Original Research Article

Genetic variability, character association and path analysis studies in Rice Genotypes (*Oryza sativa* L.)

Abstract

Forty rice genotypes were evaluated for their genetic variability, correlation and path analysis studies with respect to yield and its attributing traits at the Agricultural Research Station, Vadgaon Maval (Pune). The magnitude for test weight exhibited the highest GCV and PCV per cent, followed by flag leaf length, flag leaf breadth, infertile spikelets per panicle, fertile spikelets per panicle, grain yield per plant. High heritability (h^2) along with higher genetic advance (GA) as per-cent of mean was recorded for the characters *viz*., fertile spikelets per panicle, total spikelets per panicle, panicle length, flag leaf length, flag leaf breadth and test weight. The grain yield per plant was positively and significantly correlated with productive tillers per plant, panicle length, flag leaf breadth, spikelet fertility % and test weight. Days to 50% flowering observed significant positive correlation with days to maturity and plant height. Days to maturity found positive correlation with plant height and productive tillers per plant, plant height with panicle length, flag leaf length and flag leaf breadth, productive tillers per plant with fertile spikelets per panicle, total spikelets per panicle, spikelet fertility, fertile spikelets per panicle with total spikelets per panicle and infertile spikelets per panicle with only total spikelets per panicle. The trait test weight observed highest direct positive effect on grain yield per plant followed by total spikelets per panicle, productive tillers per plant, days to maturity, flag leaf breadth, infertile spikelets per panicle, spikelet fertility %, and plant height. The trait flag leaf length indicated positive indirect effect on grain yield through days to 50% flowering, days to maturity and productive tillers per plant. Flag leaf breadth indicated significant positively correlation with grain yield through positive direct effect *via* indirect influence of plant height, panicle length, flag leaf length, spikelet fertility and test weight.

Keywords: Correlation, Direct effect, Genetic advance, Genotypic and Phenotypic Coefficient of variation, Heritability, Indirect effect

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Introduction

For the majority of the world's population, particularly in Asia, rice is the most extensively consumed staple food as a cereal grain. According to the United States Department of Agriculture, it is the agricultural crop with the third-highest global output, with 513.1 million metric tonnes produced in 2021-22 on an area of 165.7 million hectares. India is second only to China in terms of global rice production. With more than one-fifth of all calories taken by humans globally coming from rice, it is the most significant grain in terms of human nutrition and calorie consumption. Enhancing productivity, reducing yield loss through risk assessment, processing, adding value and commercialization majorly based on market information, should be the goals of rice research strategies. However, there are various constraints in rice production which must be understood in order to fulfill the demands of the growing population and sustain self-sufficiency. To achieve food security in the country and to increase in production which is possible by exploiting heterosis where genetic diversity plays important role in plant breeding. Assessment of variability present in any crop species is an essential prerequisite for formulating an effective breeding program. The existing variability can be used to further enhancement of yield. Moreover, characters that are part of the yield exhibit associations both with one another and with the yield. By studying the genetic make-up of current cultivars' germplasms in contrast to those of their forebears and similar species is crucial. This would clearly show not only how strongly related phylogenetically, but it will also show if there is a likelihood of discovering new and beneficial genes since the enlistments with their most distinctive genetic information seem to be likely to have better concentration of novel alleles.

Yield is a complex trait and dependent on many component traits. Hence, it is necessary to have knowledge on the extent of association between yield and yield contributing characters. The degree of proximity and the linear link between two variables are measured by correlation, which also serves as a measure of their mutual relationship. The splitting of correlations into the direct and indirect effect of different characters on yield is made easier by path analysis. The benefit of path analysis is that it enables the separation of the correlation coefficient into its various components, one of which is the path coefficient, which measures the direct impact of a predictor variable on its response variable, and the other of which is the indirect effect of a variable on the dependent variables through yet another dependent variable [1]. Plant breeders have utilized path analysis to help those observing features that may be used as screening criteria to increase crop output in agriculture [1]. The selection procedure will be aided by knowledge of character associations and the direct and indirect impacts that each character has on yield. To forecast the best overall cross combinations and choose the optimum plant type with the highest yield, plant breeders must discover substantial connections between yield component characteristics as well as the impact of yield component characters on grain production [2]. Keeping the above aspects in consideration the present investigation was done to estimate genetic variability, character association and path analysis in rice.

Materials and Methods

The present experiment was conducted at the Agricultural Research Station, Vadgaon (Maval), Pune. Forty (40) genotypes of rice originating from different regions and showing phenotypic variability for different agronomic and yield characters were used from Agricultural Research Station, Vadgaon (Maval). The list of promising genotypes along with released varieties used for studies are given in **Table 1.** The experiment was conducted during the *kharif* season of 2020. Each genotype was sown in three rows of 4 m length following a spacing of 20 cm between the rows and 15 cm between the plants in randomized block design (RBD) with three replications. Standard agronomic practices were performed uniformly for all the experimental units. Crop was raised following recommended package of practices. Phenological data on days to 50% flowering was recorded for plots of each genotype. At maturity, five plants from each accession were selected randomly for recording data on grain yield per plant and yield component traits, namely, plant height, productive tillers per plant, panicle length, grains per panicle and test weight. In contrast, observations for test weight were obtained from a random grain sample drawn from each plot and replication using standard procedures. The statistical analysis was done by the standard statistical method suggested by [3]. Mean performance of the genotypes were calculated and the genotypic (GCV) and phenotypic (PCV) coefficients of variation were estimated by using the formula given by [4]. The estimates of PCV and GCV were classified as low (0-10%), moderate (10-20%) and high (>20%) according to [5]. Heritability in broad sense (h^2b) was estimated according to the formula suggested by [4] and classified as per [6]. Estimation of genetic advance was carried out following the formula given by [7]. The genotypic correlation coefficients were worked out by adopting the method described by [8]. Path coefficient analysis was done according to the procedure suggested by [1].

Results and Discussion

The variation between genotypic and phenotypic characteristics indicates the influence of environmental factors. Formulating selection criteria will help with information on heredity and genetic advance. In **Table 2,** the estimates of genotypic coefficient of variation, range of variability and phenotypic coefficients of variation, the percentage of heritability in a broad sense, and the genetic advance reported as a percentage of mean were given. For each of the traits examined in the current analysis, a significant range of variance was observed. In forty genotypes, overall high significant differences were identified in total spikelets per panicle (265.50-154.50), followed by fertile spikelets per panicle (237.50-135), plant height (104.50-59.50), days to maturity (144-107), days to 50% flowering (80-110), flag leaf length (23.75-50.80), test weight (12.70-29.85), infertile spikelet per panicle (16-32), panicle length (17-30.60), grain yield (16.30-27.45), spikelet fertility % (85.75-91.85), productive tiller per plant (5.10-7.60), and flag leaf breadth (1.25-2.85). This was observed that there was a large amount of space for these features to be exploited, as reported earlier: grains per panicle, productive tillers per plant, panicle length, seed yield per plant, 1000 grain weight and plant height [9]. For all characters, it was observed that estimate for genotypic coefficients of variation (GCV) were lower than phenotypic coefficients of variation (PCV). For spikelet fertility % exhibited the lowest GCV (1.616) as well as PCV (1.958), whereas test weight (1000 grain weight) exhibited the highest GCV (23.837) and PCV (24.259).

The highest GCV and PCV difference was recorded for grain yield per plant. However, lowest GCV and PCV difference was recorded for days to maturity followed by flag leaf length and days to 50% flowering. Highest value of GCV (23.837) and PCV (24.259) for test weight were followed by flag leaf length GCV (21.432) and PCV (21.675), flag leaf breadth GCV (18.195) and PCV (18.561), infertile spikelets per panicle GCV (18.195) and PCV (19.770), fertile spikelets per panicle GCV (15.795) and PCV (16.470), grain yield per plant GCV (13.913) and PCV (16.113), plant height GCV (12.797) and PCV (13.797), panicle length GCV (11.614) and PCV (12.061), productive tillers per plant GCV (9.592) and PCV (10.179), days to 50% flowering GCV (8.094) and PCV (8.198), days to maturity GCV (7.449) and PCV (7.519). The larger difference between GCV and PCV showed by the characters were influenced due to the environment. It observed that PCV was higher than the GCV for all characters. [9, 10, 11, 12, 13]

Days to maturity observed the highest broad sense heritability (98.13%) and followed by flag leaf length (97.76%). Days to 50% flowering showed heritability (97.48%) followed by test weight (96.55%), flag leaf breadth (96.10%), total spikelets per panicle (93.05%), panicle length (92.73%), fertile spikelets per panicle (91.97%), followed by high heritability in some characters such as productive tiller per plant (88.80%), plant height (86.03%), infertile spikelets per panicle (84.70%), grain yield per plant (74.56%) and spikelet fertility (%) (68.15%) character. High heritability estimates suggest that these characters were least influenced by the environment. The character, total spikelets per panicle observed highest genetic advance at 5% selection intensity (61.378), followed by fertile spikelets per panicle (55.244) and days to maturity (19.614). The lowest genetic advance (GA) was showed for flag leaf breadth (0.658), followed by productive tillers per plant (1.157), followed by spikelet fertility % (2.427). The highest genetic advance (GA) as per cent of mean was showed for the traits plant height (24.451), panicle length (23.038), flag leaf length (43.653), flag leaf breadth (36.743), fertile spikelets per panicle (31.205), infertile spikelets per panicle (34.496), total spikelets per panicle (30.632), test weight (42.248) and grain yield per plant (24.748).The moderate genetic advance (GA) as per cent of mean was showed to traits days to 50% flowering (16.462), days to maturity (15.200) and productive tillers per plant (18.620). The low genetic advance (GA) as per cent of mean showed to trait spikelet fertility % (2.748). High heritability (h^2) with moderate genetic advance as per cent of mean showed for the characters days to 50 % flowering, days to maturity and productive tillers per plant suggested that both additive and non-additive gene effects were involved in the genetic regulation of these traits. High heritability (h^2) along with higher genetic advance (GA) as per-cent of mean was recorded for the characters viz., fertile spikelets per panicle, total spikelets per panicle indicated that these traits were under control of additive gene action. The selection could be practised in all these traits for higher magnitude of genotype. Similar result was reported by [14] for test weight, [15] for plant height, flag leaf length, spikelets per panicle.

Correlations studies:

Information on nature as well as magnitude of associations between various component characters and grain production can be obtained using correlation analysis. Also, it helps in understanding of how the individual component characteristics interact with one another. Ultimately, the breeder might use this kind of information to design his choice to increase grain yield. In **Table 3** the genotypic correlation coefficient between yield & its related characters in all possible comparisons were given. It is revealed that the significant positive correlation among grain yield per plant and productive tillers per plant (0.2710), panicle length (0.2596), flag leaf breadth (0.3461), spikelet fertility (0.3793) and highly significant with test weight (0.6757). Days to maturity (0.0435), plant height (0.1657) and flag leaf length (0.0651) also showed non-significant positive correlation with grain yield per plant. When making selections to improve yield, it is recommended that these characters be given top priority. The results are conformity with [16] for number of productive tillers per plant, 1000 grain weight, panicle and [10] for test weight. Days to 50% flowering indicated positive and significant correlation with days to maturity (0.9819), plant height (0.3055) and productive tillers per plant (0.2898). The number of days to maturity has the significant positive corelation with plant height (0.2769), productive tillers per plant (0.3406).Plant height observed direct eff correlated with panicle length (0.5039), flag leaf length (0.5543), flag leaf breadth (0.3048) but non-significant correlation with productive tillers per plant (0.0730), fertile spikelets per panicle (0.0772), total spikelets per panicle (0.0547), test weight (0.0509) and grain yield per plant (0.1657). Number of productive tillers per plant observed the significant positive correlation with fertile spikelets per panicle (0.2735), total spikelets per panicle (0.2551), spikelet fertility % (0.2479) and grain yield per plant (0.2710) also non-significant correlation with infertile spikelets per panicle (0.0544). Panicle length showed significant positive correlation with flag leaf length (0.5660), flag leaf breadth (0.2527), test weight (0.2392) and grain yield per plant (0.2596) also non-significant correlation with spikelet fertility % (0.0781). Flag leaf length showed positive significant correlation only with flag leaf breadth (0.5239) and non-significant correlation with fertile spikelets per panicle (0.1063), infertile spikelets per panicle (0.0208), total spikelets per panicle (0.0991), spikelet fertility % (0.0700), test weight (0.0335) and grain yield per plant (0.0651). Flag leaf breadth showed positive significant correlation with grain yield per plant (0.3461) and followed by spikelet fertility % (0.2259) along with test weight (0.3033). Fertile spikelets per panicle showed highly positively significant correlation to total spikelets per panicle (0.9945). It also showed the significant correlation with spikelet fertility % (0.2604) and infertile spikelets per panicle (0.6488). Infertile spikelets per panicle observed positive significant correlation with total spikelets per panicle (0.7249). Days to 50 per cent flowering had showed significant positive association with days to maturity. This result was in conformity with the earlier findings of [17, 18]

Path analysis studies:

To determine the actual influence of each character on the yield, it is essential to divide the connection into direct and indirect impacts. Correlation and path analysis together may thus provide a better understanding of the causes and effect relationship among various character pairs. This will help in breeding programmes that simultaneously boost character and grain productivity. The path coefficient evaluation using genotypic correlation indicates the interrelationships between the characters, which are illustrated in **Table 4**. The character test weight (1.5760) observed highest direct positive effect on grain yield per plant and followed by total spikelets per panicle (0.9820), productive tillers per plant (0.5909), days to maturity (0.5186), flag leaf breadth (0.1290), infertile spikelets per panicle (0.0668), spikelet fertility % (0.0516), plant height (0.0075). Hence, direct selection for these characters will be beneficial for yield improvement programme. The characters days to 50% flowering (-0.5102), panicle length (-0.0163), flag leaf length (-0.0512) and fertile spikelets per panicle (-0.1613) observed negative direct effect on grain yield per plant. [19] and [20] reported test weight (1000 grain weight) recorded maximum positive direct effect to yield. [18] for total number spikelets or grain per panicle and fertile spikelets per panicle [17] for infertile spikelets per panicle, plant height and days to 50% flowering reported similar findings. [21] for Days to 50% flowering showed negative correlation with grain yield (-0.0427) might due to negative indirect effect with days to maturity (-0.5009), plant height (-0.1559), productive tillers plant (-0.1478), fertile spikelets panicle (-0.0686) and infertile spikelets per panicle (-0.0078). Productive tillers per plant showed significant positive correlation (0.2710) with grain yield, it also had the significantly positive direct effect (0.5909) on grain yield. The character influences the yield positively indirect effect with days to 50% flowering (0.1713), days to maturity (0.2013), fertile spikelets per panicle (0.1616), infertile spikelets per panicle (0.0322), total spikelets per panicle (0.1508), spikelet fertility (0.1465). Flag leaf length indicated positive indirect effect on grain yield with days to 50 percent flowering (0.0013), days to maturity (0.0045), productive tillers per plant (0.0048). Flag leaf breadth had positive direct effect (0.1290) on grain yield. It also showed significant positive correlation with grain yield (0.3461), which was due to positive indirect effect through plant height (0.0393), panicle length (0.0326), flag leaf length (0.0676), spikelet fertility (0.0292) and test weight (0.0391). Total spikelets per panicle had significant positive direct effect (0.9820) on grain yield per plant and indirect effect through days to 50% flowering (0.0150), plant height (0.0537), productive tillers per plant (0.2505), flag leaf length (0.0973), fertile spikelets per panicle (0.9766), infertile spikelets per panicle (0.7118), spikelet fertility (0.1562). It also observed that character had negative indirect effect like days to maturity (-0.0491), panicle length (-0.1123), flag leaf breadth (-0.1220) and test weight (-0.8442). Test weight had highest direct effect (1.5760) on grain yield per plant and also had positive significant correlation (0.6757) on grain yield. It had positive indirect effect through plant height (0.0803), panicle length (0.3770), flag leaf breadth (0.4780), spikelet fertility % (0.0620). The negative indirect effect through days to 50% flowering (-0.2176), days to maturity (-0.1232), productive tillers per plant (-0.5530), fertile spikelets per panicle (-1.3192), infertile spikelets per panicle (-1.1683), total spikelets per panicle (-1.3549).

The residual effect determines how well the causal factors account for the variability of the dependent factors, in this case, the grain yield. The residual effect in the current study was relatively low (0.1678), indicating that the characters selected were sufficient for explaining variability in rice grain yield. It is evident from the previous discussion that days to maturity, productive tillers per plant, total spikelets per panicle and test weight identified as important components of rice grain yield. Similar type of association were recorded by [18] for number of grain per panicle and days to maturity and, Shahadat *et al.* (2018) [17] for number grain per panicle and [22] and [23] for productive / effective tillers per plant and test weight.

Conclusion:

It observed that PCV was higher than the GCV for all characters that means observed variation in the trait is influenced by both genetic and environmental factors. High heritability (h^2) along with higher genetic advance (GA) as per-cent of mean was for the characters fertile spikelets per panicle and total spikelets per panicle was largely controlled by additive genetic factors and selection for these traits results in substantial and predictable genetic gain. The traits Flag leaf breadth, infertile spikelets per panicle exhibited the high heritability and low genetic advance (GA) as per-cent of mean suggest that the traits is primarily influenced by non-additive genetic effect. selection is not effective for these traits. The grain yield per plant was positively and significantly correlated with productive tillers per plant, panicle length, flag leaf breadth, spikelet fertility % and test weight. The breeders should focus on selecting the plants with those traits to improve the overall productivity. The residual effect in the current study was relatively low (0.1678), indicating that the characters selected were sufficient for explaining variability in rice grain yield. The character test weight (1.5760) and total spikelets per panicle (0.9820) observed highest direct positive effect on grain yield per plant indicates direct selection for these characters will be beneficial for yield improvement programme.

Table 1. List of Rice genotypes studied

Sr. No.	Genotype	Sr. No.	Genotype
1	RTN 1409-1	21	RDN 20-10
2	RTN 2012-5	22	IGP 14-2
3	TKR 34	23	IGP 12-1
4	RTN 1410-1	24	VDN 1822
5	KJT-184	25	Indrayani
6	KJT 11012-8	26	RTN 15 M6-22
7	VDN 1902	27	IGP Local
8	IGP 13-11	28	Super Basmati 1
9	VDN 1930	29	KJT 5-4
10	Karjat 3	30	VDN 1832
11	KJT 7	31	RDN 20-03
12	RTN 14 01-4	32	Ratnagiri 5
13	KJT R-3	33	Phule Radha
14	SKL 09-30	34	Kundalika
15	VDN 1848	35	KJT TCR 39
16	Phule Samruddhi	36	PKV Ganesh
17	KJT 2	37	VDN 1942
18	RP 4-14	38	Ratnagiri-24
19	RTN 4	39	Karjat 5
20	RTN 1513-2	40	Palghar 1

Table 2. Estimates of genetic variability parameters for 13 different characters.

Sr. No.	Name of the Character	Range	Mean	G.C.V. (%)	P.C.V. (%)	Heritability (h^2) (bs) %	Genetic advance (at 5% K)	GA as % of mean (at 5% K)
1.	Days to 50% flowering	80.50 – 110.00	99.21	8.094	8.198	97.48	16.333	16.462
2.	Days to maturity	107.50 – 144.00	129.03	7.449	7.519	98.13	19.614	15.200
3.	Plant height	59.50 – 104.50	79.77	12.797	13.797	86.03	19.506	24.451
4.	Productive tillers/plant	5.10 – 7.60	6.21	9.592	10.179	88.80	1.156	18.620
5.	Panicle length	17.00 – 30.60	22.63	11.614	12.061	92.73	5.213	23.038
6.	Flag leaf length	23.75 – 50.80	34.14	21.432	21.675	97.76	14.904	43.653
7.	Flag leaf breadth	1.25 – 2.85	1.79	18.195	18.561	96.10	0.658	36.743
8.	Fertile spikelets per panicle	135.00 – 237.50	177.03	15.795	16.470	91.97	55.244	31.205
9.	Infertile spikelets per panicle	16 – 32	23.33	18.195	19.770	84.70	8.051	34.496
10.	Total spikelets per panicle	154.50 – 265.50	200.37	15.415	15.980	93.05	61.378	30.632
11.	Spikelet fertility %	85.75 – 91.85	88.30	1.616	1.958	68.15	2.427	2.748
12.	Test weight (1000 grain weight)	12.70 – 29.85	20.84	23.837	24.259	96.55	10.059	48.248
13.	Grain yield / plant	16.30 – 27.45	21.27	13.913	16.113	74.56	5.264	24.748

Table 3. Genotypic correlation coefficients of 12 characters of 40 genotypes of rice on grain yield.

Sr. No.	**Days to 50% flowering**	**Days to maturity**	**Plant height**	**Productive tillers per plant**	**Panicle length**	**Flag leaf length**	**Flag leaf breadth**	**Fertile spikelets per panicle**	**Infertile spikelets per panicle**	**Total spikelets per panicle**	**Spikelet fertility %**	**Test weight**	**Grain yield per plant**
	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**
1.	**1.000**	0.9819**	0.3055**	0.2898**	0.0357	-0.0255	-0.1190	-0.0036	0.1345	0.0153	-0.1467	-0.1381	-0.0427
2.		**1.000**	0.2769*	0.3406**	0.0467	-0.0878	-0.1355	-0.0644	0.0603	-0.0500	-0.1127	-0.0782	0.0435
3.			**1.000**	0.0730	0.5039**	0.5543**	0.3048**	0.0772	-0.1108	0.0547	0.2016	0.0509	0.1657
4.				**1.000**	-0.0217	-0.0928	-0.1875	0.2735*	0.0544	0.2551*	0.2479*	-0.3509	0.2710*
5.					**1.000**	0.5660**	0.2527*	-0.1033	-0.1514	-0.1143	0.0781	0.2392*	0.2596*
6.						**1.000**	0.5239**	0.1063	0.0208	0.0991	0.0700	0.0355	0.0651
7.							**1.000**	-0.0977	-0.2603	-0.1242	0.2259*	0.3033**	0.3461**
8.								**1.000**	0.6488**	0.9945**	0.2604*	-0.8371	-0.3329
9.									**1.000**	0.7249**	-0.5581	-0.7413	-0.5614
10										**1.000**	0.1590	-0.8597	-0.3786
11											**1.000**	0.0393	0.3793**
12												**1.000**	0.6757**

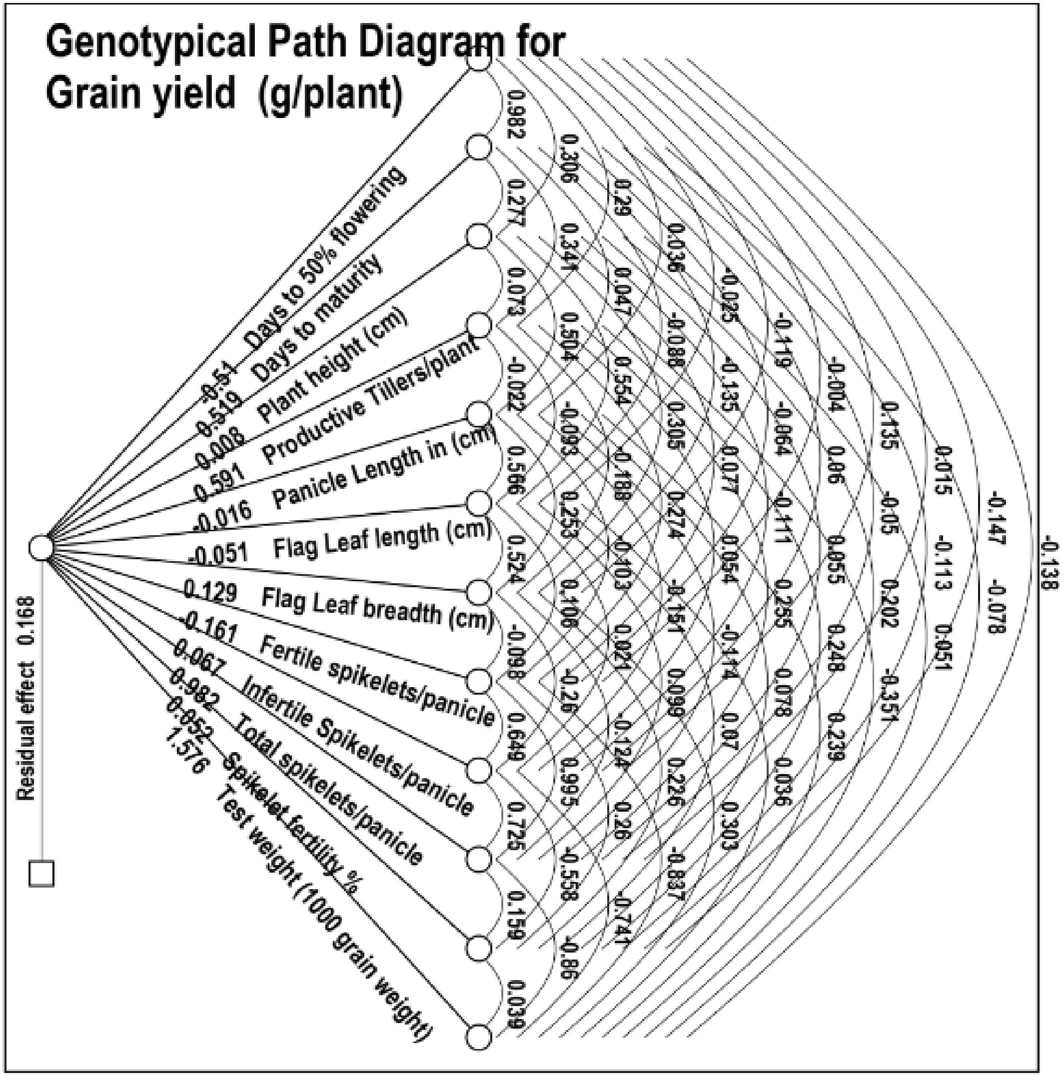
*, ** Significant at 5(0.2199) and 1(0.2864) per cent respectively

Table 4. Direct (diagonal) and indirect (above and below diagonal) path effects of different characters towards grain yield at genotypic level in rice.

Sr. No.	Days to 50% flowering	Days to maturity	Plant height	Productive tillers per plant	Panicle length	Flag leaf length	Flag leaf breadth	Fertile spikelets per panicle	Infertile spikelets per panicle	Total spikelets per panicle	Spikelet fertility %	Test weight	Grain yield per plant
	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**
1.	**-0.5102**	-0.5009	-0.1559	-0.1478	0.0130	0.0607	0.0018	-0.0686	-0.0078	0.0078	0.0749	0.0705	-0.0427
2.	0.5092**	**0.5186****	0.1436	0.1766	0.0242	-0.0455	-0.0702	-0.0334	0.0313	-0.0259	-0.0584	-0.0406	0.0435
3.	0.0023	0.0021	**0.0075**	0.0005	0.0038	0.0042	0.0023	0.0006	-0.0008	0.0004	0.0015	0.0004	0.1657
4.	0.1713	0.2013	0.0431	**0.5909****	-0.0128	-0.0549	-0.1108	0.1616	0.0322	0.1508	0.1465	-0.2073	0.2710*
5.	-0.0006	-0.0008	-0.0082	0.0004	**-0.0163**	-0.0092	-0.0041	0.0017	0.0025	0.0019	-0.0013	-0.0039	0.2596*
6.	0.0013	0.0045	-0.0284	0.0048	-0.0290	**-0.0512**	-0.0268	-0.0054	-0.0011	-0.0051	-0.0036	-0.0018	0.0651
7.	-0.0154	-0.0175	0.0393	-0.0242	0.0326	0.0676	**0.1290**	-0.0126	-0.0336	-0.0160	0.0292	0.0391	0.3461**
8.	0.0006	0.0104	-0.0125	-0.0441	0.0167	-0.0172	0.0158	**-0.1613**	-0.1047	-0.1605	-0.0420	0.1351	-0.3329
9.	0.0090	0.0040	-0.0074	0.0036	-0.0101	0.0014	-0.0174	0.0433	**0.0668**	0.0484	-0.0373	-0.0495	-0.5614
10	0.0150	-0.0491	0.0537	0.2505*	-0.1123	0.0973	-0.1220	0.9766**	0.7118**	**0.9820****	0.1562	-0.8442	-0.3786
11	-0.0076	-0.0058	0.0104	0.0128	0.0040	0.0036	0.0117	0.0134	-0.0288	0.0082	**0.0516**	0.0020	0.3793**
12	-0.2176	-0.1232	0.0803	-0.5530	0.3770	0.0560	0.4780	-1.3192	-1.1683	-1.3549	0.0620	**1.5760****	0.6757**

(Residual effect = 0.1678) *, ** Significant at 5 and 1 per cent respectively

Fig 1. Genotypical path diagram for grain yield per plant in rice



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Option 1:

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