	0.24	0.01	-0.03	-0.09	-0.23	0.01	-0.01	0.33
PH	0.14	-0.35	**-0.57**	0.33	0.03	0.48	-0.09	0.01	0.01	-0.01
NT	-0.04	0.01	-0.39	**0.48**	0.02	0.61	-0.22	0.01	-0.01	0.47
PL	0.28	-0.35	-0.25	0.17	**0.07**	0.35	0.48	0.03	0.00	0.09
BPP	0.16	0.056	0.21	-0.23	0.02	**-1.30**	0.45	0.02	0.01	-0.62
SG	0.26	-0.29	0.084	-0.16	0.05	-0.88	**0.04**	0.03	0.01	-0.85
FG	0.08	0.048	-0.15	0.13	0.06	-0.61	0.56	**0.65**	0.000	0.76
TGW	-0.27	0.39	0.24	0.17	-0.02	0.51	-0.13	0.01	**-0.01**	0.83

IFL= Initial flowering, **DH**= Days to heading, **PH**= Plant height (cm), **NT**= Number of tillers, **PL**=Panicle Length(cm), **B/P**= Branches per panicle, **SG**= Sterile gains, **FG**= Fertile grains, **TGW**= Thousands grain weight(g)

Conclusion

It can be concluded from this study that rice lines have wide range of variability for most of the characters. This provides a good source of base material for further improvement in final grain yield. Rice genotypes had stability of characters across the years suggesting that environment had little influence in the final expression of the character and genetic heritability of characters. The path analysis and correlation studies manifested that yield was much influenced by primary yield contributing characters and also through indirect effect of other yield related traits. IR6-2013A/3, IR6-2012A/1and OD-10B/2 performed well than check varieties-Shandar and NIA Mehran.

References

Agong, S.G., S. Schittenhelm and W. Fried. 2001. Genotypic variation of Kenyan tomato (*Lycopersicon esculentum* Mill.) germplasm. *J. Food Tech. Afr.*, 6(1): 13-17.

Allard, R.W. 1975. Principles of plant breeding, John Wiley and Sons Incorporation, New York.

Anonymous. 2002. Standard evaluation system for rice. International Rice Research Institute, Manila.

Anonymous. 2018. Food and Agriculture Organization of the United Nation. http://www.fao.org/faostat/en/#data. Accessed 8 Mar 2018.

Bala, A. 2001. Genetic variability, association of characters and path coefficient analysis of saline and alkaline rice genotypes under rainfed conditions. *Madras Agric. J.*, 88(4-6): 365-367.

Bekele, B.D., G.K. Naveen, S. Rakhi and H.E. Shashidhar. 2013. Genetic evaluation of recombinant inbred lines of rice (*Oryza sativa* L.) for grain zinc concentrations, yield related traits and identification of associated SSR markers. *Pak. J. Biol. Sci.*, 16(23): 1714-1721.

Bhandru, D., D.L. Reddy and M.S. Ramesha. 2010. Correlation and path coefficient analysis of yield and yield contributing traits in rice hybrids and their parental lines. *Elect. J. Pl. Breed.*, 2(1): 112-116.

Bidhan, R., M. Hossain, F. Hossain and B. Roy. 2001. Genetic variability in yield components of rice (*Oryza sativa* L.). *Environ. & Ecol*., 19(1): 168-189.

Brar D.S. and G.S. Khush. 2003. Utilization of wild species of genus oryzae in rice improvement. *In. J. Sci. Nand.,* 2(1): 283-309.

Burton, G.W. 1952. Quantitative inheritance in grasses. *Proc. 6th International Grassland Cong*., 1: 277-283.

Chandra, B.S., T.D. Reddy, N.A. Ansari and S.S. Kumar. 2009. Correlation and path analysis for yield and yield components in rice (*Oryza sativa* L.) *Agri. Sci. Digest*., 29(11): 45-47.

Comstock, R., H. Robinson and J. Gowen. 1952. Estimation of average dominance of genes, Heterosis, 494-516.

Fentie, D.B., B.B. Abera and H.M. Ali. 2021. Association of agronomic traits with grain yield of lowland rice (*Oryza sativa* L.) genotypes. *Int. J. Agric. Sci.*, 8: 161-175.

Fiyaz, R.A., K.T. Ramya, Chikkalingaiah and R.S. Kularni. 2011. Genetic variability, correlation and pathncoefficient analysis studies in rice (*Oryza sativa* L.) under alkaline soil condition. *Elect. J. Pl. Breed.*, 2(4): 531-537.

Gnanasekaran, M., P. Vevekanandan and S. Muthuramu. 2008. Correlation and path analysis in two line rice hybrids. *Adv. Pl. Sci.*, 21(2): 689-692.

Habib, S.H., M.K. Hossain, M.A. Hoque and M.M. Khatun. 2007. Character association and path analysis in hybrid rice. *J. Subtrop. Agric. Res. & Dev.,* 5(3): 305-308.

Hanson, W.D. 1961. Heritability, statistical genetics and plant breeding, National Academy of Science, *National Research Council, Washington,* pp. 125-140.

Hooker, J.D. 1979. The Flora of British India. Vol: 2. Reeve Co Kent, England 25.

Johnson, H.W., H.F. Robinson and R.E. Comstock. 1955. Estimation of genetic and environmental variability in soybeans. *Agron. J.*, 47: 314-318.

Joshi, M., A. Singh, P.M. Ram, B. Thapa and P.K. Singh. 2015. Assessment of genetic parameters for yield and yield components in rice germplasm. *Bioinfolet.,* 12(3A): 665-671.

Ketema, W. and N. Geleta. 2022. Studies on genetic variability of common bean varieties for yield and yield related traits in Western Ethiopia. *Int. J. Appl. Agric*., 8: 41.

Kole, P.C., N.R. Chakraborty and J.S. Bhat. 2008. Analysis of variability, correlation and path coefficients in induced mutants of aromatic nonbasmati rice. *Trop. Agric. Res. & Extention.*, 11: 60-64.

Li, R., M. Li, U. Ashraf, S. Liu and J.J.Zhang. 2019. Exploring the relationships between yield and yield-related traits for rice varieties released in China from 1978 to 2017. *Front. Plant Sci.*, 10: 543.

Manomani, S. and A.K. Fazlullah Khan. 2003. Studies on combining ability and heterosis in rice. *Madras Agric. J.*, 90: 228-231.

Mary, S.S. and A. Gopalan. 2006. Dissection of genetic attributes yield traits of fodder cowpea in F3 and F4. *J. App. Sci. Res.,* 2: 805-808.

Meena, O.P. and V. Bahadur. 2013. Assessment of breeding potential of tomato (*Lycopersicon esculentum* Mill.) germplasm using D2 analysis. *The Bioscan*., 8: 1145-1148.

Meena, O.P. and V. Bahadur. 2014. Assessment of genetic variability, heritability and genetic advance among tomato (*Solanumlycopersicum* L.) germplasm. *Agr. Sci. Digest*., 27: 185-192.

Minnie, C., M. Reddy, T. Dayakar and C.H.R. Surinder. 2013. Correlation and path analysis for yield and its components traits (*Oryza sativa* L.). *J. Res. Angrau.,* 41: 132-134.

Monalisa, M. Ali and B.G. Sasmal. 2006. Variability, correlation and path coefficient analysis in some important traits of lowland rice. *Crop Res*., 31(3): 153-156.

Poehlman, J.M. and D.A. Sleper. 1995. Breeding Field Crops. Panima Publishing Corporation, New Delhi, India 278.

Ragvendra, T., B.G. Suresh, V.K. Mishra, A. Kumar and A. Kumar .2011. Genetic variability and character association in direct seeded upland rice. *Environ. & Ecol*., 29(4A): 2132-2135.

Ranganatha, H.M., S.S. Patil, S.M. Manjula and B.N. Arvindkumar. 2013. Genetic variability studies in segregating generation of upland cotton (*Gossypium hirsutum* L.). *Mol. Pl. Breed.*, 4: 84-88.

Singh, A.K., R. Nandan and P.K. Singh. 2013. Genetic variability and association analysis in rice germplasm under rainfed conditions. *Crops Res.*, 47(1-3): 7-11.

Singh, D.N., A. Sahu and A.K. Parida. 1997. Genetic variability and correlation studies in tomato (*Lycopersicon esculentum* Mill.). *J. Environ. & Ecol.*, 15: 135-141.

Subbaiah, P.V., M.R. Sekhar, K.H.P. Reddy and N.P.E. Reddy. 2011. Variability and genetic parameters for grain yield and its components and kerenel quality attributes in CMS based rice hybrids (*Oryza sativa* L.). *Int. J. Appl. Biol. & Pharm. Tech*., 2(3): 603-609.

Wright, S. 1921. Correlation and causation. *J. Agri. Res.*, 20: 557-85.

Yared, S. and T. Misteru. 2016. Variability, heritability and genetic advance analysis for some morphological characters in oilseed brassica breeding lines. *Mol. Pl. Breed*., 7(20): 1-8.

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