Original Research Article

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

ABSTRACT

The present investigation with thirty-four accessions of rice (*Oryza sativa* L.) genotypes (26 Advanced breeding lines (ABL's),7 Dhan varieties and one check) were investigated to study variability, correlation and path analysis for yield contributing characters carried out at the Field Experimentation Centre, 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. NDR 359 rice variety was used as the check. The data was recorded for 13 quantitative traits *viz* Days to 50% flowering, Plant height (cm), Flag leaf length (cm), Flag leaf width (cm), Number of total tillers per hill, Number of panicles per hill, Panicle length (cm), Number of spikelets per panicle, Days to maturity, Biological index, Harvest index (%), Test weight (g), Grain yield per hill (g) using agro-morphological traits. The mean sum of squares due to genotypes was highly significant for all the quantitative characters in ANOVA. 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 positive significance with flag leaf length, number of spikelets per panicle, biological yield, harvest index, number of tillers per hill, biological yield because it help in determining the nature and extent of the relationship existing between the yield and its contributing components and their association.Path analysis further proved about the direct and indirect effect of characters on grain yield. Days to 50% flowering, flag leaf width, number of panicles per hill, biological yield, harvest index showed positive direct effect at both genotypic and phenotypic level indicating their importance in breeding programme. So direct selection of the above characters will be rewarding.

Key words: Advanced Breeding Lines (ABL's), Genotypic, Phenotypic, Character association, Path coefficient.

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. The genus *Oryza* contains 24 recognized species, of which two are distinct types of domesticated rice, *Oryza* *sativa* or Asian rice and *Oryza glaberrima* or African rice are cultivated. The genus *Oryza* contains 22 wild relatives of the domesticated rice. The genus is divided into four species complexes: The *O. sativa, O. officialis, O. ridelyi* and *O. granulate* species complexes. More than 90% of the world rice is grown and consumed in Asia, known as rice bowl of the world, where 60% of the earth's people and two third of world's poor live. For meeting the dietary requirements of increasing population, genetic improvement of rice with higher yield, good grain quality, resistance to biotic and abiotic stresses is the most logical and promising approach **(Palaniyappan *et al.*2020).** Since it is a staple food crop, it accounts for about 48 percent of total food grain production in India.

Global production of milled rice was 507.24 million metric tonnes during 2020-2021. According to the most recent official data, with a production volume of over 211 million metric tons in 2020, China was the world's leading paddy rice producer, followed by India and Bangladesh **(Stastista, 2020**). The Indian population will reach 1.53 billion by 2030 AD and hence to feed these extra mouths, the rice production has to be increased by at least 70 per cent in next three decades to meet out the growing demand.

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. 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. Heritability helps indicating that selection will be effective based on these traits because they were under the influence of additive and additive x additive type of gene action (**Kumar *et al.* 2017).**

Simultaneously, understanding the relationship between yield and its components is of paramount importance for making the best use of these relationships in selection. 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. Path analysis indicated that characters exhibited positive direct effects on grain yield at both genotypic and phenotypic level (**Parimala *et al.* 2019).** The characters exhibiting high direct effects for grain yield also exhibited high degree of positive correlation with grain yield. 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. The genotypic path analysis shows that the characters have positive direct effect which could be considered as good selection criteria for yield improvement. (**Jeyaprakash*et al.* 2020**).

OBJECTIVES

1. To estimate the genetic variability parameters, heritability and genetic advance for various quantitative characters in ABL’s
2. To study the association, direct and indirect effects of yield attributing traits, quality traits on yield in ABL’s
3. To study the nature of character associations of yield and yield attributing traits by means of correlation coefficientsand to assess the direct and indirect contribution of yield components on grain yield through path-coefficient analysis

MATERIAL AND METHODS

This study was conducted using 34 diverse genotypes of advanced breeding lines of rice during Kharif 2021 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. This Southern part of Uttar Pradesh is very fertile due to annual low level floods in the Ganges. Prayagraj is located in the South-East part of Uttar Pradesh, India. The site of experiment located at 25.57^0 N latitude, 81.51^0E longitude and 98 meter above the sea level. The nursery was sown 20^{TH} June, 2021 and twenty one days old seedlings were transplanted in the main field. Normal recommended cultural practices with spacing of (20X15) cm were followed for raising a good and healthy crop. 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 plants were selected from the middle rows, excluding border plants. The observation recorded as per the following procedure. Recording from five plants were averaged replication-wise and the mean data was used for statistical analysis for thirteen quantitative traits

The data thus generated were subjected to statistical analysis for the objectives to assess the genetic variability, genetic parameters, character association and path analysis 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. "R- Language software was used here to carry out analysis.

Table 1: List of Experimental materials (34 Rice genotypes)

S.NO.	NOTATION	S.NO.	NOTATION	S.NO.	NOTATION
1.	ABLR-1	14.	ABLR-14	27	SHUATS DHAN -01
2.	ABLR-2	15.	ABLR-15	28.	SHUATS DHAN -02
3.	ABLR-3	16.	ABLR-16	29.	SHUATS DHAN -03
4.	ABLR-4	17.	ABLR-17	30.	SHUATS DHAN -04
5.	ABLR-5	18.	ABLR-18	31.	SHUATS DHAN -05
6.	ABLR-6	19.	ABLR-19	32.	SHUATS DHAN -06
7.	ABLR-7	20.	ABLR-20	33.	SHUATS DHAN -07
8.	ABLR-8	21.	ABLR-21	34.	NDR 359 (Check)
9.	ABLR-9	22.	ABLR-22		
10.	ABLR-10	23.	ABLR-23		
11.	ABLR-11	24.	ABLR-24		
12.	ABLR-12	25.	ABLR-25		
13.	ABLR-13	26.	ABLR-26		

RESULT AND DISCUSSION

Analysis of variance for 13 quantitative characters showed significant differences 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).**

Anova for the characters is represented in Table 2.The mean sum of square due to genotypes was highly significant for all the quantitative characters (α=0.01).

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. A wide range of variation for all the traits revealed the mean values, coefficient of variation (C.V), Standard error of the mean (S.Em+), critical difference (C.D.) at 5% and 1%, for 13 quantitative characters represented in in table 3 and figure 1.

Table2: Analysis of variance for 13 quantitative characters of 34 rice germplasm during *Kharif*-2021

Character	Mean sum of squares		
	Replication	Treatment	Error
	2	33	66
Days to 50 flowering	2.330	122.572**	23.383
Plant height	22.5540	245.921**	9.185
Flag leaf length	1.6420	74.448**	6.886
Flag leaf width	0.0060	0.089**	0.006
Number of total tillers per hill	0.6740	16.764**	1.033
Number of panicles per hill	0.0420	13.565**	1.349
Panicle length	0.4570	20.523**	0.765
Number of spikelets per panicle	857.7970	10432.575**	431.019
Days to maturity	0.7110	174.179**	5.311
Biological yield	50.0950	751.28**	34.189
Harvest Index	22.0140	354.549**	21.427
Test weight	2.9620	75.186**	3.822
Grain yield per hill	8.9460	313.96**	15.819

****Significant at P<0.01, respectively**

Table 3: Genetic parameters for 13 quantitative characters of rice genotypes during *Kharif*– 2021

Traits	GCV	PCV	h^2 (Broad Sense)	Genetic Advancement	Gen.Adv as % of Mean
Days to 50 flowering	6.442	8.417	58.574	9.065	10.156
Plant height	6.801	7.186	89.574	17.319	13.26
Flag leaf length	12	13.712	76.582	8.555	21.632
Flag leaf width	13.478	14.792	83.027	0.313	25.3
Number of total tillers per hill	20.458	22.383	83.544	4.312	38.521
Number of panicles per hill	18.553	21.408	75.109	3.603	33.123
Panicle length	9.27	9.794	89.597	5.004	18.076
Number of spikelets per panicle	28.362	30.14	88.552	111.928	54.98
Days to maturity	6.284	6.573	91.379	14.774	12.373
Biological yield	22.521	24.078	87.487	29.79	43.394
Harvest Index	22.258	24.311	83.824	19.874	41.98
Test weight	20.928	22.547	86.157	9.326	40.017
Grain yield per hill	30.79	33.15	86.268	19.074	58.912

GCV: Genotypic coefficient of variation**, PCV:** Phenotypic coefficient of variation**, h^2:** Heritability**, Gen. Adv as% of Mean:** Genetic Advance at percent of mean

Figure 1: Comparison of GCV, PCV, Heritability and Genetic advance for 13 quantitative characters

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. Similar findings were found in **Lavanya *et al.* (2011), Jadav *et al.* (2011).**

High GCV is observed for grain yield per hill (30.7%) followed by number of spikelets per panicle (20.87%).PCV (%) followed a similar pattern. The phenotypic coefficient of variation was found higher in 13 quantitative characters for grain yield per hill (33.15%) followed by number of spikelets per panicle (30.14%), harvest index (24.31%), biological yield (24.31%), test weight (22.55%) and number of total tillers per hill (22.38%).**Harsh *et al.* (2015), Saha *et al.* (2019).**

Among these high heritable characters, the highest values (>60%) were recorded for the character days to maturity (91.379), panicle length (89.597), plant height (89.574), number of spikelets per panicle (88.552), biological yield (87.487), grain yield per hill (86.268), test weight (86.157), harvest index (83.824), number of total tillers per hill (83.544), flag leaf width (83.027), flag leaf length (76.582), number of panicles per hill (75.109).**Thirumeni *et al.* (2018), Kumar *et al.* (2020).**

The estimation of Genetic Advance was highest in number of spikelets per panicle (111.928%), biological yield (29.79%), harvest Index (19.874%), grain yield per hill (19.074%), plant height (17.319%) for 13 quantitative characters of 34 genotypes. **Mian *et al.* (2016), Singh *et al.* (2017).** High Genetic Advance as percent mean were observed for grain yield per hill (58.912%), number of Spikelet's per panicle (54.98%), biological yield (43.394%), harvest index (41.98%), test weight (40.017%), number of total tillers per hill (33.123%), flag leaf width (25.3%). **Joshi *et al.* (2020), Prajapathi *et al.* (2011).**

Grain yield per plant showed positive highly significant correlation with number of spikelets per panicle (rg = 0.469**, rp =0.425**), biological yield (rg = 0.709**, rp = 0.688**) and harvest index (rg = 0.662**,0.668**). The traits were plant height (rg = 0.248*, rp = 0.214*) and number of panicles per hill (rg =0.291*, rp = 0.242*) both at genotypic and phenotypic level. While days to 50% flowering (rg = 0.0469, rp = 0.0503), flag leaf width (rg = 0.1108, rp = 0.1120), number of total tillers per hill (rg = 0.1811, rp = 0.1696), panicle length (rg= 0.1813, rp = 0.1855), and test weight (rg = 0.1131, rp = 0.1174) showed non- significant positive relation with grain yield both at genotypic and phenotypic level (table 4).It indicates that the characters are positively governed by additive gene action and useful improvement **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. Only significant characters were put forwarded for path analysis.

The results of path analysis showed that the traits which had positively direct effect were days to 50% flowering (0.0104), flag leaf width (0.0043), number of panicle per hill (0.0396), panicle length (0.0134), days to maturity (0.0034), biological yield (0.7646), harvest index (0.7319) at genotypic level. While the traits like plant height (-0.0130), flag leaf length (-0.0283), number of total tillers per plant (-0.0091), number of spikelets per panicle (-0.0620), test weight (-0.0218) showed negative direct effect with grain yield. These traits were influencing grain yield with the help of other indirect traits.The traits likedays to 50% flowering (0.0172), flag leaf width (0.0096), number of panicle per hill (0.0503), biological yield (0.7462), harvest index (0.7428) showed positive direct effect at phenotypic level. Negative direct effects were showed by traits like plant height (-0.0013), flag leaf length (-0.0161), number of total tillers per plant (-0.0224), number of spikelets per panicle (-0.0547), test weight (-0.0218). **Saxena *et al.* (2017)**, **Abida *et al.* (2020).**

TRAITS		DF50	PH	FLL	FLW	NTTPH	NPPH	PL	NSPP	DM	BY	HI	TW	GYPH
DF50	P	1	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}
	G	1	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	P		1	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*
	G		1	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	P			1	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*
	G			1	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	P				1	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}
	G				1	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	P					1	0.901**	-0.0735^{NS}	-0.0185^{NS}	0.385**	0.262*	-0.0783^{NS}	-0.237*	0.1696^{NS}
	G					1	0.907**	-0.1292^{NS}	-0.0202^{NS}	0.444**	0.284*	-0.0966^{NS}	-0.277*	0.1811^{NS}
NPPH	P						1	-0.0303^{NS}	-0.0368^{NS}	0.448**	0.317*	-0.0427^{NS}	-0.1728^{NS}	0.242*
	G						1	-0.0741^{NS}	-0.0409^{NS}	0.544**	0.359**	-0.0351^{NS}	-0.207*	0.291*
PL	P							1	0.1259^{NS}	-0.1288^{NS}	0.0248^{NS}	0.246*	0.1213^{NS}	0.1855^{NS}
	G							1	0.1468^{NS}	-0.1611^{NS}	-0.0219^{NS}	0.291*	0.0998^{NS}	0.1813^{NS}
NSPP	P								1	-0.0475^{NS}	0.363**	0.273*	-0.311*	0.425**
	G								1	-0.0599^{NS}	0.420**	0.283*	-0.354**	0.469**
DM	P									1	0.270*	-0.319*	-0.225*	-0.0106^{NS}
	G									1	0.293*	-0.343**	-0.258*	0.0057^{NS}
BY	P										1	-0.0655^{NS}	-0.1721^{NS}	0.688**
	G										1	-0.0490^{NS}	-0.230*	0.709**
HI	P											1	0.348**	0.668**
	G											1	0.408**	0.662**
TW	P												1	0.1174^{NS}
	G												1	0.1131
GYP	P													1
	G													1

TRAITS		DFF-50	PH	FLL	FLW	NTTPH	NPPH	PL	NSPP	DM	BY	HI	TW
DFF-50	P	**0.0172**	0.0006	0.0037	0.0029	0.0057	0.0065	-0.0006	-0.0014	0.0129	0.0033	-0.0028	-0.0018
	G	**0.0104**	0.0006	0.0032	0.0031	0.0048	0.0058	-0.0003	-0.0009	0.0111	0.0031	-0.003	-0.0016
PH	P	0	**-0.0013**	-0.0002	-0.0004	0.0001	0.0002	-0.0004	-0.0003	0	-0.0003	-0.0001	-0.0002
	G	-0.0007	**-0.013**	-0.0025	-0.0043	0.0011	0.0023	-0.0041	-0.0026	-0.0003	-0.0037	-0.0012	-0.0021
FLL	P	-0.0034	-0.0029	**-0.0161**	-0.0031	-0.0031	-0.0029	-0.0055	-0.0023	-0.0031	-0.0057	-0.0016	-0.0006
	G	-0.0086	-0.0055	**-0.0283**	-0.0052	-0.0065	-0.006	-0.0108	-0.0045	-0.0067	-0.0111	-0.0037	-0.0003
FLW	P	0.0016	0.0031	0.0019	**0.0096**	0.0027	0.0012	0.0015	0.0033	0.0007	0.0016	0	-0.0005
	G	0.0013	0.0014	0.0008	**0.0043**	0.0014	0.0006	0.0007	0.0016	0.0004	0.0007	0	-0.0003
NTTPH	P	-0.0074	0.0015	-0.0043	-0.0062	**-0.0224**	-0.0201	0.0016	0.0004	-0.0086	-0.0059	0.0017	0.0053
	G	-0.0042	0.0008	-0.0021	-0.0029	**-0.0091**	-0.0083	0.0012	0.0002	-0.004	-0.0026	0.0009	0.0025
NPPH	P	0.0191	-0.0068	0.0091	0.0065	0.0453	**0.0503**	-0.0015	-0.0019	0.0225	0.0159	-0.0021	-0.0087
	G	0.0218	-0.0071	0.0084	0.0057	0.0359	**0.0396**	-0.0029	-0.0016	0.0215	0.0142	-0.0014	-0.0082
PL	P	0.0001	-0.0007	-0.0008	-0.0004	0.0002	0.0001	**-0.0024**	-0.0003	0.0003	-0.0001	-0.0006	-0.0003
	G	-0.0004	0.0042	0.0051	0.0022	-0.0017	-0.001	**0.0134**	0.002	-0.0022	-0.0003	0.0039	0.0013
NSPP	P	0.0044	-0.0104	-0.008	-0.0185	0.001	0.002	-0.0069	**-0.0547**	0.0026	-0.0199	-0.015	0.017
	G	0.0055	-0.0124	-0.0098	-0.0229	0.0013	0.0025	-0.0091	**-0.062**	0.0037	-0.0261	-0.0176	0.0219
DM	P	-0.0065	-0.0001	-0.0017	-0.0006	-0.0033	-0.0038	0.0011	0.0004	**-0.0086**	-0.0023	0.0027	0.0019
	G	0.0036	0.0001	0.0008	0.0004	0.0015	0.0019	-0.0005	-0.0002	**0.0034**	0.001	-0.0012	-0.0009
BY	P	0.143	0.1833	0.2645	0.1205	0.1957	0.2361	0.0185	0.271	0.2017	**0.7462**	-0.0489	-0.1284
	G	0.2237	0.216	0.3014	0.129	0.2172	0.2748	-0.0167	0.3215	0.2243	**0.7646**	-0.0375	-0.1761
HI	P	-0.1203	0.0515	0.0732	0.0005	-0.0581	-0.0317	0.183	0.2031	-0.2366	-0.0487	**0.7428**	0.2584
	G	-0.2089	0.0662	0.0968	-0.0002	-0.0707	-0.0257	0.2126	0.2074	-0.2512	-0.0359	**0.7319**	0.2987
TW	P	0.0025	-0.0037	-0.001	0.0012	0.0058	0.0043	-0.003	0.0077	0.0055	0.0042	-0.0086	**-0.0247**
	G	0.0034	-0.0035	-0.0002	0.0017	0.006	0.0045	-0.0022	0.0077	0.0056	0.005	-0.0089	**-0.0218**
GYP	P	0.0503	0.214*	0.320*	0.112	0.1696	0.242*	0.1855	0.425**	-0.0106	0.688**	0.668**	0.1174
	G	0.0469	0.248*	0.374**	0.1108	0.1811	0.291*	0.1813	0.469**	0.0057	0.709**	0.662**	0.1131

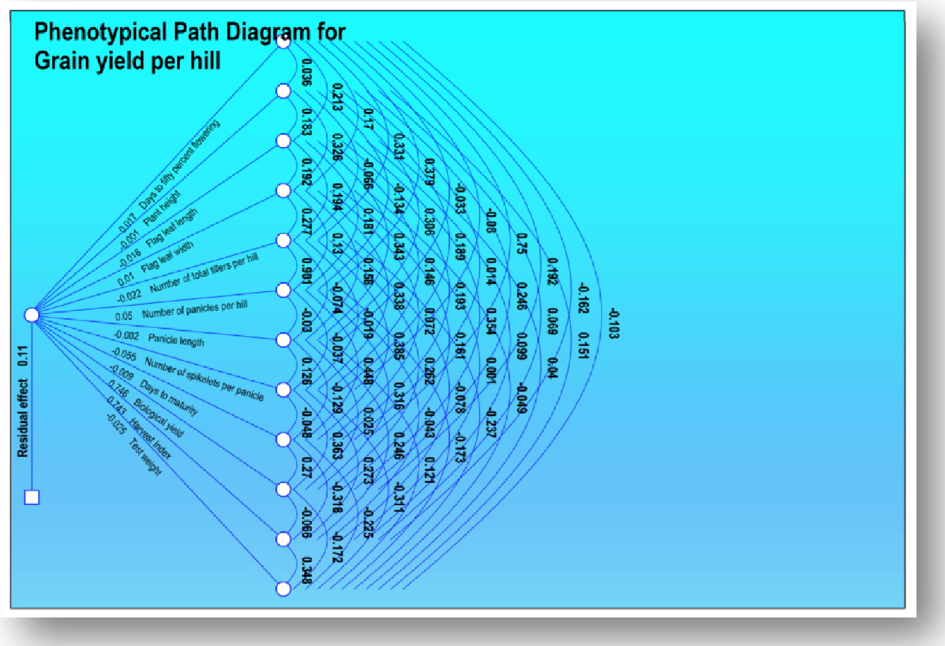

Figure-2: Genotypical Path Diagram

Figure-3: Phenotypical Path Diagram

CONCLUSION

The above criteria of plant type may be considered at the initial stage for selecting the desired genotypes. There were more variation among genotypes. From this investigation, it is concluded that Analysis of Variance showed significant variation to all the characters. Based on this investigation 34 genotypes were evaluated in terms of all genetic parameters. So genetic variability is the basic requirement for making progress in crop breeding. 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 in which number of spikelet per panicle, biological yield, harvest index, plant height, number of panicles per hill 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.

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