

Original Research Article

<https://doi.org/10.20546/ijcmas.2019.810.120>

Genetic Variability, Correlation and Path Coefficient Studied for Yield and Quality Traits in JNPT Lines of Rice (*Oryza sativa* L.)

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ABSTRACT

In present study, sixty-seven JNPT (Jawahar New Plant Type) lines were evaluated for twenty-eight morphological and quality traits planted in Randomized Complete Block Design with three replications. The experiment was conducted during *kharif* seasons of 2018 at Seed Breeding Farm, Department of Plant Breeding and Genetics, College of Agriculture, JNKVV, Jabalpur (M.P.), India. Observations were recorded on the basis of middle five random competitive plants selected from each line in every replication for yield and quality traits to study the genetic variability parameters, correlation coefficient and path coefficient for yield and its attributing traits. The values of PCV for all the traits were found to be more than GCV and very small difference was present in between GCV and PCV revealing little influence of environment for their expression. High heritability accompanied with high genetic advance was observed for the traits thousand grain weight (g), head rice recovery (%), spikelet fertility (%), harvest index (%), number of spikelets/panicle, fertile spikelets/panicle, spikelet density, grain yield /plant (g), panicle weight/plant (g), number of tillers/plant and number of productive tillers/plant. Based on the results from correlation and path coefficient analysis, it is concluded that number of tillers/plant, spikelet fertility and panicle weight/plant showed positive correlation with grain yield and at same time exhibited high positive direct effect towards yield. Therefore, they seem to be primary yield contributing character and thus can be used as direct selection to improve genetic yield potential of rice.

Keywords

Genetic variability,
Correlation and
path coefficient,
JNPT Lines
Oryza sativa

Article Info

Accepted:
07 September 2019
Available Online:
10 October 2019

Introduction

Rice (*Oryza sativa* L.) is one of the most important crops that feed more than half the population of the world. The biggest consuming areas are Asia, Sub-Saharan Africa, and South America. Globally, after China, India is first in rice cultivation and

second in rice production. It adds 26.9% of rice production globally. Rice occupies one-quarter of the total crop area within the country, contributes around 40 to 43 per cent of total food grain production, and continues to play an important role in the domestic food and livelihood security framework. In Asia, 90% of all rice is cultivated and eaten. World

paddy production has steadily increased from around 220 million tons in 1960 to over 759.6 million tons in 2017, and rice production in 2017 is 503.9 million tons. At this level, global production would exceed the 2016 record by a modest 0.6% or 4.5 million tons (FAOSTAT, 2018).

The present investigation was undertaken to gather some useful information on genetic variability character association and path coefficient analysis in a set of sixty-seven JNPT lines of rice genotypes. Heritability (h^2) is an index of transmissibility of the characters from the parents to offspring and has a predictive role in crop breeding programs (Khan and Naqvi, 2011). Improvement in the mean genotypic value of selected plants over the parental population is known as genetic advance. The genetic advance for the studied traits is dependent on the extent of genetic variability, heritability and selection intensity (Allard, 1960). It is not necessary that a character showing high heritability will also exhibit high genetic advance (Johnson, *et al.*, 1955). Selection of parents based on yield alone is often misleading. Hence, knowledge about relationship between yield and its contributing characters is needed for an efficient selection strategy for the plant breeders to evolve an economic variety. Correlation studies provide better understanding about yield contributing characters. Path coefficient analysis provide information about influence of each contributing trait to yield directly as well as indirectly and also enables breeders to rank the genetic attributes according to their contribution.

Materials and Methods

The experimental material consists of 67 new JNPT lines (Table 1) derived from *Indica X Japonica* subspecies crosses (F_8 - F_9 BC₃ generation) developed by Rice Improvement Project, JNKVV, Jabalpur were grown during

Kharif season of 2018 at Seed Breeding Farm, JNKVV, Jabalpur (M.P.), India. These lines were planted in Randomized Complete Block Design with three replications. Twenty-one days old seedlings were transplanted in the experimental site with spacing of 15 cm between plant to plant and 20 cm between the rows, keeping single seedling per hill. Gap filling was done within a week so as to keep uniform plant population. Fertilizer dose of 120 kg N, 60 kg P₂O₅ and 60 kg K₂O was applied. The standard agronomic practices were adopted for normal crop growth.

Twenty-eight quantitative and quality characteristics were used to characterize and assess the genetic diversity of JNPT lines as per rice DUS guideline. Five plants were randomly chosen from each replication in each genotype for yield assessment and quality attribute traits. The observations were recorded as per the standard procedure and subjected to statistical analysis using mean values of five randomly selected plants.

Statistical analysis

The data on quantitative characters were statistically analysed on the basis of model described by Cochran and Cox (1950) for randomized complete block design. Parameters of genetic variability include mean, range, genotypic and phenotypic coefficient of variation were calculated by the method suggested by Burton (1952) and the estimate of PCV and GCV were classified as low, moderate and high according to Sivasubramanian and Madhavamenon (1973).

Heritability for broad sense is the ratio of genotypic variance to the total phenotypic variance. Expected genetic advance was calculated by the method suggested by Johnson *et al.*, (1955) and genetic advance as percentage of mean was calculated by the following formula:

GA as percentage of mean =

$$\frac{\text{Genetic advance}}{\text{General mean}} \times 100$$

Correlation coefficients were calculated for all quantitative character combinations at phenotypic, genotypic and environmental level by the formula given by Miller *et al.*, (1958).

$$r_{x_i \times x_j} = \frac{\text{Cov}X_i X_j}{\sqrt{(\text{Var}X_i)} \cdot \sqrt{(\text{Var}X_j)}}$$

The significance of phenotypic correlation coefficients was tested against 'r' values given by Fisher and Yates (1963).

$$t_{cal} = \frac{r\sqrt{n-2}}{\sqrt{1-r^2}}$$

The direct and indirect contribution of various characters to yield were calculated through path coefficient analysis as suggested by Wright (1921) and elaborated by Dewey and Lu (1959). The path coefficients were rated based on the scales given below (Lenka and Mishra, 1973).

>1.00	=	Very high
0.3-0.99	=	High
0.2-0.29	=	Moderate
0.1-0.19	=	Low
0.0-0.09	=	Negligible

Results and Discussion

Genetic variability parameters

Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV)

The magnitude of variation between genotypes was reflected by high values of mean and range for genotypic traits studied

(Table 3). The value of GCV and PCV were obtained high for number of spikelets/panicle, spikelet density, grain yield/plant, fertile spikelets/panicle, biological yield /plant and panicle weight/plant. This was in agreement with the finding reported by Shrivastava *et al.*, (2015), Gautam *et al.*, (2016), Devi *et al.*, (2017), Srujana *et al.*, (2017) and Choudhary *et al.*, (2018). In this study, moderate GCV and PCV were observed for harvest index, thousand grain weight, number of tillers/plant, number of productive tillers/plant, head rice recovery, flag leaf width, stem thickness, spikelet fertility, this was in agreement with Choudhary *et al.*, (2018) and partial agreement with Devi *et al.*, (2017). Similarly, harvest index recorded a high magnitude of GCV and PCV with the findings reported by Shrivastava *et al.*, (2015). Stem length, decorticated grain l/b ratio, flag leaf length, plant height, grain breadth, decorticated grain breadth, grain length, decorticated grain length, days to 50% flowering, panicle length, panicle index, days to maturity, milling percentage and hulling percentage showed low GCV and PCV (<10%) which was in agreement with the Hossain *et al.*, (2015) for days to 50% percent flowering, Sohgaura *et al.*, (2014) for milling percentage, days to 50% percent flowering and days to maturity.

Heritability and genetic advance analysis

In our study, most of the characters exhibited high broad sense heritability except flag leaf length which recorded low broad sense heritability. High heritability coupled with high genetic advance showed by thousand grain weight, head rice recovery, spikelet fertility, harvest index, number of spikelets/panicle, fertile spikelets/panicle, spikelet density, grain yield/plant, panicle weight/plant, number of tillers/plant and number of productive tillers/plant. This was partially in consonance with the findings of Dongre *et al.*, (2014); Jha *et al.*, (2014) for

fertile spikelets/panicle. Similar results were reported by Debnath *et al.*, (2015) for thousand grain weight, panicle weight/plant, fertile spikelets/panicle and grain yield /plant; Devi *et al.*, (2017) for number of productive tillers/plant, fertile spikelets/panicle, thousand grain weight, grain yield /plant and head rice recovery; Vinoth *et al.*, (2016) for fertile spikelets/panicle and fertile spikelets/panicle; Rajesh *et al.*, (2016) for number of productive tillers/plant, fertile spikelets/panicle, number of spikelets/panicle, grain yield /plant and panicle weight/plant; Kumar *et al.*, (2018) for thousand grain weight, spikelet fertility, spikelets per panicle, harvest index, grain yield/plant, biological yield/plant and number of productive tillers/plant.

High heritability coupled with moderate genetic advance were found for grain length, decorticated grain length, days to maturity, days to 50% flowering, grain width, decorticated grain l/b ratio, decorticated grain breadth, panicle index, stem length and plant height. This study was in consonance with the findings of Sharma *et al.*, (2014) for days to 50% flowering and days to maturity.

High heritability accompanied with low genetic advance exhibited by milling percentage and hulling percentage. This was in confirmation with the findings reported by Sohgaure *et al.*, (2014) and Choudhary (2016) for hulling percentage.

Correlation coefficient analysis

In present investigation, genotypic correlation coefficients were higher in magnitude than phenotypic correlation coefficients in the same direction and magnitude indicated that there is a strong inherent association between each pair of character(s) which might be due to masking or modifying effect of the environment (Table 2).

Grain yield/plant revealed significant and positive association with panicle weight/plant, followed by biological yield/plant, harvest index, number of tillers/plant, number of productive tillers/plant, panicle index, number of fertile spikelets/panicle, number of spikelets/panicle, spikelet fertility and spikelet density. It indicates strong association of these traits with grain yield per plant and selection for such traits will be useful in improving grain yield. A positive correlation between desirable characters is favourable because it helps in simultaneous improvement of both the characters. Similar results were previously confirmed by Ketan and Sarkar (2014), Sohgaure *et al.*, (2014), Dongre *et al.*, (2014), Shrivastava *et al.*, (2015), Yadav *et al.*, (2015), Sameera *et al.*, (2016), Vinoth *et al.*, (2016), Kumar *et al.*, (2017), Onyia *et al.*, (2017), Shamim *et al.*, (2017) and Pratap *et al.*, (2018).

However, negative and highly significant correlation of grain yield/plant was also observed with days to 50% flowering followed by days to maturity. This finding was in confirmation with the results of Lingaiah *et al.*, (2014), Sohgaure *et al.*, (2014), Onyia *et al.*, (2017) and Hosagoudar *et al.*, (2018).

Path coefficient analysis

The present investigation revealed that the highest positive direct effect towards grain yield/plant was observed for spikelet density followed by number of tillers/plant, spikelet fertility, panicle weight/plant, decorticated grain length/breadth ratio, flag leaf length, decorticated grain width, milling percentage, panicle length, stem length, stem thickness, days to maturity and thousand grain weight. Similar results were reported by Chakraborty *et al.*, (2010) for Spikelet density and spikelet fertility. Whereas, Kumar *et al.*, (2017) confirmed the highest positive direct effect of spikelet fertility on grain yield/plant.

Table.1 Parameters of genetic variability for yield, yield attributing and quality traits in NPT lines of rice

S.No.	TRAITS	Mean	Range		Coefficient of variation		h ² (bs) %	Genetic Advance (GA)	Genetic advance as 5% of mean
			Max.	Min.	GCV (%)	PCV (%)			
1	DTF	107.10	122.33	95.67	5.799	5.896	96.8	12.59	11.75
2	DTM	134.16	154.33	124.67	5.205	5.271	97.5	14.20	10.59
3	TPP	7.35	7.84	2.50	13.166	15.525	71.9	1.69	23.00
4	PTPP	7.33	7.34	2.05	13.083	15.43	71.9	1.68	22.85
5	PH	101.15	121.73	83.07	7.727	9.155	71.2	13.59	13.43
6	SL	75.91	93.53	58.47	9.525	11.236	71.9	12.63	16.63
7	PL	25.24	29.20	22.33	5.714	7.858	52.9	2.16	8.56
8	ST	5.78	7.87	4.60	11.321	13.764	67.7	1.11	19.18
9	FLL	49.74	63.00	39.00	8.648	12.446	48.3	6.16	12.38
10	FLW	1.41	1.83	1.03	11.878	15.887	55.9	0.26	18.30
11	BYPP	58.02	127.67	35.00	22.07	24.134	83.6	24.12	41.58
12	PWPP	26.83	56.67	16.40	21.979	24.923	77.8	10.71	39.93
13	NSPP	214.79	465.67	135.33	27.637	29.497	87.8	114.58	53.34
14	FSPP	182.60	346.67	118.33	23.014	25.718	80.1	77.47	42.43
15	SF	86.33	97.43	38.30	10.385	10.843	91.7	17.69	20.49
16	SD	8.51	16.03	5.67	25.437	27.924	83	4.06	47.73
17	TGW	24.85	34.03	14.53	16.632	16.636	99.9	8.51	34.25
18	PI	74.51	84.65	62.97	5.635	6.444	76.5	7.57	10.15
19	HI	34.86	60.30	24.78	17.807	18.948	88.3	12.02	34.47
20	GL	9.49	11.25	7.19	6.611	6.633	99.3	1.21	13.57
21	GW	2.90	3.59	2.19	7.168	7.415	93.5	0.37	14.27
22	DGL	6.59	8.14	5.98	6.145	6.196	98.3	0.81	12.55
23	DGW	2.29	3.04	2.03	7.017	7.414	89.6	0.30	13.68
24	DLBR	2.91	3.44	2.08	8.876	9.303	91.0	0.52	17.45
25	HP	80.07	87.72	72.01	3.131	3.566	77.1	4.45	5.66
26	MP	71.64	77.70	62.72	4.833	5.099	89.8	6.91	9.44
27	HRR	50.57	59.86	40.58	11.935	12.024	98.5	15.09	24.40
28	GYPP	20.02	42.20	12.47	23.26	26.129	79.2	8.54	42.66

DTF- Days to 50% flowering, **DTM**- Days to maturity, **TPP**- Number of tillers per plant, **PTPP**- Productive tillers per plant, **PH**- Plant height, **SL**- Stem length, **PL**- Panicle length, **CT**- Culm thickness, **FLL**- Flag leaf length, **FLW**- Flag leaf width, **BYPP**- Biological yield per plant, **PWPP**- Panicle weight per plant, **NSPP**- Number of spikelet per panicle, **FSPP**- Fertile spikelet per panicle, **SF**- Spikelet fertility, **SD**- Spikelet density, **TGW**- Thousand grain weight, **PI**- Panicle index, **HI**- Harvest index, **GL**- Grain length, **GW**- Grain width, **DGL**- Decorticated grain length, **DGW**- Decorticated grain width, **DLBR**- Decorticated length breadth ratio, **HP**- Hulling percentage, **MP**- Milling percentage, **HRR**- Head rice recovery, **GYPP**- Grain yield per plant.

Table.2(a) Estimates of phenotypic correlation coefficient for various yield and attributing traits

TRAITS	DTF	DTM	TPP	PTPP	PH	SL	PL	ST	FLL	FLW	BYPP	PWPP	NSPP	FSPP
DTF		0.940**	0.036	0.034	-0.035	-0.004	-0.144*	0.264**	0.228**	-0.306**	-0.134	-0.190**	0.126	0.106
DTM			0.093	0.092	-0.006	0.036	-0.178*	0.247**	0.182**	-0.350**	-0.083	-0.156*	0.068	0.064
TPP				0.999**	-0.074	-0.038	-0.186**	-0.009	-0.114	-0.122	0.381**	0.326**	-0.220**	-0.114
PTPP					-0.077	-0.041	-0.190**	-0.011	-0.119	-0.121	0.373**	0.315**	-0.228**	-0.125
PH						0.978**	0.461**	0.118	0.371**	0.121	0.199**	0.025	0.110	0.055
SL							0.268**	0.088	0.343**	0.088	0.185**	-0.002	0.053	0.021
PL								0.172*	0.258**	0.189**	0.134	0.127	0.286**	0.165*
ST									-0.023	-0.201**	0.243**	0.124	0.154*	0.060
FLL										0.324**	-0.011	-0.066	0.208**	0.130
FLW											-0.082	0.009	0.203**	0.240**
BYPP												0.771**	0.162*	0.231**
PWPP													0.210**	0.291**
NSPP														0.882**
FSPP														
SF														
SD														
TGW														
PI														
HI														
GL														
GW														
DGL														
DGW														
DLBR														
HP														
MP														
HRR														
GYPP	-0.225**	-0.194**	0.370**	0.360**	-0.004	-0.022	0.077	0.078	-0.073	0.061	0.733**	0.968**	0.172*	0.282**

* Significant at 5 % level; ** Significant at 1 % level

Table.2(b) Estimates of phenotypic correlation coefficient for various yield and attributing traits (continue)

TRAITS	SF	SD	TGW	PI	HI	GL	GW	DGL	DGW	DLBR	HP	MP	HRR
DTF	-0.152*	0.178*	-0.456**	-0.191**	-0.127	-0.153*	-0.440**	-0.200**	-0.263**	0.077	-0.219**	-0.307**	0.296**
DTM	-0.095	0.128	-0.469**	-0.180*	-0.145*	-0.136	-0.428**	-0.149*	-0.276**	0.117	-0.198**	-0.329**	0.319**
TPP	0.276**	-0.183**	0.080	0.242**	0.022	-0.065	0.147*	-0.051	0.178*	-0.148*	0.076	0.062	-0.005
PTPP	0.275**	-0.190**	0.084	0.247**	0.019	-0.062	0.147*	-0.049	0.179*	-0.148*	0.075	0.062	-0.008
PH	-0.099	-0.016	-0.181*	-0.146*	-0.270**	-0.165*	-0.113	0.006	-0.091	0.062	-0.129	-0.100	0.172*
SL	-0.046	-0.019	-0.203**	-0.110	-0.273**	-0.206**	-0.093	-0.023	-0.056	0.020	-0.134	-0.115	0.128
PL	-0.262**	0.009	0.027	-0.211**	-0.084	0.118	-0.128	0.130	-0.182**	0.204**	-0.020	0.030	0.245**
ST	-0.223**	0.112	-0.141*	-0.173*	-0.195**	0.135	-0.175*	0.135	-0.117	0.192**	-0.151*	-0.175*	0.168*
FLL	-0.220**	0.140*	-0.234**	-0.078	-0.104	-0.149*	-0.169*	-0.180*	-0.108	-0.032	-0.115	-0.158*	0.156*
FLW	0.055	0.155*	-0.032	0.160*	0.165*	-0.126	-0.033	-0.149*	0.029	-0.120	-0.020	0.041	-0.170*
BYPP	0.097	0.132	0.033	0.001	-0.230**	0.186**	0.036	0.184**	-0.026	0.136	0.077	0.012	0.119
PWPP	0.097	0.180*	0.013	0.070	0.383**	0.120	0.080	0.110	0.004	0.079	0.047	-0.058	0.016
NSPP	-0.486**	0.957**	-0.497**	-0.113	0.051	-0.151*	-0.493**	-0.273**	-0.456**	0.174*	0.059	-0.054	0.176*
FSPP	-0.033	0.881**	-0.440**	0.009	0.114	-0.130	-0.448**	-0.271**	-0.400**	0.130	0.091	0.037	0.200**
SF		-0.416**	0.273**	0.316**	0.109	0.052	0.228**	0.065	0.257**	-0.162*	0.095	0.236**	-0.034
SD			-0.536**	-0.061	0.068	-0.196**	-0.491**	-0.319**	-0.435**	0.131	0.063	-0.075	0.113
TGW				0.086	-0.020	0.540**	0.649**	0.569**	0.511**	-0.039	0.175*	0.309**	-0.170*
PI					0.455**	-0.190**	0.222**	-0.189**	0.349**	-0.395**	0.323**	0.378**	-0.096
HI						-0.151*	0.107	-0.157*	0.144*	-0.199**	0.116	0.072	-0.136
GL							0.170*	0.799**	-0.133	0.587**	-0.001	0.086	-0.009
GW								0.224**	0.649**	-0.327**	0.153*	0.297**	-0.103
DGL									-0.082	0.665**	-0.015	0.034	-0.118
DGW										-0.787**	0.304**	0.277**	-0.117
DLBR											-0.258**	-0.212**	0.007
HP												0.755**	0.186**
MP													0.332**
HRR													
GYPP	0.167*	0.155*	0.033	0.313**	0.480**	0.064	0.130	0.053	0.094	-0.028	0.111	0.036	-0.0022

* Significant at 5 % level; ** Significant at 1 % level

Table.3(a) Estimates of genotypic path coefficient for various yield and quality attributing traits on grain yield/plant

TRAITS	DTF	DTM	TPP	PTPP	PH	SL	PL	ST	FLL	FLW	BYPP	PWPP	NSPP	FSP
DTF	-2.2034	-2.0794	-0.0885	-0.0787	0.0736	-0.0081	0.4393	-0.7273	-0.7431	0.9407	0.3116	0.4576	-0.3041	-0.2714
DTM	0.7428	0.7871	0.0833	0.0813	0.0019	0.0408	-0.1944	0.2561	0.2006	-0.3768	-0.0651	-0.1313	0.0644	0.065
TPP	0.2357	0.6209	5.8666	5.8676	-0.9299	-0.5554	-2.2543	-0.1044	-1.5629	-1.05	2.3312	1.886	-1.9633	-1.3194
PTPP	-0.1851	-0.535	-5.1828	-5.182	0.8128	0.4776	2.0099	0.088	1.4135	0.9432	-2.0154	-1.6082	1.7687	1.2105
PH	0.0711	-0.0051	0.3376	0.334	-2.1296	-2.0969	-1.0283	-0.1899	-1.3335	-0.5875	-0.376	0.054	-0.1885	0.0209
SL	0.0046	0.0642	-0.1172	-0.1141	1.2193	1.2384	0.3993	0.0784	0.7373	0.295	0.2082	-0.0623	0.0192	-0.0711
PL	-0.3955	-0.49	-0.7623	-0.7694	0.9578	0.6396	1.9837	0.329	0.8103	0.5966	0.2261	0.2272	0.7968	0.4652
ST	0.2854	0.2812	-0.0154	-0.0147	0.0771	0.0547	0.1434	0.8645	-0.0094	-0.228	0.2759	0.0996	0.1634	0.0552
FLL	0.8534	0.645	-0.6741	-0.6902	1.5844	1.5065	1.0336	-0.0275	2.5304	0.8301	0.022	-0.1471	0.8733	0.5707
FLW	0.2406	0.2697	0.1008	0.1026	-0.1554	-0.1342	-0.1695	0.1486	-0.1848	-0.5634	0.0724	-0.0032	-0.1385	-0.1681
BYPP	0.591	0.3457	-1.6609	-1.6256	-0.738	-0.7027	-0.4763	-1.3337	-0.0363	0.5372	-4.1796	-3.2268	-0.386	-0.5989
PWPP	-1.0122	-0.8127	1.5668	1.5125	-0.1236	-0.245	0.5583	0.5614	-0.2833	0.0281	3.7627	4.8737	0.6842	1.0075
NSPP	-0.6674	-0.3958	1.6185	1.6507	-0.428	-0.0751	-1.9426	-0.9141	-1.6691	-1.1887	-0.4466	-0.6789	-4.8363	-4.2336
FSP	-1.1967	-0.8022	2.1852	2.2697	0.0952	0.5575	-2.2786	-0.6203	-2.1912	-2.8991	-1.3923	-2.0086	-8.5053	-9.716
SF	-0.882	-0.55	1.8022	1.8031	-0.8644	-0.5301	-2.0264	-1.5267	-1.9264	0.3931	0.3284	0.309	-3.1145	-0.623
SD	3.1357	2.3577	-4.421	-4.5214	-0.2592	-0.8774	2.9936	2.4588	4.2345	2.9433	1.1461	1.7946	15.2393	13.9358
TGW	-0.0872	-0.0894	0.0175	0.0182	-0.0402	-0.0448	0.0069	-0.032	-0.0633	-0.0083	0.0067	0.0028	-0.1001	-0.0929
PI	0.1805	0.169	-0.2839	-0.2841	0.1951	0.1488	0.3112	0.1967	0.1082	-0.1654	0.0208	-0.1004	0.1197	0.0056
HI	0.2282	0.2611	-0.016	-0.0112	0.5544	0.5518	0.2382	0.5118	0.2292	-0.3785	0.4573	-0.6044	-0.0508	-0.1559
GL	0.0281	0.0247	0.0142	0.0136	0.0348	0.0431	-0.0275	-0.0295	0.0391	0.0309	-0.0362	-0.0246	0.0282	0.0253
GW	0.4995	0.4815	-0.201	-0.2012	0.134	0.1038	0.2054	0.2059	0.247	0.0601	-0.0337	-0.0903	0.593	0.5626
DGL	0.1928	0.1453	0.0645	0.0613	0.0025	0.0344	-0.1587	-0.1614	0.2536	0.2015	-0.1922	-0.1129	0.2912	0.3084
DGW	-0.7004	-0.7369	0.5934	0.5953	-0.2883	-0.1746	-0.6869	-0.3619	-0.4103	0.1076	-0.0595	0.0664	-1.2276	-1.1299
DLBR	0.2252	0.3306	-0.5241	-0.5216	0.1958	0.0567	0.7767	0.5947	-0.1242	-0.4673	0.3892	0.1805	0.4582	0.3448
HP	0.2492	0.2213	-0.1326	-0.1361	0.2198	0.2266	0.0549	0.1778	0.2411	-0.0272	-0.0964	-0.1115	-0.074	-0.112
MP	-0.7041	-0.7424	0.2166	0.2176	-0.2912	-0.3318	0.0853	-0.4093	-0.5982	0.118	0.0437	-0.0745	-0.1289	0.0905
HRR	0.0221	0.0238	0.0004	0.0001	0.0145	0.0107	0.025	0.0162	0.0161	-0.0169	0.0098	0.0025	0.0138	0.0163
GYPP	-0.2482	-0.2102	0.3877	0.3772	-0.0747	-0.085	0.0213	0.0498	-0.0752	0.0682	0.7189	0.9689	0.0955	0.1921
R SQUARE = 0.9835														
RESIDUAL EFFECT = 0.1286														

Table.3(b) Estimates of genotypic path coefficient for various yield and quality attributing traits on grain yield/plant (continue)

TRAITS	SF	SD	TGW	PI	HI	GL	GW	DGL	DGW	DLBR	HP	MP	HRR
DTF	0.3527	-0.4411	1.0203	0.4983	0.2967	0.3528	1.0275	0.446	0.6348	-0.1946	0.5464	0.739	-0.6635
DTM	-0.0786	0.1185	-0.374	-0.1667	-0.1213	-0.1108	-0.3538	-0.1201	-0.2386	0.102	-0.1733	-0.2783	0.2557
TPP	1.9186	-1.6558	0.5447	2.0863	0.0555	-0.4751	1.1009	-0.3974	1.432	-1.2057	0.7739	0.6052	0.0282
PTPP	-1.6955	1.4958	-0.5015	-1.8443	-0.0342	0.4004	-0.9735	0.3338	-1.269	1.0601	-0.7016	-0.5371	-0.0084
PH	0.334	0.0352	0.4548	0.5205	0.6968	0.4226	0.2664	0.0056	0.2526	-0.1636	0.4657	0.2954	-0.4223
SL	-0.1191	-0.0694	-0.295	-0.2308	-0.4033	-0.3043	-0.1201	-0.0447	-0.089	0.0276	-0.2792	-0.1957	0.1811
PL	-0.7295	0.3791	0.0731	-0.7735	-0.2788	0.3102	-0.3803	0.3306	-0.5605	0.6043	-0.1084	0.0806	0.6777
ST	-0.2395	0.1357	-0.1469	-0.213	-0.2611	0.1454	-0.1662	0.1465	-0.1287	0.2016	-0.153	-0.1685	0.1913
FLL	-0.8845	0.6841	-0.8505	-0.3429	-0.3422	-0.5629	-0.5834	-0.6738	-0.4271	-0.1233	-0.607	-0.721	0.5572
FLW	-0.0402	-0.1059	0.0249	-0.1168	-0.1258	0.099	0.0316	0.1192	-0.0249	0.1033	-0.0153	-0.0317	0.13
BYPP	-0.2491	-0.3058	-0.1493	0.1089	1.128	-0.8622	-0.1316	-0.8433	0.1023	-0.638	-0.4008	-0.0871	-0.5588
PWPP	0.2733	0.5584	0.0732	0.6132	1.7383	0.682	0.4107	0.5777	0.1331	0.3449	0.5407	-0.1731	0.1665
NSPP	2.7333	-4.7053	2.5718	0.7255	-0.145	0.7772	2.6772	1.4784	2.4422	-0.869	-0.3562	0.2969	-0.9085
FSPP	1.0985	-8.6444	4.7928	0.0678	-0.894	1.4026	5.1031	3.1462	4.5157	-1.314	-1.0825	-0.4187	-2.1586
SF	5.5107	-2.7971	1.5706	2.0433	0.5694	0.3036	1.3978	0.3522	1.5276	-0.948	0.5718	1.4094	-0.1962
SD	-7.9504	15.6633	-9.238	-1.2394	0.8007	-3.3444	-8.867	-5.6832	-7.7499	2.1298	1.2766	-1.3787	1.9325
TGW	0.0537	-0.111	0.1883	0.0179	-0.0039	0.102	0.1267	0.108	0.1016	-0.0077	0.0376	0.0616	-0.0323
PI	-0.296	0.0632	-0.0757	-0.7982	-0.4287	0.1745	-0.2112	0.1741	-0.3156	0.3541	-0.339	-0.365	0.0905
HI	-0.1751	-0.0866	0.0347	-0.9102	-1.6946	0.2738	-0.1958	0.3036	-0.2892	0.3971	-0.3292	-0.1834	0.227
GL	-0.0097	0.0375	-0.0952	0.0384	0.0284	-0.1756	-0.0304	-0.1419	0.0252	-0.1086	0.0014	-0.0153	0.0017
GW	-0.2717	0.6064	-0.7209	-0.2834	-0.1238	-0.1857	-1.0712	-0.2492	-0.7587	0.3812	-0.1845	-0.3428	0.1169
DGL	-0.0609	0.3456	-0.5465	0.2078	0.1706	-0.7697	-0.2216	-0.9525	0.0812	-0.6572	0.0228	-0.0308	0.1162
DGW	0.6739	-1.2028	1.3126	0.9612	0.4148	-0.3484	1.7219	-0.2072	2.431	-1.8873	0.843	0.7376	-0.3171
DLBR	-0.4386	0.3467	-0.1044	-1.1312	-0.5975	1.5769	-0.9075	1.7595	-1.9795	2.5498	-0.7546	-0.5911	0.0288
HP	-0.1043	-0.0819	-0.2009	-0.4269	-0.1953	0.0081	-0.1731	0.024	-0.3485	0.2975	-1.0051	-0.7597	-0.1641
MP	0.537	-0.1848	0.6866	0.96	0.2273	0.1832	0.6719	0.0678	0.637	-0.4867	1.5868	2.0995	0.6651
HRR	-0.0026	0.009	-0.0126	-0.0083	-0.0098	-0.0007	-0.008	-0.0089	-0.0096	0.0008	0.012	0.0232	0.0733
GYPP	0.1404	0.0865	0.0369	0.3634	0.4673	0.0747	0.1408	0.0512	0.1277	-0.0496	0.189	0.0704	0.0099
R SQUARE = 0.9835													
RESIDUAL EFFECT = 0.1286													

Number of tillers/plant had positive direct effect on grain yield/plant this result collaborated with the finding of Dongre *et al.*, (2014). While, panicle weight/plant exhibited positive direct effect on grain yield/plant was in agreement with the result of Kumar *et al.*, (2014) and Yadav *et al.*, (2015). Decorticated grain length/breadth ratio and milling percentage recorded positive direct effect on grain yield/plant was in confirmation with the findings of Haque *et al.*, (2014) and Devi *et al.*, (2017) respectively.

Panicle length had positive direct effect on grain yield/plant was in agreement with the results of Lingaiah *et al.*, (2014) and Pratap *et al.*, (2018) with positive direct effect. Whereas, stem length recorded positive direct on grain yield/plant was in confirmation with the findings of Dongre *et al.*, (2014) and Kumar *et al.*, (2014). Days to maturity had positive direct effect on grain yield/plant. This was in consonance with the finding of Sohgaure *et al.*, (2014), Karim *et al.*, (2016), Kumar *et al.*, (2017) and Shamim *et al.*, (2017). The positive direct effect of thousand grain weight was in confirmatory with the results of Dongre *et al.*, (2014), Lingaiah *et al.*, (2014), Sohgaure *et al.*, (2014), Debnath *et al.*, (2015), Devi *et al.*, (2017) and Pratap *et al.*, (2018).

In conclusion, the mean sum of squares due to genotypes for all the characters was highly significant for all the traits under study and indicated that the genotypes possessed inherent genetic differences. The values of PCV for all the traits were found to be more than GCV and very small difference was present in between GCV and PCV revealing little influence of environment for their expression. High heritability accompanied with high genetic advance was observed for the traits thousand grain weight (g), head rice recovery (%), spikelet fertility (%), harvest index (%), number of spikelets/panicle, fertile

spikelets/panicle, spikelet density, grain yield /plant (g), panicle weight/plant (g), number of tillers/plant and number of productive tillers/plant. It indicates that the heritability is most likely due to additive gene effect and direct selection for these traits may be effective. Based on the results from correlation and path coefficient analysis, it is concluded that number of tillers/plant, spikelet fertility and panicle weight/plant showed positive correlation with grain yield and at same time exhibited high positive direct effect towards yield. Therefore, they seem to be primary yield contributing character and thus can be used as direct selection to improve genetic yield potential of rice.

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How to cite this article:

Shivangi Rahangdale, Yogendra Singh, G.K. Koutu and Tiwari, S. 2019. Genetic Variability, Correlation and Path Coefficient Studied for Yield and Quality Traits in JNPT Lines of Rice (*Oryza sativa* L.). *Int.J.Curr.Microbiol.App.Sci.* 8(10): 1025-1037.

doi: <https://doi.org/10.20546/ijcmas.2019.810.120>