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Correlation and path analysis studies in recombinant inbred lines (F₈) of Langulmota/Sambamahsuri derivatives

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Abstract

Recombinant inbred lines (F8) derivatives of Langulmota/Sambamahsuri were tested for interrelationship of yield attributing characters along with parental lines and three check varieties during *kharif*-2016 using nineteen quantitative traits. Correlation analysis revealed that grain yield showed highly positive significant correlation with number of panicles per plant, panicle weight, number of florets per panicle, number of grains per panicle, number of primary branches per panicle, floret fertility percentage and 1000 grain weight, selection of these traits will directly leads to increase in yield. Path analysis revealed that Grain L/B ratio imparted the highest positive direct effect on yield followed by grain breadth, number of florets per panicle, florets fertility%, kernel L/B ratio, kernel breadth. Therefore, these characters should be taken into consideration for simultaneous, indirect selection models in rice improvement programme.

Keywords: Recombinant inbred lines, correlation analysis, path analysis

Introduction

Rice (*Oryza sativa* L.) is a self-pollinated cereal crop belonging to the family Gramineae, with a diploid chromosome number of 2n=24. It is the most important crop of the Indian subcontinent and the staple food for a large population, feeding more than 60% population especially in Asia. World's population is increasing in geometric proportion. In order to meet the fastest growing demand for food, there is a necessity of development of high yielding genotypes with desirable agronomic traits for diverse ecosystem.

Population of Recombinant Inbred Lines (RILs) are the recombinant output from which superior stabilized segregants can be directly used as breeding lines and can serve as a powerful tool to cover the complexity of yield related traits. Yield is a complex trait and is a result of the interaction of a number of components (Sarawgi *et al.*, 1997)^[30]. Some of these components affect the yield directly while others contribute indirectly. In plant breeding programme, direct selection for yield may be sometimes misleading thus indirect selection may supplement the selection criteria and can be reliable. Correlation coefficient and path analysis provide a better understanding of the association of different characters through other related characters by partitioning the correlation coefficient (Dixet and Dubey, 1984)^[9]. The present study was aimed at understanding the interrelationship among different traits for selection of desirable genotypes of rice suitable for the Gangetic plains of West Bengal by assessing the RILs of Langulmota/Sambamahsuri derivatives and understanding the direct, indirect effects with respect to yield and its attributing characters.

Material and Methods

30 F8 progenies developed from Langulmota/Sambamahsuri derivatives developed at Regional Research Station, new alluvial zone, sub center- Chakdah, Nadia, along with two parents and three check varieties viz., Dhanrasi, SwarnaSub-1, Sabita were used in the present research for the correlation and path analysis studies. The experiment was conducted during Aman (Kharif) season of year 2015-16 at Instructional farm, Bidhan Chandra Krishi Viswavidyalya, Jaguli, Nadia following Randomised Block Design. The seedlings were transplanted at a spacing of 20cm from row to row and 15cm from plant to plant. Recommended agronomic package of practices were followed during the crop growth period. A sample consisting of five plants were drawn at random for recording the observations from each replication of each genotype for the 19 characters namely Days to 50% flowering, Days to maturity, Plant height (cm), Number of panicles per plant, Panicle weight(g), Panicle length (cm), Number of primary branch per panicle, Number of secondary branch per panicle,

Number of florets per panicle, Number of grains per panicle, Florets fertility (%),1000 grain weight (g), Grain length (mm), Grain breadth (mm), Grain L/B ratio, Kernel length (mm), Kernel breadth (mm), Kernel L/B ratio, Grain yield per plant. The genotypic and phenotypic correlations were estimated by the method described by Johnson *et al.*, (1955) and Path coefficient analysis was carried out at the genotypic level as subjected by Wright (1921) and discussed by Dewey and Lu (1959). The statistical analysis was done using the software OPSTAT.

Result and Discussion Correlation

To identify the important trait to use in crop improvement programme through suitable breeding method, one should select the trait based on the direction and magnitude of association between yield and yield attributing characters.

The genotypic and phenotypic correlation coefficients among different biometrical traits are presented in (Table 1). Grain yield has shown highly positive significant correlation with number of panicles per plant, panicle weight, number of florets per panicle, number of grains per panicle, number of primary branches per panicle, fertility percentage and 1000 grain weight, while number of secondary branches per panicle, panicle length only at genotypic level. This finding is in agreement with that of Sawarkar and Senapati (2014)^[31] for number of grains per panicle and floret fertility percentage, for number of florets per panicle and number of grains per panicle, Sameera et al., (2016)^[28] and Rajamadhan et al., (2016)^[24] for number of grains per panicle, Bagati et al., (2016)^[4] for fertility percentage and number of grains per panicle, Srijan et al., (2016)^[33] for panicle weight, Anis et al., (2016) for number of panicles per plant, Das and Sarma (2015)^[5] for 1000 grain weight.

Days to 50 per cent flowering showed highly significant and positive correlation with days to maturity and grain breadth. It also had high significant negative correlation with grain L/B ratio and number of secondary branches per panicle. Significant positively correlation was observed for days to maturity with grain breadth. Number of secondary branches per panicle (only at genotypic level) and grain L/B ratio significantly and negatively correlated with days to maturity. Highly significant positive correlation was observed for plant height with panicle weight, number of primary branches per panicle, number of secondary branches per panicle, number of florets per panicle and grains per panicle. It had significant negative correlation with kernel length (only genotypic level) and number of panicles per plant.

Number of panicles per plant showed significant positive correlation with panicle length and grain L/B ratio only at genotypic level. It also showed high significant and negative correlation with panicle weight, number of florets per panicle, number of grains per panicle, yield per plant both at genotypic and phenotypic levels, while only at genotypic level with 1000 grain weight, grain breadth and only at phenotypic level with number of secondary branches per panicle. A highly significant positive correlation was observed for panicle weight with number of primary branches per panicle, number of secondary branches per panicle, number of secondary branches per panicle, number panicle, grain yield per plant (this character can be used for direct selection of high yielding lines), and grain breadth (genotypic level only). Significant negative correlation with number of florets per panicle (only genotypic level) was also noticed.

Panicle length showed highly significant positive correlation with primary branches per panicle, secondary branches per panicle, kernel breadth and grain yield per plant. It had negative significant correlation with grain length (at genotypic level only). Highly significant positive correlation was observed for primary branches per panicle with number of secondary branches per panicle, number of grains per panicle, grain yield per plant and number of florets per panicle (only genotypic level). It also had significant negative correlation with grain length, kernel length, kernel L/B ratio and grain L/B ratio (only phenotypic level).

Secondary branches per panicle showed high and significant positive correlation with number of florets per panicle, number of grains per panicle, grain yield per plant (only genotypic level). It also showed significant negative correlation with floret fertility (%). Number of florets per panicle showed highly significant positive correlation with number of grains per panicle and grain yield per plant. It also had significant negative correlation with floret fertility%, 1000 grain weight, grain length, kernel length, grain L/B ratio (only genotypic level). Highly significant negative correlation was observed for number of grains per panicle with grain yield per plant. It also had significant negative correlation with 1000 grain weight, grain length, kernel length, grain L/B ratio (only genotypic level).

Secondary branches per panicle showed high and significant positive correlation with number of florrets per panicle, number of grains per panicle, grain yield per plant (only genotypic level). It also showed significant negative correlation.

Florets fertility showed highly significant positive correlation with 1000 grain weight, grain length, and grain yield per plant. 1000 grain weight showed significant positive correlation with grain length, grain breadth, kernel length, kernel breadth and yield per plant at genotypic and phenotypic level. Grain length incurred highly significant and positive correlation with grain L/B ratio, kernel length and kernel L/B ratio. It also showed significant negative correlation with kernel breadth. Grain breadth showed significant correlation with kernel breadth. It also had significant negative correlation with grain L/B ratio and kernel L/B ratio. Grain L/B ratio showed highly significant positive correlation with kernel length and kernel L/B ratio and significant negative correlation with kernel breadth. Kernel length showed high significant positive correlation with kernel L/B ratio while kernel breadth showed significant negative correlation.

The traits that showed high positive correlation with yield can be used for indirect selection as well as conforming the phenotypic values of yield. The characters that have exhibited significant negative correlation with yield can be selected against to achieve higher yield. The correlation data can be used to establish the relative utility of the contributing characters towards yield.

Table 1: Genotypic (G) and Phenotypic (P) correlations among yield and quality traits in Langulmota/Sambamahsuri derivatives along with parents and check varieties

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Characters		Days to maturity	Plant height at maturity(cm)	Number of	Panicle weight(g)	Panicle length(cm)	No. of primary branches/Plant	No. of secondary branches/plant	Number of Florets/ plant	Number of grains/ plant	Floret Fertility (%)	1000 grain weight (g)	Grain length (mm)	Grain breadth (mm)	Grain L/B ratio	Kernel length (mm)	Kernel breath (mm)	Kernel L/B ratio	Seed yield/ plant(g)
Days to 50% flowering	G	0.972**	0.037	-0.017	0.052	-0.204	-0.041	-0.261*	-0.056	0.007	-0.008	0.127	-0.056	0.591**	- 0.443**	-0.143	-0.114	0.040	-0.069
	Р	0.929**	0.029	0.037	0.039	-0.116	0.011	0.243*	-0.053	-0.016	-0.030	0.123	-0.054	0.454**	-0.391*	-0.134	-0.106	0.042	0.069
Days to maturity	G		0.012	0.186	0.032	-0.090	0.157	-0.301*	-0.070	0.018	0.023	0.048	-0.097	0.508**	- 0.423**	-0.231	-0.117	-0.017	0.020
	Р		0.019	0.088	0.022	-0.075	0.092	-0.225	-0.069	0.014	0.033	0.030	-0.115		- 0.316**		-0.127	0.015	0.021
Plant height (cm)				-0.619**	0.606**	0.102	0.49**	0.586**	0.458**	0.548**	0.165	0.013	-0.169	-0.128	-0.063	-0.275*	-0.222	-0.029	0.072
	Р			-0.410**	0.423**	0.057	0.39**	0.452**	0.440**	0.455**	0.052	-0.026	-0.163	-0.097	-0.051	-0.228	-0.186	-0.007	0.029
No. of Panicles/ Plant	G				-0.716**	0.454**	-0.049	-0.164				- 0.389**	0.074	-0.362**	0.299*	0.153	-0.174	0.230	0.460**
	Р				-0.333**	-0.018	-0.145	-0.268*	-0.314**		0.002	-0.137	0.073	-0.081	0.105	0.069	-0.108		0.319**
Panicle weight(g)	G P					0.060 0.089	0.54** 0.40**	0.579** 0.467**	-0.737** 0.631**	0.719** 0.723**	-0.026 0.021	0.345** 0.295*	0.012 0.010	0.362** 0.219	-0.220 -0.147	-0.073 -0.025	0.184		0.601** 0.460**
Panicle	P G					0.089	0.40***	0.261*	-0.166	-0.098	-0.021	0.293*	-0.240*	-0.046	-0.147		0.175	-0.134	0.460***
length(cm)	Р						0.255*	0.299*	-0.051	0.005	-0.038	0.159	-0.124	0.054	-0.074	0.105	0.306**	-0.166	0.142
No.of Pri.Branch/panicl							0.235	0.602**	0.288*	0.483**	0.180	0.072	0.436**	-0.225	0.000	0.456**			0.524**
e	Р							0.301*	0.220	0.361**	0.140	-0.022	- 0.311**	0.054	-0.270*	- 0.326**	0.103		0.355**
No.of Sec.Branch/panicl e	G								0.650**	0.561**	-0.380**	-0.176	-0.200	-0.176	-0.053	-0.207	-0.095	-0.097	0.260*
	Р								0.559**	0.464**	-0.327**	-0.067	-0.177	-0.097	-0.038	-0.193	0.001	-0.134	0.172
No. Florets/ Panicle	G									0.915**	-0.515**	- 0.336**	- 0.332**	-0.070	-0.243*	- 0.362**	-0.096	-0.203	0.318**
	Р									0.857**	-0.470**	- 0.336**	-0.299*	-0.063	-0.167	- 0.315**	-0.050	-0.183	0.282*
No. of grains/ Panicle	G										-0.182	- 0.343**	- 0.353**	-0.041	-0.281*	- 0.430**	-0.113	-0.221	0.576**
	Р										-0.095	-0.288*	-0.289*	-0.043	-0.173	- 0.352**	-0.071	-0.177	0.489**
Floret fertility (%)	G											0.286*	0.289*	0.176	0.105	0.081	-0.121	0.164	0.390**
	Р											0.274*	0.247*	0.101	0.079	0.058	-0.088	0.118	0.331**
1000 grain weight(g)	G												0.491**	0.618**		0.592**		0.142	0.511**
	Р												0.465**	0.467**	0.001	0.538**	0.350**	0.082	0.442**
Grain length(mm)																	0.550.	0.841**	
	Р													0.019	0.647**	0.724**	-0.254*	0.667**	-0.030

Grain breadth(mm)	G					- 0.004	0.411**	-0.268*	0.082
	Р					- 0.739** -0.031	0.289*	-0.218	0.061
Grain L/B ratio	G					0.662**	- 0.474**	0.821**	-0.109
	Р							0.595**	
Kernel length(mm)	G							0.721**	-0.045
	Р						0.009	0.613**	-0.061
Kernel breadth(mm)	G							- 0.690**	-0.051
	Р							- 0.768**	-0.024
Kernel L/B ratio	G								-0.012
	Р								-0.032

** Significant at 1% level of significance

* Significant at 5% level of significance

Character	Days to 50% flowering	Daystu	ar		Panicle weight(g)		No. of Primary branches/Plant	No. of Secondary branches/plant	of florets/	Number of grains/ plant	Floret fertility(%)	1000 grain weight (g)	length	Grain breadth (mm)		Kernel length (mm)	Kernel breath (mm)	Kernel L/B ratio	Seed yield / Plant(g)
Days to 50% flowering	-0.366	0.368	-0.011	0.008	-0.013	0.002	-0.003	-0.059	-0.098	0.001	-0.011	0.0001	0.200	1.797	-1.894	0.040	-0.065	0.036	-0.068
Days to maturity	-0.356	0.378	-0.003	0.091	-0.008	0.0005	0.015	-0.068	-0.124	-0.003	0.030	0.00005	0.346	1.545	-1.808	0.065	-0.066	-0.015	0.019
Plant height(cm)	-0.013	0.004	-0.311	-0.306	-0.160	-0.001	0.048	0.133	0.807	-0.089	0.087	0.00001	0.604	-0.389	-0.268	0.078	-0.126	-0.026	0.072
No.of panicles/plant	-0.006	0.070	0.192	0.494	0.190	-0.005	-0.004	-0.037	-0.425	0.081	-0.062	-0.0004	-0.264	-1.102	1.277	-0.043	-0.099	0.208	0.460**
Panicle weight(g)	-0.019	0.012	-0.188	-0.354	-0.265	-0.0007	0.052	0.132	1.299	-0.117	-0.034	0.0003	-0.041	1.101	-0.949	0.020	0.105	-0.156	0.601**
Panicle length(cm)	0.074	-0.034	-0.031	0.224	-0.015	-0.012	0.039	0.059	-0.293	0.015	-0.027	0.0002	0.858	-0.140	-0.533	-0.059	0.316	-0.192	0.247*
No.of Pri.Branch/plant	0.014	0.059	-0.154	-0.024	-0.142	-0.005	0.097	0.137	0.507	-0.078	0.244	- 0.00007	1.560	-0.684	-0.857	0.297	0.082	-0.362	0.524**
No.of Sec.Branch/plant	0.095	-0.114	-0.182	-0.081	-0.153	-0.003	0.058	0.228	1.146	-0.091	-0.514	-0.0001	0.717	-0.536	-0.226	0.058	-0.054	-0.088	0.260*
No.Florets/Panicle	0.020	-0.026	-0.142	-0.234	-0.195	0.002	0.027	0.148	1.763	-0.149	-0.697	-0.0003	1.188	-0.211	-1.039	0.103	-0.054	-0.183	0.318**
No.of grain\s/ Panicle	0.002	0.006	-0.170	-0.245	-0.190	0.001	0.046	0.128	1.614	-0.163	-0.246	-0.0003	1.262	-0.124	-1.202	0.122	-0.064	-0.199	0.576**
Floret fertility(%)	0.003	0.008	-0.020	-0.022	0.006	0.0002	0.017	-0.086	-0.907	0.029	1.356	0.0003	-1.036	0.536	0.447	-0.023	-0.069	0.149	0.390**
1000 grain weight(g)	-0.046	0.018	-0.004	-0.192	-0.091	-0.002	-0.006	-0.040	-0.393	0.056	0.388	0.001	-1.358	1.881	0.107	-0.168	0.234	0.128	0.511**
Grain length(mm)	0.020	-0.036	0.052	0.036	-0.003	0.003	-0.042	-0.045	-0.585	0.057	0.392	0.0005	-3.581	0.067	3.260	-0.225	-0.188	0.762	-0.055
Grain breadth(mm)	-0.216	0.192	0.039	-0.179	-0.096	0.0005	-0.021	-0.040	-0.122	0.006	0.239	0.0006	-0.079	3.043	-2.670	0.001	0.234	-0.242	0.082
Grain L/B ratio	0.162	-0.159	0.019	0.146	0.058	0.001	-0.019	-0.011	-0.428	0.045	0.141	0.00003	-2.728	-1.903	4.279	-0.218	-0.270	0.744	-0.109
Kernel length(mm)	0.052	-0.087	0.085	0.075	0.019	-0.002	-0.442	-0.047	-0.638	0.027	0.109	0.0006	-2.830	-0.013	2.833	-0.284	0.002	0.653	-0.045
Kernel breadth(mm)	0.041	-0.044	0.068	-0.085	-0.048	-0.007	0.014	-0.021	-0.168	0.018	-0.164	0.0004	1.181	1.250	-2.029	-0.001	0.570	-0.625	-0.051
Kernel L/B ratio	-0.014	-0.006	0.008	0.113	0.045	0.002	-0.038	-0.022	-0.357	0.036	0.222	0.0001	-3.011	-0.814	3.515	-0.205	-0.393	0.906	-0.012

Residual effects R²=0.0723

** Significant at 1% level of significance

* Significant at 5% level of significance

Path analysis

Based on the interaction between the yield attributing traits, grain yield architecture is determined. The association between yield attributing traits among themselves and with yield is crucial selection criteria for yield improvement. Correlation gives only the simple relation between the two variables but not provide the true contribution of each trait towards the yield. Whereas the path coefficient analysis partitions the correlation into direct effect and indirect effects through other attributes.

Path analysis (Table 2) based on correlation coefficients using grain yield per plant as the dependent factor (effect) and fix other quantitative characters as independent factor (causes) calculated. The correlation coefficient of each was independent quantitative character was partitioned into direct and indirect effect towards grain yield. The direct and indirect effects were rated as negligible (0.00-0.09). Low (0.10-0.19), Moderate (0.20-0.29), High (more than 1.00) as suggested by Lenka and Mishra (1973)^[18], as the residual effect was very low (0.072), it is therefore, indicated that the number of characters chosen for the study were very much appropriate for determination of yield in rice. Nearly half of the characters viz., days to maturity, number of panicles per plant, number of primary branches, number of secondary branches, number of florets per panicle, florets fertility%, 1000 grain weight, grain breadth, grain L/B ratio, kernel breadth and kernel L/B ratio showed positive direct effects towards grain yield. While the rest of the characters namely days to 50% flowering, plant height, panicle weight, panicle length, number of grains per panicle imparted negative direct effect on grain yield per plant. This finding was in agreement with that of Sadeghi (2011)^[27], Sanghera and Kashyap (2012)^[29], Pandey et al., (2017)^[22], Dhurai *et al.*, (2014)^[7], and Dhurai *et al.*, (2016)^[8] for days to maturity, Kiani (2012)^[14], Nagaraju *et al.*, (2013)^[20], Sawarkar and Senapati (2014)^[31], and Allam *et al.*, (2015)^[1] for number of panicles per plant, Yadav *et al.*, (2010)^[35], Babu *et al.*, (2011)^[3], Reddy *et al.*, (2013)^[19], Ketan et al., (2014)^[13], Allam et al., (2015)^[1] for number of florets per panicle, Laxuman et al., (2011) [17], Awneet kumar and Senapati (2013)^[16], and Allam et al., (2015)^[1] for floret fertility%, Sadeghi (2011) ^[27], Pandey *et al.*, (2012) ^[22], Osman *et al.*, (2012) ^[21], Reddy *et al.*, (2013) _[20], Karim *et al.*, (2014), Jambhulkar *et al.*, (2014) ^[10], Allam *et al.*, (2015) ^[1], Rajamadhan *et al.*, (2016) ^[24], Rukmini *et al.*, (2017) ^[26] for 1000 grain weight, Awneet kumar and Senapati (2013) ^[16] for grain breadth, Awneet kumar and Senapati (2013) ^[16] for grain L/B ratio, Sawarkar and Senapati (2014) [31], Dhurai et al., (2014)^[7] for kernel breadth and Dhurai et al., (2014)^[7] for kernel L/B ratio.

Grain yield per plant was positively and significantly correlated with number of panicles per plant, panicle weight, panicle length, and number of primary branches per plant, number of secondary branches per plant, number of florets per panicle, number of grains per panicle, floret fertility% and 1000 grain weight. This finding was in agreement with that of of Sawarkar and Senapati (2014) ^[31] for number of grains per panicle and floret fertility percentage for number of florets per panicle and number of grains per panicle, Sameera *et al.*, (2016) ^[28] and Rajamadhan *et al.*, (2016) ^[24] for number of grains per panicle. Correlation coefficient of grain yield with number of panicles per plant (0.460**) and number of secondary branches of plant (0.280*) was almost equal to their direct effects (0.495 & 0.228 respectively). Thus, it explained the true relationship and a direct selection through

these characters would be effective for yield improvement in rice. In addition to these, number of florets per panicle and florets fertility% imparted very high positive direct effect on grain yield along with a highly significant correlation; therefore, direct selection against these characters will be effective for yield improvement in rice.

Number of grains per panicle, panicle length, and panicle weight had significantly positive correlation with yield per plant but their direct effects were negative. It indicated that indirect effects would be the cause of correlation in this situation the indirect casual factors were to be considered simultaneously for selection. Therefore, it would be better to consider the characters that showed high indirect effect on grain yield per plant.

Conclusion

Grain yield, the most economic quantitative trait exhibited highly positive association with number of panicles per plant, panicle weight, number of florets per panicle, number of grains per panicle, number of primary branches per panicle, fertility percentage and 1000 grain weight. Correlation studies conclude that traits that are with direct positive effects with yield and also among themselves can be used for simultaneous selections, leading to improvement of yield. Path analysis revealed that Grain L/B ratio imparted the highest positive direct effect on yield followed by grain breadth, number of florets per panicle, florets fertility%, kernel L/B ratio, kernel breadth. The residual effect results was 0.0723 indicated that the contribution of component characters on grain yield was 92.77%, by the 19 characters studied in path analysis, the rest 07.23% was the contribution of other factors such as traits not studied. Therefore, the selection of higher intensities of these traits can also lead to the increase in yield.

References

- 1. Allam CR, Jaiswal HK, Qamar A. Character association and path analysis studies of yield and quality parameters in basmati rice (*Oryza sativa* L.). Journal of the Bio Scan. 2015; 9(4):1733-1737.
- Anis GB, EL Namaki RA, Ashkar AL, Barutcular IM C, EL Sabagh A. Yield potential and correlation analysis of some rice hybrids for yield and its component traits. Journal of Animal and Plant Sciences. 2016; 30(2):4748-4757.
- 3. Babu GS, Lavanya GR, Singh AP. Genetic variability for grain yield and character association studies in upland rice (*Oryza sativa* L.) germplasm. Environment and Ecology. 2011; 29(1):164-1160.
- 4. Bagati S, Singh AK, Salgotra RK, Bhardwaj R, Sharma M, Rai SK *et al.* A genetic variability, heritability and correlation coefficients of yield and its component traits in basmati rice (*Oryza sativa* L.). Journal of Breeding and Genetics. 2016; 48(4):445-452.
- Das S, Sarma D. Correlation and path analysis of morpho physiological and yield traits in boro rice (*Oryza sativa* L.). Agricultural Science Digest. 2015; 35(4):256-262.
- Dewey OR, Lu KH. "A correlation and path coefficient analysis of components of crested wheat grass and production". Indian Journal of Agronomy. 1959; 57:515-518.
- Dhurai SY, Reddy DM, Bhati PK. Correlation and path coefficient analysis for yield and quality traits under organic fertilizer management in rice (*Oryza sativa* L.). Electronic Journal of Plant Breeding. 2014; 5(3):581-587.

- 8. Dhurai SY, Mohan DR, Ravi S. Correlation and path analysis for yield and quality characters in rice (*Oryza sativa* L.). Rice Genomics and Genetics. 2016; 7(4):143-146.
- 9. Dixet P, Dubey DK. Path analysis in lentil (Lens culinaris Med.), Lens Newsletter. 1984; 11:15-17.
- 10. Jambhulkar NN, Bose LK. Genetic variability and association of yield attributing traits with grain yield in upland rice. Genetika. 2014; 46(3):831-838.
- Johnson HW, Robinson HF, Comstock RE. Estimation of genetic and environmental variability in soyabean. Agronomy Journal. 1955; 47:314-318.
- 12. Karim D, Noor EA, Siddique MD, Umakanto S, Zakir HMD, Jakia S. Phenotypic and genotypic correlation coefficient of quantitative characters and character association of aromatic rice. Journal of Bioscience and Agriculture Research, 2014; 01(01):34-46.
- 13. Ketan R, Sarkar G. Studies on variability, heritability, genetic advance and path analysis in some indigenous Aman rice (*Oryza sativa* L.). Journal of Crop and Weed. 2014; 10(2):308-315.
- 14. Kiani G. Character association and path coefficient analysis of yield component in rice varieties. Research on Crops. 2012; 13(2):552-555.
- 15. Krishna V, Vijaya L, Ramana JV. Variability and association studies for yield components and quality parameters in rice genotypes. Journal of Rice Research, 2013, 6(2).
- 16. Kumar A, Senapati BK. Genetic parameters and association studies for important quantitative traits in advance line of Sambamahsuri derivatives. Journal of Crop and Weed. 2013; 9(1):156-163.
- 17. Laxuman Salimath PM, Shashidhar HE, Mohankumar HD, Patil SS, Vamadeaiah HM, Janagoudar BS. Character association and path coefficient analysis among the backcross inbred lines derived from Indica x NERICA cross for productivity traits in rice (*Oryza sativa* L.). Karnataka Journal of Agricultural Sciences. 2011; 24(5):626-628.
- Lenka D, Mishra B. Path coefficient analysis of yield in rice varieties. Indian Journal of Agricultural Science. 1973; 43:376-379.
- 19. Minnie CM, Reddy TD, Raju CS. Correlation and path analysis for yield and its components in rice (*Oryza sativa* L.). Journal of Research Angrau. 2013; 41(1):132-134.
- 20. Nagaraju C, Sekhar M, Reddy KH, Sudhakar. Correlation between traits and path analysis coefficient for grain yield and other components in rice (*Oryza sativa* L.) genotypes. International journal of Applied Biology and Pharmacutical Technology. 2013; 9(11):137-142.
- Osman KA, Mustafa AM, Ali F, Zheng YL, Qiu FAZ. Genetic variability for yield and related attributes of upland rice genotypes in semi-arid zone (Sudan). African journal of Agricultural Research. 2012; 7(33):4613-4619.
- 22. Pandey VR, Singh PK, Verma OP, Pandey P. Interrelationship and path coefficient estimation in rice under salt stress environment. International Journal of Agricultural Research. 2012; 7(4):169-184.
- 23. Patel JR, Saiyad MR, Prajapati KN, Patel RA, Bhavani R. Genetic variability and character association studies in rainfed upland rice (*Oryza sativa* L.). Electronic Journal of Plant Breeding. 2014; 5(3):531-537.
- 24. Rajamadhan R, Murugan. Genetic Variability, Correlation and Path Coefficient Studies for Grain Yield

and Other Yield Attributing Traits in Rice (*Oryza sativa* L.). Journal of Advances in Life Science. 2016; 9:2145-2150.

- 25. Reddy, Suresh, Sravan, Ashok Reddy. Interrelationship and Cause-Effect Analysis of Rice Genotypes in North East Plain Zone. The Bio scan. 2013; 8(4):1141-1144.
- Rukmini DK, Chandra B, Satish, Lingaiah N, Hari Y, Venkanna V. Analysis of variability, correlation and path coefficient studies for yield and quality traits in rice (*Oryza sativa* L.). Agricultural Science Digest. 2017; 37(1):1-9.
- Sadeghi SM. Heritability, phenotypic correlation and path coefficient studies for some agronomic characters in landrace rice varieties. World Applied Sciences Journal. 2011; 13(5):1229-1233.
- Sameera SK, Rajesh A, Prasanna Jayalakshmi V, Nirmala PJ, Srinivas T. Genetic Variabily Studies for Yield and Yield Components in Rice (*Oryza sativa* L.). Electronic Journal of Plant Breeding. 2016; 6(1):81-85.
- 29. Sanghera GS, Kashyap SC. Genetic parameters and selection indices in F3 progenies of hill rice genotypes. Notulae Scientia Biologicae. 2012; 4(4):110-114.
- Sarawgi AK, Rastogi NK, Soni DK. Correlation and path analysis in rice accessions from Madhya Pradesh. Field Crops Res. 1997; 52:161-167.
- 31. Sawarkar A, Senapati BK. Polygenic variations and cause effect relationship in some photo-insensitive recombinant inbred lines (RIL's) of Basmati derivative. African Journal of Biotechnology. 2014; 13(1):112-118.
- 32. Senapati, Awneet kumar. Genetic assessment of some phenotypic variants of rice (Oryza sps) for some quantitative characters under the Gangatic plains of West Bengal. African journal of biotechnology. 2015; 14(3):87-201.
- Srijan AS, Sudheer Kumar, DamodarRaju CH. Studies on Gene Action and Combining Ablility in Rice (*Oryza* sativa L.). Environment and Ecology. 2016; 34(4):1749-1755.
- 34. Wright S. Correlation and causation. Journal of Agricultural Research. 1921; 20:57-585.
- 35. Yadav SK, Suresh BG, Pandey P, Kumar B. Assessment of genetic variability, correlation and path association in rice. Journal of biological sciences. 2010; 18:1-8.