Unraveling The Genetics Of Rice (Oryza Sativa L.) Yield And Its Component Traits

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Abstract

In the Hadoti region of Rajasthan, rice (*Oryza sativa* L.) crosses were grown in a Randomized Block Design for the purpose of estimating correlation and path coefficient in an experimental study. An examination of variance data demonstrated that there were noteworthy distinctions among all genotypes with respect to the traits that were studied. The correlation or association studies disclosed that the relation of grain yield per plant was positively and significantly at phenotypic and genetic level with characters viz. number of effective tillers per plant, panicle length, number of spikelets per panicle, test weight and kernel length. The highest positive direct impression/ effect on grain yield was recorded for number of spikelets per panicle, panicle length, kernel length and number of effective tillers per plant.

Keywords: path analysis, grain yield per plant, *Oryza sativa*, correlation

Introduction:

Rice is a self-pollinating, short-day plant originating from Southeast Asia, belonging to the Poaceae family and Oryzoidae subfamily. It functions as a primary dietary source for more than half of the global population, as stated by Khush in 2005, with a rich nutritional profile encompassing carbohydrates, proteins, minerals, dietary fiber, and vitamins like riboflavin, thiamine and niacin (Verma et al.). Rice, in particular, serves as the predominant dietary foundation for over 50 percent of the world's population, with Southeast Asia, where 90 percent of the population relies on rice for their main energy source (Anonymous 2018). In India, rice cultivation covers a vast 44 million hectares, yielding a substantial annual production of 116×10^6 tons and 2700 kilograms per hectare productivity recorded (Anonymous 2021). In essence, rice's historical roots in Southeast Asia, its global prevalence as a dietary staple, and its vital role in nourishing millions underline its significance in the world's food landscape. In Rajasthan, rice cultivation spans approximately 2.19×10^5 hectares, yielding a production of 4.80×10^5 tonnes, with an average productivity of 2180 kg/ha (Anonymous 2019-20). The rice-growing landscape in Rajasthan can be broadly categorized into four zones. The first zone is the irrigated area, known as the humid southeastern plain zone (Zone Vth), encompassing districts like Kota, Baran, Bundi and Jhalawar, traversed by the Chambal river canal system. Within this zone, the agricultural university in Kota falls under the Zone Vth of Rajasthan. Here, rice is cultivated across 1.16×10^5 hectares, resulting in a production of 3.03×10^5 tonnes and a productivity of 2320 kg per ha (Anonymous 2019-20). In summary, rice cultivation in Rajasthan encompasses diverse zones, with the irrigated, humid southeastern plain zone being one of the prominent regions, contributing significantly to the state's rice production and productivity. Enhancing this yield through direct selection proves challenging since grain yield per plant is a assorted, polygenic attribute heavily impressed by multiple component traits and surrounded habitat factors. Consequently, it becomes imperative to evaluate the correlation or association between yield and its component attributes, as well as the interrelationships among these component traits.

Materials and Methods

The study was carried out in the Ummedganj Agricultural Farm, Kota (Rajasthan), during the *Kharif* season of 2020. The Meteorological data is given in figure 1 and figure 2. The experimental setup followed RBD with 3 replications. To maintain uniformity, a R×R spacing of 20 cm and a P×P spacing of 10 cm were adhered to. Data were recorded from 5 randomly or conjecturally selected competitive plants among the 45 crosses in every replication for all characters, excluding for the days to 50% flowering, which was collected on seed bed basis. Statistical analysis of the experimental design was performed utilizing the technique recommended by Panse and Sukhatme (1985) for variance determination. Genotypic and phenotypic correlation coefficients or quotient were determined using the method outlined by Singh and Chaudhary (1979). The path coefficient analysis, proposed by Wright (1921) and expanded upon by Dewey and Lu (1959), was employed to compute the direct and indirect effect measure.
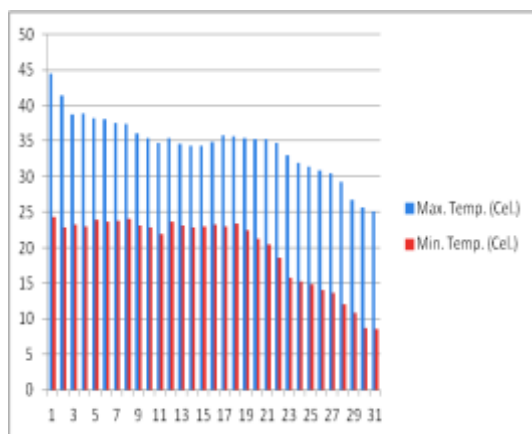
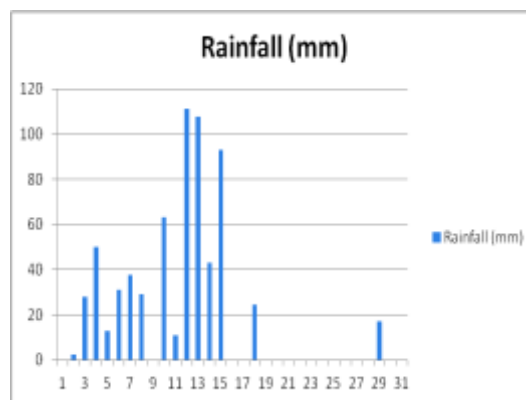**Fig. 1** Maximum and Minimum Temperature on Weekly Basis

Fig. 2 Rainfall on weekly basis

Result and Discussion:

To enhance the effectiveness of the selection process, it is advantageous to concurrently consider traits that exhibit correlations with crop yield. This approach can significantly raise the outcomes of breedings. In the context of quantitative traits, it's essential to understand that the genotype of a plant is not solely responsible for determining its traits. Environmental factors show a crucial contribution in influencing the statement of these traits. Consequently, the environment can impact not only the phenotypic expression of individual traits but also their associations with one another. This means that the environment can influence the direction and magnitude of the relationships between various traits. Having knowledge about the magnitude and direction of these correlations is invaluable for plant breeders. It allows them to make informed decisions about how improvements in one particular trait may lead to simultaneous changes in other traits. In essence, this information helps in predicting the overall impact of a breeding strategy on the plant's performance. A particularly important aspect to consider is the magnitude of the positive correlation coefficient at the genotypic level between individual traits and grain yield. This is essential for indirect selection, where breeders choose to enhance a particular trait by selecting for another trait that is strongly correlated with it. When there is a high positive correlation between a component trait and yield at the genetic level, it indicates that improvements in the component trait will likely result in higher yield. It's worth noting that while genotypic correlation coefficients are valuable for breeding purposes, there isn't a suitable statistical test available to determine the significance of these coefficients. Consequently, the focus in breeding programs has predominantly been on phenotypic correlation coefficients, which provide practical insights into trait relationships and their potential impact on grain yield. This emphasis on phenotypic correlations ensures that breeding decisions are based on tangible and observable traits, even though the underlying genetic correlations may not be as precisely quantified.

In our study, we observed that genotypic correlation factor/ coefficients tend to be higher than their corresponding/ commensurate phenotypic counterparts. This discrepancy likely arises from the environmental influence on the relationship between traits at the phenotypic level. It's important to consider this when selecting for crop yield, as merely targeting yield itself may not yield the most effective results. This is because yield is often the result of a complex interplay of multiple genes and their interactions. To make more informed breeding decisions, it's crucial to descry the relationships between yield and its attributes. By selecting for one component, we can inadvertently trigger changes in others. Therefore, a strategic approach to enhancing yield involves gathering data on character associations. In the context of our current investigation, we focused on determining both phenotypic correlation quotient/ coefficients and genotypic correlation quotient/ coefficients for grain production and its related characteristics. This analysis is essential for comprehending how these traits interact and influence one another at the genetic and phenotypic levels. Ultimately, it allows us to make more precise and effective choices in our efforts to renovate grain production and its related traits.

Significantly positive correlations were identified between grain production and other traits such as the number of effective tillers per plant, panicle length, number of spikelets per panicle, 1000-grain weight, and kernel length, at both the phenotypic level and genotypic level. On the other hand, a significantly negative correlation was observed with plant height at both levels and with kernel breadth at the genotypic level. These characters need due consideration during any selection programme. Similar findings of correlation reported earlier by Ahmed et al. (2021) and Das (2021). Days to 50% flowering, elongation ratio and amylose content showed non signification association with grain yield both levels. The correlation of days to 50% flowering was positive significantly associated or correlated with plant height and test weight at genotypic levels. It was positive correlated with no. of effective tillers/ plant, panicle length, elongation ratio. It was negatively associated with no. of spikelets/ panicle, kernel length, kernel breadth, amylose percentage and grain production per plant. Plant height was positive or direct significant correlated with days to 50% flowering and kernel breadth at genotypic level and phenotypic level. It was negatively or unfavourable and remarkably/ significantly associated by number of effective tillers/ plant, no. of spikelets/ panicle and grain output/ plant at genotypic level and phenotypic level. It was positively associated with kernel breadth. These findings support

the observation made by Tiwari et. al. (2019) and Subbulakshmi and Muthuswamy (2018). Number of effective tillers per plant was significantly and positively associated with panicle length, number of spikelets per panicle, test weight, kernel length and grain output/ plant at both genotypic level an phenotypic level. Grain yield exhibited positive and statistically significant association with various traits, namely the number of effective tillers per plant, panicle length, number of spikelets per panicle, test weight, and kernel length, at both the phenotypic level and genotypic level. Conversely, a significant negative correlation was observed with plant height at both levels and with kernel breadth at the genotypic level. It was positive correlated by elongation ratio at genotypic level and phenotypic level. No. of spikelets per panicle was significantly positive associated by elongation ratio and grain yield per plant. It found positive correlated with test weight, kernel length and amylose content. test weight was significantly positive related with no. of effective tillers per plant, panicle length, kernel length, elongation ration and grain output/ plant. It was positively related with no. of effective tillers per plant, kernel breadth and amylose content. Kernel length was significantly positively related by no. of effective tillers per plant, panicle length, test weight and grain production per plant at genotypic level and phenotypic level. It was positive or straight associated by no. of spikelets per panicle and elongation ratio. Kernel breadth was significantly positive correlated with plant height, elongation ratio and amylose content. It was significantly negatively correlated by no. of effective tillers per plant and grain production/ plant. Elongation ratio was significantly positive correlated with no. of spikelets/ panicle and test weight. It was negatively related by plant height, no. of effective tillers/ plant and grain production per plant. Significantly positive relations were observed between amylose content and kernel breadth. Furthermore, amylose content showed positive relation with the number of spikelets per panicle, kernel length, kernel breadth, elongation ratio, and grain yield per plant. Additionally, grain production per plant exhibited significantly positive correlations with the number of effective tillers per plant, panicle length, the number of spikelets per panicle, test weight, and kernel length. Conversely, it had negative associations with days to 50% flowering, plant height, kernel breadth, and elongation ratio. These consistent results were also documented by Lakshmi et al. (2020) and Gour et al. (2017) in their research on rice.

Amylose content was positively and significantly associated with kernel breadth. It was positively associated with no. of spikelets/ panicle, kernel length, kernel breadth, elongation ratio, amylose content, grain yield/ plant. Grain yield/ plant was positively and significantly correlated with no. of effective tillers/ plant, panicle length, no. of spikelets/ panicle, 1000-grain weight and kernel length. It was negatively associated with days to 50% flowering, plant height, kernel breadth and elongation ratio. Similar results were also reported by Lakshmi et. al. (2020) and Gour et. al. (2017) in rice.

Correlation analysis, while informative, presents an incomplete picture by merely revealing associations without delving into their underlying causes. Complex traits, like grain yield, are influenced by a multitude of component traits working in concert. To truly comprehend the genetic architecture of such complex characteristics, a more nuanced approach is required. This is where causal analysis, specifically path coefficient analysis as devised by Wright in 1921, comes into play. Path coefficient analysis serves as a valuable tool for dissecting the intricate web of direct and indirect causal factors contributing to correlations. It unravels the specific forces at play behind observed associations and quantifies the relative significance of each causal element. This method transcends the limitations of basic correlation analysis, offering a more comprehensive understanding of the genetic dynamics shaping complex traits. In practical terms, path coefficient analysis enables researchers to assign weighted importance to individual attributes when formulating strategies for genetic improvement. By discerning the true nature of character associations, this approach guides the allocation of resources and efforts toward the most influential genetic components. It transforms the analysis from a mere statistical exercise to a practical basis for informed decision-making. Although correlation analysis provides a valuable initial step in genetic research, path coefficient analysis stands out as an essential instrument in this field. It illuminates the complex web of causal relationships underpinning intricate traits, enabling the development of more refined and potent genetic improvement strategies. This methodology empowers researchers to tap into the complete potential of their investigations, moving beyond superficial associations to reveal the profound genetic mechanisms at work.

In this investigation, we conducted path coefficient analyses at both genotypic level and phenotypic level for all the traits. The aim of the analysis was to disentangle the correlation coefficients between these characteristics, specifically in relation to grain yield. By doing so, we aimed to assess the individual contributions of each characteristic to the overall grain production. The results of our investigation shed light on the direct and indirect effect or consequences of different traits on grain production. These findings highlighted a consistent alignment between the direction and magnitude of the direct effects of these characteristics and their correlations with grain yield. As a result, it is reasonable to anticipate a significant enhancement in grain yield through the selection of component traits that exhibit strong positive direct effects. In the phenotypic analysis, the most prominent direct positive influence or effect on grain production was associated with the number of effective tillers per plant, followed by the number of spikelets per panicle, test weight, kernel length, panicle length, and amylose content. While highest direct negative effect was recorded for plant height followed by days to 50% flowering, kernel breadth and elongation ratio. These findings support the observation made earlier by Kumar et. al. (2020) and Tiwari et. al. (2019). In the genotypic evaluation, the most substantial direct positive impact on grain production was linked to the number of effective tillers per plant, with panicle length, the number of spikelets per panicle, test weight, kernel length, and amylose content following closely. Meanwhile, the most pronounced direct negative effect was associated with plant height, succeeded by kernel breadth, days to 50% flowering, and elongation ratio.

Further examination through path analysis showed that the number of spikelets per panicle, panicle length, kernel length, and the number of effective tillers per plant had significant direct effects on grain yield. The strong positive relationships between grain yield and the other attributes were primarily due to their substantial indirect impact via these traits. These results emphasized that grain production is primarily shaped by a combination of direct and indirect impacts/ effects. In contrast, the negative associations of plant height, kernel breadth, days to 50% flowering, and elongation ratio with grain production were predominantly influenced by their adverse indirect effects. If direct effect is more and positive then put more emphasis on the use of that character in selection programme. Otherwise restricted selection is to be used for characters having high indirect effects.

Table 1 Computation of phenotypic (P) and genotypic (G) correlation coefficients for 11 traits in rice.

Characters		Days to 50% flowering	Plant height (cm)	No. of effective tillers/ plant	Panicle length (cm)	No. of spikelets/ panicle	1000-Grain weight (g)	Kernel length (mm)	Kernel breadth (mm)	Elongation ratio	Amylose content (%)	Grain yield/ plant (g)
Days to 50% flowering	P		0.144	0.051	0.024	-0.005	0.081	-0.023	-0.162	0.042	-0.044	-0.075
	G		0.407**	0.019	0.041	-0.136	0.319**	0.034	-0.244	0.004	-0.254	-0.142
Plant height (cm)	P			-0.317**	-0.083	-0.320**	0.047	-0.002	0.172*	-0.081	-0.096	-0.400**
	G			-0.413**	-0.192	-0.420**	-0.021	-0.039	0.212	-0.144	-0.130	-0.547**
No. of effective tillers/ plant	P				0.246**	0.319**	0.474**	0.333**	-0.230**	0.017	0.025	0.596**
	G				0.484**	0.430**	0.631**	0.445**	-0.308*	-0.015	0.040	0.766**
Panicle length (cm)	P					0.240**	0.176*	0.171**	-0.123	0.039	-0.106	0.263**
	G					0.422**	0.370**	0.313*	-0.277	0.280	-0.166	0.550**
No. of spikelets/ panicle	P						0.141	0.055	-0.109	0.295**	0.148	0.447**
	G						0.186	0.078	-0.110	0.427**	0.160	0.532**
1000-Grain weight (g)	P							0.423**	0.027	0.171**	0.114	0.429**
	G							0.557**	0.026	0.215	0.132	0.481**
Kernel length (mm)	P								-0.093	0.133	-0.123	0.319**
	G								-0.113	0.297*	-0.185	0.385**
Kernel breadth (mm)	P									0.166	0.457**	-0.226**
	G									0.344*	0.546**	-0.229
Elongation ratio	P										0.040	-0.009
	G										0.067	-0.055
Amylose content (%)	P											0.026
	G											0.026
Grain	P											

Table 2 Estimation of the path coefficients for grain yield per plant, taking into account both phenotypic (P) and genotypic (G) factors related to various traits.

Characters		Days to 50% flowering	Plant height (cm)	No. of effective tillers/ plant	Panicle length (cm)	No. of spikelets/ panicle	1000-Grain weight (g)	Kernel length (mm)	Kernel breadth (mm)	Elongation ratio	Amylose content (%)	Grain yield/ plant (g)
Days to 50% flowering	P	**-0.078**	-0.033	0.013	0.001	-0.001	0.022	-0.003	0.011	-0.007	0.001	-0.075
	G	**0.117**	-0.203	0.002	0.014	-0.066	0.048	0.011	-0.113	-0.003	0.051	-0.142
Plant height (cm)	P	-0.011	**-0.232**	-0.080	-0.004	-0.090	0.012	0.000	-0.011	0.013	0.002	-0.400
	G	0.048	**-0.498**	-0.037	-0.065	-0.205	-0.003	-0.012	0.098	0.101	0.026	-0.547
No. of effective tillers/ plant	P	-0.004	0.073	**0.251**	0.011	0.090	0.126	0.037	0.015	-0.003	-0.001	0.596
	G	0.002	0.205	**0.089**	0.163	0.210	0.095	0.141	-0.142	0.011	-0.008	0.766
Panicle length (cm)	P	-0.002	0.019	0.062	**0.046**	0.067	0.047	0.019	0.008	-0.006	0.002	0.263
	G	0.005	0.096	0.043	**0.336**	0.206	0.056	0.099	-0.128	-0.196	0.033	0.550
No. of spikelets/ panicle	P	0.000	0.074	0.080	0.011	**0.281**	0.038	0.006	0.007	-0.047	-0.003	0.447
	G	-0.016	0.209	0.038	0.142	**0.488**	0.028	0.025	-0.051	-0.299	-0.032	0.532
1000-Grain weight (g)	P	-0.006	-0.011	0.119	0.008	0.040	**0.266**	0.046	-0.002	-0.028	-0.003	0.429
	G	0.037	0.010	0.056	0.124	0.091	**0.151**	0.177	0.012	-0.151	-0.027	0.481
Kernel length (mm)	P	0.002	0.000	0.084	0.008	0.015	0.112	**0.110**	0.006	-0.022	0.003	0.319
	G	0.004	0.019	0.040	0.105	0.038	0.084	**0.317**	-0.052	-0.208	0.037	0.385
Kernel breadth (mm)	P	0.013	-0.040	-0.058	-0.006	-0.031	0.008	-0.011	**-0.065**	-0.026	-0.011	-0.226
	G	-0.029	-0.106	-0.027	-0.093	-0.053	0.004	-0.036	**0.462**	-0.241	-0.110	-0.229
Elongation ratio	P	-0.003	0.019	0.004	0.002	0.083	0.046	0.015	-0.011	**-0.162**	-0.001	-0.009
	G	0.000	0.072	-0.001	0.094	0.208	0.032	0.094	0.159	**-0.700**	-0.014	-0.055
Amylose content (%)	P	0.003	0.022	0.006	-0.005	0.042	0.030	-0.013	-0.030	-0.006	**-0.023**	0.026
	G	-0.030	0.065	0.004	-0.056	0.078	0.020	-0.059	0.252	-0.047	**-0.201**	0.026

Digonal values in Bold are direct effects Residual effects: Phenotypic : 0.4500Genotypic : 0.1099

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