__Original Research Article__

ESTIMATION OF VARIABILITY, CORRELATION COEFFICIENT AND PATH ANALYSIS IN IMPROVED RESTORER LINES OF RICE (*Oryza sativa* L.)

Abstract

The present investigation was conducted to estimate genetic variability parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2) and genetic advance (GA) along with correlations and path coefficients from data collected on 40 F_4 segregating populationderived from a cross between aerobic restorer AR 9-18and blast resistant donorMSM 1212 possessing *Pi54*. Analysis of variance indicated significant differences among the genotypes for all the characters studied. Moderate GCV and PCV was observed for number of productive tillers per plant, number of grains per panicle, per day productivity and single plant yield. High heritability coupled with high genetic advance as percent of mean were observed for number of productive tillers per plant, number of grains per panicle, per day productivity and single plant yield,whereas high heritability coupled with moderate genetic advance as percent of mean were observed for panicle length, spikelet fertility, thousand grain weight and plant height. Grain yield per plant showed positive correlation with per day productivity, days to 50% flowering, panicle length, number of productive tillers per plant, thousand grain weight and spikelet fertility, while, negative association with number of grains per panicle and plant height. The trait per day productivity had highest direct effect on single plant yield followed by days to 50% flowering, panicle length, number of productive tillers per plant, thousand grain weight, spikelet fertility (%). Hence, per day productivity and number of productive tillers per plant are identified as key traits for developing high yielding genotypes of rice for future breeding programme.

Keywords: *PCV, GCV, Correlation coefficient, Path analysis, Rice.*

Introduction

Rice(*Oryza sativa* L.) is the staple food for more than 1.25 billion people in most parts of India. An increase in rice production is necessary to bring self-sufficiency in the country to feed the burgeoning population (Kumar *et al.*2017). Rice hybridshave yield superiority of about 15–20 % over the best commercial inbred varieties (Virmani 1996) and large-scale adoption of hybrid rice production is one of the feasible options to meet the food security challenges in India (Pranathi *et al.*2016). However, the major problems in hybrid rice breeding are the limited number of parental lines with specific desirable traits. Therefore, improving parental lines must be an integral part of hybrid rice breeding programmes. Highmagnitude of variability in a population provides the opportunity for selection to evolve a variety having desirable characters.

Planning and execution of any breeding program for improvement on quantitative traits depends on magnitude of genetic variability. Therefore, success on plant breeding activities entirely depends on the existence of genetic variability with respect to desired traits and selection skill of plant breeder (Adhikari *et al.*, 2018). Variability, expected genetic advances and heritability of the traits are therefore key basis for genetic improvement of the trait. Correlation and path analysis establish the extent of association between yield and its components and also bring out relative importance of their direct and indirect effects, thus giving an obvious understanding of their association with grain yield. Ultimately, this kind of analysis could help the breeder to design his selection strategies to improve grain yield (Babu *et al.*, 2012). In the light of the above scenario, the present investigation conducted to identify the most important characters for breeding programme by exploiting the genetic variability parameters, heritability, genetic advance as percent of mean, correlation coefficient and path analysis in restorer lines of rice.

MATERIALS AND METHODS

The research was carried out at ICAR-Research Farm, Indian Institute of Rice Research (IIRR), Hyderabad, Telangana during the *kharif*, 2021. For the present genetic study, the experimental material consists of 40 segregating F_4 population derived from a cross between aerobic restorer, AR 9-18 and blast resistant donor,MSM 1212 possessing *Pi54*.The experiment was conducted using randomized complete block design with two replications. Thirty days old seedlings of F_4 population along with check were transplanted with 15 × 20 cm spacing between the plants and rows. Phenotypic data was recorded for nine yield and its attributing traits *viz*., days to 50 % flowering, plant height (cm), number of productive tillers per plant, panicle length (cm), spikelet fertility(%),number of grains per panicle, thousandgrain weight (g), per day productivity(kg/ha/day) and single plant yield (g) on all the fourty F_4 segregating population and check based on flowering duration and maturity. During the experiment for raising a healthy nursery and main crop recommended cultural practices and crop protection measures were taken up.

Analysis of variance (ANOVA) for the randomized complete block design was computed using the method of Panse and Sukhatme (1985), genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were computed using the method of Burton and Dewane (1953). Variation ranges were classified as high (> 20%), moderate (10-20%), or low (< 10%) as proposed by Sivasubramanian and Madhavamenon(1973). Broad sense heritability (h^2 (bs)) was estimated as the ratio of genotypic variance to total variance, categorized as high (> 60%), moderate (30-60%), or low (0-30%) based on Robinson *et al*. (1949).Geneticadvance was calculated and categorized as high (> 20%), moderate (10-20%), or low (< 10%) following Johnson et al. guidelines (1955).Simple correlations were computed using Weber and Moorthy's formula (1952), and path analysis was computed using the method suggested by Dewey and Lu (1959).

Results and discussion

The analysis of variance carried out for the single plant yield and its attributing traits. The variations among the treatments were highly significant for all the characters under study indicating the existence of considerable genetic variation in the experimental material. The analysis of variance was calculated using the method of Panse and Sukhatme (1985) and presented in Table 1.

To uncover the role of environmental effect on different traits GCV and PCV values are vital (Akinwale *et al*., 2011). For all the traits studied it was observed that PCV values in comparison with GCV values were slightly higher which indicates that the expression of traits was influenced less by the environmental factors.Moderate PCV and GCV were recorded for number of productive tillers per hill, number of grains per panicle, per day productivity and single plant yield. Similar results of moderate PCV and GCV was reported by Dhanwani*et al.*(2013), Yadav *et al.* (2017), Lingaiah *et al.* (2018) for number of productive tillers per plant and number of grains per panicle, Yadav *et al.* (2017) and Sudeepthi *et al.* (2020) for single plant yield.

The traits *viz.*, days to 50 percent flowering, panicle length, plant height, spikelet fertility, thousand grain weight recorded low levels of PCV and GCV, which suggest that these traits exhibited less variability so, the selection may not be fruitful based on these traits. Similar results were given by Sravan *et al.* (2012) Yadav *et al.* (2017) for thousandgrain weight, days to 50 percent flowering, panicle length, spikelet fertility, Savitha and Usha Kumari (2015), Sala and Shanthi (2016), Singh and Varma (2018), Abhilash *et al.* (2018) for plant height.

All the studied traits exhibited high heritability.The traits *viz.*, number of productive tillers per plant, number of grains per panicle, single plant yield and per day productivity recorded high heritability with high genetic advance, which favours additive gene action. Earlier researchers, Savitha and Usha Kumari (2015), Ali *et al.* (2018), Pradeep *et al.* (2018), Subbulakshmi and Muthuswamy (2018),reported similar findings for productive tiller number per plant, number of grains per panicle and single plant yield.

The traits *viz.*,panicle length, spikelet fertility and thousandgrain weight and plant height showed high heritability but genetic advance was moderate which limits further improvement through direct selection. Panwar and Mathur (2007) reported similar findingsfor spikelet fertility, panicle length, thousandgrain weight and Nath *et al.*(2021) reported similar findings with plant height.

Correlation analysis provides information regarding nature and degree of relationship among various traits and decides the component traits, on the basis of which traits can be chosen to improve grain yield genetically. In this study, correlations between yield and its related traits namely days to 50 % flowering, plant height, number of productive tillers per plant, panicle length, spikelet fertility, number of grains per panicle, thousandgrain weight, per day productivity and single plant yield were computed. Correlation coefficient results were represented in Table 3 which was done by considering single plant yield as dependent variable.

Thousand grain weight exhibited positive and significant correlation with spikelet fertility, per day productivity, panicle length and single plant yield. Similar results were reported by Prasad *et al.* (2017) for single plant yield, Gautam *et al.* (2018) and Tripathi *et al.* (2018) with number of productive tillers per plant and number of grains per panicle,Ghazy*et al.* (2020) with panicle length.Days to 50 percent flowering exhibited negative and significant correlation with per day productivity. Plant height exhibited negative and significant correlation with number of grains per panicle, similar results were reported by Muthuvijayaragavan and Murugan (2020). Number of productive tillers per plant exhibited significant positive correlation with single plant yield and per day productivity, similar results were reported by Saha *et al.* (2019) Kiruthikadevi*et al.* (2020). Panicle length showed positive and significant correlation with thousand grain weight, per day productivity and single plant yieldSimilar results were reported by Prasad *et al.* (2017).Spikelet fertility exhibited positive and significant correlation with number of grains per panicle and thousand grain weight. Similar results were reported by Tripathi*et al.* (2018). Per day productivity revealed positive and significant correlation with thousand grain weight, number of grains per panicle, number of productive tillers per plant, panicle length and single plant yield and negative significant correlation with days to 50% flowering. Similar results were reported by

Bhadru*et al.* (2011) with single plant yield and days to 50 % flowering. Thousand grain weight, number of productive tillers per plant, panicle length, per day productivity and number of grains per panicle exhibited significant and positive association with single plant yield. This suggests that ultimate increase in yield may be due to improvement of these traits. Similar results were reported by Touhiduzzaman*et al.* (2016) with days to 50 % flowering, Shrivatsav *et al.* (2020) with plant height, number of grains per panicle and panicle length, Padmaja *et al.* (2011) with number of productive tillers per plant and thousandgrain weight, Parimala *et al.* (2019) with spikelet fertilityandBhadru*et al.* (2011) with per day productivity.

Path coefficient analysis explains the direct and indirect causes of association using other attributes by dividing the correlations for explaining the cause-andeffect relationship clearly (Wright, 1921). Table 4 depicts the path coefficient analysis estimates for yield and its attributing traits. Per day productivity exerted highest positive direct effect on plant yield followed by days to 50% flowering, panicle length, number of productive tillers per plant, thousand grain weight, spikelet fertility, indicates yield improvement is directly associated with these traits. Similar results of direct positive effect on plant yield were reported by Padmaja *et al.* (2011) with number of productive tillers per plant and panicle length, Kalaiselvan *et al.* (2019) with thousand grain weight, spikelet fertility and days to 50% flowering.

Negative direct effect on single plant yield was exhibited by plant height and number of grains per panicle. Similar results of negative direct results were reported by Shrivatsav *et al.* (2020). At phenotypic level the residual effect was 0.19. The trait per day productivity exhibited highest positive direct effect among all the yield attributing traits. Hence, it can be considered as major contributor to plant yield. Phenotypical path diagram for plant yield was represented in Fig. 3.

Table 1: Analysis of variance for yield & yield attributing traits in F_4 population of AR 9-18 × MSM 1212

Source of variation	**D.F**	**Mean sum of squares**								
		TGW	**TG**	**SF**	**PH**	**PL**	**PT**	**DFF**	**PDP**	**SPY**
Replication	2	0.2325	796.53	0.248	0.144	4.145	0.0959	55.04	0.000048	0.1110
Treatment	42	5.811**	1198.0**	41.19**	85.48**	3.706**	1.7163**	74.32**	0.001487**	23.5851**
Error	84	1.2387	262.26	3.083	5.430	0.358	0.1531	17.99	0.000233	2.491

DFF- Days to 50% flowering, **PH**- Plant height (cm), **PT**-Number of productive tillers per plant, **PL**-Panicle length (cm), **TG**-Number of grains per panicle, **SF**-Spikelet fertility (%), **TGW**- Thousand grain weight (g), **PDP-**Per day productivity, **SPY**- Single plant yield (g).

Table 2. Genetic variability parameters for yield and related traits in the F_4 population of AR 9-18 × MSM 1212.

Traits	**General mean**	**Range**		**PCV (%)**	**GCV (%)**	**Heritability in broad sense (h2) (%)**	**Genetic Advance as percent of mean (at 5%)**
		Minimum	**maximum**				
TGW	23.98	16.04	20.94	8.96	7.22	64.86	11.97
TG	162.30	112.00	231.00	16.54	13.24	64.08	21.84
SF	82.88	72.77	92.01	5.67	5.26	86.08	10.06
PH	117.15	101.83	128.50	5.75	5.40	88.06	12.23
PL	22.43	18.33	25.86	6.35	5.76	82.37	10.78
PT	8.27	6.00	10.00	11.68	10.68	83.62	20.13
DFF	106.78	88.00	121.0	6.36	4.96	61.01	7.99
PDP	0.20	0.11	0.26	13.51	11.70	75.00	20.87
SPY	27.42	15.33	33.56	13.16	11.84	80.89	21.93

DFF- Days to 50% flowering, **PH**- Plant height (cm), **PT**-Number of productive tillers per plant, **PL**-Panicle length (cm), **TG**-Number of grains per panicle, **SF**-Spikelet fertility (%), **TGW**- Thousand grain weight (g), **PDP-**Per day productivity, **SPY**- Single plant yield (g).

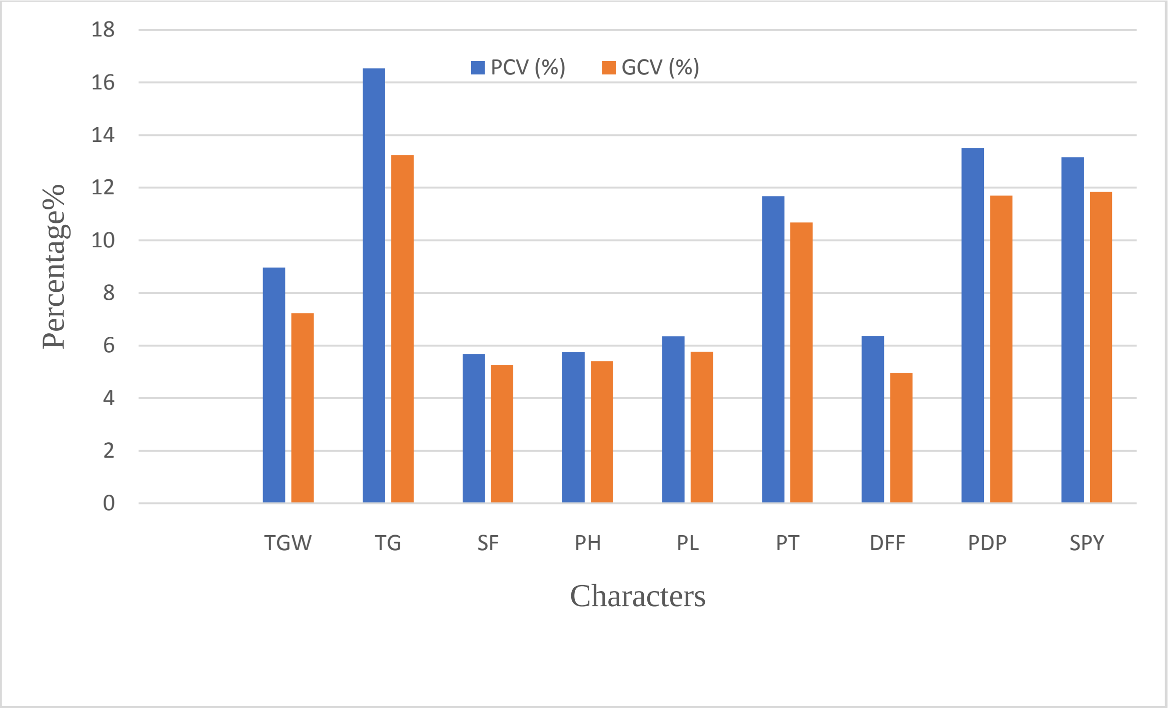

Figure.1. Graphical representation of PCV and GCV for yield contributing traits

DFF- Days to 50% flowering, **PH**- Plant height (cm), **PT**-Number of productive tillers per plant, **PL**-Panicle length (cm), **TG**-Number of grains, **SF**-Spikelet fertility (%), **TGW**-Thousand grain weight (g), **PDP**-Per day productivity, **SPY**- Single plant yield (g)

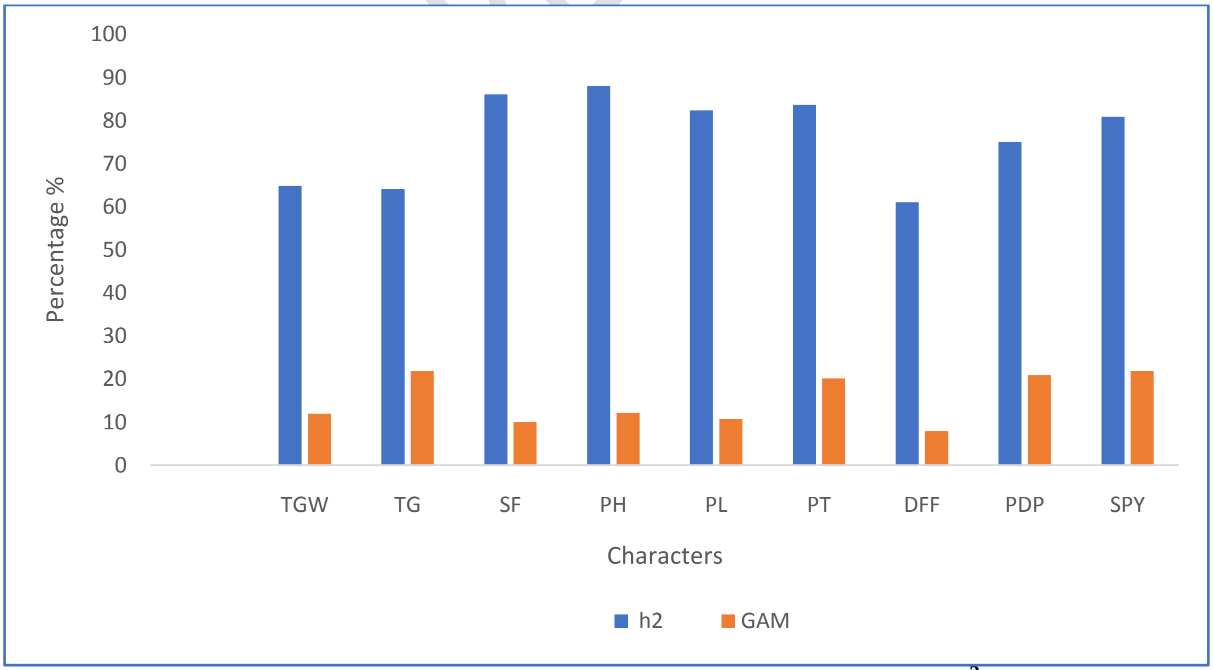

Figure.2. Graphical representation of heritability in broad sense (h^2) and genetic advance as per cent of mean (GAM) (5%). for yield contributing traits

DFF- Days to 50% flowering, **PH**- Plant height (cm), **PT**-Number of productive tillers per plant, **PL**-Panicle length (cm), **TG**-Number of grains, **SF**-Spikelet fertility (%), **TGW**-Thousand grain weight (g), **PDP-**Per day productivity, **SPY**- Single plant yield (g)

Table 3. Correlation analysis among yield and related traits in F_4 population of AR 9-18 × MSM 1212.

Traits	**TGW**	**TG**	**SF**	**PH**	**PL**	**PT**	**DFF**	**PPD**	**SPY**
TGW	1 **	0.0973	0.2220 *	-0.0410	0.2602 *	0.1274	-0.2053	0.42051 ***	0.3993***
TG		1 **	0.3353 **	-0.2503 *	-0.0140	0.1570	-0.1453	0.2836 **	0.2353 *
SF			1 **	-0.0966	0.1146	0.1619	-0.0460	0.1778	0.1842
PH				1 **	0.1864	-0.0030	0.0660	-0.1229	-0.1329
PL					1 **	0.1229	-0.2089	0.3522**	0.3645***
PT						1 **	-0.1709	0.3092 **	0.2906 **
DFF							1 **	-0.2705 *	-0.0224
PPD								1 **	0.94735***
SPY									1 **

DFF- Days to 50% flowering, **PH**- Plant height (cm), **PT**-Number of productive tillers per plant, **PL**-Panicle length (cm), **TG**-Number of grains per panicle, **SF**-Spikelet fertility (%), **TGW**- Thousand grain weight (g), **PDP-**Per day productivity, **SPY**- Single plant yield (g).

Table 4. Phenotypic path coefficient analysis representing direct and indirect effects on single plant yield by its related traits in F_4 population of AR 9-18 × MSM 1212

	TGW	TG	SF	PH	PL	PT	DFF	PPD	SPY
TGW	**0.0188**	0.0018	0.0042	-0.0008	0.0049	0.0024	-0.0039	0.0079	0.3993
TG	-0.0022	**-0.0225**	-0.0075	0.0056	0.0003	-0.0035	0.0033	-0.0064	0.2354
SF	0.0020	0.0030	**0.0089**	-0.0009	0.0010	0.0014	-0.0004	0.0016	0.1842
PH	0.0020	0.0122	0.0047	**-0.0487**	-0.0091	0.0001	-0.0032	0.0060	-0.1330
PL	0.0198	-0.0011	0.0087	0.0142	**0.0763**	0.0094	-0.0159	0.0269	0.3645
PT	0.0031	0.0038	0.0040	-0.0001	0.0030	**0.0245**	-0.0042	0.0076	0.2906
DFF	-0.0546	-0.0387	-0.0122	0.0176	-0.0555	-0.0454	**0.2659**	-0.0719	-0.0224
PPD	0.4103	0.2767	0.1735	-0.1200	0.3437	0.3018	-0.2639	**0.9757**	0.9474

Direct effects are represented in bold values

Residual effect: 0.191

DFF- Days to 50% flowering, **PH**- Plant height (cm), **PT**-Number of productive tillers per plant, **PL**-Panicle length (cm), **TG**-Number of grains per panicle, **SF**-Spikelet fertility (%), **TGW**- Thousand grain weight (g), **PDP-**Per day productivity, **SPY**- Single plant yield (g)

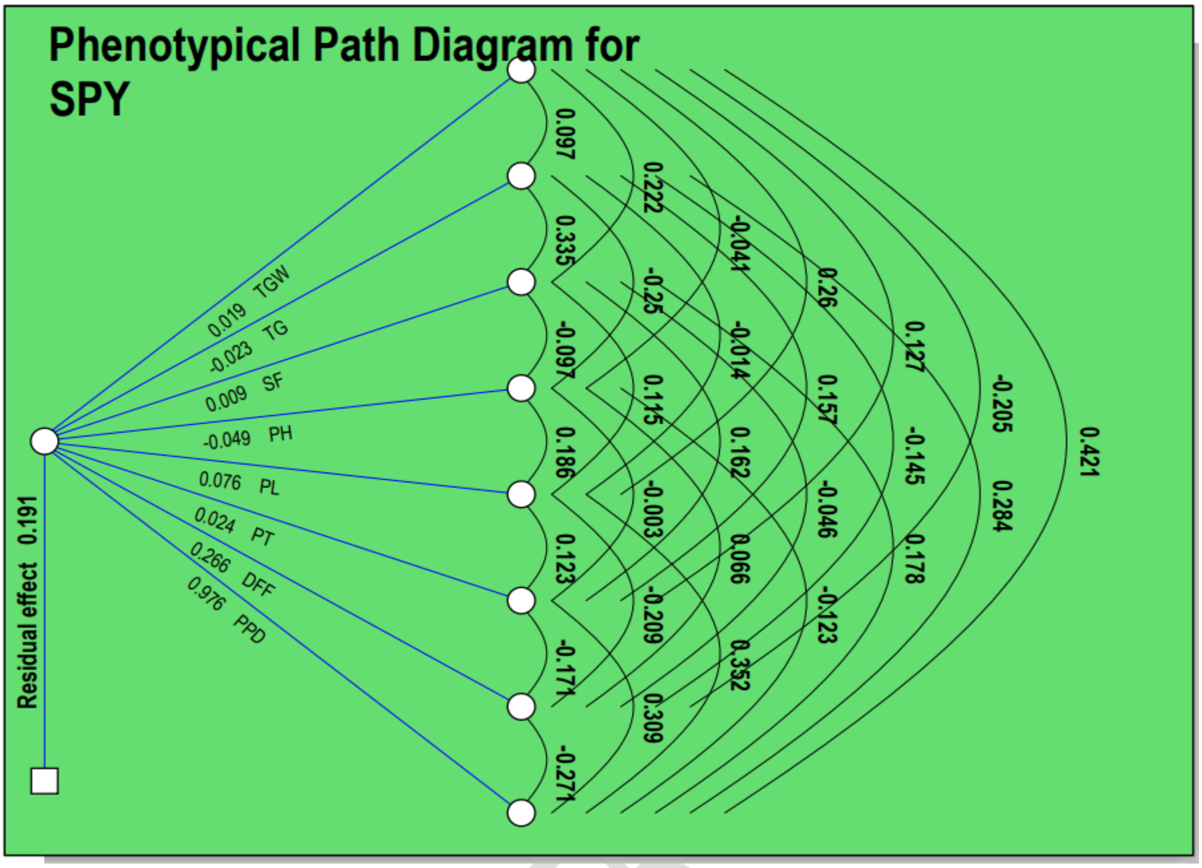

Fig. 3. Phenotypical path diagram for yield related traits

DFF- Days to 50% flowering, **PH**- Plant height (cm), **PT**-Number of productive tillers per plant, **PL**-Panicle length (cm), **TG**-Number of grains per panicle, **SF**-Spikelet fertility (%), **TGW**- Thousand grain weight (g), **PPD**-Per day productivity, **SPY**- Single plant yield (g).

Conclusion

Analysis of variance revealed significant differences among the treatments for all the characters under study indicating the existence of considerable genetic variation in the experimental material. Moderate PCV and GCV were recorded for number of productive tillers per plant, number of grains per panicle, per day productivity and single plant yield which signifies fair level of selection in these characters. Number of productive tillers per plant, number of grains per panicle, per day productivity and single plant yield showed high heritability with high genetic advance as per cent of mean which signifies predominance of additive gene action in their genetic control. So, for improvement of these traits simple selection would be productive. Analysis of correlation and path coefficient together revealed that among the yield traits studied, per day productivity and number of productive tillers per plant were considered as most critical ones as they exhibited higher correlation coefficients and direct positive effects in association to plant yield.

References

Akinwale, M.G., Gregorio, G., Nwilene, F., Akinyele, B.O., Ogunbayo, S.A and Odiyi, A.C. (2011). Heritability and correlation coefficient analysis for yield and its components in rice (Oryza sativa L.). *African Journal of Plant Science*, 5(3): 207-212.

Abhilash, R., Thirumurugan, T., Sassikumar, D and Chitra, S. (2018). Genetic studies in F2 for biometrical traits in Rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*, 9 (3): 1067-1076.

Adhikari, B.N., Joshi, B.P., Shrestha, J. and Bhatta, N.R. (2018). Genetic variability, heritability, genetic advance and correlation among yield and yield components of rice (*Oryza sativa* L.). *Journal of Agriculture and Natural Resources*, *1*(1):149-160.

Ali, E.N., Rajeswari, S., Saraswathi, R and Jeyaprakash, P. (2018). Genetic variability and character association for earliness, yield and its contributing traits in F2 population of rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*, 9(3): 1163-1169.

Burton, G.W and Devane. (1953). Estimating heritability in tall tissue (FestulaarundnaceaL.) from replicated clonal material. *Agronomy Journal*, 45: 478 -481.

Bhadru, D., Reddy, D.L. and Ramesha, M.S. (2011). Correlation and path coefficient analysis of yield and yield contributing traits in rice hybrids and their parental lines. *Electronic Journal of Plant Breeding*, *2*(1):112-116.

Babu, V.R., Shreya, K., Dangi, K.S., Usharani, G. and Shankar, A.S. (2012). Correlation and path analysis studies in popular rice hybrids of India. *International Journal of Scientific and Research Publications*, *2*(3):1-5.

Dewey, D. R and Lu, K. H. (1959). A correlation and path analysis of components of crested wheat grass seed production. *Agronomy Journal*, 51: 513-516.

Dhanwani, R.K., Sarawgi, A.K., Solanki, A. and Tiwari, J.K. (2013). Genetic variability analysis for various yield attributing and quality traits in rice (*O. sativa* L.). *The Bioscan*, *8*(4) :1403-1407.

Gautam, D., Kandel, B.P and Adhikari, B. B. (2018). Performance of rice genotypes in western mid hill of Nepal. *Journal of Plant Breeding and Genetics*, 6(3): 111–116.

Ghazy, M. I., Salem, K. F. M and Sallam, A. (2020). Utilization of genetic diversity and marker-trait to improve drought tolerance in rice (*Oryza sativa* L.). *Molecular Biology Reports*, 48(1): 157–170.

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

Kumar, A., Bhowmick, P.K., Singh, V.J., Malik, M., Gupta, A.K., Seth, R., Nagarajan, M., Krishnan, S.G. and Singh, A.K. (2017). Marker-assisted identification of restorer gene (s) in iso-cytoplasmic restorer lines of WA cytoplasm in rice and assessment of their fertility restoration potential across environments. *Physiology and Molecular Biology of Plants*, *23*: 891-909.

Kalaiselvan, S., Subramanian, A., Thirumurugan, T. and Rajanbabu, V. (2019). Genetic variability and association studies in F2 population of rice under sodicity. *Electronic Journal of Plant Breeding*, *10*(2):.601-613.

Kiruthikadevi, U., Banumathy, S., Arunachalam, P., Renuka, R and Thirumurugan, T. (2020). Correlation, path analysis and stress indices studies of saltolintrogressed lines of rice for salinity tolerance. *Electronic Journal of Plant Breeding*, 11(1): 230–237.

Lingaiah, N. (2018). Variability studies in F2 population of Rice (*Oryza sativa* L.). *International Journal of Agriculture Sciences*, *ISSN*, *10*(9):0975-3710.

Muthuvijayaragavan, R and Murugan, E. (2020). Association analysis of F_2 generation in rice (*Oryza sativa* L.) under salinity condition. *Electronic Journal of Plant Breeding*. 11(1): 283-289.

Nath, S. and Kole, P.C. (2021). Genetic variability and yield analysis in rice. *Electronic Journal of Plant Breeding*, *12*(1):253-258.

Panse, V. G and Sukhatme, P. V. 1985. Statistical Methods for Agricultural Workers. *Indian Council of Agricultural Research Publication*, 87-89.

Panwar, L.L and Mathur, S.S. (2007). Variability studies in segregating populations of Rice (*Oryza sativa* L.). *Annals of Agricultural Research*, 28 (1).

Padmaja, D., Radhika, K., Rao, L.V. and Padma, V. (2008). Studies on variability, heritability and genetic advance for quantitative characters in rice (*Oryza sativa* L.). *Indian Journal of Plant Genetic Resources*, *21*(3):196-198.

Pranathi, K., Viraktamath, B.C., Neeraja, C.N., Balachandran, S.M., Hari Prasad, A.S., Koteswara Rao, P., Revathi, P., Senguttuvel, P., Hajira, S.K., Balachiranjeevi, C.H. and Bhaskar Naik, S. (2016). Development and validation of candidate gene-specific markers for the major fertility restorer genes, Rf4 and Rf3 in rice. *Molecular Breeding*, *36* :1-14.

Prasad, K.R., Krishna, K.R., Kumar, S.S., Senguttuvel, P and Rao, L.S. (2017). Screening of Lines for Restoring Fertility Genes Rf3 and Rf4 with SSR Markers in Rice (*Oryza sativa* L.). *International Journal of Pure and Applied Bioscience*, 5 (4): 647-650.

Parimala, K and Devi, K. R. (2019). Estimation of variability and genetic parameters in indica and japonica genotypes of rice (*Oryza sativa* L.). *International Journal of Current Microbiology and Applied Sciences*, 8(03): 1138–1142.

Robinson, F. A., Comstock, R. E and Harvey, P. H. (1949). Estimation of heritability and degree of dominance in corn. *Agronomy Journal*, 41: 353-359.

Sivasubramanian, S and Madhavamenon, P. (1973). Genetic analysis of quantitative characters in rice through diallel crosses. *Madras Agricultural Journal*, 60: 1097-1098.

Sravan, T., Rangare, N.R., Suresh, B.G. and Kumar, S.R. (2012). Genetic variability and character association in rainfed upland rice (*Oryza sativa* L.). *Journal of Rice Research*, *5*(1), p.2.

Savitha, P and Usha Kumari, R. (2015). Assessment of genetic variability and correlation studies among traditional land races and improved cultivars for segregating generations of rice (*Oryza sativa* L.). *International Journal of Science and Nature*, 6 (2): 135-140.

Sala, M and Shanthi, P. (2016). Variability, heritability and genetic advance studies in F2 population of rice (*Oryza sativa* L.). *International Journal of Forestry and Crop Improvement*, 7 (1): 57-60.

Sumanth, V., Suresh, B.G., Ram, B.J. and Srujana, G. (2017). Estimation of genetic variability, heritability and genetic advance for grain yield components in rice (*Oryza sativa* L.). *Journal of Pharmacognosy and Phytochemistry*, *6*(4):1437-1439.

Singh, N. and Verma, O.P. (2018). Genetic variability, heritability and genetic advance in rice (*Oryza sativa* L.) under salt stressed soil. *Journal of Pharmacognosy and Phytochemistry*, *7*(3): 3114-3117.

Subbulakshmi, K and Muthuswamy, A. (2018). Estimation of genetic variability, heritability and correlation studies in F2 and F3 populations for yield and quality traits in rice (*Oryza sativa* L.) *Life Sciences Leaflets*, 95: 1-11.

Saha, S., Hassan, L., Haque, M., Islam, M and Rasel, M. (2019). Genetic variability, heritability, correlation and path analyses of yield components in traditional rice (Oryza sativa L.) landraces. *Journal of the Bangladesh Agricultural University*, 17(1): 26-32.

Shrivastav, S. P., Verma, O. P., Singh, V and Lal, K. (2020). Interrelationships among yield and its contributing traits in rice (*Oryza sativa* L.) under sodic soil. *Electronic Journal of Plant Breeding*, 11(4): 1044–1052.

Sudeepthi, K., Srinivas, T.V.S.R., Kumar, B.R., Jyothula, D.P.B. and Umar, S.N. (2020). Assessment of genetic variability, character association and path analysis for yield and yield component traits in rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*, *11*(01):144-148.

Touhiduzzaman, S.R., Asif, M., Mehraj, H and Uddin, A.J. (2016). Correlation and genetic distance on sixteen rice varieties grown under SRI. *Advances In Plants and Agriculture Research*, 3(3): 95-99.

Tripathi, N., Verma, O.P., Singh, P.K. and Rajpoot, P. (2018). Studies on correlation and path coefficient analysis for yield and its components in rice (*Oryza sativa* L.) under salt affected soil. *Journal of Pharmacognosy and Phytochemistry*, *7*(3): 1626-1629.

Virmani SS (1996) Hybrid rice. *Advances in Agronomy*,57:377–462

Wright, S. 1921. Correlation and causation. Journal of Agricultural Research, 20: 557-585.

Weber, C.R and Moorthy, B.R. (1952). Heritability and non- heritability relationships and variability of oil content and agronomic characters in the F_2 generation of soybean crosses. *AgronomyJournal*, 44: 202-209.

Yadav, R., Rajpoot, P., Verma, O.P., Singh, P.K., Singh, P. and Pathak, V. (2017). Genetic variability, heritability and genetic advance in Rice (*Oryza sativa* L.) for grain yield and itâ€™ s contributing attributes under sodic soil. *Journal of Pharmacognosy and Phytochemistry*, *6*(5):1294-1296.

Sala, M and Shanthi, P. (2016). Variability, heritability and genetic advance studies in F_2 population of rice (*Oryza sativa* L.). *International Journal of Forestry and Crop Improvement*, 7 (1): 57-60.