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Association and path analysis for yield and its attributing traits in long duration rice genotypes (*Oryza sativa* L.) in Chhattisgarh plain region

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Abstract

The present study was undertaken to determine the relationship between grain yield and yield related traits in 40 long duration rice genotypes for 15 quantitative traits. The correlation study revealed that yield per hectare (q/ha) had strong positive association with tillers per hill, biological yield (q/ha), harvest index (%), spikelet fertility (%) and 1000 grain weight (g). The path coefficient analysis between yield per hectare (q/ha) as dependent variable and its related traits revealed that biological yield (q/ha), harvest index (%), 1000 grain weight (g), main panicle length (cm) showed high positive direct effect. Hence selection of these traits should be beneficial for improvement of grain yield in long duration rice genotypes.

Keywords: Correlation coefficient analysis, path coefficient analysis, long duration rice

Introduction

Rice is world's second most important staple food and it feed 2/3rd of the India's population. India is the 2nd largest producer of rice in the world, India's total production was 124.37 million metric tonnes from 45.77 mha area with 4.08 metric tonnes/hectare productivity (USDA 2022) [17]. The primary goal of rice breeding programmes is yield improvement. Correlation and path analysis is a biometrical tool used by breeders to discriminate the yield attributing trait and aids in development of genetically improved varieties. Grain yield is a combination of several other characteristics. The yield contributing traits are known as yield components having low heritability. Selection of such traits which directly influence yield is quite difficult. Yield is a function of total dry matter and harvest index. Thus, enhancing either the total dry matter or harvest index or both can increase the yield (Shobhana *et al.* 2017) [13]. An efficient breeding programme requires an understanding of the genetic variability of yield contributing traits, how they interact, and how they are related to yield (Nayak *et al.* 2016) [9]. The correlation analysis reveals the interaction between different traits, allowing us to interpret the component character on which the entire selection process is based. Path coefficient analysis is used to separate the coefficient of correlation into indirect and direct effects. Hence the present study is carried out to study the yield and yield attributing traits in rice genotypes.

Materials and Methods

The present investigation was scheduled during *kharif* season of 2022-23 at experimental farm of "B.T.C. College of Agriculture and Research Station (IGKV) Bilaspur, (C.G)". The experimental material contained forty rice genotypes along with four checks *viz.*, Swarna, MTU 1318, Pooja, Jaldubi. These forty genotypes were used for research work and all the rice genotypes were raised as a seedling in nursery bed and transplanted. The important quantitative traits recorded for study were days to 50% flowering, days to maturity, plant height (cm), tillers per hill, main panicle length (cm), peduncle length (cm), grains per main panicles, 1000 grain weight (g), biological yield (q/ha), harvest index (%), grain length (mm), grain width (mm), L/B ratio of grain and yield per ha (q/ha). Correlation was analysed using the Miller *et al.* (1958) [8] formula and path coefficients using the Dewey and Lu (1959) [3] technique. All the regular agronomic practices and plant protection measures were followed in experimental field to ensure uniform, healthy and stable crop growth. The observations were made on five competing plants from each genotype in each block that was randomly labelled. Finally, average values were calculated and statistical analysis was performed.

Results and Discussion

Correlation Analysis

In the present investigation correlation studies revealed that character viz. tillers per hill ($r_g = 0.920^{**}$ $r_p = 0.747^{**}$), biological yield ($r_g = 0.368^{**}$ $r_p = 0.641^{**}$), harvest index ($r_g = 0.784^{**}$ $r_p = 0.798^{**}$), spikelet fertility ($r_g = 0.825^{**}$ $r_p = 0.606^{**}$) and 1000 grain weight ($r_g = 0.476^{**}$ $r_p = 0.291^{**}$) were observed highly significant positive correlation with yield at both genotypic and phenotypic level. Therefore, direct selection of these trait can be practised for improving grain yield. Highly significant negative correlation was observed between grain yield and plant height ($r_g = -0.674^{**}$ $r_p = -0.467^{**}$), days to maturity ($r_g = -0.368^{**}$ $r_p = -0.225^{*}$), days to 50% flowering ($r_g = -0.419^{**}$ $r_p = -0.212^{*}$) at both genotypic and phenotypic level. Similar results were obtained by Prakash *et al.* (2019) [10] for harvest index, biological yield; Sudeepti *et al.* (2020) [15] for tiller per hill, spikelet fertility and 1000 grain weight; Kujur *et al.* (2023) [4] days to 50% flowering, days to maturity, biological yield, harvest index and spikelet fertility; Bhattacharya *et al.* (2019) [2] for harvest index, biological yield, 1000 grain weight; Lakshmi *et al.* (2017) [6] for plant height and days to 50% flowering. Days to 50% flowering had highly positive and significant correlation with days to maturity ($r_g = 0.823^{**}$ $r_p = 0.665^{**}$) while tillers per hill was positive and significantly correlated with harvest index % ($r_g = 0.757^{**}$ $r_p = 0.590^{**}$). Similar results were obtained by Sravan *et al.* (2012) [14] and Williams *et al.* (2021) [16] for harvest index; Mahto *et al.* (2018) [7] for days to maturity. The correlation analysis is represented in table 1.

Path Coefficient Analysis

The path coefficient analysis revealed that highest positive direct effect on grain yield per hectare at genotypic level was exhibited by biological yield (0.6719) followed by harvest index % (0.8150), 1000 grain weight (0.3929), main panicle length (0.2501), L/B ratio of grain (0.1419), plant height (0.1119). The highest direct but negative effect at genotypic level was exhibited by tillers per hill (-0.4838), grain length (-0.2891), grain width (-0.2858), spikelet fertility (-0.1183), days to 50% flowering (-0.0974), grains per main panicle (-0.0747), peduncle length (-0.0712). At phenotypic level

highest positive direct effect was exhibited by harvest index % (0.8250) followed by biological yield (0.6659). The above results were in accordance with Kumar *et al.* (2018) [5] for harvest index and biological yield and Singh *et al.* (2018) [12] for plant height, harvest index and biological yield; Basavraja *et al.* (2011) [1] and Pushkarnath *et al.* (2022) [11] for tiller per hill. Tillers per hill had moderate positive indirect effect through plant height (0.2646), days to 50% flowering (0.1359), days to maturity (0.1102) at genotypic level. Harvest index had high to moderate indirect effect through tillers per hill (0.6005), grain per main panicle (0.4859), spikelet fertility (0.4719), main panicle length (0.4038), grain width (0.3636), 1000 grain weight (0.2254), at genotypic level. At phenotypic level harvest index had high to negligible positive indirect effect through tillers per hill (0.6334), grain per main panicle (0.5310), spikelet fertility (0.4840), grain width (0.3446), 1000 grain weight (0.2437). Biological yield has high indirect effect through, days to maturity (0.9509), days to 50% flowering (0.6552) while moderate through plant height (0.4238), spikelet fertility (0.3819), tillers per hill (0.2350), grain length (0.2285), 1000 grain weight (0.2141) at genotypic level. At phenotypic level biological yield had moderate to low positive indirect effect through days to 50% flowering (0.2750), spikelet fertility (0.1884), days to maturity (0.1739), plant height (0.1480), tillers per hill (0.1357), grain length (0.1008). The remaining traits showed low to negligible direct and indirect effects. The direct and indirect effect of all traits are presented in table 2 and table 3. The genotypic and phenotypic path diagram is presented in Fig 1 and Fig 2.

The residual effect determines how best the causal factors account for the variability of the resultant factor. In the present study the residual effect was 0.172 and 0.150 at phenotypic and genotypic level respectively. Residual effect (0.172 and 0.150) indicated that the characters which were selected in this study contributed 83% and 85% at phenotypic and genotypic level respectively to the yield. Besides, some other factors, which have not been considered here, need to be included in this analysis to account fully that directly or indirectly influences the grain yield.

Table 1: Genotypic and phenotypic correlation matrix. (Above diagonal = Phenotypic correlation, Below diagonal = Genotypic correlation)

	DFE	DM	PH	TPH	MPL	PL	GPMP	TGW	BY	HI	GL	GW	LBR	SPF	YPH
DFE	1.000	0.665**	0.335*	-0.225*	-0.354*	-0.373**	-0.499**	0.012	0.413**	-0.437**	-0.006	-0.089	0.031	-0.060	-0.212
DM	0.823**	1.000	0.276*	-0.107	-0.303*	-0.324*	-0.295*	-0.066	0.261*	-0.357*	-0.060	-0.088	0.015	-0.024	-0.225*
PH	0.425**	0.612**	1.000	-0.441**	-0.217	0.215	-0.218	-0.296*	0.222*	-0.580**	-0.230*	-0.213	-0.020	-0.204	-0.467**
TPH	-0.281*	-0.228*	-0.547**	1.000	0.368**	0.056	0.396**	0.341*	0.204	0.590**	0.304*	0.251*	-0.013	0.546**	0.747**
MPL	-0.654**	-0.778**	-0.416**	0.541**	1.000	0.374**	0.379**	0.222*	-0.309*	0.389**	0.348*	-0.059	0.251*	0.211	0.228*
PL	-0.651**	-0.571**	0.380**	0.238*	0.496**	1.000	0.421**	-0.049	-0.007	0.080	0.141	-0.247*	0.274*	0.105	0.089
GPMP	-0.617**	-0.522**	-0.359*	0.491**	0.546**	0.619**	1.000	-0.067	-0.036	0.495**	0.152	-0.048	0.079	0.329*	0.487**
TGW	-0.010	-0.051	-0.427**	0.498**	0.337*	-0.250*	-0.114	1.000	0.090	0.227*	0.582**	0.545**	-0.030	0.310*	0.291*
BY	0.603**	0.876**	0.390**	0.216	-0.568**	0.052	0.028	0.197	1.000	-0.368**	0.151	0.068	0.027	0.283*	0.239*
HI	-0.715**	-0.817**	-0.863**	0.757**	0.566**	0.190	0.560**	0.312*	-0.287*	1.000	0.054	0.321*	-0.256*	0.451**	0.798**
GL	0.044	-0.004	-0.296*	0.398**	0.467**	0.206	0.150	0.665**	0.210	0.080	1.000	0.063	0.600**	0.235*	0.169
GW	-0.045	-0.171	-0.344*	0.366**	-0.072	-0.264*	-0.037	0.761**	0.041	0.564**	0.030	1.000	-0.673**	0.292*	0.349*
LBR	0.065	0.107	-0.023	0.019	0.345*	0.220	0.119	-0.032	0.050	-0.329*	0.675**	-0.738**	1.000	-0.104	-0.214
SPF	-0.085	0.127	-0.405**	0.816**	0.254*	0.232*	0.517**	0.445**	0.352*	0.786**	0.293*	0.557**	-0.294*	1.000	0.606**

*Significant at 5% probability level, ** Significant at 1% probability level, R critical value at 5% level of significance- ± 0.2199, R critical value at 1% level of significance- ±0.36107 DFE= Days to 50% flowering, DM= Days to maturity, PH= Plant height (cm), TPH= Tillers per hill, MPL= Main panicle length (cm), PL= Peduncle length (cm), GPMP= Grains per main panicle, TGW= 1000 grain weight (g), BY= Biological yield (q/ha), HI= Harvest index (%), GL= Grain length (mm), GW= Grain width (mm), LBR = L/B ratio of grain, SPF= Spikelet fertility, YPH= Yield per ha (q/ha).

Table 2: Genotypic path coefficient analysis showing direct effect (bold and diagonal values) and indirect effect (non-bold and off diagonal values).

	DFE	DM	PH	TPH	MPL	PL	GPMP	TGW	BY	HI	GL	GW	LBR	SPF	YPH
DFE	-0.0974	-0.1231	-0.0414	0.0274	0.0637	0.0634	0.0601	0.0010	-0.0587	0.0696	-0.0042	0.0044	-0.0063	0.0082	-0.419**
DM	0.0784	0.0620	0.0379	-0.0141	-0.0482	-0.0354	-0.0323	-0.0032	0.0543	-0.0506	-0.0003	-0.0106	0.0066	0.0079	-0.368**
PH	0.0476	0.0685	0.1119	-0.0612	-0.0465	0.0425	-0.0401	-0.0478	0.0436	-0.0965	-0.0331	-0.0385	-0.0026	-0.0453	-0.674**
TPH	0.1359	0.1102	0.2646	0.4838	-0.2618	-0.1149	-0.2375	-0.2410	-0.1047	-0.3661	-0.1923	-0.1769	-0.0090	-0.3948	0.920**
MPL	-0.1636	-0.1945	-0.1040	0.1353	0.2501	0.1239	0.1365	0.0842	-0.1421	0.1416	0.1168	-0.0180	0.0864	0.0634	0.238*
PL	0.0464	0.0407	-0.0271	-0.0169	-0.0353	-0.0712	-0.0441	0.0178	-0.0037	-0.0135	-0.0147	0.0188	-0.0157	-0.0165	0.253*
GPMP	0.0461	0.0390	0.0268	-0.0367	-0.0408	-0.0463	-0.0747	0.0085	-0.0021	-0.0419	-0.0112	0.0027	-0.0089	-0.0386	0.604**
TGW	-0.0039	-0.0202	-0.1678	0.1957	0.1323	-0.0982	-0.0449	0.3929	0.0774	0.1226	0.2614	0.2990	-0.0125	0.1748	0.476**
BY	0.6552	0.9509	0.4238	0.2350	-0.6169	0.0559	0.0307	0.2141	0.6719	-0.3116	0.2285	0.0450	0.0545	0.3819	0.368**
HI	-0.4840	-0.3923	-0.6661	0.6005	0.4038	0.0856	0.4859	0.2254	-0.3906	0.8150	0.0522	0.3636	-0.2613	0.4719	0.784**
GL	-0.0126	0.0013	0.0857	-0.1149	-0.1350	-0.0595	-0.0434	-0.1924	-0.0608	-0.0232	-0.2891	-0.0087	-0.1950	-0.0846	0.247*
GW	0.0129	0.0488	0.0984	-0.1045	0.0205	0.0754	0.0105	-0.2175	-0.0118	-0.1613	-0.0086	-0.2858	0.2110	-0.1592	0.594**
LBR	0.0092	0.0152	-0.0033	0.0027	0.0490	0.0312	0.0169	-0.0045	0.0071	-0.0467	0.0957	-0.1048	0.1419	-0.0417	-0.259*
SPF	0.0100	-0.0150	0.0479	-0.0965	-0.0300	-0.0275	-0.0611	-0.0526	-0.0416	-0.0930	-0.0346	-0.0659	0.0348	-0.1183	0.825**

Table 3: Phenotypic path coefficient analysis showing direct effect (bold and diagonal values) and indirect effect (non-bold and off diagonal values)

	DFE	DM	PH	TPH	MPL	PL	GPMP	TGW	BY	HI	GL	GW	LBR	SPF	YPH
DFE	-0.0501	-0.0333	-0.0168	0.0113	0.0177	0.0187	0.0250	-0.0006	-0.0207	0.0219	0.0003	0.0045	-0.0016	0.0030	-0.2121
DM	0.0162	0.0243	0.0067	-0.0026	-0.0074	-0.0079	-0.0072	-0.0016	0.0064	-0.0087	-0.0015	-0.0021	0.0004	-0.0006	-0.225*
PH	0.0038	0.0031	0.0114	-0.0050	-0.0025	0.0024	-0.0025	-0.0034	0.0025	-0.0066	-0.0026	-0.0024	-0.0002	-0.0023	-0.467**
TPH	-0.0029	-0.0014	-0.0056	0.0127	0.0047	0.0007	0.0050	0.0043	0.0026	0.0075	0.0039	0.0032	-0.0002	0.0070	0.747**
MPL	-0.0068	-0.0058	-0.0041	0.0070	0.0191	0.0072	0.0072	0.0042	-0.0059	0.0074	0.0067	-0.0011	0.0048	0.0040	0.228*
PL	0.0022	0.0019	-0.0013	-0.0003	-0.0022	-0.0059	-0.0025	0.0003	0.0000	-0.0005	-0.0008	0.0015	-0.0016	-0.0006	0.0888
GPMP	0.0134	0.0079	0.0058	-0.0106	-0.0101	-0.0113	-0.0268	0.0018	0.0010	-0.0132	-0.0041	0.0013	-0.0021	-0.0088	0.487**
TGW	0.0001	-0.0005	-0.0023	0.0026	0.0017	-0.0004	-0.0005	0.0076	0.0007	0.0017	0.0044	0.0041	-0.0002	0.0024	0.291*
BY	0.2752	0.1739	0.1480	0.1357	-0.2057	-0.0049	-0.0239	0.0596	0.6659	-0.2452	0.1008	0.0450	0.0176	0.1884	0.239*
HI	-0.4690	-0.3831	-0.6231	0.6334	0.4171	0.0859	0.5310	0.2437	-0.3953	0.8250	0.0579	0.3446	-0.2750	0.4840	0.798**
GL	0.0000	-0.0002	-0.0008	0.0011	0.0012	0.0005	0.0005	0.0021	0.0005	0.0002	0.0036	0.0002	0.0021	0.0008	0.1689
GW	0.0011	0.0011	0.0027	-0.0031	0.0007	0.0031	0.0006	-0.0068	-0.0008	-0.0040	-0.0008	-0.0125	0.0084	-0.0036	0.349*
LBR	0.0008	0.0004	-0.0005	-0.0003	0.0068	0.0074	0.0021	-0.0008	0.0007	-0.0069	0.0162	-0.0182	0.0270	-0.0028	-0.2138
SPF	0.0039	0.0015	0.0131	-0.0352	-0.0136	-0.0067	-0.0212	-0.0200	-0.0183	-0.0291	-0.0152	-0.0189	0.0067	-0.0645	0.606**

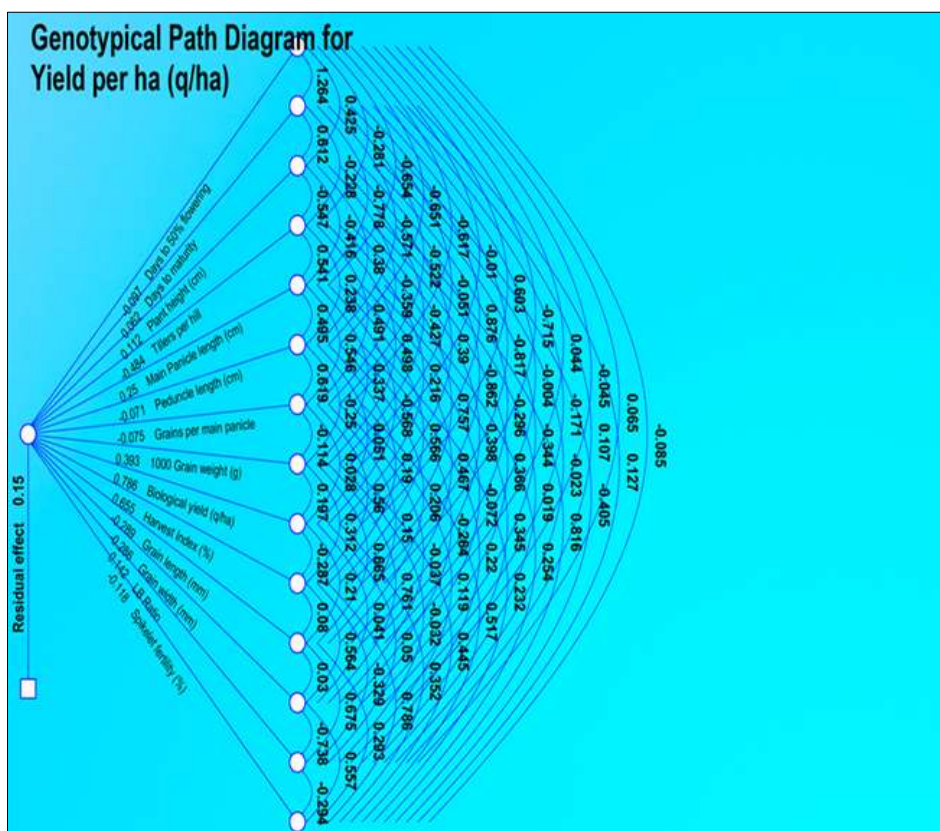


Fig 1: Genotypic Path Diagram

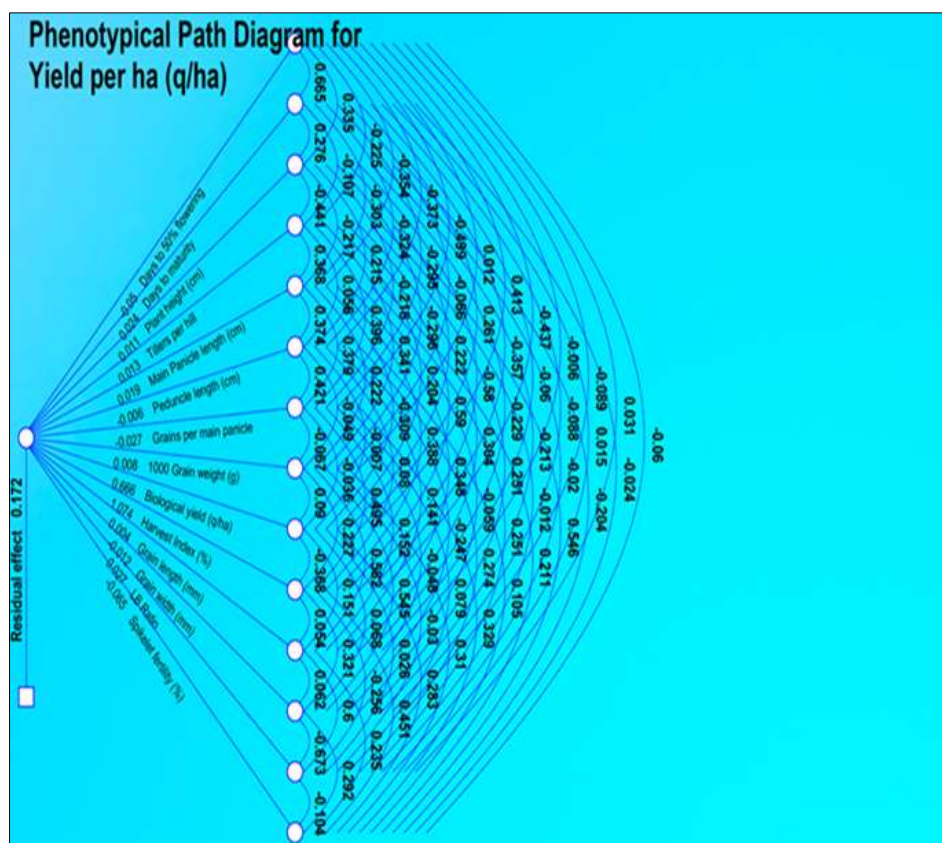


Fig 2: Phenotypic Path Diagram

Conclusion

The correlation study revealed that yield per hectare (q/ha) had strong positive association with tillers per hill, biological yield (q/ha), harvest index (%), spikelet fertility (%), 1000 grain weight (g). The path coefficient analysis between yield per hectare as dependent variable and its related traits indicated biological yield (q/ha), harvest index (%), 1000 grain weight (g), main panicle length (cm), L/B ratio of grain and plant height (cm). Hence these were most important traits which should be given priority during further selection programmes for the improvement of grain yield in long duration rice genotypes.

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