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## Study of genetic variability using correlation and heritability in F<sub>2</sub> populations of rice

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### Abstract

Rice (*Oryza sativa* L.) is one of the most consumed cereal grain in the world constituting the dietary staple food for more than half of the human population. More than 90% of the world's rice is grown and consumed in Asia. The investigation was carried out with 200 lines of F<sub>2</sub> segregating generation of Rice in RCBD design with three replications in *kharif* 2016. The analysis of variation revealed significant differences in the genotypes for all the characters studied. High heritability was observed in panicle weight/plant followed by thousand grain weight, spikelet density, days to flowering, days to maturity, flag leaf width and thousand grain weight showed maximum genetic advance as percentage of mean followed by stem thickness, flag leaf length, grain yield/plant, spikelet density, number of productive panicles/plant, number of tillers/plant, number of productive tillers/plant, panicle weight/plant, fertile spikelets/plant, stem length, number of spikelets/plants, biological yield. Correlation studies revealed positive and significant association of grain yield/plant with panicle weight/plant followed by panicle index, biological yield/plant, number of tillers/plant, number of productive tillers/plant, number of panicles/plant, harvest index, fertile spikelets/panicle, panicle length, grain breadth, spikelet fertility, flag leaf width, stem length, amylose content. While, it showed negative and significant with days to 50% flowering, thousand grain weight and decorticated grain breadth.

**Keywords:** Correlation, heritability, quantitative traits, genetic advance

### 1. Introduction

Success of any breeding programme depends on the magnitude of genetic variability present in the population. 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) [7]. The genetic advance for the studied traits is dependent on the extent of genetic variability, heritability and selection intensity (Allard, 1960) [3]. Correlation studies provide better understanding of yield components. Keeping all these in view, an attempt was, therefore, made to have some information on extent of genetic variation, nature of association between yield and its component traits in rice crop. To achieve genetic improvement in yield traits, it is imperative to generate information on variability, its heritable proportion and also interrelationships existing there in the breeding material handled. The F<sub>2</sub> generation is critical for success of the breeding programme, as there are remote chances of recovering superior recombinants in advanced generations, if proper selection is not exercised to spot out useful segregants in F<sub>2</sub>. The present investigation was undertaken with 25 F<sub>2</sub> populations to study various genetic parameters.

### 2. Material and method

The experiment was carried out at Seed Breeding Farm under Rice Improvement Project, Department of Genetics and Plant Breeding, College of Agriculture, J.N.K.V.V., Jabalpur (M.P.). The experimental material consists 8 lines each of 25 crosses a total of 200 lines derived from Indica × Japonica subspecies of F<sub>2</sub> generation, developed by Rice Improvement Project, JNKVV, Jabalpur. These lines were planted in Randomized Complete Block Design with three replications. A detail of these lines is given in table 1

**Table 1:** List of lines used in study

S.N.	Lines	S.N.	Lines	S.N.	Lines
1.	NPT 13-01 × CANP 318 -1	64.	Danteswari × NPT 14-8 -8	127.	IR 64 × NPT(S) 6-2 -7
2.	NPT 13-01 × CANP 318 -2	65.	Danteswari × WGL 32100 -1	128.	IR 64 × NPT(S) 6-2 -8
3.	NPT 13-01 × CANP 318 -3	66.	Danteswari × WGL 32100 -2	129.	IR 64 × MTU 1081 -1
4.	NPT 13-01 × CANP 318 -4	67.	Danteswari × WGL 32100 -3	130.	IR 64 × MTU 1081 -2
5.	NPT 13-01 × CANP 318 -5	68.	Danteswari × WGL 32100 -4	131.	IR 64 × MTU 1081 -3
6.	NPT 13-01 × CANP 318 -6	69.	Danteswari × WGL 32100 -5	132.	IR 64 × MTU 1081 -4
7.	NPT 13-01 × CANP 318 -7	70.	Danteswari × WGL 32100 -6	133.	IR 64 × MTU 1081 -5
8.	NPT 13-01 × CANP 318 -8	71.	Danteswari × WGL 32100 -7	134.	IR 64 × MTU 1081 -6
9.	NPT 13-01 × CANP 58 -1	72.	Danteswari × WGL 32100 -8	135.	IR 64 × MTU 1081 -7
10.	NPT 13-01 × CANP 58 -2	73.	Danteswari × CANP 549 -1	136.	IR 64 × MTU 1081 -8
11.	NPT 13-01 × CANP 58 -3	74.	Danteswari × CANP 549 -2	137.	IR 64 × WGL 32100 -1
12.	NPT 13-01 × CANP 58 -4	75.	Danteswari × CANP 549 -3	138.	IR 64 × WGL 32100 -2
13.	NPT 13-01 × CANP 58 -5	76.	Danteswari × CANP 549 -4	139.	IR 64 × WGL 32100 -3
14.	NPT 13-01 × CANP 58 -6	77.	Danteswari × CANP 549 -5	140.	IR 64 × WGL 32100 -4
15.	NPT 13-01 × CANP 58 -7	78.	Danteswari × CANP 549 -6	141.	IR 64 × WGL 32100 -5
16.	NPT 13-01 × CANP 58 -8	79.	Danteswari × CANP 549 -7	142.	IR 64 × WGL 32100 -6
17.	MTU 1010 × Menka -1	80.	Danteswari × CANP 549 -8	143.	IR 64 × WGL 32100 -7
18.	MTU 1010 × Menka -2	81.	Danteswari × CANP 535 -1	144.	IR 64 × WGL 32100 -8
19.	MTU 1010 × Menka -3	82.	Danteswari × CANP 535 -2	145.	IR 64 × NPT 14-6 -1
20.	MTU 1010 × Menka -4	83.	Danteswari × CANP 535 -3	146.	IR 64 × NPT 14-6 -2
21.	MTU 1010 × Menka -5	84.	Danteswari × CANP 535 -4	147.	IR 64 × NPT 14-6 -3
22.	MTU 1010 × Menka -6	85.	Danteswari × CANP 535 -5	148.	IR 64 × NPT 14-6 -4
23.	MTU 1010 × Menka -7	86.	Danteswari × CANP 535 -6	149.	IR 64 × NPT 14-6 -5
24.	MTU 1010 × Menka -8	87.	Danteswari × CANP 535 -7	150.	IR 64 × NPT 14-6 -6
25.	MTU 1010 × CANP 554 -1	88.	Danteswari × CANP 535 -8	151.	IR 64 × NPT 14-6 -7
26.	MTU 1010 × CANP 554 -2	89.	IR64 × 25 A ×NPT 70 -1	152.	IR 64 × NPT 14-6 -8
27.	MTU 1010 × CANP 554 -3	90.	IR64 × 25 A ×NPT 70 -2	153.	IR 64 × CANP 554 -1
28.	MTU 1010 × CANP 554 -4	91.	IR64 × 25 A ×NPT 70 -3	154.	IR 64 × CANP 554 -2
28.	MTU 1010 × CANP 554 -5	92.	IR64 × 25 A ×NPT 70 -4	155.	IR 64 × CANP 554 -3
30.	MTU 1010 × CANP 554 -6	93.	IR64 × 25 A ×NPT 70 -5	156.	IR 64 × CANP 554 -4
31.	MTU 1010 × CANP 554 -7	94.	IR64 × 25 A ×NPT 70 -6	157.	IR 64 × CANP 554 -5
32.	MTU 1010 × CANP 554 -8	95.	IR64 × 25 A ×NPT 70 -7	158.	IR 64 × CANP 554 -6
33.	MTU-1010 × CANP 551 -1	96.	IR64 × 25 A ×NPT 70 -8	159.	IR 64 × CANP 554 -7
34.	MTU-1010 × CANP 551 -2	97.	IR 64 × SPS 71 × IR 42342 -1	160.	IR 64 × CANP 554 -8
35.	MTU-1010 × CANP 551 -3	98.	IR 64 × SPS 71 × IR 42342 -2	161.	IR 64 × CANP 535 -1
36.	MTU-1010 × CANP 551 -4	99.	IR 64 × SPS 71 × IR 42342 -3	162.	IR 64 × CANP 535 -2
37.	MTU-1010 × CANP 551 -5	100.	IR 64 × SPS 71 × IR 42342 -4	163.	IR 64 × CANP 535 -3
38.	MTU-1010 × CANP 551 -6	101.	IR 64 × SPS 71 × IR 42342 -5	164.	IR 64 × CANP 535 -4
39.	MTU-1010 × CANP 551 -7	102.	IR 64 × SPS 71 × IR 42342 -6	165.	IR 64 × CANP 535 -5
40.	MTU-1010 × CANP 551 -8	103.	IR 64 × SPS 71 × IR 42342 -7	166.	IR 64 × CANP 535 -6
41.	JR 201 × CANP 212 -1	104.	IR 64 × SPS 71 × IR 42342 -8	167.	IR 64 × CANP 535 -7
42.	JR 201 × CANP 212 -2	105.	IR 64 × NPT 40-01 × Pusa Basmati -1	168.	IR 64 × CANP 535 -8
43.	JR 201 × CANP 212 -3	106.	IR 64 × NPT 40-01 × Pusa Basmati -2	169.	IR 64 × CANP 521 -1
44.	JR 201 × CANP 212 -4	107.	IR 64 × NPT 40-01 × Pusa Basmati -3	170.	IR 64 × CANP 521 -2
45.	JR 201 × CANP 212 -5	108.	IR 64 × NPT 40-01 × Pusa Basmati -4	171.	IR 64 × CANP 521 -3
46.	JR 201 × CANP 212 -6	109.	IR 64 × NPT 40-01 × Pusa Basmati -5	172.	IR 64 × CANP 521 -4
47.	JR 201 × CANP 212 -7	110.	IR 64 × NPT 40-01 × Pusa Basmati -6	173.	IR 64 × CANP 521 -5
48.	JR 201 × CANP 212 -8	111.	IR 64 × NPT 40-01 × Pusa Basmati -7	174.	IR 64 × CANP 521 -6
49.	Danteswari × NPT(s) 6-2 -1	112.	IR 64 × NPT 40-01 × Pusa Basmati -8	188.	IR 64 × CANP 440 -4
50.	Danteswari × NPT(s) 6-2 -2	113.	IR 64 × NPT 40-01 -1	189.	IR 64 × CANP 440 -5
51.	Danteswari × NPT(s) 6-2 -3	114.	IR 64 × NPT 40-01 -2	190.	IR 64 × CANP 440 -6
52.	Danteswari × NPT(s) 6-2 -4	115.	IR 64 × NPT 40-01 -3	191.	IR 64 × CANP 440 -7
53.	Danteswari × NPT(s) 6-2 -5	116.	IR 64 × NPT 40-01 -4	192.	IR 64 × CANP 440 -8
54.	Danteswari × NPT(s) 6-2 -6	117.	IR 64 × NPT 40-01 -5	193.	IR 64 × CANP 212 -1
55.	Danteswari × NPT(s) 6-2 -7	118.	IR 64 × NPT 40-01 -6	194.	IR 64 × CANP 212 -2
56.	Danteswari × NPT(s) 6-2 -8	119.	IR 64 × NPT 40-01 -7	195.	IR 64 × CANP 212 -3
57.	Danteswari × NPT 14-8 -1	120.	IR 64 × NPT 40-01 -8	196.	IR 64 × CANP 212 -4
58.	Danteswari × NPT 14-8 -2	121.	IR 64 × NPT(S) 6-2 -1	197.	IR 64 × CANP 212 -5
59.	Danteswari × NPT 14-8 -3	122.	IR 64 × NPT(S) 6-2 -2	198.	IR 64 × CANP 212 -6
60.	Danteswari × NPT 14-8 -4	123.	IR 64 × NPT(S) 6-2 -3	199.	IR 64 × CANP 212 -7
61.	Danteswari × NPT 14-8 -5	124.	IR 64 × NPT(S) 6-2 -4	200.	IR 64 × CANP 212 -8
62.	Danteswari × NPT 14-8 -6	125.	IR 64 × NPT(S) 6-2 -5		
63.	Danteswari × NPT 14-8 -7	126.	IR 64 × NPT(S) 6-2 -6		

Observation were recorded on 24 quantitative and 8 quality traits. The mean data were subjected to standard statistical

technique for which heritability was calculated in broad sense by adopting the formula as suggested by Hanson *et al.* (1956)

[6] and correlation coefficients were calculated for all quantitative characters combinations at phenotypic, genotypic and environmental level by the formula given by Miller *et al.* (1958) [8].

### 3. Result and discussion

Heritability measures the contribution of genetic variability to the phenotypic variability observed for quantitative traits and it is good index for the transmission of characters from parents to their offspring. Genetic advance (GA) is the

improvement in the mean genotypic value of selected individual over the parental population. It is the measure of genetic gain under selection. Thus, estimates of  $h^2$  and GA are the important for predicting gains from selection.

In the study high heritability with high genetic advance were found for the character decorticated grain length, length breadth ratio, decorticated grain breadth, flag leaf length, flag leaf width, thousand grain weight, plant height, stem length and amylose content. The heritability estimates along with genetic advance in present study were categorized in table 2

**Table 2:** Estimate of heritability along with genetic advance for different traits.

Characteristics	Traits
High Heritability with High Genetic Advance	Decorticated grain length, length breadth ratio, decorticated grain breadth, flag leaf length, flag leaf width, thousand grain weight, amylose content, plant height, stem length.
High Heritability with Moderate Genetic Advance	Days to fifty percent flowering, days to maturity.
Moderate Heritability with High Genetic Advance	Stem thickness, stem density, number of spikelets/panicle.
Moderate Heritability with Low Genetic Advance	Panicle length
Low Heritability with High Genetic Advance	Number productive panicles/plant, fertile spikelets/panicle, number of productive tillers/plant, number of tillers/plant, biological yield/plant, grain yield/plant.
Low Heritability with Moderate Genetic Advance	Grain breadth, grain length.
Low Heritability with Low Genetic Advance	Spikelet fertility, panicle index, harvest index.

The result revealed higher estimate of phenotypic correlation coefficient than genotypic correlation coefficient for almost all the characters studied. Correlation studies revealed positive and significant association of grain yield/plant with panicle weight/plant followed by panicle index, biological yield/plant, number of tillers/plant, number of productive tillers/plant, number of panicles/plant, harvest index, fertile spikelets/panicle, panicle length, grain breadth, spikelet fertility, flag leaf width, stem length, amylose content. While, it showed negative and significant with days to 50% flowering, thousand grain weight and decorticated grain breadth. This finding for high heritability along with high genetic advance confirms in earlier studies of Saxena *et al.* (2005) [10], Narinder (2006), Bhagat (2007) [5] and Abdul Fiyaz

*et al.* (2011) [11] and Patil and Sarawgi (2005) [9]. Plant height recorded as high heritability coupled with high genetic advance. This result was in agreement with the findings of Patil and Sarawgi (2005) [9] and Anis *et al.* (2016) [4]. Correlation of flag leaf width with grain yield/plant was positive and significant. This result was in confirmation with the reports of Shrivastava *et al.* (2014) [11], Kumar *et al.* (2014) [12], Sohgaura *et al.* (2014) [12]. Grain yield per plant was correlated significantly and positively with panicle length. The result was in agreement as reported by Khan *et al.* (2009) [7], Basavaraja *et al.* (2011). Phenotypic and genotypic correlations for various yield and quality attributing traits were estimated and presented in table3.

**Table 3a:** Estimates of phenotypic correlation coefficient for various yield and attributing traits

Char.	DFP	DM	NTPP	NPTPP	PH	SL	FLL	FLW	PL
DFP	1.0000	0.7590**	-0.2171**	-0.2363**	-0.0357	-0.0089	0.1529**	0.0743	-0.1712**
DM		1.0000	-0.0704	-0.0836*	-0.0638	-0.0301	0.2398***	0.1143**	-0.2195**
NTPP			1.0000	0.9822**	-0.0744	-0.0864*	-0.0794	0.0210	0.0540
NPTPP				1.0000	-0.0800	-0.0930*	-0.0859*	0.0083	0.0587
PH					1.0000	0.9877**	0.0319	-0.0369	0.3222**
SL						1.0000	0.0508	-0.0172	0.1701**
FLL							1.0000	-0.0667	-0.1062**
FLW								1.0000	-0.1284**
PL									1.0000
PWPP									
BYPP									
HI									
PI									
ST									
NSPP									
FSPP									
SF									
SD									
NPPP									
GL									
GB									
DGL									
DGB									
L/B									
TGW									
AC									
GYPP	-0.1013**	-0.0088	0.6780**	0.6645**	0.0595	0.0405*	-0.0256	0.0426*	0.1301*

\* Significant at 5% level, \*\* Significant at 1% level

**Table 3b:** Estimates of phenotypic correlation coefficient for various yield and attributing traits (continue)

Char.	PWPP	BYPP	HI	PI	ST	NSPP	FSPF	SF	SD
DFF	-0.1013*	-0.1093**	-0.0186	-0.1048*	0.4221**	0.1513**	0.0932*	-0.1017	0.2044**
DM	-0.0088	0.0039	-0.0074	0.0032	0.3673**	0.1846**	0.1299**	-0.0821	0.2635**
NTPP	0.6780**	0.6706**	0.2401**	0.5605**	-0.2038**	-0.0394	-0.0505	-0.0400	-0.0533
NPTPP	0.6645**	0.6569**	0.2389**	0.5607**	-0.2126**	-0.0226	-0.0333	-0.0370	-0.0392
PH	0.0595	0.2480**	-0.1825**	0.0649	0.1823**	-0.2009**	-0.2380**	-0.1172**	-0.2985**
SL	0.0405	0.2367**	-0.1995**	0.0430	0.2148**	-0.2165**	-0.2501**	-0.1116**	-0.2567**
FLL	-0.0256	-0.0758	0.0782	-0.0002	0.1453**	0.0736	0.0810*	-0.0210	0.1046*
FLW	0.0426	0.0666	0.0022	0.0406	0.0597	-0.1014*	-0.1395**	-0.1014*	-0.0433
PL	0.1301**	0.1296**	0.0575	0.1487**	-0.1519**	0.0450	0.0140	-0.0630	-0.3269**
PWPP	1.0000	0.8299**	0.5851**	0.8778**	-0.1005*	0.0830*	0.1042*	0.0470	0.0365
BYPP		1.0000	0.0875*	0.7341**	-0.0252	-0.0113	-0.0331	-0.0656	-0.0475
HI			1.0000	0.6130**	-0.1143**	0.1728**	0.2415**	0.1820**	0.1363**
PI				1.0000	-0.1193**	0.0921*	0.1250**	0.0780	0.0358
ST					1.0000	0.1628**	0.1128**	-0.0617	0.2161**
NSPP						1.0000	0.8668**	-0.0524	0.9246**
FSPF							1.0000	0.4308**	0.8093**
SF								1.0000	-0.0302
SD									1.0000
NPPP									
GL									
GB									
DGL									
DGB									
L/B									
TGW									
AC									
GYPP	1.0000**	0.8299**	0.5851**	0.8778**	-0.1005	0.0830	0.1042*	0.0470*	0.0365

\* Significant at 5% level, \*\* Significant at 1% level

**Table 3c:** Estimates of phenotypic correlation coefficient for various yield and quality attributing traits

Char.	NPPP	GL	GB	DGL	DGB	L/B	TGW	AC
DFF	-0.2329**	0.0301	0.3480**	-0.0118	0.0000	-0.0052	-0.0776	-0.0088
DM	-0.0808*	0.0418	0.2679**	0.0092	0.0501	-0.0237	-0.1017*	-0.0031
NTPP	0.9800**	-0.0245	0.0969*	-0.0537	-0.0154	-0.0366	-0.0475	-0.0723
NPTPP	0.9967**	-0.0352	0.0833*	-0.0501	0.0054	-0.0493	-0.0406	-0.0815*
PH	-0.0776	0.0509	0.0607	0.0387	-0.0017	0.0196	-0.0038	0.0476
SL	-0.0912*	0.0381	0.0412	0.0340	0.0055	0.0105	-0.0011	0.0421
FLL	-0.0899*	-0.0551	0.0755	0.0248	-0.0268	0.0277	0.0407	0.1658**
FLW	0.0070	-0.0123	0.0797	0.0454	-0.0107	0.0490	-0.1636**	0.1007*
PL	0.0632	0.0897*	0.1330**	0.0379	-0.0441	0.0599	-0.0174	0.0456
PWPP	0.6664**	-0.0315	0.0780	-0.0304	-0.0721	0.0137	-0.0521	0.0242
BYPP	0.6580**	-0.0315	0.0683	-0.0384	-0.0478	-0.0042	-0.0677	-0.0081
HI	0.2410**	-0.0312	0.0828*	-0.0068	-0.0467	0.0184	-0.0058	0.0692
PI	0.5627**	-0.0760	0.1677**	-0.0056	-0.0598	0.0250	-0.0678	0.0666
ST	-0.2132**	0.0372	0.0140	0.0510	0.0613	0.0029	-0.0893*	-0.0114
NSPP	-0.0210	0.0262	0.0081	0.0092	-0.0190	0.0166	-0.0094	0.0419
FSPF	-0.0261	-0.0072	-0.0448	0.0268	-0.0300	0.0411	0.0098	0.0229
SF	-0.0262	-0.0750	-0.0288	0.0265	-0.0167	0.0397	0.0246	-0.0514
SD	-0.0397	-0.0115	-0.0014	-0.0054	-0.0038	-0.0060	-0.0026	0.0198
NPPP	1.0000	-0.0364	0.0836*	-0.0455	0.0050	-0.0455	-0.0409	-0.0774
GL		1.0000	0.0984*	0.1359**	0.0332	0.0888*	0.0702	0.0170
GB			1.0000	0.0579	0.1539**	0.0116	-0.0231	0.1344**
DGL				1.0000	0.0401	0.7290**	0.0641	0.0020
DGB					1.0000	-0.6411**	-0.0016	-0.0103
L/B						1.0000	0.0362	0.0094
TGW							1.0000	0.0020
AC								1.0000
GYPP	0.6664**	-0.0315	0.0721*	-0.0304	-0.0721**	0.0137	-0.0521*	0.0242*

\* Significant at 5% level, \*\* Significant at 1% level

#### 4. Conclusion

High heritability was observed in panicle weight/plant followed by thousand grain weight, spikelet density, days to flowering, days to maturity. flag leaf width and thousand grain weight showed maximum genetic advance as percentage of mean followed by stem thickness, flag leaf length, gain

yield/plant, spikelet density, number of productive panicles/plant, number of tillers/plant, number of productive tillers/plant, panicle weight/plant, fertile spikelets/plant, stem length, number of spikelets/plants, biological yield. Correlation studies revealed positive and significant association of grain yield/plant with panicle weight/plant

followed by panicle index, biological yield/plant, number of tillers/plant, number of productive tillers/plant, number of panicles/plant, harvest index, fertile spikelets/panicle, panicle length, grain breadth, spikelet fertility, flag leaf width, stem length, amylose content. While, it showed negative and significant with days to 50% flowering, thousand grain weight and decorticated grain breadth.

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