

RESEARCH ARTICLE

CORRELATION AND PATH COEFFICIENT ANALYSIS FOR GRAIN YIELD IN RICE (*ORYZA SATIVA* L.) GENOTYPES

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Received-03.06.2023, Revised-15.06.2023, Accepted-26.06.2023

Abstract: The current study investigated the relationship between GY of rice and its related attributing characters in twenty five different rice crop genotypes. As a consequence of correlation, it was found that the PTPP showed a very strong association that is positive with GYPP, followed by TW, PL, PH, DF50% and DM at the genotypic as well as phenotypic levels, respectively, demonstrate how GY can be increased with choosing genotypes with greater amounts for these characteristics. The outcome of the analysis of the path co-efficient showed that the PTPP had the greatest direct positive impact on GYPP, followed by the TW, PL, PH, DM, and DF 50%. These features should be regarded as a crucial selection criterion for maximizing crop output because they also played a significant influence in the indirect impacts for the majority of constituent traits on grain yield per plant.

Keywords: Correlation coefficient, Grain yield, Path analysis, Rice

INTRODUCTION

Rice (*Oryza sativa* L.) is a self-pollinating and an annual cereal crop. Rice belongs to the *Poaceae* family. It has chromosomal number $2n=24$. There are 25 recognised species in the genus *Oryza*, *Oryza sativa* and *Oryza glaberrima* are two of the 23 species that are wild, respectively grown as crops. Above the 60% of the world's people eats rice as a food regularly, making it the 2nd most popular food grain crop or a staple food that provides about 75% of their daily calories and 55% of their protein. The Asian continent is known as the world's rice bowl since it produces around 90% of the world's rice. In India, rice output totaled 116.42 million tonnes, and the crop's productivity was close to 2650 kg per ha. It took up about 43.79 mha of land (Anonymous 2018–2019). In Rajasthan, crop rice was grown on 0.199 mh along with a productivity of 2310 kg/ha and a production of 0.46 million tonnes in (Anonymous 2018–19). Due to unrestricted population growth, rice demand is continually rising. Numerous new varieties these are could break the yield ceiling are urgently needed to be developed the need to deal

given the existing rising population, achieve rice output suffers due to oneself and potentially maintain price steadiness. A complex polygenic characteristic known as yield that is strongly influenced by the environmental factor's and each of its component properties. Estimating the yield's association with its component characteristics and among them becomes crucial as a result. If selection is done simultaneously for yield-related characters, the effectiveness of selection can be increased. In quantitative traits, the environment has an impact on the genotypes, which in turn affects the phenotypic expression, association or ultimately, direction of the characters' associations with one another. Ability to gauge the strength and direction of a correlation is utilized to assess whether a change in one character will lead to a change in contrast characters at the same time. The information provided by the correlation analysis is incomplete in that it does not shed any insight on the underlying factors that are responsible for the numerous interrelationships. The interaction of a multitude of component qualities determines how a complicated trait, like grain yield per plant, is expressed. Through the examination of causal networks, a clearer picture

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of how each element contributes to the overall a complicated character's genetic makeup can be acquired. As a result, in this case, Wright's (1921) path coefficient analysis was helpful in separating direct from indirect causes of association, allowing for a more in-depth analysis of the specific forces at work to create a specific correlation and quantify the relative value of each causative factor. Such a study offers a reasonable basis for allocating weight to each trait when choosing an appropriate genetic improvement criterion. Identification of acceptable features for yield enhancement is greatly aided by the correlation and path co-efficient analysis.

MATERIALS AND METHODS

At the Agriculture Research Station in Kota, Rajasthan, the experiment was conducted. The experimental materials included 25 different rice genotypes. During *Kharif* 2019, these genotypes were cultivated using a RBD (Randomized Block Design) with 3 reps. Seedlings that were 24 days old were transplanted into 10 rows that were each 5 M long with a plant to plant distance of 20 CM and a row to row distance of 10 CM, respectively. To maintain a uniform plant population in each treatment and replication, all necessary precautions were performed. DF 50%, DM, PH, PTPP, PL, GPP, TW, amylose%, protein% and GYPP were all noted as observations for the traits. Character association by Singh and Chaudhary (1979) and path co-efficient analysis by Dewey and Lu (1959), respectively.

RESULTS AND DISCUSSION

According to the results of the association, genotypic correlation coefficients were larger than their corresponding phenotypic correlation coefficients, which may be due to the environment's modifying effect on the relationship of characters at the phenotypic level (Table 1).At both the phenotypic and genotypic levels, grain yield per plant was positively and significantly correlated with characters such as DF50%, DM, PH, PTPP, PL and TW, indicating that grain yield of rice can be improved by

choosing genotypes with higher values for these traits. These findings were consistent with those of Rajamadhan *et al.* (2011), Edukondalu *et al.* (2017), Sangare (2017), Priya *et al.* (2017), Kumar and Sonali (2018).

DF50% were positively and significantly correlated with DM, PH, PTPP, PL, GYPP and TW, while DM were positively and significantly correlated with PH, PTPP, PL, GYPP and test weight. The PTPP, PL, GPP, TW and GYPP were all substantially and positively linked with PH.At the genotypic level, a positive and substantial association between the PTPP and PH, weight, and quantity of GPP was found. The number of GPP had a positive and significant link with test weight, while the length of the panicle had a positive and significant correlation with GYPP.TW was positively and significantly correlated with amylose per cent, protein per cent, and GYPP. Protein per cent and amylose per cent had a positive and substantial correlation. The results of the path coefficient analysis (Table 2) showed that the PTPP had the greatest direct positive effect on GYPP, followed at both levels by the TW, PL, PH, DM, and DF50%.

The findings of Sowjanya *et al.* (2017), Hijam *et al.* (2017) and Khare *et al.* (2015) are in agreement with these findings. The large indirect effect through these qualities also contributed to the higher positive relationship of grain yield per plant with other characters. On the other hand, at the genotypic level, PL, GPP, and protein content per cent showed a negative direct effect on GYPP, whereas at the phenotypic level, PL, GPP, amylose content per cent and protein percent showed a negative direct effect. PTPP (0.93360) had the greatest direct impact among all the features at the genotypic level, followed by PH (0.24020), test weight (0.17320), amylose content (0.06630), DF50% (0.06070), and DM (0.01990). However, negative direct effects were seen for the PL (-0.22480), the GPP (-0.20510), and the protein content (-0.05210). PTPP (0.78260) had the most direct effect at the phenotypic level, followed by DF50% (0.57710), DM (0.54310), test weight (0.35130), and PH (0.0380).

Table 1. Estimation of the correlation between phenotypic (P) and genotypic (G) characteristics for 10 characters of rice

| Characters | r | DF 50% | DM | PH | PTPP | PL | GPP | 1000-GW | Amylose content | Protein content | GYPP |
|------------|---|---------------|---------------|---------------|---------------|---------|---------|---------|-----------------|-----------------|---------|
| DF 50% | P | 1.0000 | 0.976** | 0.754** | 0.302** | 0.585** | 0.694** | 0.362** | -0.446** | -0.0740 | 0.294** |
| | G | 1.0000 | 0.999** | 0.926** | 0.329** | 0.631** | 0.961** | 0.372** | -0.481** | -0.0890 | 0.308** |
| DM | P | | 1.0000 | 0.767** | 0.323** | 0.632** | 0.677** | 0.415** | -0.418** | -0.0400 | 0.293** |
| | G | | 1.0000 | 0.941** | 0.348** | 0.668** | 0.988** | 0.430** | -0.446** | -0.0360 | 0.325** |
| PH | P | | | 1.0000 | 0.280* | 0.567** | 0.526** | 0.411** | -0.331** | -0.1010 | 0.284* |
| | G | | | 1.0000 | 0.383** | 0.705** | 0.859** | 0.534** | -0.433** | -0.1330 | 0.409** |
| PTPP | P | | | | 1.0000 | 0.396** | 0.1970 | 0.527** | 0.1170 | 0.2140 | 0.881** |
| | G | | | | 1.0000 | 0.484** | 0.233* | 0.577** | 0.1240 | 0.2100 | 0.993** |

| | | | | | | | | | | | |
|------------------------|---|--|--|--|--|---------------|---------------|---------------|---------------|---------------|---------------|
| PL | P | | | | | 1.0000 | 0.375** | 0.622** | 0.0480 | 0.0310 | 0.369** |
| | G | | | | | 1.0000 | 0.518** | 0.677** | 0.0570 | 0.0580 | 0.459** |
| GPP | P | | | | | | 1.0000 | 0.262* | -0.334** | 0.0660 | 0.1460 |
| | G | | | | | | 1.0000 | 0.340** | -0.488** | 0.0670 | 0.2040 |
| 1000- GW | P | | | | | | | 1.0000 | 0.284* | 0.420** | 0.607** |
| | G | | | | | | | 1.0000 | 0.293** | 0.456** | 0.645** |
| Amylose content | P | | | | | | | | 1.0000 | 0.384** | 0.1390 |
| | G | | | | | | | | 1.0000 | 0.412** | 0.1570 |
| Protein content | P | | | | | | | | | 1.0000 | 0.1780 |
| | G | | | | | | | | | 1.0000 | 0.1850 |
| GYPP | P | | | | | | | | | | 1.0000 |
| | G | | | | | | | | | | 1.0000 |

* 5% significant level

** 1% significant level

Table 2. genotypic and phenotypic path coefficient for grain yield per plant in rice

| Characters | | DF 50% | DM | PH | PTPP | PL | GPP | 1000- GW | Amylose content | Protein content | GYPP |
|-------------------------|---|----------------|---------------------|----------------|----------------|---------------------|---------------------|----------------|-----------------|---------------------|---------|
| DF 50% | P | 0.57710 | - 0.53020 | 0.00290 | 0.23670 | - 0.07110 | - 0.05850 | 0.12730 | 0.00150 | 0.00780 | 0.294** |
| | G | 0.06070 | 0.01990 | 0.22240 | 0.30670 | - 0.14180 | - 0.19710 | 0.06450 | -0.03190 | 0.00470 | 0.308** |
| DM | P | 0.56330 | - 0.54310 | 0.00300 | 0.25250 | - 0.07680 | - 0.05700 | 0.14570 | 0.00140 | 0.00410 | 0.293** |
| | G | 0.06060 | 0.01990 | 0.22610 | 0.32480 | - 0.15030 | - 0.20250 | 0.07450 | -0.02950 | 0.00190 | 0.325** |
| PH | P | 0.43500 | - 0.41670 | 0.00380 | 0.21900 | - 0.06890 | - 0.04430 | 0.14430 | 0.00110 | 0.01060 | 0.284* |
| | G | 0.05620 | 0.01870 | 0.24020 | 0.35800 | - 0.15840 | - 0.17630 | 0.09250 | -0.02870 | 0.00690 | 0.409** |
| PTPP | P | 0.17450 | - 0.17520 | 0.00110 | 0.78260 | - 0.04810 | - 0.01660 | 0.18510 | -0.00040 | - 0.02240 | 0.881** |
| | G | 0.01990 | 0.00690 | 0.09210 | 0.93360 | - 0.10870 | - 0.04780 | 0.10000 | 0.00820 | - 0.01090 | 0.993** |
| PL | P | 0.33780 | - 0.34340 | 0.00220 | 0.31000 | - 0.12140 | - 0.03160 | 0.21830 | -0.00020 | - 0.00330 | 0.369** |
| | G | 0.03830 | 0.01330 | 0.16930 | 0.45140 | - 0.22480 | - 0.10620 | 0.11730 | 0.00380 | - 0.00300 | 0.459** |
| GPP | P | 0.40050 | - 0.36750 | 0.00200 | 0.15400 | - 0.04550 | - 0.08430 | 0.09220 | 0.00110 | - 0.00690 | 0.14600 |
| | G | 0.05830 | 0.01970 | 0.20650 | 0.21760 | - 0.11640 | - 0.20510 | 0.05900 | -0.03240 | - 0.00350 | 0.20400 |
| 1000- GW | P | 0.20920 | - 0.22520 | 0.00160 | 0.41250 | - 0.07550 | - 0.02210 | 0.35130 | -0.00090 | - 0.04380 | 0.607** |
| | G | 0.02260 | 0.00860 | 0.12830 | 0.53880 | - 0.15230 | - 0.06980 | 0.17320 | 0.01950 | - 0.02380 | 0.645** |
| Amylose content% | P | - 0.25750 | 0.22720 | - 0.00130 | 0.09190 | - 0.00580 | - 0.02820 | 0.09970 | -0.00330 | - 0.04010 | 0.13900 |
| | G | - 0.02920 | - 0.00890 | - 0.10400 | 0.11580 | - 0.01280 | - 0.10010 | 0.05080 | 0.06630 | - 0.02150 | 0.15700 |
| Protein content% | P | - 0.04290 | 0.02150 | - 0.00040 | 0.16770 | - 0.00380 | - 0.00550 | 0.14740 | -0.00130 | - 0.10440 | 0.17800 |
| | G | - 0.00540 | - 0.00070 | - 0.03200 | 0.19560 | - 0.01290 | - 0.01380 | 0.07900 | 0.02730 | - 0.05210 | 0.18500 |

Phenotypic residual effect = 0.1623, Genotypic residual effect = 0.18190

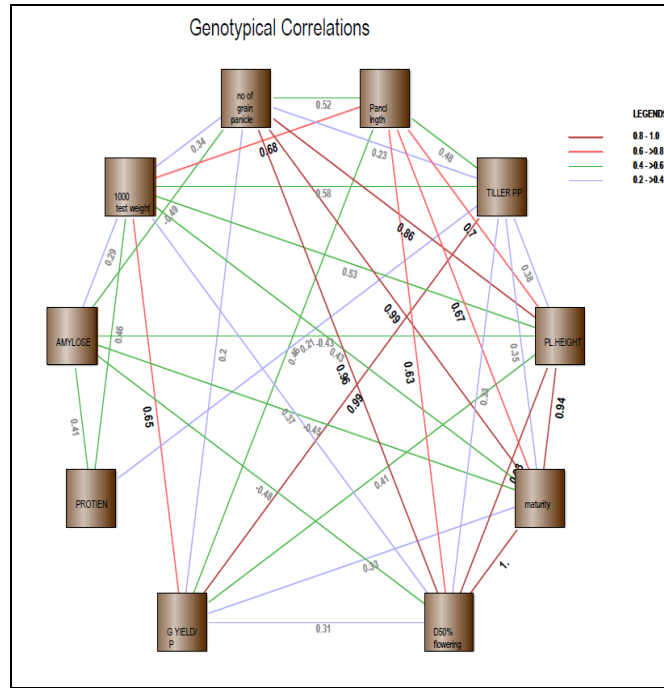


Fig 1. Genotypic correlation co-efficient diagram for ten characters in rice genotypes.

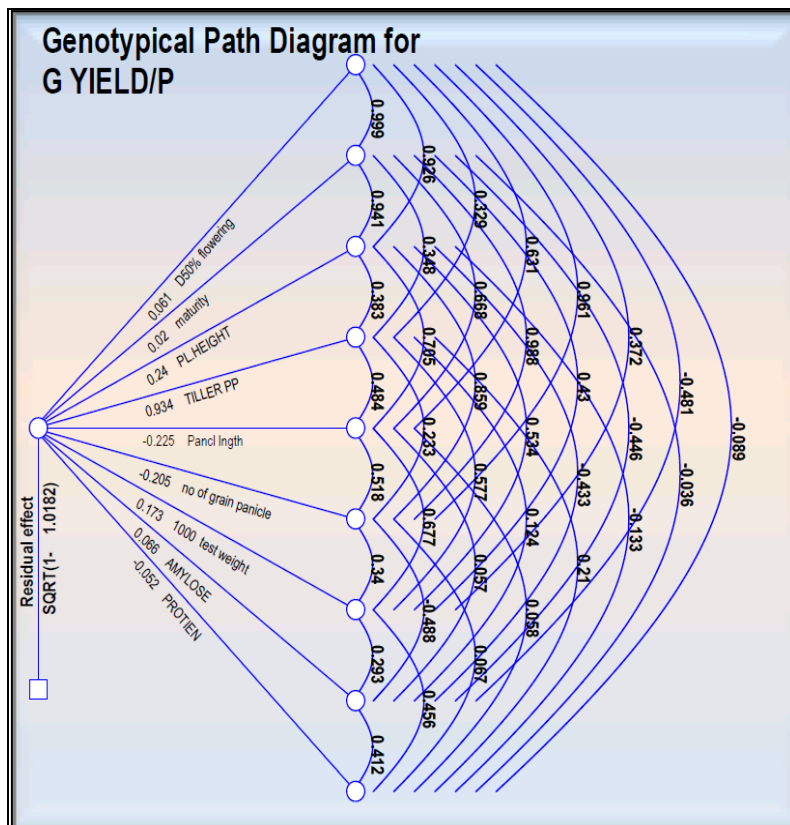


Fig 2. Genotypic path diagram for grain yield per plant for rice genotypes

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