Direct and Indirect Effects of Yield Contributing Traits in Rice (*Oryza sativa* L.)

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Original Research Article

ABSTRACT

At the Field Experimentation Centre of the Department of Genetics and Plant Breeding, 20 rice genotypes, including one check variety, were assessed in order to research genetic variability, heritability, genetic progress, correlation, and path coefficient for 13 quantitative features. In Kharif 2022, the experiment was carried out utilising a Randomised Block Design with three replications. Over the NDR 359 (check), BRRI DHAN-75 (26.133) and A.K.DHAN (23.067) demonstrated a greater yield. Number of spikelets per hill, Number of panicles per hill, Biological yield, Number of tillers per hill, Grain yield per hill, Harvest index, Panicle length, Test weight, Days to maturity, and Plant height all had high to moderate estimations of GCV, PCV, and Genetic Advance as Percent Mean. Estimates of heritability ranging from high to moderate, genetic progress for the quantity of spikelets per panicle, biological yield, plant height, and days to 50% blooming. At both the

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phenotypic and genotypic levels, grain yield showed a strong positive connection with biological yield, the number of spikelets per panicle, and harvest index. Harvest index and biological yield showed both genotypic and phenotypic positive significant direct influences on grain yield per hill. Thus, in the current experimental materials, these qualities are recognised as the effective and prospective for indirect selection for the increase of rice yield.

1. INTRODUCTION

Rice is a self-pollinated cereal crop with chromosomal number 2n=24 that belongs to the family Gramineae (Poaceae), order Cyperales, and class Monocotyledon. There are 25 recognised species in the genus Oryza, including Oryza sativa and *Oryza glaberrima*, two cultivated species, and 23 wild species. The sticky, short-grained japonica variety and the nonsticky, long-grained indica rice variety are the two main subspecies of Oryza sativa. A third subspecies, which is broad-grained and thrives in tropical environments, was discovered based on morphology and was first dubbed javanica [1-3].

The small genome of rice (430 Mb) made it a model plant for studying cereal genetics. With an alarming increase in the population throughout the world, the demand for rice will continue to increase in near future; therefore, rice breeders across the world aim at increasing the grain yield in rice (Singh et al. 2007).

Rice is one of the most important food crops in the world, supporting 21% of the total calorie intake of the world population and up to 76% of that of Southeast Asia (Miura et al., 2011).

Genetic variability is the life blood of plant breeding. Genetic advance and exceleration of its relative potential depends on its genetic variation. The presence of a wide genetic variability in rice varieties is a pre- requisit in initiating successful breeding programme Partitioning of observed variability into heritable and non-heritable component by suitable genetic parameters such as genetic coefficient of variation, heritability estimates and genetic advance has been found useful and fruitful.

Heritability (h^2bs) is an index of transmissibility of the characters from the parents to offspring and has a predictive role in crop breeding programme.

Correlation studies helps in better understanding of yield components. Is the measure of the mutual relationship between two variables. The

study of correlations may help the plant breeder to know how the improvement of one character will bring simultaneous improvement in other characters. Path coefficient analysis is a standardized regression coefficient and measures the direct influence of one variable upon the other [4,5].

1.1 Objectives

1. To evaluate 20 rice genotypes for Genetic Variability of grain yield component characters
2. To estimate the association among grain yield characters
3. To study direct and indirect effects of yield contributing traits on grain yield

2. MATERIALS AND METHODS

The study, which was carried out in Kharif 2022 at the Field Experimentation Centre of the Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, U.P., included 20 genotypes of rice from various geographical origins that were transplanted in a Randomised block design with three replications. The crop was cared for in accordance with accepted agronomic principles. On June 21, 2021, the genotypes were sowed in raised beds. 20 × 15 cm is the recommended plant spacing from row to row and from plant to plant.13 quantitative features, such as days to 50% blooming, days to maturity, were noted in the field.Flag leaf dimensions (cm), flag leaf width (cm), plant height (cm), Number of tillers per hill, Number of panicles per hill, panicle length (cm).Test weight(g), Biological yield(g), Harvest Index(%), Grain yield per hill(g)

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance for Quantitative Characters in Rice (*Oryza sativa* L.)

All 13 yield characters had very significant genotype-level differences, which indicated that there was a sizable amount of variation among

the studied characters, according to the analysis of variance (Table 1). A sizable level of diversity in the original breeding material ensures the creation of acceptable recombinants for crop improvement. Among 20 Rice genotypes BRRI DHAN-75 (69.17 gm), DHAN-47 (56.02 gm), DHAN-55 (55.97 gm), BINADHAN-17 (54.41 gm) and A.K. DHAN (50.82 gm) were found to be superior in grain yield.

Variability is a measure by estimation of genotypic coefficient of variations (GCV), Phenotypic coefficient of variations (PCV), Heritability (h2) in the broad sense, Genetic advance and Genetic advance as a percentage of mean.

The characters studied in the present investigation exhibited low (less than 10%), moderate (10-20%), and high (more than 20%) phenotypic and genotypic coefficient of variation as proposed by Sivasubramaniam and Menon (1973).

High PCV estimates for grain yield per hill (31.312), biological yield (27.207), number of spikelets per panicle (25.142), number of panicles per hill (24.389), number of tillers per hill (21.309).High estimates of GCV were recorded Grain yield per hill (29.005), biological yield (25.313), number of spikelets per panicle (23.837), number of panicles per hill (22.923) [6,7].

3.2 Heritability

Heritability (in the broad sense) varied from 62.536 to 89.893 and was classified as low by

Johnson et al. (1955) (60%). The highest heritability (above 60%) was observed for number of spikelets per panicle (89.893), number of panicles per hill (88.34) ,biological yield (86.56), number of tillers per hill (86.446), grain yield per hill (85.807), harvest index (72.897), panicle length (71.839) , flag leaf length (64.799), flag leaf width (64.366), test weight (64.326), days to maturity (62.827), plant height (62.568) and days to 50% flowering (62.536). No values for low and medium heritability exist [8].

3.3 Genetic Advance as Percent Mean

The estimation of genetic advance as percent mean is classified to be low (20%) as proposed by Johnson et al., 1955.

Highest GAM was recorded for grain yield per hill (55.348), biological yield (48.514), number of spikelets per panicle (46.557), number of panicles for hill (44.384), number of tillers per hill (37.947) and harvest index (27.61). Moderate estimates of genetic advance as per cent mean was recorded for flagleaf width (18.278), test weight (18.206), panicle length (17.347), flag leaf (16.319), plant height (14.188), days to maturity (13.163) and days to 50%flowering(11.593).

3.4 Correlation Coefficient of Analysis

Both phenotypic and genotypic correlation coefficient analysis revealed that grain yield per hill exhibited positive and significant correlation with Plant height, Harvest index, Number of panicles per hill, Number of panicles per hill, and Number of panicles per hill. The genotypic correlation coefficients were generally higher

Table 1. Analysis of Variance for 13 quantitative characters of 20 rice genotypes during *kharif, 2022*

SI.No.	Source	Replication	Treatment	Error
	Degrees of freedom	**2**	**19**	**38**
1	Days to 50% flowering	6.0170	243.442**	40.522
2	Days to maturity	30.4170	333.785**	54.986
3	Plant height (cm)	155.780	469.734**	78.1
4	Flag leaf length (cm)	14.0830	46.074**	7.064
5	Flag leaf width (cm)	0.0160	0.051**	0.008
6	Number of tillers per hill	0.6330	9.709**	0.482
7	Number of panicles per hill	1.2450	9.97**	0.42
8	Panicle length (cm)	1.350	22.603**	2.612
9	Number of spikelets per panicle	86.2060	2509.917**	90.664
10	Test weight (g)	1.6660	23.142**	3.611
11	Biological yield (g)	32.5430	331.81**	16.329
12	Harvest Index (%)	10.3320	181.964**	20.065
13	Grain yield per hill	12.4020	94.724**	4.95

* and ** indicate Significant at 5% and 1% level of significance

Table 2. Estimation of variability and genetic parameters for 13 quantitative characters in rice genotypes during for kharif 2022

SI.No.	Characters	GCV	PCV	h² (Broad Sense)	Genetic advancement 5%	Gen.Adv as % of Mean 5%
1	Days to 50% flowering	7.117	8.999	62.536	13.398	11.593
2	Days to maturity	8.061	10.17	62.827	15.741	13.163
3	Plant height	8.707	11.008	62.568	18.618	14.188
4	Flag leaf length	9.841	12.225	64.799	5.98	16.319
5	Flag leaf width	11.059	13.785	64.366	0.198	18.278
6	Number of tillers per hill	19.812	21.309	86.446	3.359	37.947
7	Number of panicles per hill	22.923	24.389	88.34	3.455	44.384
8	Panicle length	9.935	11.722	71.839	4.507	17.347
9	Number of spikelets per panicle	23.837	25.142	89.893	55.464	46.557
10	Test weight	11.019	13.739	64.326	4.216	18.206
11	Biological yield	25.313	27.207	86.56	19.654	48.514
12	Harvest Index	15.698	18.386	72.897	12.921	27.61
13	Grain yield per hill	29.005	31.312	85.807	10.439	55.348

h² =Heritability, GCV= Genotypic Coefficient of Variation, PCV=Phenotypic Coefficient of Variation

than their phenotypic correlation coefficients, indicating the association was largely due to genetic reason [9,10].

3.5 Path Analysis

At the phenotypic and genotypic levels of the path analysis, the diagonal values demonstrated a direct, strong, and positive impact on the harvest index, biological yield, test weight, flag leaf width, plant height, and days to maturity with grain yield per hill.

It had a direct, significant, and adverse impact on the quantity of grains per panicle, flag leaf length, and days to 50% blooming [11-13].
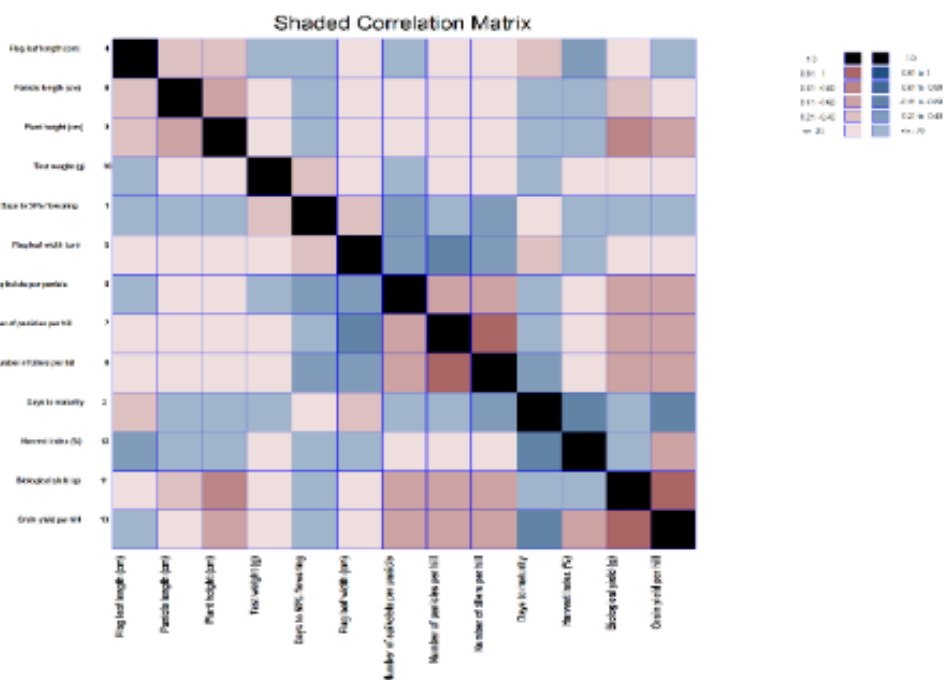

Fig. 1. Phenotypical correlation matrix

Table 3. Correlation coefficient analysis

TRAITS		FT	DM	PH	FLL	FLW	NTT	NPT	PL	NGPP	TW	BM	H.I	GYP
DFT	P	1.0000	0.0684	-0.0039	-0.0614	0.2115	-0.262*	-0.1655	-0.1161	-0.310*	0.2335	-0.1565	-0.0980	-0.1910
	G	1.0000	0.262*	-0.0557	-0.0716	0.342*	-0.460**	-0.272*	-0.0827	-0.405*	0.294*	-0.285*	-0.1813	-0.334*
DM	P		1.0000	-0.0880	0.2256	0.2001	-0.336*	-0.1503	-0.1018	-0.0148	-0.0570	-0.1620	-0.486**	-0.407*
	G		1.0000	-0.0724	0.431**	0.2183	-0.431**	-0.1716	-0.1392	-0.0006	-0.308*	-0.1371	-0.658**	-0.453**
PH	P			1.0000	0.2285	0.0531	0.0600	0.1086	0.450**	0.1719	0.1935	0.609**	-0.0050	0.502**
	G			1.0000	0.2107	0.0346	0.0588	0.1622	0.699**	0.1835	0.2304	0.787**	-0.0531	0.617**
FLL	P				1.0000	0.0667	0.0753	0.0593	0.2301	-0.1308	-0.1065	0.0231	-0.285*	-0.1573
	G				1.0000	0.0167	0.0597	0.0582	0.305*	-0.2075	-0.0576	0.0973	-0.595**	-0.264*
FLW	P					1.0000	-0.350*	-0.449**	0.0888	-0.355*	0.0349	0.0677	-0.0641	0.0144
	G					1.0000	-0.577**	-0.678**	0.1204	-0.461**	0.0722	0.0385	-0.1775	-0.0809
NTT	P						1.0000	0.852**	0.1173	0.523**	0.0616	0.410*	0.1879	0.466**
	G						1.0000	0.883**	0.1929	0.569**	0.0503	0.450**	0.0948	0.439**
NPT	P							1.0000	0.1919	0.586**	0.0057	0.475**	0.0139	0.422**
	G							1.0000	0.2011	0.634**	0.0168	0.553**	-0.1237	0.420**
PL	P								1.0000	0.1558	0.0934	0.371*	-0.1762	0.1900
	G								1.0000	0.1983	0.1629	0.501**	-0.299*	0.255*
NGPP	P									1.0000	-0.0179	0.507**	0.1312	0.506**
	G									1.0000	-0.0073	0.563**	0.1072	0.539**
TW	P										1.0000	0.0324	0.1552	0.1226
	G										1.0000	0.0584	0.255*	0.1953
BM	P											1.0000	-0.0623	0.807**
	G											1.0000	0.0008	0.843**
H.I	P												1.0000	0.532**
	G												1.0000	0.535**

DF50: Days to 50% Flowering, DM: Days to Maturity, PH: Plant Height, FLL: Flag Leaf Length, FLW: Flag Leaf Width, NTT: Number of Total Tillers, NPT: Number of Productive Tillers, PL: Panicle Length, BM: Biological Yield, H.I: Harvest Index, NGPP: Number of Grains per Panicle, TW: Test Weight, GYP: Grain Yield per Plant,
P: Phenotypic, G: Genotypic
*, ** indicates 5% and 1% significant, respectively

Table 4. Path coefficient analysis

TRAITS	DF50	DM	PH	FLL	FLW	NTT	NPT	PL	NGPP	TW	BY	H.I	
DF50	-0.0077	-0.0005	0.0000	0.0005	-0.0016	0.0020	0.0013	0.0009	0.0024	-0.0018	0.0012	0.0008	-0.1910
	-0.0809	-0.0211	0.0045	0.0058	-0.0276	0.0372	0.0220	0.0067	0.0328	-0.0238	0.0231	0.0147	-0.334*
DM	0.0016	0.0233	-0.0020	0.0053	0.0047	-0.0078	-0.0035	-0.0024	-0.0003	-0.0013	-0.0038	-0.0113	-0.407*
	0.0423	0.1618	-0.0117	0.0698	0.0353	-0.0697	-0.0278	-0.0225	-0.0001	-0.0499	-0.0222	-0.1065	-0.453**
PH	0.0000	-0.0003	0.0035	0.0008	0.0002	0.0002	0.0004	0.0016	0.0006	0.0007	0.0021	0.0000	0.502**
	-0.0005	-0.0006	0.0081	0.0017	0.0003	0.0005	0.0013	0.0056	0.0015	0.0019	0.0064	-0.0004	0.617**
FLL	0.0009	-0.0035	-0.0035	-0.0153	-0.0010	-0.0012	-0.0009	-0.0035	0.0020	0.0016	-0.0004	0.0044	-0.1573
	0.0057	-0.0344	-0.0168	-0.0799	-0.0013	-0.0048	-0.0046	-0.0244	0.0166	0.0046	-0.0078	0.0475	-0.264*
FLW	0.0001	0.0001	0.0000	0.0000	0.0005	-0.0002	-0.0002	0.0000	-0.0002	0.0000	0.0000	0.0000	0.0144
	0.0281	0.0179	0.0028	0.0014	0.0822	-0.0474	-0.0557	0.0099	-0.0379	0.0059	0.0032	-0.0146	-0.0809
NTT	-0.0013	-0.0017	0.0003	0.0004	-0.0017	0.0049	0.0042	0.0006	0.0026	0.0003	0.0020	0.0009	0.466**
	0.0275	0.0257	-0.0035	-0.0036	0.0345	-0.0597	-0.0528	-0.0115	-0.0340	-0.0030	-0.0269	-0.0057	0.439**
NPT	-0.0043	-0.0039	0.0028	0.0016	-0.0118	0.0223	0.0262	0.0050	0.0153	0.0001	0.0124	0.0004	0.422**
	-0.0718	-0.0452	0.0427	0.0153	-0.1785	0.2327	0.2635	0.0530	0.1671	0.0044	0.1456	-0.0326	0.420**
PL	0.0023	0.0020	-0.0090	-0.0046	-0.0018	-0.0024	-0.0038	-0.0200	-0.0031	-0.0019	-0.0074	0.0035	0.1900
	-0.0069	-0.0116	0.0581	0.0254	0.0100	0.0160	0.0167	0.0832	0.0165	0.0136	0.0417	-0.0249	0.255*
NGPP	0.0062	0.0003	-0.0034	0.0026	0.0071	-0.0104	-0.0117	-0.0031	-0.0199	0.0004	-0.0101	-0.0026	0.506**
	0.0449	0.0001	-0.0203	0.0230	0.0511	-0.0630	-0.0702	-0.0219	-0.1107	0.0008	-0.0623	-0.0119	0.539**
TW	0.0014	-0.0003	0.0011	-0.0006	0.0002	0.0004	0.0000	0.0005	-0.0001	0.0058	0.0002	0.0009	0.1226
	0.0085	-0.0089	0.0067	-0.0017	0.0021	0.0015	0.0005	0.0047	-0.0002	0.0289	0.0017	0.0074	0.1953
BY	-0.1326	-0.1372	0.5154	0.0195	0.0574	0.3472	0.4020	0.3140	0.4296	0.0274	0.8469	-0.0528	0.807**
	-0.2110	-0.1014	0.5820	0.0719	0.0285	0.3326	0.4086	0.3704	0.4165	0.0432	0.7396	0.0006	0.843**
H.I	-0.0576	-0.2856	-0.0029	-0.1673	-0.0377	0.1104	0.0082	-0.1036	0.0771	0.0912	-0.0366	0.5876	0.532**
	-0.1199	-0.4350	-0.0351	-0.3932	-0.1174	0.0627	-0.0818	-0.1978	0.0709	0.1688	0.0006	0.6614	0.535**

DF50: Days to 50% Flowering, DM: Days to Maturity, PH: Plant Height, FLL: Flag Leaf Length, FLW: Flag Leaf Width, NTT: Number of Total Tillers, NPT: Number of Productive Tillers, PL: Panicle Length, B.Y: Biological Yield, H.I: Harvest Index, NGPP: Number of Grains per Panicle, TW: Test Weight, GYP: Grain Yield per Plant, P: Phenotypic, G: Genotypic *, ** indicates 5% and 1% significant
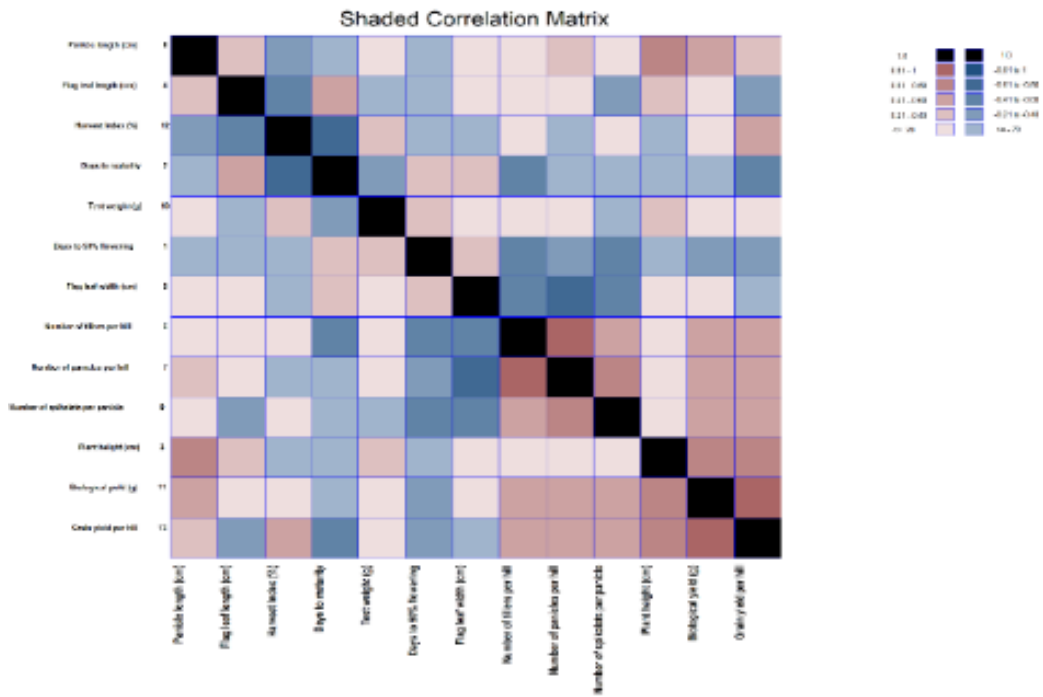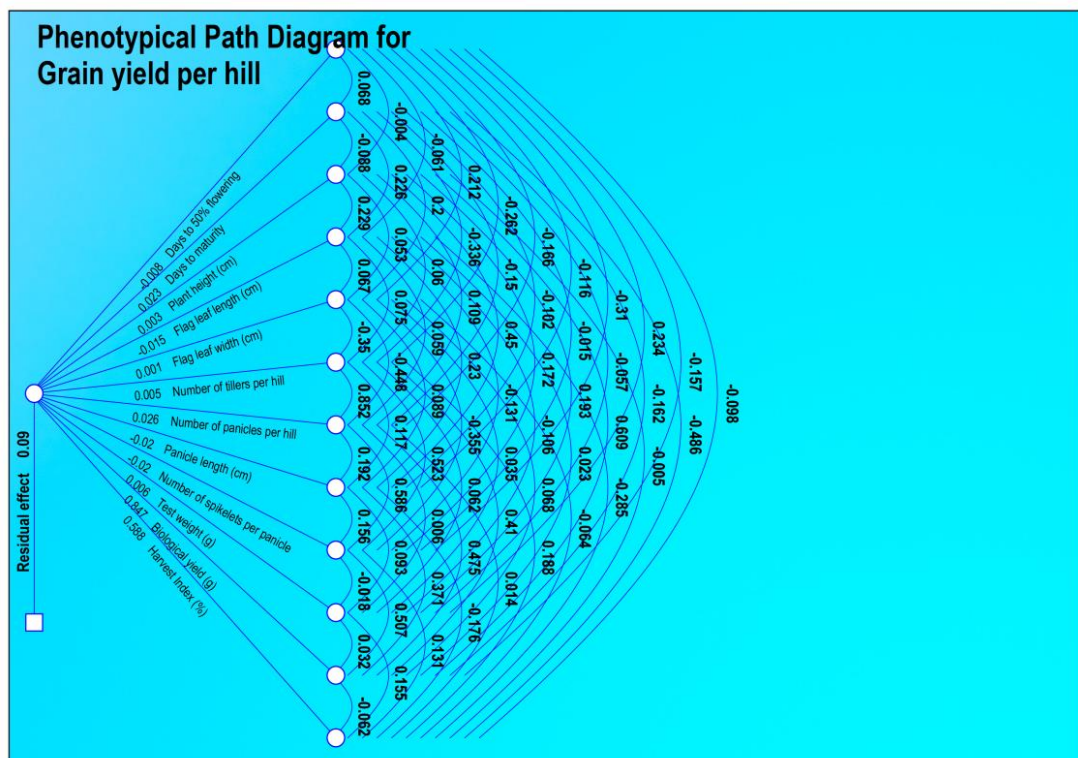
Fig. 2. Genotypical correlation matrix

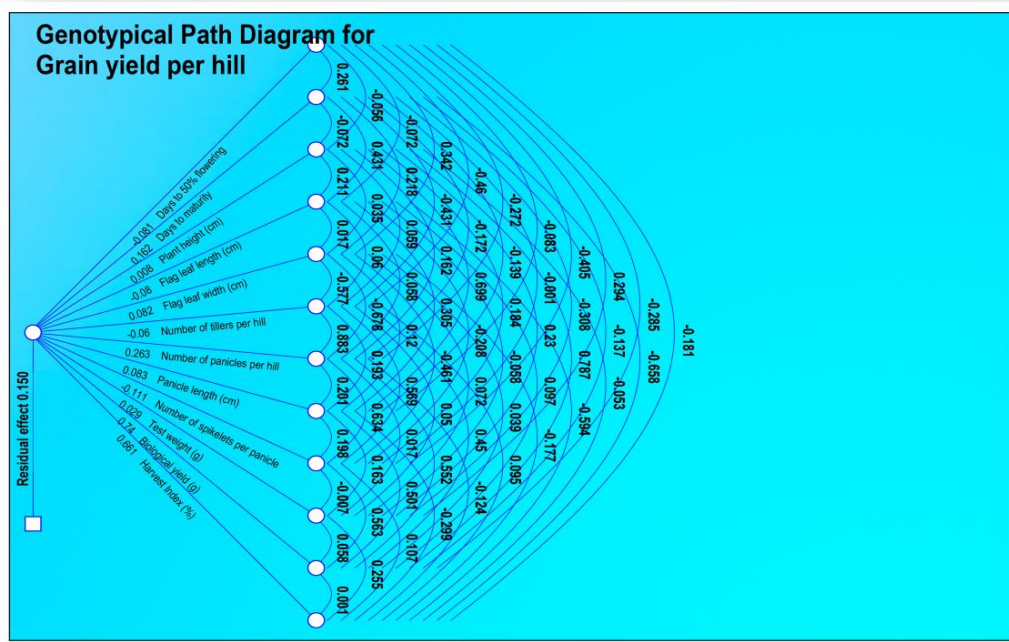**Fig. 3. Phenotypical path diagrams for grain yield per hill**

Fig. 4. Genotypical path diagram for grain yield per hill

4. CONCLUSION

Among 20 genotypes of rice, BRRI-DHAN-75, A.K.DHAN were found superior for Grain yield per hill over the check (NDR-359). High PCV, GCV, and Genetic Advance as Percent of Mean were recorded for grain yield per hill and high Heritability, Genetic advance for number of spikelets per panicle indicating predominance of additive genes effect. Correlation at both genotypic and phenotypic level,Grain yield per hill showed highly positive significant association with biological yield, number of spikelets per panicle and harvest index. In Path analysis, at both phenotypic and genotypic level the diagonal values showed Direct, high and Positive effect at harvest index, biological yield, test weight, flag leaf width, plant height and days to maturity with grain yield per hill. These traits offer a wide range of diversity in segregation and might be employed as parents in a future hybridization programme to create desired genotypes for rice genotypes that would increase grain production.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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