Original Research Article

"VARIABILITY, CORRELATION AND PATH ANALYSIS FOR GRAIN YIELD CHARACTERS OF RICE (*Oryza sativa* L.) GENOTYPES"

ABSTRACT

Thirty- four accessions of rice (*Oryza sativa* L.) genotypes (26 Advanced breeding lines, 7 Dhan varieties and one check) were investigated out at the Field Experimentation Center, Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj during *Kharif*-2021 in Randomized Block Design with three replications to study variability, correlation and path analysis for yield contributing characters. NDR 359 rice variety was used as the check. The data was recorded for 13 quantitative traits using agro-morphological traits.The characters with high range estimates of GCV and PCV (Grain yield per hill), heritability (days to maturity) and genetic advance as percent mean (number of spikelets per panicle,) should be given top priority during selection. For character association, grain yield per hill showed highly positive significance with flag leaf length, number of spikelets per panicle, biological yield, harvest index, number of tillers per hill, biological yield. Days to 50% flowering, flag leaf width, number of panicle per hill, biological yield, harvest index showed positive direct effect at both genotypic and phenotypic level indicating their importance in breeding programme.

Key words: Rice, Advanced Breeding Lines (ABL's), Genetic variability, heritability, Genetic advance, Correlation, Path-coefficient analysis.

INTRODUCTION

Rice (*Oryza sativa* L.) is the principal food crop, feeds over half of the world population providing employment to millions of people with enormous societal impacts. Rice is the main source of food for approximately half of the world's population and hence, may be the most important plant on the earth (**Shimamoto, 1995; Goff, 1999**). Since it is a staple food crop, it accounts for about 48 percent of total food grain production in India. Hence, we must produce 40 percent more rice by 2025 to satisfy the growing demand without adversely affecting the resource base (**Khush, 2006**). Grain yield is a complex character, which depends on its main components *viz.*, number of effective tillers, panicle length, number of grains per panicle and 1000 grain weight.

Comment [A1]: Pages should be vertical

Comment [A2]: At the beginning of the abstract, describe in one line what was the problem when the experiment was performed

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The variability parameters such as coefficient of variation, heritability and genetic advance are used for devising suitable selection strategy for high yield in rice crop while making selection for high yielding genotypes, the choice of parents plays a vital role for successful breeding programme. Knowledge concerning heritability helps the plant breeders to predict the nature of the succeeding generation, to make an appropriate selection and to assess the magnitude of genetic improvement through selection (**Tuhina-Khatun *et al*. 2007**). Heritability along with genetic advance is considerate in estimating the genetic gain under selection than heritability estimates alone (**Karim *et al.* 2007**). Character association derived by correlation coefficient helps in evaluation of relative influence of various component characters on grain yield. Correlation coefficient measures the mutual relationship between various plant characters and determines the component characters on which selection can be based for genetic improvement in yield and quality. Path coefficient analysis picks out correlation into direct and indirect effects. In path analysis, the correlation coefficient between two traits is separated into the components which measure the direct and indirect effects (**Ahmadizadeh *et al.* 2011**). Path co-efficient analysis provides an exact picture of the relative importance of direct and indirect effects of each of the component character towards yield. To study the interrelationships between different yield attributing traits, the direct and indirect effects of different characters were worked out using path analysis.

Comment [A6]: The abstract is very short.
The problem is not well stated. The necessity of investigation and study in this field should be stated.
Old references should be deleted and new references should be replaced.
Refer to the results of other researchers.
At the end of the introduction, the purpose of this experiment should be stated clearly.

MATERIAL AND METHODS

34 diverse genotypes of rice aimed to develop high yielding from different geographical origin were transplanted in the Randomized block design with 3 replications conducted at the Experimental Farm of the Department of Genetics and Plant Breeding, Naini Agricultural Institute, Prayagraj, Uttar Pradesh during *Kharif*-2021. Twenty one days old seedlings were transplanted by adopting a spacing of 15cm between plants and 20cm between rows. Important precautions were taken to maintain uniform plant growth population in each treatment. All the observations were recorded and analysis done. Observations were recorded on randomly selected five plants for 13 quantitative traits *viz.*, days to 50% flowering, plant height (cm), number of tillers per hill, number of panicles per hill, panicle length (cm), flag leaf length (cm), flag leaf width (cm), number of spikelet's per panicle, days to maturity, biological yield per hill (g), harvest index, test weight and grain yield per hill (g). The data thus generated were subjected to statistical analysis for the objectives to assess the genetic variability, genetic diversity and to identify the high yielding lines besides divergent parents for future hybridization programme. Analysis for the characters were done by using **Singh and Chaudhary (1995)**. Correlation coefficient by **Falconer (1964)**and **Dewey and Lu (1959)** for path analysis.

Comment [A7]: Materials and methods should be presented comprehensively.
The soil test results should be presented in the table and mentioned in the text.
The characteristics of cultivars (origin, length of growth period, etc.) should be presented comprehensively (preferably in a table).
Agricultural management during the experiment should be explained comprehensively.
The method of measuring traits should be fully explained.
Introduce the statistical software used

RESULT AND DISCUSSION

Analysis of variance showed significant differences among the 34 genotypes which indicates the possibility to select promising lines from the existing germplasm. The presence of high amount of variability might be due to diverse source of materials taken as well as environmental influence affecting the phenotypes (**Marker *et al.* (2016).**

The mean data of 34 genotypes revealed that the genotypes SHUATS DHAN-6 (62.133 gm), SHUATS DHAN-2 (51.467 gm), SHUATS DHAN-3 (46.733 gm), SHUATS DHAN-7 (43 gm), ABLR-21 (42.07gms), were found to be superior in grain yield. The mean performance of grain yield was ranged from 16.68g to 62.13g. **(Lavanya *et al.* (2011), Jadav *et al.* (2011).**

The estimates GCV and PCV revealed that phenotypic coefficient of variance higher than genotypic coefficient of variance, which indicate presence of environment effects on expression on characters studied. High GCV is observed for grain yield per hill (30.7%) followed by number of spikelets per panicle (20.87%) and for 10 superior ones 10 superior genotypes, GCV found high in Starch (53.8%) followed by amylose content (38.78%). PCV (%) followed a similar pattern. It ranged from grain yield per hill (33.15%) to number of total tillers per hill (22.38%).In case of superior one, PCV ranged from starch (53.988%) to grain yield per hill (20.048%) (**Krishna *et al.* (2014),Harsh *et al.* (2015), Saha *et al.* (2019).**

Estimates of heritability in broad sense revealed that the highest heritability ranged from days to maturity (91.379), to Number of panicles per hill (75.109). For the best 10 superior genotypes, high heritability ranged from amylose (99.836) to grain yield per hill (63.433%) **Thirumeni *et al.* (2018), Kumar *et al.* (2020**).

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Genetic advance as percent mean estimates revealed maximum range from Number of spikelet's per panicle (111.928%) to Flag leaf width (0.313%) and for eight biochemical character, high GA ranged from number of spikelets per panicle (146.6%) to biological yield (39.91%) and low found ranged from panicle length (8.435%) to protein (0.153%) **Mian *et al.* (2016), Singh *et al.* (2017).**High Genetic Advance as percent mean were ranged from grain yield per hill (58.912) to flag leaf width (25.3%). Low genetic advance as percent mean was not observed. **Joshi *et al.* (2020), Prajapathi *et al.* (2011).**

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Correlation between grain yield and other traits showed the positive high significant genotypic and phenotypic correlation fornumber of spikelet per panicle (0.425**), biological yield (0.688**) and harvest index (0.668**) for 13 quantitative characters indicate that the characters are positively governed by additive gene action and useful improvement **Suresh *et al.* (2015), Ansari *et al.* (2017), Abida*et al.* (2020).**As the correlation coefficient is in sufficient to explain true relationship for an effective multiplication of the characters path coefficient was worked out.The results of path analysis showed that the traits which had positively direct effect were days to 50% flowering, flag leaf width, number of panicle per hill, panicle length, days to maturity, biological yield, harvest index at genotypic level. The traits likedays to 50% flowering, flag leaf width, number of panicle per hill, biological yield, harvest index at phenotypic level**Saxena *et al.* (2017)**, **Abida *et al.* (2020).**

Comment [A11]: The results and discussion are very weak.
Explain each attribute separately.
Mention scientific reasons for the obtained results be matched with the results of other researchers (new reference)
Reports of other people's tests should be provided

Table1.1:ANOVA for 13 quantitative characters of rice germplasm during *Kharif*- 2021

Sl.No.	Character	Mean sum of squares		
		Replication (Df=2)	Treatment (Df=33)	Error (Df=66)
1	Days to 50 flowering	2.330	122.572**	23.383
2	Plant height	22.5540	245.921**	9.185
3	Flag leaf length	1.6420	74.448**	6.886
4	Flag leaf width	0.0060	0.089**	0.006
5	Number of total tillers per hill	0.6740	16.764**	1.033
6	Number of panicles per hill	0.0420	13.565**	1.349
7	Panicle length	0.4570	20.523**	0.765
8	Number of spikelets per panicle	857.7970	10432.575**	431.019
9	Days to maturity	0.7110	174.179**	5.311
10	Biological yield	50.0950	751.28**	34.189
11	Harvest Index	22.0140	354.549**	21.427
12	Test weight	2.9620	75.186**	3.822
13	Grain yield per hill	8.9460	313.96**	15.819

Comment [A12]: Insert the coefficient of variation in the table

* and ** indicates significant at 5% and 1% level of significance, respectively

S.No.	Traits	GCV	PCV	h² (Broad Sense)	Genetic Advancement	Gen.Adv as % of Mean
1	Days to 50 flowering	6.442	8.417	58.574	9.065	10.156
2	Plant height	6.801	7.186	89.574	17.319	13.26
3	Flag leaf length	12	13.712	76.582	8.555	21.632
4	Flag leaf width	13.478	14.792	83.027	0.313	25.3
5	Number of total tillers per hill	20.458	22.383	83.544	4.312	38.521
6	Number of panicles per hill	18.553	21.408	75.109	3.603	33.123

Comment [A13]: These abbreviations are explained in the table below

7	Panicle length	9.27	9.794	89.597	5.004	18.076
8	Number of spikelets per panicle	28.362	30.14	88.552	111.928	54.98
9	Days to maturity	6.284	6.573	91.379	14.774	12.373
10	Biological yield	22.521	24.078	87.487	29.79	43.394
11	Harvest Index	22.258	24.311	83.824	19.874	41.98
12	Test weight	20.928	22.547	86.157	9.326	40.017
13	Grain yield per hill	30.79	33.15	86.268	19.074	58.912

Traits	**PH**	**FLL**	**FLW**	**NTTPH**	**NPPH**	**PL**	**NSPP**	**DM**	**BY**	**HI**	**TW**	**GYPH**
DFF-50	0.0569^{NS}	0.305*	0.294*	0.458**	0.551**	-0.0281^{NS}	-0.0879^{NS}	0.754**	0.293*	-0.285*	-0.1569^{NS}	0.0469^{NS}
PH	1.0000	0.1931^{NS}	0.331**	-0.0847^{NS}	-0.1807^{NS}	0.312*	0.200*	0.0248^{NS}	0.283*	0.0904^{NS}	0.1618^{NS}	0.248*
FLL		1.0000	0.1855^{NS}	0.231*	0.213*	0.381**	0.1587^{NS}	0.238*	0.394**	0.1323^{NS}	0.0099^{NS}	0.374**
FLW			1.0000	0.315*	0.1444^{NS}	0.1623^{NS}	0.369**	0.1038^{NS}	0.1687^{NS}	-0.0002^{NS}	-0.0783^{NS}	0.1108^{NS}
NTTPH				1.0000	0.907**	-0.1292^{NS}	-0.0202^{NS}	0.444**	0.284*	-0.0966^{NS}	-0.277*	0.1811^{NS}
NPPH					1.0000	-0.0741^{NS}	-0.0409^{NS}	0.544**	0.359**	-0.0351^{NS}	-0.207*	0.291*
PL						1.0000	0.14[illegible]	-0.161[illegible]	-0.0219	0.29[illegible]	0.0998	0.1813
NSPP							1.0000	-0.0599	0.420*	0.283*	[illegible]4**	[illegible]9**
DM								[illegible]000	[illegible]93*	[illegible]343**	[illegible]58*	[illegible]57^{NS}
BY									[illegible]000	[illegible]490^{NS}	[illegible]30*	[illegible]9**
HI										[illegible]000	[illegible]8**	[illegible]2**
TW											[illegible]00	[illegible]131

	PH	**FLL**	**FLW**	**NTTPH**	**NPPH**	**PL**	**NSPP**	**DM**	**BY**	**HI**	**TW**	**GYPH**
DFF-50	0.0358^{NS}	0.213*	0.1700^{NS}	0.331**	0.380**	-0.0328^{NS}	-0.0804^{NS}	0.750**	0.1917^{NS}	-0.1620^{NS}	-0.1031^{NS}	0.0503^{NS}
PH	1.0000	0.1827^{NS}	0.326**	-0.0659^{NS}	-0.1342^{NS}	0.306*	0.1892^{NS}	0.0144^{NS}	0.246*	0.0694^{NS}	0.1512^{NS}	0.214*
FLL		1.0000	0.1921^{NS}	0.1937^{NS}	0.1814^{NS}	0.344**	0.1457^{NS}	0.1927^{NS}	0.355**	0.0986^{NS}	0.0399^{NS}	0.320*
FLW			1.0000	0.277*	0.1295^{NS}	0.1578^{NS}	0.338**	0.0724^{NS}	0.1614^{NS}	0.0007^{NS}	-0.0487^{NS}	0.1120^{NS}
NTTPH				1.0000	0.901**	-0.0735^{NS}	-0.0185^{NS}	0.385**	0.262*	-0.0783^{NS}	-0.237*	0.1696^{NS}
NPPH					1.0000	-0.0303^{NS}	-0.0368^{NS}	0.448**	0.317*	-0.0427^{NS}	-0.1728^{NS}	0.242*
PL						1.0000	0.1259^{NS}	-0.1288^{NS}	0.0248^{NS}	0.246*	0.1213^{NS}	0.1855^{NS}
NSPP							1.0000	-0.0475^{NS}	0.363**	0.273*	-0.311*	0.425**
DM								1.0000	0.270*	-0.319*	-0.225*	-0.0106^{NS}
BY									1.0000	-0.0655^{NS}	-0.1721^{NS}	0.688**
HI										1.0000	0.348**	0.668**
TW											1.0000	0.1174^{NS}

Comment [A14]: All abbreviations are explained in the table below

To measure correlation, it is better to enter the average of the data in the software and then calculate the correlation. In the present table, numbers less than 0.45 are significant, which is not correct. Edit based on new results and modify in the text

Traits	**DFF-50**	**PH**	**FLL**	**FLW**	**NTTPH**	**NPPH**	**PL**	**NSPP**	**DM**	**BY**	**HI**	**TW**	**GYPH**
DFF-50	**0.0104**	0.0006	0.0032	0.0031	0.0048	0.0058	-0.0003	-0.0009	0.0111	0.0031	-0.0030	-0.0016	0.0469
PH	-0.0007	**-0.0130**	-0.0025	-0.0043	0.0011	0.0023	-0.0041	-0.0026	-0.0003	-0.0037	-0.0012	-0.0021	0.248*
FLL	-0.0086	-0.0055	**-0.0283**	-0.0052	-0.0065	-0.0060	-0.0108	-0.0045	-0.0067	-0.0111	-0.0037	-0.0003	0.374**
FLW	0.0013	0.0014	0.0008	**0.0043**	0.0014	0.0006	0.0007	0.0016	0.0004	0.0007	0.0000	-0.0003	0.1108
NTTPH	-0.0042	0.0008	-0.0021	-0.0029	**-0.0091**	-0.0083	0.0012	0.0002	-0.0040	-0.0026	0.0009	0.0025	0.1811
NPPH	0.0218	-0.0071	0.0084	0.0057	0.0359	**0.0396**	-0.0029	-0.0016	0.0215	0.0142	-0.0014	-0.0082	0.291*
PL	-0.0004	0.0042	0.0051	0.0022	-0.0017	-0.0010	**0.0134**	0.0020	-0.0022	-0.0003	0.0039	0.0013	0.1813
NSPP	0.0055	-0.0124	-0.0098	-0.0229	0.0013	0.0025	-0.0091	**-0.0620**	0.0037	-0.0261	-0.0176	0.0219	0.469**
DM	0.0036	0.0001	0.0008	0.0004	0.0015	0.0019	-0.0005	-0.0002	**0.0034**	0.0010	-0.0012	-0.0009	0.0057
BY	0.2237	0.2160	0.3014	0.1290	0.2172	0.2748	-0.0167	0.3215	0.2243	**0.7646**	-0.0375	-0.1761	0.709**
HI	-0.2089	0.0662	0.0968	-0.0002	-0.0707	-0.0257	0.2126	0.2074	-0.2512	-0.0359	**0.7319**	0.2987	0.662**
TW	0.0034	-0.0035	-0.0002	0.0017	0.0060	0.0045	-0.0022	0.0077	0.0056	0.0050	-0.0089	**-0.0218**	0.1131

GYPH	0.0469	0.248*	0.374**	0.1108	0.1811	0.291*	0.1813	0.469**	0.0057	0.709**	0.662**	0.1131	**1.0000**

Traits	**DFF-50**	**PH**	**FLL**	**FLW**	**NTTPH**	**NPPH**	**PL**	**NSPP**	**DM**	**BY**	**HI**	**TW**	**GYPH**
DFF-50	0.0172	0.0006	0.0037	0.0029	0.0057	0.0065	-0.0006	-0.0014	0.0129	0.0033	-0.0028	-0.0018	0.0503
PH	0.0000	-0.0013	-0.0002	-0.0004	0.0001	0.0002	-0.0004	-0.0003	0.0000	-0.0003	-0.0001	-0.0002	0.214*
FLL	-0.0034	-0.0029	-0.0161	-0.0031	-0.0031	-0.0029	-0.0055	-0.0023	-0.0031	-0.0057	-0.0016	-0.0006	0.320*
FLW	0.0016	0.0031	0.0019	0.0096	0.0027	0.0012	0.0015	0.0033	0.0007	0.0016	0.0000	-0.0005	0.1120
NTTPH	-0.0074	0.0015	-0.0043	-0.0062	-0.0224	-0.0201	0.0016	0.0004	-0.0086	-0.0059	0.0017	0.0053	0.1696
NPPH	0.0191	-0.0068	0.0091	0.0065	0.0453	0.0503	-0.0015	-0.0019	0.0225	0.0159	-0.0021	-0.0087	0.242*
PL	0.0001	-0.0007	-0.0008	-0.0004	0.0002	0.0001	-0.0024	-0.0003	0.0003	-0.0001	-0.0006	-0.0003	0.1855
NSPP	0.0044	-0.0104	-0.0080	-0.0185	0.0010	0.0020	-0.0069	-0.0547	0.0026	-0.0199	-0.0150	0.0170	0.425**
DM	-0.0065	-0.0001	-0.0017	-0.0006	-0.0033	-0.0038	0.0011	0.0004	-0.0086	-0.0023	0.0027	0.0019	-0.0106
BY	0.1430	0.1833	0.2645	0.1205	0.1957	0.2361	0.0185	0.2710	0.2017	0.7462	-0.0489	-0.1284	0.688**
HI	-0.1203	0.0515	0.0732	0.0005	-0.0581	-0.0317	0.1830	0.2031	-0.2366	-0.0487	0.7428	0.2584	0.668**
TW	0.0025	-0.0037	-0.0010	0.0012	0.0058	0.0043	-0.0030	0.0077	0.0055	0.0042	-0.0086	-0.0247	0.1174
GYPH	0.0503	0.214*	0.320*	0.1120	0.1696	0.242*	0.1855	0.425**	-0.0106	0.688**	0.668**	0.1174	1.0000

CONCLUSION

The above criteria of plant type may be considered at the initial stage for selecting the desired genotypes, in which number of spikelet per panicle, biological yield, harvest index and yield can form the basis of selection criteria. These characters were highly significant and put forwarded for further processs. Direct effect and indirect effect on yield is estimated on the basis of path analysis.

Comment [A15]: be rewritten

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