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Genetic variability, character association and path analysis of advanced breeding lines (Magic lines) of rice (*Oryza sativa* L.)

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Abstract
Rice is a staple food for more than half of the world's population, but the production is severely affected by the impact of abiotic stresses due to frequent change in climate. Hence there is a need to combine desirable traits of different varieties using Multi-parent advanced generation inter-cross population (Magic) and identify high yielding rice genotypes suited to varied topographic regions. The present investigation was carried out at ZAHRS, Shivamogga by using multi-parent advanced breeding lines of the MF$_6$ generation developed by crossing eight diverse varieties having desirable traits. The variability studies among the lines revealed a higher GCV, PCV, heritability and genetic advance as per cent of mean for majority of yield attributing traits. The correlation and path coefficient studies on yield and its contributing traits revealed majority of the traits were positively associated with yield.

Keywords: Genetic variability, Magic lines, *Oryza sativa* L.

Introduction

Rice, *Oryza sativa* is one the most important crop in Asia and is the staple food for more than half of the world's population. It belongs to the family *Gramineae* and is grown in about 120 countries with China and India together accounting for more than 50 percent of the rice production globally. Rapid population growth is imparting increased pressure on already strained food-producing resources. According to the reports of the UN Department of economic and social affairs, India's population may reach 1.5 billion by 2030 and 1.64 billion by 2050. Currently the production of rice in India is 121.46 MT and the demand of rice is estimated to increase to 197.40 MT by 2050 (FAOSTAT, 2018). In addition to this, elevating drift in climate change like rise in temperature, altered precipitations, melting of glaciers and shifting seasons are threat to agriculture and food security to the growing population. It is necessary to develop new technologies in order meet this need and contribute to global efforts which are directed towards poverty alleviation.

In order to increase the rice production there is a need to identify suitable high yielding varieties which can be cultivated in different topographical conditions and also develop high yielding, nutritionally superior and biotic and abiotic stress tolerant varieties. Hence, there is a need to combine all the desirable traits of different varieties using Multi-parent advanced generation inter-cross population (MAGIC) and identify suitable rice genotypes suited to different topographic regions. MAGIC – combines high diversity (from multiple parents) with high recombination and also has the potential to increase the speed and efficiency of breeding. Magic populations can serve as source material for extraction and development of breeding lines and varieties with several agronomic ally beneficial traits. These populations bring model shift toward QTL analysis, gene mapping, variety development etc. in plant species.

The Association of different characters was essential to determine their contribution towards yield. The knowledge about genetic variability of yield contributing characters, inter relationship among them and their relation with yield are necessary for an effective breeding programme. Moreover knowledge of heritability was used for selection, as it indicates the extent of transmissibility of trait in to future generations. The correlation coefficient also help to identify characters that have little or no importance in the selection programme where as path coefficient analysis helps in determining the direct and indirect cause of association and permit to examine the specific forces acting to produce the given correlation.

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Correlation and path coefficient analysis together have been successfully used for plant selection for increasing yield and provide information about cause and effect relationship between direct pair of variables. Therefore, the present investigation was undertaken to estimate the variability, heritability, genetic advance as percentage of mean, correlation among the traits and their path coefficient analysis for grain yield and yield attributing traits among the genotypes.

Materials and Methods
Plant material and location of the Experimental site
Thirty multi-parent advanced breeding lines of MF$_6$ developed from crossing eight parents (JGL1798 × KPR2, Hemavathi × Gandhasali, BPT5204 × H3, Jaya × Mysore Mallige) in structured mating design along with six checks *viz.,* JGL1798, KPR2, Hemavathi, Gandhasali, BPT5204 and Mysore mallige were collected from the Department Of Genetics and Plant Breeding, KSNUAHS, College of Agriculture, Shivamogga, Karnataka, India. The list of the multi-parent advanced breeding lines along with the six checks used in the present investigation is presented in Table 1. The study was conducted during *Kharif* 2020 at KSNUAHS, College of Agriculture, Shivamogga, Karnataka, India). Twenty-one days old seedlings were transplanted manually into the main field with single seedling per hill in Randomized block design with two replications with spacing of 20 cm row to row and 15 cm plant to plant. The recommended package of practices was followed to maintain a healthy and good crop stand. Five plants were randomly selected from each multi-parent advanced line and labelled for recording the observations in each treatment. Mean of the observations recorded on these five plants was considered for statistical analysis. The characters for which observations were recorded are as follows: days to 50% flowering, plant height (cm), number of tillers per plant, number of productive tillers per plant, number of spikelets per panicle, number of filled grains, panicle fertility (%), test weight (gm) and grain yield (kg/ha).

Table 1: List of MF$_6$ rice advanced lines taken for the experiment

Line No.	Genotype	Line No.	Genotype
1	ML1-2-3-1-6	16	ML3-5-2-1-105
2	ML1-2-5-1-8	17	ML3-6-7-1-107
3	ML1-6-1-1-22	18	ML3-7-1-1-108
4	ML1-6-3-1-23	19	ML3-7-3-1-110
5	ML1-7-2-1-26	20	ML3-7-9-1-113
6	ML1-8-1-1-31	21	ML1-2-7-4-121
7	ML1-11-4a-2-45	22	ML1-7-1-1-126
8	ML1-11-5-1-49	23	ML2-5-21-3-154
9	ML1-11-9-1-50	24	ML2-7-2-2-156
10	ML1-12-6-1-52	25	ML2-7-2-3-160
11	ML1-14-1-1-54	26	ML2-7-3-2-164
12	ML1-15-3A-1-17	27	ML2-5-21-2-152(P2*)
13	ML2-5-3-1-19	28	ML2-8-10-1-177(P2*)
14	ML2-6-1-1-76	29	ML2-8-13-2-178(P2*)
15	ML3-2-4-4-96	30	ML1-11-4a-3-47(P1)

Statistical Analysis: The experimental data were compiled by their mean value over randomly selected plants from all the three replication and subjected to statistical analysis for genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) as per procedure given by Burton and De Vane (1953) and heritability and genetic advance by Johanson *et al*. (1955). Correlation coefficient was worked as per and path analysis given by Dewey and Lu (1959) [13].

Results and Discussion
Presence of variability in genotypes is of prime most importance in breeding programmes for improvement of crop plants for desired characters. Hence, assessment of magnitude of variability available in gene pool is the first and foremost step involved in breeding program. The analysis of variance for various characters studied reported the presence of significant difference among the rice advanced lines for those characters showing that they were genetically diverse and selection will be effective. Similar results were proclaimed by Afrin *et al*. (2017), Sudeepthi *et al* (2020) and Bhargava *et al* (2021) [6].

Table 2: Analysis of variance for yield and its component characters in multi-parent advanced lines of rice in MF$_6$ generation

Source of variation	df	Days to 50% flowering	Days to maturity	Plant height (cm)	Total number of tillers per plant	Number of productive tillers per plant
Replication	1	2.722	3.556	1.125	0.681	0.500
Genotype	35	73.784**	74.386**	260.957**	14.223**	12.022**
Error	35	0.951	0.927	2.239	0.537	0.300
CD (5%)		1.979	1.955	3.037	1.488	1.112
CD (1%)		2.676	2.622	4.076	1.997	1.492
CV (%)		1.885	1.686	2.373	4.471	3.435

Table 3: Analysis of variance for yield and its component characters in multi-parent advanced lines of rice in MF$_6$ generation

Source of variation	Df	Panicle length (cm)	Total no. of spikelets per panicle	No. of filled grains per panicle	Panicle fertility (%)	Test weight (g)	Grain yield (Kg/ha)
Replication	1	0.681	24.500	22.220	0.180	0.056	28203
Genotype	67	13.947*	875.000**	1038.41**	40.687**	7.627**	6004001**
Error	67	0.480	51.360	44.710	1.291	0.427	341291
CD (5%)		1.407	14.548	13.574	2.307	1.326	1185.991
CD (1%)		1.888	19.520	18.213	3.095	1.779	1591.250
CV (%)		2.958	3.087	3.268	1.290	3.927	9.652

In the present study, PCV was greater than GCV for all the traits with a narrow range of gaps, indicating little environmental influence on these traits. The high estimates of PCV and GCV with high heritability coupled with high Genetic advance mean(GAM) were recorded for most of the traits *viz.,* plant height, number of tillers, number of

productive tillers, panicle length, number of spikelets per panicle, number of filled grains per panicle, test weight and grain yield. This result indicated that practicing selection for these traits could be effective as these traits respond to section. Prasad *et al.* (2017) observed moderate GAM for

days to 50 percent flowering, days to maturity and panicle length, high GAM for plant height, number of tillers per plant, number of productive tillers per plant, number of filled grains per panicle, test weight and grain yield.

Table 4: Estimation of mean, range, variability, heritability and genetic advance as percent mean for yield and yield related traits in MF$_6$ generation

Sl. No	Characters	Mean ± SE$_m$	Range		PCV (%)	GCV (%)	h^2 (bs) (%)	GAM (%)
			Min	Max				
1	Days to 50 percent flowering	110.22 ± 0.689	98.00	118.00	5.54	5.47	97.46	11.13
2	Days to maturity	140.24 ± 0.680	128.00	148.00	4.37	4.32	97.54	8.79
3	Plant height (cm)	109.01 ± 1.058	89.00	138.00	10.52	10.43	98.23	21.31
4	Number of tillers per plant	16.403 ± 0.518	10.00	21.00	16.66	15.95	92.71	31.63
5	Number of productive tillers per plant	15.944 ± 0.387	10.00	19.00	15.56	15.18	95.13	30.51
6	Panicle length (cm)	23.431 ± 0.490	17.00	28.00	11.46	11.07	99.34	22.04
7	Total number of spikelets per panicle	232.111 ± 5.067	199.00	270.00	9.18	8.64	88.69	16.77
8	Number of filled grains per panicle	204.583 ± 4.728	170.00	248.00	11.37	10.89	91.74	21.49
9	Panicle fertility (%)	88.08 ± 0.804	72.31	96.11	5.20	5.04	93.85	10.05
10	Test weight (g)	16.472 ± 0.462	12.00	22.00	12.18	11.52	89.40	22.43
11	Grain yield (kg/ha)	6052 ± 875	2334	8534	29.43	27.79	89.24	54.09

Plant yield is a complex trait and highly influenced by environmental fluctuations; hence, direct yield selection is ineffective. Correlation studies provide information about yield contributing characters. This information is helpful to plant breeders in the selection of elite genotypes from diverse genetic populations.

A significant positive association was found between grain yield with number of tillers per plant (r = 0.9079), number of productive tillers per plant (r = 0.8843), panicle length (r = 0.7954), number of filled grains per panicle (r = 0.6776), total number of spikelets per panicle (r = 0.7529), test weight (r = 0.7784). A non-significant positive association was found between grain yield with days to 50 percent flowering (r =

0.1673), days to maturity (0.1646), and panicle fertility (r = 0.1344). Whereas a negative non-significant association of grain was found with plant height(r = -0.0037). The present study indicated that yield could be increased by selecting the following traits: days to 50% flowering, days to maturity, number of tillers, number of productive tillers, panicle length, spikelets per panicle, number of filled grains per panicle, and test weight. Similar results were observed by Williams *et al.* (2021) and Singh *et al.* (2017) [19], and Mahamadali *et al.* (2020) [20]. Patil *et al.* (2020) [21] reported a significant positive association of test weight with the yield. Lakshmi *et al.* (2014) observed a positive correlation between plant height with yield.

Table 5: Phenotypic correlation among yield and yield related characters in MF$_6$ generation

	X$_1$	X$_2$	X$_3$	X$_4$	X$_5$	X$_6$	X$_7$	X$_8$	X$_9$	X$_{10}$	X$_{11}$
X$_1$	1.000	0.996**	-0.027	0.212	0.181	0.189	0.098	0.075	-0.007	0.189	0.167
X$_2$		1.000	-0.032	0.209	0.177	0.186	0.100	0.077	-0.007	0.187	0.165
X$_3$			1.000	-0.056	-0.006	0.181	0.129	0.121	0.039	-0.120	-0.004
X$_4$				1.000	0.894**	0.688**	0.653**	0.619**	0.179	0.684**	0.908**
X$_5$					1.000	0.637**	0.580**	0.499**	0.053	0.607**	0.884**
X$_6$						1.000	0.781**	0.748**	0.231	0.654**	0.795**
X$_7$							1.000	0.879**	0.147	0.627**	0.753**
X$_8$								1.000	0.599**	0.570**	0.678**
X$_9$									1.000	0.122	0.134
X$_{10}$										1.000	0.778**
X$_{11}$											1.000

X$_1$= Days to 50 percent flowering	X$_5$= Number of productive tillers per plant	X$_9$= Panicle fertility (%)
X$_2$= Days to maturity	X$_6$= Panicle length (cm)	X$_{10}$= Test weight (g)
X$_3$= Plant height (cm)	X$_7$= Total number of spikelets per panicle	X$_{11}$= Grain yield (kg/ha)
X$_4$= Number of tillers per plant	X$_8$= Number of filled grains per panicle	

Path coefficient analysis was carried out at the phenotypic level to measure the direct and indirect effect of various independent characters on a dependent character yield. Based on the obtained result, it may be suggested that selection for days to maturity, number of tillers per plant, number of productive tillers per plant, panicle length, number of

spikelets per panicle, panicle fertility and test weight may be given priority as they exhibited a direct positive effect on yield. Similar results were reported by Kumar *et al.* (2018), Parimala *et al.* (2019) [12], Chhangte *et al.* (2019) [10] and Lakshmi *et al.* (2020).

Table 6: Path coefficient analysis for advanced breeding lines of rice in MF_6 generation

	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}
X_1	-0.4226	0.3833	0.0002	0.0598	0.0617	0.0357	0.0562	-0.0437	-0.0019	0.0384
X_2	-0.4225	0.3835	0.0003	0.0590	0.0606	0.0351	0.0571	-0.0445	-0.0018	0.0378
X_3	0.0116	-0.0121	-0.0095	-0.0157	-0.0021	-0.0341	-0.0741	-0.0698	0.0101	-0.0243
X_4	-0.0897	0.0803	0.0005	0.2820	0.3052	0.1296	0.3730	-0.3586	0.0468	0.1387
X_5	-0.0764	0.0680	0.0001	0.2520	0.3415	0.1201	0.3315	-0.2894	0.0137	0.1231
X_6	-0.0801	0.0714	-0.0017	0.1938	0.2175	0.1885	0.4463	-0.4331	0.0602	0.1325
X_7	-0.0416	0.0383	-0.0012	0.1842	0.1982	0.1472	0.5712	-0.5088	0.0383	0.1271
X_8	-0.0319	0.0295	-0.0011	0.1746	0.1706	0.1409	0.5019	-0.5789	0.1562	0.1156
X_9	0.0032	-0.0027	-0.0004	0.0507	0.0180	0.0435	0.0840	-0.3471	0.2606	0.0246
X_{10}	-0.0801	0.0716	0.0011	0.1929	0.2073	0.1232	0.3579	-0.3301	0.0316	0.2027
r value	0.1673	0.1646	-0.0037	0.9079	0.8843	0.7954	0.7529	0.6776	0.1344	0.7784

Residual effect = 0.1734 r = correlation coefficient of component traits with grain yield per plant

Where,
X_1 = Days to 50 percent flowering
X_2 = Days to maturity
X_3 = Plant height (cm)
X_4 = Number of tillers per plant
X_5 = Number of productive tillers per plant
X_6 = Panicle length (cm)
X_7 = Total number of spikelets per panicle
X_8 = Number of filled grains per panicle
X_9 = Panicle fertility (%)
X_{10} = Test weight (g)
X_{11} = Grain yield (kg/ha)

The highest direct negative effect was exhibited by plant height. The results were in accordance with the findings of Gour *et al.* (2017) [19] for days to 50 percent flowering.

Conclusion
Yield is a complex trait that is influenced by various environmental factors hence, direct yield selection is ineffective. Adequate information of yield and its associating traits is of great importance in breeding program in order to select superior genotypes. The present study indicated that yield could be increased by selecting the following traits: plant height, number of tillers, number of productive tillers, panicle length, number of spikelets per panicle, number of filled grains per panicle, and test weight.

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