

Original Research Article

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Harnessing the Genetic Variability and Trait Association of Yield and Yield Related Traits in Rice (*Oryza sativa* L.)

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ABSTRACT

The present investigation was conducted to examine the 17 bread rice genotypes including one check to study the genetic parameters, correlation and genetic diversity. The experiment was carried out in Research Farm Genetics & Plant Breeding of AKS University, Satna, M.P., during *kharif* season, 2021-22 in Randomized Block Design (RBD) with three replications. Analysis of variance showed highly significant differences among 17 bread rice genotypes for 14 characters studied. The statistical analysis of variance showed significant differences among genotypes for all 14 traits, including days to 50% flowering, plant height, effective tillers per plant, flag leaf length, maturity, panicle length, kernel length and width, test weight, harvest index, biological yield per plant and grain yield per plant. The results showed that these genotypes of rice crops have short flowering period, tall plant height, many effective tillers per plant, long flag leaf, long panicle and high grain yield per plant. The coefficients of variation were low, indicating little variation within the genotypes for each trait. The study results suggest significant variations in the characteristics of different genotypes of rice crops and can be useful for crop improvement. The genotypic correlation coefficients were generally higher than the phenotypic ones. Traits related to reproductive growth, such as number of effective tillers per plant, number of seeds per panicle, and harvest index, had positive effects on grain yield per plant, while traits related to vegetative growth, such as days to 50% flowering and plant height, had negative effects. The path coefficient analysis indicated that biological yield per plant and harvest index had the maximum positive effect on grain yield per plant, while spikelet's per spike, grain per spike, effective tiller per plant, days to maturity, and days to 50% flowering had the maximum negative effect. These findings provide valuable insights for rice crop improvement.

Keywords

Rice, genetic parameters, correlation and path analysis

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Introduction

Rice is an ancient staple food crop of the world covering an area 143.69 mha. Rice belongs to genus *Oryza* of Gramineae family. The genus *Oryza* has 24

wild sub-species in which two cultivable species (*Oryza sativa* and *Oryza galberima*). Chromosome contain ($2n=24$). *Oryza sativa* is a cultivated diploid species. The sativa rice varieties of the world are commonly divided into three sub-species i.e., indica,

japonica, and javanica. It provides about 80% calories for more than two billion people of Asia including India (Subhashchandra, *et al.*, 2009) and 1/3 calories intake of nearly one billion people in Africa and Latin America. On global basis, It provides about 22% of the world supply of calories. Rice is also a major source of protein (17%). Rice occupies 1/3 of the area planted to cereals in the developing countries which is about 50% more than area under wheat, (Singh, 1986).

India has the largest area (40.99 million hectare) constituting 28% of the land under rice in the world (Anonymous, 1986) and ranks second in total production (89.58 million tonnes), next to China. Rice is a very unique crop, widely adopted and grown under wide range of agroclimatic conditions. Reduced genetic variability, improved cultural practices and continuous rice cropping factors for increased rice production have increased the genetic vulnerability of the crop. The productivity of rice in 2022 is 42.8% in India.

China is the world's leading rice producer with nearly 125 million tonnes production. India largest rice area (43.86 mts) producing nearly a quarter of Asia production occupying second position after China. In India rice production and productivity showed a steady increase from the first five-year plan to tenth five-year plan. However, it is difficult to devise direct approaches to determine the relative importance of the source capacity and sink strength in contributing to the grain yield in wheat. Therefore, a better understanding of source-sink interactions would help to propose strategies to improve yield potential using genetic approaches.

Sink limitation has been reported to be a limiting factor to yield potential of wheat and barley in the environments with the absence of serious post-anthesis stress (Anwar, *et al.*, 2009; Birhanu Mecha *et al.*, 2017; Ansari, *et al.*, 2005). The ration of genotypic variance to the phenotypic variance or total variance is known as heritability. It is generally expressed in percentage. Thus, heritability is the heritable portion of phenotypic variance. Estimates

of heritability are useful in predicting the transmission of character from the parents to their off springs. Estimates of heritability are free from genetical assumptions. Heritability estimates are based on empirical results. The broad sense heritability can be estimated from parental as well as hybrid populations. Heritability helps in the selection of elite types from the mixed parental population or segregating populations. Narrow sense heritability gives an idea about the additive genetic variance. Heritability estimates can be worked out from both in-breeders as well as out-breeders.

Estimates of genetic advance are based on empirical results and are free from genetical assumptions. It is reliable measure of genetic improvement under selection for polygenic traits. Genetic advance can be estimated both from parental as well as segregating populations. Estimates of genetic advance help in understanding the types of gene action involved in the expression of various polygenic characters. High values of genetic advance are indicative of additive gene action. It also helps in deciding a breeding procedure for the genetic improvement of various polygenic traits by determining the gene action.

Correlation studies provide information about yield contributing characters. This information is useful to plant breeder in selection of elite genotypes from diverse genetic populations (Robinson *et al.*, 1951; Khaliq *et al.*, 2004). Mass selection has been used to improve grain yield in several crops through indirect selection of highly heritable traits which are associated with yield. Path coefficient analysis helps in indirect selection for genetic improvement of yield. Selection for a component trait for yield improvement is called indirect selection. While, straight selection for is termed as direct selection.

Materials and Methods

The materials used for present investigation comprised of 17 bread rice genotypes, collected from various Sources and the research was conducted at the Research Farm Genetics & Plant

Breeding of AKS University, Satna, M.P during the *kharif* season of 2022. The details of these 17 rice genotypes are given in a table below.

Experimental Design and Trial Management

All the 17 genotypes were grown in Randomized Block Design (RBD) with 3 replications. In each replication, genotypes were sown in 3 rows of 1-meter length with row to row and plant to plant spacing of 25 cm and 20 cm respectively. Recommended fertilizer in the forms of Urea and DAP was applied to each plot in the shallow furrow depths and mixed with soil at the same time during sowing. For data collection, the middle rows were used.

The central rows were harvested for grain yield and biomass yield from each plot leaving boarder rows to avoid boarder effects. All other agronomic practices were undertaken uniformly to the entire plot as recommended for wheat production in the area during the growing season.

Results and Discussion

The present investigation was carried out to estimate the nature and magnitude of variability parameters, characters associations and path analysis among 17 genotypes of rice for 14 characters. The experiment was laid out in Randomized Completely Block Design (RBD) with 3 replications during Rabi, 2021-22. The experiment data obtained was subjected to statistical analysis.

Analysis of Variance (ANOVA)

The Analysis of variance (ANOVA) indicated that the mean sum of squares due to genotypes were highly significant for all the traits viz., days to 50% flowering, plant height, no. of effective tillers / plant, flag leaf length, flag leaf, days to maturity, no. of spikelet's/panicle, panicle length, kernel length, kernel width, test weight, harvest index, biological yield per plant, economic yield. The mean sum of squares due to replication showed non-significant

differences for all the traits under study indicating good homogeneity among replications. Mean sum of square from analysis of variance for various traits are given in Table no.1.

The similar finding have been reported by Devi Bineeta *et al.*, (2012); Bhusan *et al.*, (2013); Asif *et al.*, (2004); Kumar and Kerkhi (2015); Tabassum Ahmad *et al.*, (2013); Mollasadeghi *et al.*, (2013) and Lal *et al.*, (2009).

Mean Performance of the Genotypes

Mean performance of genotypes and range for all the 14 characters are presented in Table no.2.

The results of this study show that the genotypes of rice crops had mean days to 50% flowering of 86.18, with a minimum of 60.00 days (IR-64) and a maximum of 94.33 days (RNR - 29325). The plant height had a mean of 98.21 cm, with a minimum of 82.13 cm (JGL-3828) and a maximum of 108.53 cm (MTU-1280). The number of effective tillers per plant had a mean of 19.03, with a minimum of 13.47 (DURGA PADDY) and a maximum of 25.40 (KNM - 118). The flag leaf length had a mean of 33.53 cm, with a minimum of 26.30 cm (KNM - 118) and a maximum of 42.27 cm (MTU - 1190). The flag leaf width had a mean of 1.80 cm, with a minimum of 1.39 cm (IR - 64) and a maximum of 2.02 cm (MTU - 1212). The days of maturity had a mean of 112.04 days, with a minimum of 84.00 days (IR - 64, RNR - 29325, DURGA PADDY, MTU - 1075, BPT - 5204) and a maximum of 126.00 days (RNR - 15459). The kernel length had a mean of 0.87 cm, with a minimum of 0.49 cm (RNR - 15459) and a maximum of 0.97 cm (IR - 64, WGL - 4727). The kernel width had a mean of 0.21 cm, with a minimum of 0.16 cm (RNR - 15459) and a maximum of 0.28 cm (MTU - 1281, MTU - 1280). The panicle length had a mean of 23.92 cm, with a minimum of 20.07 cm (MTU - 1075) and a maximum of 29.80 cm (SUJALA (CHECK)). The number of seeds per panicle had a mean of 285.75, with a minimum of 182.27 (SUJALA (CHECK)) and a maximum of 476.93 (RNR - 1446). The test

weight had a mean of 19.23 g, with a minimum of 9.31 g (RNR - 15459) and a maximum of 27.78 g (MTU - 1280). The harvest index had a mean of 42.10, with a minimum of 29.84 (WGL - 401) and a maximum of 47.41 (JGL - 3828). The biological yield per plant had a mean of 40.26 g, with a minimum of 35.78 g (MTU - 1281) and a maximum of 42.35 g (DURGA PADDY). The grain yield per plant had a mean of 16.87 g, with a minimum of 11.92 g (WGL - 401) and a maximum of 19.52 g (JGL - 3828).

The coefficient of variation (C.V.) for all the traits was relatively low, ranging from 3.40% to 14.49%. This suggests that there was little variation within the genotypes for each trait.

The results suggest that these genotypes of rice crops have a relatively short flowering period and a relatively tall plant height. Additionally, the genotypes had a relatively high number of effective tillers per plant and relatively long flag leaf length and width. The days to maturity were relatively long, which is desirable for certain types of rice. The kernel length and width were relatively small, but the panicle length was relatively long and had a high number of seeds per panicle. The test weight, harvest index, biological yield per plant, and grain yield per plant were all relatively high, indicating that these genotypes may have potential for crop improvement.

The study found that the genotypes of rice crops had a wide range of values for each of these characteristics, with the minimum and maximum values for each characteristic also reported. The study's results indicate that there are significant variations in the characteristics of different genotypes of rice crops, which can be useful for rice breeding programs to select and improve high-performing rice varieties. The results also indicate that there may be genotypes that excel in specific characteristics such as grain yield, harvest index or biological yield and can be used as parents in breeding programs.

The findings were quite similar to as reported by Hailegiorgis, *et al.*, (2012) for days to 50% flowering, days to maturity, grain yield per plant. Hailegiorgis, *et al.*, (2012) for plant height, grain per spike, spike length. Verma *et al.*, (2013); Ahmed *et al.*, (2014) for biological yield per plant and harvest index.

Genetic Variability Parameters

The parameters of genetic variability viz., phenotypic coefficient of variation (%), genotypic coefficient of variation (%), environmental coefficient of variation (%), heritability (%) in broad sense, genetic advancement 5% and genetic advance as % of mean 5% for each trait are presented in table 1.

Genotypic and Phenotypic coefficient of variation

In this case, the GCV values range from 3.40 (days to 50% flowering) to 27.02 (test weight), indicating a wide range of variation among genotypes for these traits. The PCV values range from 4.06 (biological yield per plant) to 27.20 (test weight) and the ECV values range from 1.88 (days of maturity) to 14.83 (number of seed per panicle). This suggests that characters such as days of maturity, kernel width and no of seed per panicle are more stable and less affected by environmental factors, while characters such as test weight, biological yield per plant and grain yield per plant are more affected by environmental factors.

The GCV values indicate the degree of variation among genotypes for a given trait. The higher the GCV value, the greater the variation among genotypes for that trait. The PCV values indicate the total variation of a trait, while the ECV values indicate the variation due to environmental factors.

Overall, the study suggests that there is a significant amount of variation among genotypes for the evaluated traits, which can be useful for rice breeding programs to select and improve high-performing rice varieties. The study also suggests

that the characters such as test weight, biological yield per plant and grain yield per plant are more affected by environmental factors, thus it is important to consider the environment while selecting parents for breeding programs.

Sachan and Singh (2003); Devi Bineeta (2016); Singh and Upadhyay (2013) reported high estimates of GCV for grain yield per plant, effective tiller per plant. Borghi *et al.*, (2016) reported low GCV for spikelet's per spike, plant height.

Hailegiorgis, *et al.*, (2012); Devi Bineeta (2016) also find similar observations.

Heritability (h^2) and Genetic advance 5%

The results show that the days to 50% flowering has a high heritability of 97.20 and a high genetic advance of 20.30, indicating that this trait is highly influenced by genetics and that selection can lead to significant progress in this trait. The plant height also has a high heritability of 80.70 and genetic advance of 12.24, indicating that this trait is also highly influenced by genetics and that selection can lead to significant progress in this trait.

The number of effective tillers per plant has a relatively lower heritability of 71.50 and genetic advance of 4.394, indicating that this trait is less influenced by genetics and that selection may not lead to as much progress in this trait. Similarly, flag leaf width has a low heritability of 74.30 and genetic advance of 0.209, indicating that this trait is less influenced by genetics and that selection may not lead to as much progress in this trait.

The days of maturity has a high heritability of 99.30 and genetic advance of 29.49, indicating that this trait is highly influenced by genetics and that selection can lead to significant progress in this trait. Similarly, grain yield per plant has a high heritability of 83.50 and genetic advance of 3.61, indicating that this trait is highly influenced by genetics and that selection can lead to significant progress in this trait. In summary, the data suggests

that selection for days to 50% flowering, plant height, days of maturity, and grain yield per plant may be effective in improving these traits in rice breeding programs. However, selection for the number of effective tillers per plant and flag leaf width may not be as effective.

Shah *et al.*, (2017) high heritability for days to maturity. Shah *et al.*, (2017) high heritability for thousand seed weight. Bhushan *et al.*, (2013); Sabit *et al.*, (2017) high heritability for biological yield per plant. Zaeifzadeh, *et al.*, (2011) reported high heritability for plant height

Bhusan *et al.*, (2013) reported high genetic advancement for biological yield per plant. Shah *et al.*, (2017) reported for plant height.

Suleiman *et al.*, (2014); Mecha *et al.*, (2016) reported high genetic advancement as % of mean for grain yield per plant. Kabir *et al.*, (2017) reported high for harvest index.

Genotypic and phenotypic correlation coefficient Analysis

Correlation coefficients at phenotypic and genotypic levels were estimated using 14 characters in 17 genotypes of bread rice to study the degree of mutual relationship between yields and its component traits. The correlation coefficients can range from -1 to 1, with positive values indicating a positive relationship, negative values indicating a negative relationship, and values close to 0 indicating little or no relationship (Table no.4 & 5).

Genotypic correlation coefficient Analysis

The strongest positive correlation is between grain yield per plant and harvest index (0.987**), indicating that an increase in harvest index is likely to result in an increase in grain yield per plant. The next strongest positive correlation is between grain yield per plant and number of effective tillers per plant (0.564*) and number of seed per panicle (0.503*).

On the other hand, the strongest negative correlation is between grain yield per plant and days to 50% flowering (-0.568*), indicating that an increase in days to 50% flowering is likely to result in a decrease in grain yield per plant. The next strongest negative correlation is between grain yield per plant and plant height (-0.229).

The genotypic correlation coefficients suggest that traits related to the reproductive growth such as number of effective tillers per plant, number of seed per panicle and harvest index have positive effects on grain yield per plant, while traits related to vegetative growth such as days to 50% flowering and plant height have negative effects on grain yield per plant.

The strongest positive correlation is between grain yield per plant and harvest index (0.954**), indicating that an increase in harvest index is likely to result in an increase in grain yield per plant. The next strongest positive correlation is between grain yield per plant and biological yield per plant (0.528*). On the other hand, the strongest negative correlation is between grain yield per plant and days to 50% flowering (-0.577**), indicating that an increase in days to 50% flowering is likely to result in a decrease in grain yield per plant. The next strongest negative correlation is between grain yield per plant and plant height (-0.188) and flag leaf width (-0.214)

Phenotypic correlation coefficient Analysis

The phenotypic correlation coefficients suggest that traits related to the reproductive growth such as harvest index, biological yield per plant have positive effects on grain yield per plant, while traits related to vegetative growth such as days to 50% flowering, plant height and flag leaf width have negative effects on grain yield per plant. Also, number of effective tillers per plant and number of seed per panicle have weak positive correlation with grain yield per plant.

It is worth noting that the phenotypic correlation

coefficient reflects the relationship between the trait and the grain yield per plant in the given population and environmental conditions. This is different from genotypic correlation coefficient, which reflects the relationship between the trait and the grain yield per plant that is inherited by the genotype of the rice plants.

Aydin *et al.*, (2010); Gelalcha and Hanchinal (2013); Phougat *et al.*, (2017) also agreed with the similar results.

Path coefficient analysis

The maximum direct positive genotypic and phenotypic path on grain yield per plant was observed in biological yield per plant followed by harvest index, spike length, thousand seed weight, and plant height. Maximum direct negative effect on grain yield per plant was observed in spikelet's per spike followed by grain per spike, effective tiller per plant, days to maturity and days to 50% flowering (Table No. 5 & 6; Figure No. 1 & 2).

Genotypic path

Days to 50% flowering trait has a direct effect of 0.299 on itself, indicating a strong positive indirect effect. It also has a positive indirect effect of 0.121 with Flag leaf length, and a negative indirect effect of -0.106 with kernel length. The plant height trait has a direct effect of -0.025 on itself, indicating a negative indirect effect. It also has a positive indirect effect of 0.006 with Biological yield per plant.

The number of effective tillers per plant trait has a direct effect of 0.005 on itself, indicating a positive indirect effect. It also has a positive indirect effect of 0.002 with kernel length and a negative indirect effect of -0.001 with biological yield per plant. The flag leaf length trait has a direct effect of 0.305 on itself, indicating a strong positive indirect effect. It also has a positive indirect effect of 0.171 with days of maturity and a negative indirect effect of -0.078 with test weight.

Table.1 List of genotypes

S. No.	Genotypes	Source
1.	RNR-1446	DRR, HYDERABAD
2.	KNM-118	DRR, HYDERABAD
3.	MTU-1212	DRR, HYDERABAD
4.	BPT-5204	DRR, HYDERABAD
5.	MTU-1311	DRR, HYDERABAD
6.	RNR-29325	DRR, HYDERABAD
7.	DURGA PADDY	DRR, HYDERABAD
8.	MTU-1280	DRR, HYDERABAD
9.	WGL-401	DRR, HYDERABAD
10.	MTU-1281	DRR, HYDERABAD
11.	MTU-1075	DRR, HYDERABAD
12.	RNR-15459	DRR, HYDERABAD
13.	WGL-4727	DRR, HYDERABAD
14.	MTU-1190	DRR, HYDERABAD
15.	JGL-3828	DRR, HYDERABAD
16.	IR-64	DRR, HYDERABAD
17.	SUJALA	A.K.S. UNIVERSITY

Table.2 Analysis of Variance of the 14 characters

Characters	Replication Df=2	Treatment Df=16	Error Df=32
Days to 50% flowering	5.71	308.30	8.60
Plant height	2.52	162.85	31.50
No. of effective tillers per plant	2.66	26.69	7.60
Flag leaf length	0.35	86.72	4.58
Flag leaf width	0.02	0.06	0.01
Days of maturity	3.55	623.95	4.42
Karnel length	0.00	0.04	0.00
Karnel width	0.00	0.00	0.00
Panicle length	6.68	18.16	3.53
No. of seed per panicle	12231.69	16585.74	1796.91
Test weight	0.73	82.06	1.08
Harvest index	0.10	60.69	15.63
Biological yield per plant	0.00	8.01	3.34
Grain yield per plant	0.05	13.24	2.18

Table.3 Means performance of the 17 rice genotypes

Genotypes	DFP	PH	NEP	FLL	FLW	DM	KL	KW	PL	NSP	TW	HI	BYP	GYP
RNR - 1446	87.33	95.40	20.20	27.87	1.93	116.00	0.87	0.17	24.33	476.93	14.41	44.41	38.88	17.15
KNM - 118	89.00	83.20	25.40	26.30	1.79	120.67	0.85	0.20	23.33	313.00	14.90	37.84	41.52	15.48
MTU - 1212	90.33	101.00	21.27	32.40	2.02	121.00	0.85	0.20	20.33	299.20	20.23	40.94	39.18	15.95
BPT - 5204	84.00	102.13	18.53	33.00	1.75	110.00	0.95	0.20	24.13	356.27	16.95	41.40	39.92	16.45
MTU - 1311	91.33	98.60	16.67	32.67	1.93	119.33	0.86	0.20	25.07	333.27	21.97	42.74	40.02	17.02
RNR - 29325	94.33	96.73	15.47	31.60	1.64	84.00	0.96	0.20	24.00	216.53	21.88	45.73	39.89	18.15
DURGA PADDY	61.33	94.40	13.47	26.93	1.76	84.00	0.92	0.20	23.73	182.67	26.43	40.21	42.35	16.89
MTU - 1280	89.67	108.53	19.47	32.47	1.79	116.00	0.91	0.28	23.33	242.37	27.78	39.41	39.49	15.49
WGL - 401	82.00	100.13	18.67	32.47	1.90	114.00	0.93	0.20	26.53	296.00	17.71	29.84	40.55	11.92
MTU - 1281	89.00	104.53	19.73	41.67	1.82	124.00	0.79	0.28	21.80	316.13	17.20	35.84	35.78	12.72
MTU - 1075	92.67	93.67	18.27	27.13	1.81	103.33	0.83	0.20	20.07	188.13	17.21	44.94	39.72	17.79
RNR - 15459	91.67	105.67	17.00	35.73	1.85	126.00	0.49	0.16	24.20	346.73	9.31	43.84	42.22	18.49
WGL - 4727	86.00	103.33	18.80	40.53	1.74	118.00	0.97	0.20	29.80	271.00	17.35	45.04	40.25	18.05
MTU - 1190	91.00	107.07	24.13	42.27	1.85	119.33	0.85	0.20	22.53	305.67	17.63	46.98	41.52	19.42
JGL - 3828	92.67	82.13	17.67	40.40	1.78	123.00	0.81	0.20	21.07	271.33	13.43	47.41	41.35	19.52
IR - 64	60.00	96.67	21.87	28.73	1.39	84.00	0.97	0.21	25.73	260.33	27.54	45.01	39.35	17.55
SUJALA(CHEC K)	92.67	96.40	16.93	37.87	1.85	122.00	0.93	0.25	26.67	182.27	24.91	44.17	42.49	18.72
Mean	86.18	98.21	19.03	33.53	1.80	112.04	0.87	0.21	23.92	285.75	19.23	42.10	40.26	16.87
Min.	60.00	82.13	13.47	26.30	1.39	84.00	0.49	0.16	20.07	182.27	9.31	29.84	35.78	11.92
Max.	94.33	108.53	25.40	42.27	2.02	126.00	0.97	0.28	29.80	476.93	27.78	47.41	42.35	19.52
C.V.	3.40	5.71	14.49	6.38	6.67	1.88	3.40	7.19	7.85	14.83	5.40	9.39	4.54	8.76
S.E.	1.69	3.24	1.59	1.24	0.07	1.21	0.02	0.01	1.08	24.47	0.60	2.28	1.06	0.85
C.D. 5%	4.88	9.33	4.59	3.56	0.20	3.50	0.05	0.03	3.13	70.50	1.73	6.57	3.04	2.46

Table.4 Genetic parameters of 14 traits

Characters	GCV	PCV	ECV	Heritability (%)	Genetic advance	Genetic as percent of mean
Days to 50% flowering	11.60	11.76	3.40	97.00	20.30	23.56
Plant height	6.74	7.50	5.71	81.00	12.24	12.47
No. of effective tillers per plant	13.25	15.67	14.49	72.00	4.39	23.09
Flag leaf length	15.61	16.03	6.38	95.00	10.49	31.29
Flag leaf width	6.54	7.59	6.67	74.00	0.21	11.60
Days of maturity	12.83	12.87	1.88	99.00	29.50	26.33
Karnel length	12.93	13.08	3.40	98.00	0.23	26.33
Karnel width	14.85	15.42	7.19	93.00	0.06	29.46
Panicle length	9.23	10.29	7.86	81.00	4.08	17.07
No. of seed per panicle	24.57	26.02	14.83	89.00	136.58	47.80
Test weight	27.02	27.20	5.41	99.00	10.63	55.29
Harvest index	9.21	10.68	9.39	74.00	6.88	16.34
Biological yield per plant	3.10	4.06	4.54	0.58	1.96	4.87
Grain yield per plant	11.38	12.45	8.76	0.84	3.61	21.42

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Table.5 Genotypic Correlation Matrix of 14 traits

Characters	DFF	PH	NEP	FLL	FLW	DM	KL	KW	PL	NSP	TW	HI	BYP	GYP
DFF	1.000	0.100	0.123	0.405	0.681**	0.664**	-0.355	0.083	-0.290	0.176	-0.501*	0.204	-0.062	-0.568*
PH		1.000	-0.148	0.434	0.135	0.171	-0.098	0.294	0.255	0.161	0.171	-0.242	-0.377	-0.229
NEP			1.000	0.021	-0.063	0.405	0.017	-0.021	-0.208	0.396	-0.236	-0.097	-0.297	0.564*
FLL				1.000	0.208	0.561*	-0.188	0.315	0.169	0.025	-0.255	0.214	-0.048	0.211
FLW					1.000	0.814**	-0.437	-0.075	-0.256	0.423	-0.449	-0.414	0.041	0.298
DM						1.000	-0.492*	0.134	-0.078	0.471	-0.564*	-0.147	-0.025	0.105
KL							1.000	0.289	0.375	-0.292	0.647*	-0.057	-0.188	0.119
KW								1.000	-0.058	-0.423	0.550	-0.327	-0.607**	0.445
PL									1.000	0.055	0.188	-0.030	0.267	0.007
NSP										1.000	-0.608**	-0.064	-0.454	0.503*
TW											1.000	-0.065	-0.049	0.066
HI												1.000	0.636	0.987**
BYP													1.000	0.487*
GYP														1.000

* & ** indicates 5% & 1% level of significance

Int.J.Curr.Microbiol.App.Sci (2023) 12(08): 126-143
Table.6 Phenotypic Correlation Matrix of 14 traits

Characters	DFE	PH	NEP	FLL	FLW	DM	KL	KW	PL	NSP	TW	HI	BYP	GYP
DFE	1.000	0.055	0.090	0.398	0.567*	0.668**	-0.343	0.082	-0.260	0.169	-0.489*	0.156	-0.060	-0.577**
PH		1.000	-0.020	0.368	0.134	0.139	-0.098	0.264	0.209	0.126	0.156	-0.137	-0.283	-0.188
NEP			1.000	0.030	-0.001	0.331	0.013	0.031	-0.160	0.372	-0.198	-0.077	-0.193	-0.138
FLL				1.000	0.149	0.544*	-0.188	0.299	0.116	0.020	-0.248	0.180	-0.060	0.173
FLW					1.000	0.694**	-0.345	-0.061	-0.250	0.344	-0.378	-0.272	0.032	-0.214
DM						1.000	-0.485*	0.128	-0.070	0.445	-0.560*	-0.135	-0.023	-0.103
KL							1.000	0.272	0.352	-0.283	0.641*	-0.061	-0.129	0.115
KW								1.000	-0.063	-0.372	0.521*	-0.310	-0.415	0.380
PL									1.000	0.026	0.180	-0.070	0.229	0.002
NSP										1.000	-0.572*	-0.084	-0.306	0.172
TW											1.000	-0.046	-0.038	0.061
HI												1.000	0.253	0.954**
BYP													1.000	0.528*
GYP														1.000

* & ** indicates 5% & 1% level of significance

Table.7 Genotypic path matrix of GYP

Characters	DFE	PH	NEP	FLL	FLW	DM	KL	KW	PL	NSP	TW	HI	BYP
DFE	0.299	0.030	0.037	0.121	0.203	0.198	-0.106	0.025	-0.087	0.053	-0.150	0.061	-0.019
PH	-0.003	-0.025	0.004	-0.011	-0.003	-0.004	0.002	-0.007	-0.006	-0.004	-0.004	0.006	0.009
NEP	0.001	-0.001	0.005	0.000	0.000	0.002	0.000	0.000	-0.001	0.002	-0.001	-0.001	-0.001
FLL	0.123	0.132	0.007	0.305	0.063	0.171	-0.057	0.096	0.051	0.008	-0.078	0.065	-0.015
FLW	-0.112	-0.022	0.011	-0.034	-0.165	-0.134	0.072	0.012	0.042	-0.070	0.074	0.068	-0.007
DM	-0.410	-0.106	-0.250	-0.346	-0.502	-0.617	0.303	-0.083	0.048	-0.290	0.348	0.091	0.016
KL	0.010	0.003	-0.001	0.005	0.012	0.014	-0.028	-0.008	-0.010	0.008	-0.018	0.002	0.005
KW	0.036	0.126	-0.009	0.135	-0.032	0.058	0.124	0.429	-0.025	-0.182	0.236	-0.140	-0.259
PL	0.075	-0.066	0.053	-0.043	0.066	0.020	-0.097	0.015	-0.257	-0.014	-0.049	0.008	-0.069
NSP	0.130	0.119	0.293	0.018	0.313	0.349	-0.216	-0.314	0.040	0.740	-0.447	-0.047	-0.336
TW	-0.050	0.017	-0.023	-0.025	-0.044	-0.056	0.064	0.054	0.019	-0.060	0.099	-0.006	-0.005
HI	0.118	-0.140	-0.056	0.124	-0.241	-0.086	-0.033	-0.190	-0.017	-0.037	-0.038	0.581	0.369
BYP	-0.049	-0.296	-0.234	-0.038	0.032	-0.020	-0.148	-0.475	0.210	-0.357	-0.038	0.500	0.787

Table.8 Phenotypic path matrix of GYP

Characters	DFF	PH	NEP	FLL	FLW	DM	KL	KW	PL	NSP	TW	HI	BYP
DFF	-0.006	0.000	-0.001	-0.002	-0.004	-0.004	0.002	-0.001	0.002	-0.001	0.003	-0.001	0.000
PH	0.001	0.010	0.000	0.004	0.001	0.001	-0.001	0.003	0.002	0.001	0.002	-0.001	-0.003
NEP	-0.001	0.000	-0.013	0.000	0.000	-0.004	0.000	0.000	0.002	-0.005	0.003	0.001	0.003
FLL	0.007	0.007	0.001	0.019	0.003	0.010	-0.004	0.006	0.002	0.000	-0.005	0.003	-0.001
FLW	0.003	0.001	0.000	0.001	0.006	0.004	-0.002	0.000	-0.002	0.002	-0.002	-0.002	0.000
DM	-0.001	0.000	-0.001	-0.001	-0.001	-0.001	0.001	0.000	0.000	-0.001	0.001	0.000	0.000
KL	0.004	0.001	0.000	0.002	0.004	0.006	-0.013	-0.003	-0.004	0.004	-0.008	0.001	0.002
KW	0.002	0.007	0.001	0.008	-0.002	0.004	0.007	0.027	-0.002	-0.010	0.014	-0.009	-0.011
PL	0.002	-0.001	0.001	-0.001	0.002	0.000	-0.002	0.000	-0.006	0.000	-0.001	0.000	-0.001
NSP	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	-0.001	0.001	0.000	0.000
TW	0.007	-0.002	0.003	0.004	0.006	0.008	-0.010	-0.008	-0.003	0.009	-0.015	0.001	0.001
HI	0.138	-0.121	-0.068	0.159	-0.239	-0.119	-0.053	-0.272	-0.062	-0.074	-0.041	0.880	0.223
BYP	-0.019	-0.090	-0.061	-0.019	0.010	-0.007	-0.041	-0.131	0.072	-0.097	-0.012	0.080	0.316

Fig.1 Genotypic path diagram

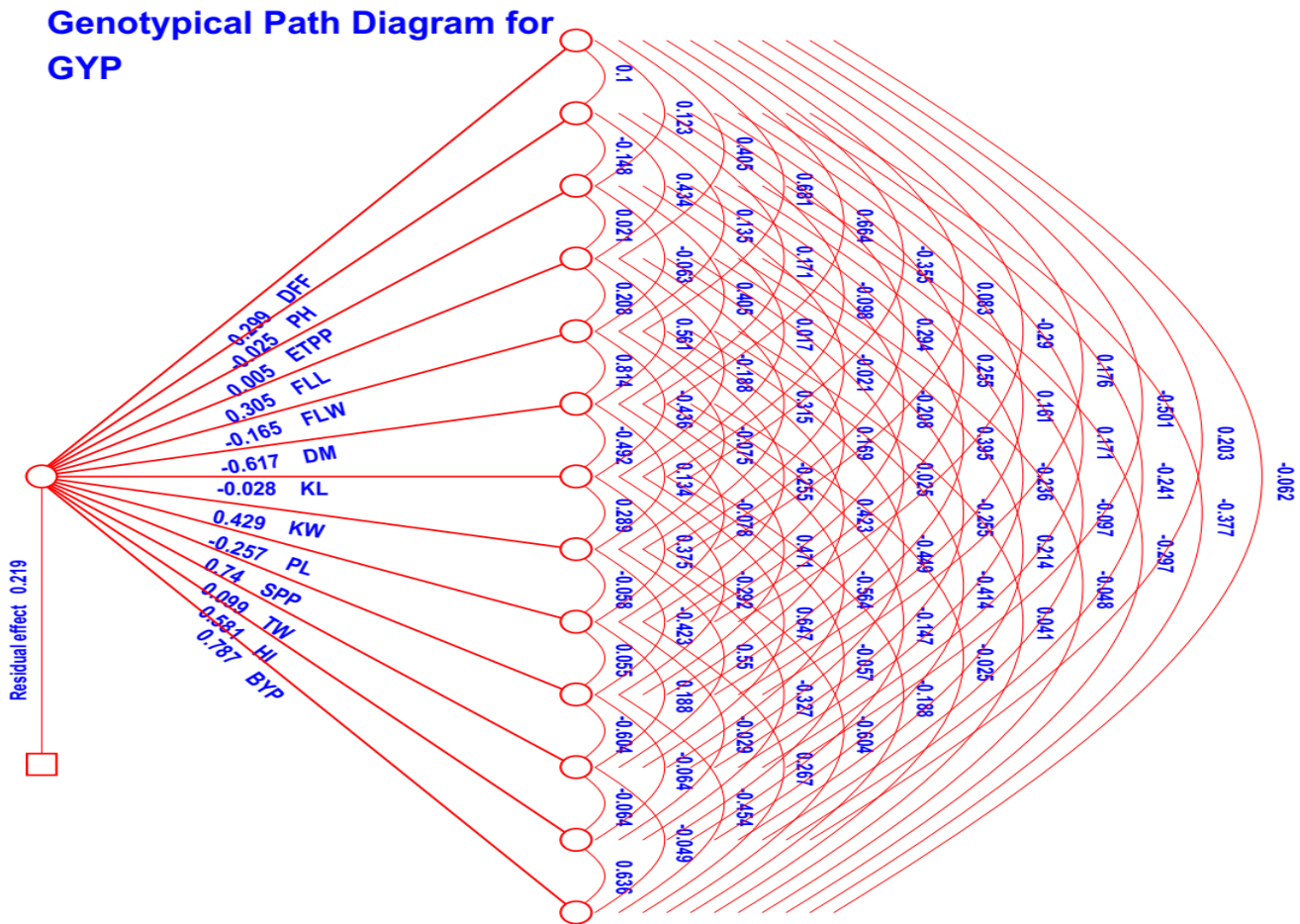
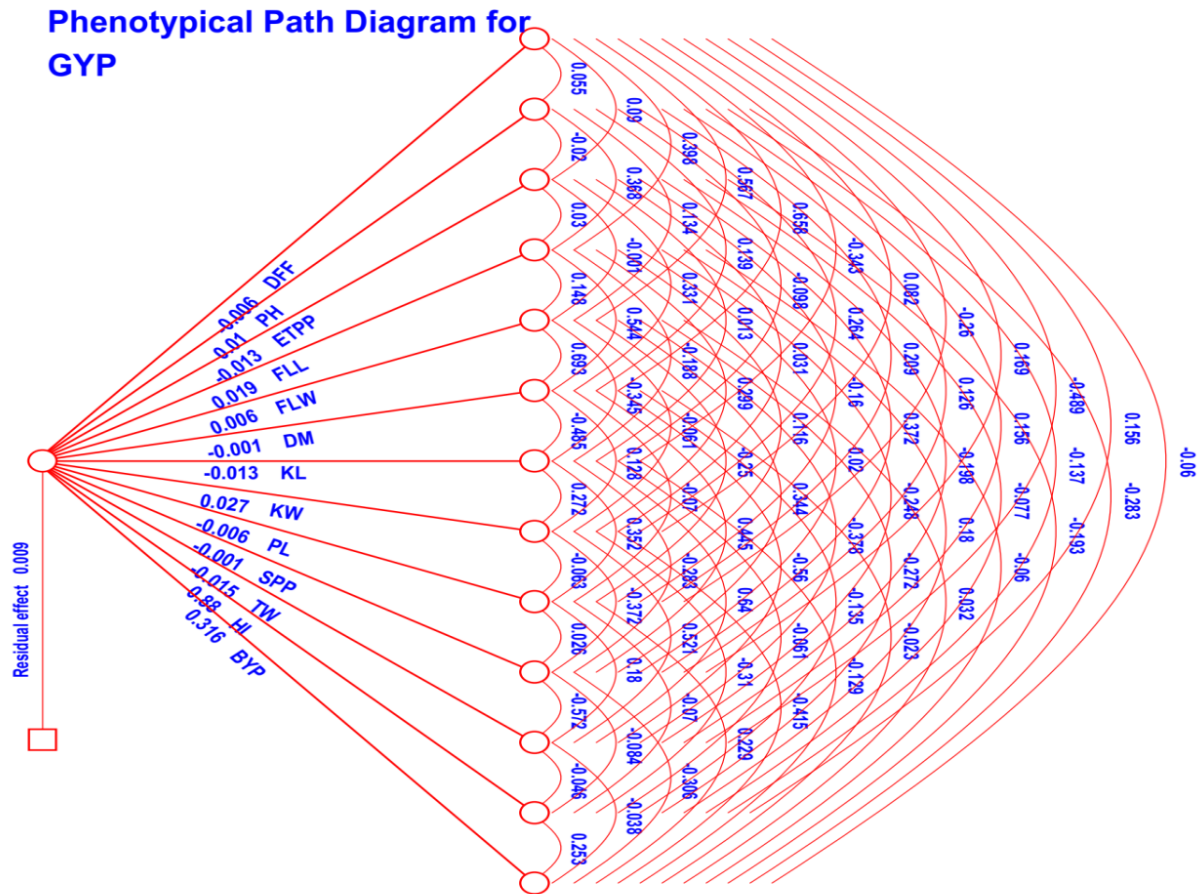


Fig.2 Genotypic path diagram



The flag leaf width trait has a direct effect of -0.165 on itself, indicating a negative indirect effect. It also has a positive indirect effect of 0.068 with Biological yield per plant. The days of maturity trait has a direct effect of -0.617 on itself, indicating a strong negative indirect effect. It also has a positive indirect effect of 0.348 with Test weight and a negative indirect effect of -0.475 with Kernel width. The Kernel length trait has a direct effect of -0.028 on itself, indicating a negative indirect effect. It also has a positive indirect effect of 0.124 with Kernel width. The Kernel width trait has a direct effect of 0.429 on itself, indicating a strong positive indirect effect. It also has a positive indirect effect of -0.259 with Biological yield per plant. The panicle length trait has a direct effect of -0.257 on itself, indicating a strong negative indirect effect. It also has a positive indirect effect of -0.014 with Number of seed per panicle.

The Number of seed per panicle trait has a direct effect of 0.74 on itself, indicating a strong positive indirect effect. It also has a negative indirect effect of -0.336 with Biological yield per plant. The Test weight trait has a direct effect of -0.060 on itself, indicating a negative indirect effect. It also has a positive indirect effect of 0.581 with Harvest index. The Harvest index trait has a direct effect of -0.037 on itself, indicating a negative indirect effect. It also has a positive indirect effect of 0.787 with Biological yield per plant. The Biological yield per plant trait has a direct effect of 0.787 on itself, indicating a strong positive indirect effect. It also has a positive indirect effect of -0.475 with Kernel width and a negative indirect effect of -0.336 with Number of seed per panicle.

Overall, this table indicates that Days to 50% flowering and Flag leaf length have a strong positive indirect effect with themselves, and a negative indirect effect with Kernel length and Days of maturity. Plant height and kernel width have a negative indirect effect with themselves, and a positive indirect effect with biological yield per plant. Number of effective tillers per plant, flag leaf width, kernel length, panicle length, and test weight have a positive indirect effect with themselves.

Phenotypic path

This table is a phenotypic path analysis for rice, which shows the indirect effect between different traits and biological yield per plant. The values in the table represent the indirect effect coefficients between each trait and the biological yield per plant, with negative values indicating a negative indirect effect and positive values indicating a positive indirect effect.

The most positively correlated traits with biological yield per plant are harvest index (0.223) and flag leaf length (0.003). This means that an increase in these traits is likely to result in an increase in the biological yield per plant.

On the other hand, the most negatively correlated traits with biological yield per plant are plant height (-0.090) and days to 50% flowering (-0.006), meaning an increase in these traits is likely to result in a decrease in the biological yield per plant. It is also worth noting that some traits do not have a significant indirect effect with biological yield per plant, such as no. of seed per panicle which has an indirect effect of 0.000. Overall, this table can be used to identify which traits are important for increasing the biological yield per plant and to help guide breeding efforts. Kaddem *et al.*, (2014); Subhani *et al.*, (2000); Phougat *et al.*, (2017); Gelalcha and Hanchinal (2013) also agreed with the similar finding.

Based on the results of this study, the best genotypes of rice crops could be IR-64 with 60 days to 50% flowering, IR-64 and WGL-4727 with 0.97 cm kernel length, MTU-1280 with 108.53 cm plant height, 27.78 g test weight and 19.52 g grain yield per plant. However, it is important to consider that the best genotype would depend on the specific requirements and environment.

The results suggest that genotypes with short flowering period, tall plant height, many effective tillers per plant, long flag leaf, long panicle and high grain yield per plant were observed. The results of

the analysis showed that traits related to reproductive growth positively impacted grain yield, while traits related to vegetative growth had a negative effect. The path coefficient analysis revealed that biological yield and harvest index had the highest positive impact on grain yield, while spikelets per spike, grain per spike, effective tiller per plant, days to maturity, and days to 50% flowering had the highest negative impact. These findings provide useful information for rice crop improvement.

References

- Ahmed, N., Khaliq, I., Chowdhry, M A., Ahsan, M., Ibrahim, M. and Maekqwq, M. (2004). Heritability estimates of some flag leaf characters in wheat. *Caderno de Pesquisa Ser. Bio. Santa Cruz do Sul.*, 16: 131–141.
- Ajmal, S. U., Nahid, Z. and Muhammad Y. M. (2009). Estimation of Genetic Parameters and Character Association in Wheat. *J. Agric. Biol. Sci.* 1(1):15-18.
- Alamerew, S., Chebotar, S., Huang, X., Roeder, M. and Boemer, A., (2004). Genetic diversity in Ethiopian hexaploid and tetraploid wheat germplasm assessed by microsatellite markers. *Genetic resources and crop evaluation*, Germany, 51 FEDERER, W. T., 1956. Augmented Designs. *Hawaii Planters Record*, 40: 191-207.
- Ansari, K. A., Soomro, Z. A., Ansari, B. A. and Leghari, M. H. (2005). Genetic variability and heritability studied for some quantitative traits in bread wheat (*Triticum aestivum L.*). *Pakistan J. Agric. Agril. Engg. Vet. Sci.*, 21: 18–24.
- Anwar, J., Ali, M. A., Hussain, M., Sabir, W., Khan, M. A., Zulkiffal, M. and Abdullah, M., (2009). Assessment of yield criteria in bread wheat through correlation and path analysis. *The Journal of Animal & Plant Sciences.* 19 (4).
- Asif M., Mujahid, M. Y., Kisana, N. S., Mustafa, S. Z. and Ahmad, I. (2004). Heritability, genetic variability and path-coefficients of some traits in spring wheat. *Sarhad Journal of Agric.*, Pakistan, 20 (1): 87-91.
- Aydin, Sermet, N., Mut, C., Bayramoglu, Z. and Ozcan, H. O., (2010). Path analyses of yield and some agronomic and quality traits of bread wheat (*Triticum aestivum L.*) under different environments. *African Journal of Biotechnology.* 9 (32): 5131-5134.
- Bhushan, B., Bharti, S., Ojha, A., Pandey, M., Gourav, S. S., Tyagi, B. S. and Singh, G. (2013) Genetic variability, correlation coefficient and path analysis of some quantitative traits in bread wheat. *Journal of Wheat Research* 06/2013; 5(1):24-29.
- Birhanu Mecha, Sentayehu Alamerew, Alemayehu Assefa, Ermias Assefa, Dargicho Dutamo Correlation and path coefficient studies of yield and yield associated traits in bread wheat (*Triticum aestivum L.*) Genotypes *Adv Plants Agric Res.* 2017; 6 (5): 128-136. <https://doi.org/10.15406/apar.2017.06.00226>
- Borghi B., Corbellini M., Cattaneo M., Fornasari M. E., L. Zucchelli (2016). Modification Of The Sink/Source Relationships In Bread Wheat and its Influence On Grain Yield And Grain Protein Content Research Work Supported By Cnr, Italy. *Special Grant I.P.R.A. Sub-Project 1.* Paper N. 675.
- Devi Bineeta. 2016. Genetic divergence analysis for quantitative traits in rice (*Oryza sativa L.*). *European Journal of Biotechnology and Bioscience.* 4(6): 01-03.
- Devi Bineeta, G M Lal., C M Singh and Prashant Yadav (2012) Genetic Architecture, Interrelationship and Path Analysis for Yield Improvement in Exotic Rice (*Oryza sativa L.*). *International J. Agric. Environment and Biotechnology.* 5(4):387-392,.
- Gelalcha, S. and Hanchinal, R. R. (2013). Correlation and path analysis in yield and yield components in spring bread wheat (*Triticum aestivum L.*) genotypes under irrigated condition in Southern India. *African Journal of Agricultural Research*, 8(24):3186-3192. <https://doi.org/10.5897/AJAR2012.6965>

- Gite, V. D. & Bankar, Deepak & K J, Yashavantha & Baviskar, Dr. Vijendra & B K, Honrao & A M, Chavan & Surve, V. D. & S S, Raskar & S S, Khairnar & J H, Bagwan & V M, Khade. (2018). Genetic variability parameters and correlation study in elite genotypes of bread wheat (*Triticum aestivum* L.). *Journal of Pharmacognosy and Phytochemistry*. 7. 3118-3123.
- Hailegiorgis, D., Mesfin, M., Genet, T., (2012) Genetic Divergence Analysis on some Bread Wheat Genotypes Grown in Ethiopia, p.344-352 *Journal of central European agriculture*. <https://doi.org/10.5513/JCEA01/12.2.922>
- Kaddem K W, Marker, S. and Lavanya G. R. (2014). Genetic variability and correlation analysis of wheat (*Triticum aestivum* L.) genotypes for grain yield and its Component traits *European academic research-vol.II, Issue 5*.
- Khaliq, I., Parveen N. and Chowdhry, M. A. (2004). Correlation and path coefficient analyses in bread wheat. *Int. J. Agric. Biol.*, 6: 633–635.
- Khan, N. and Naqvi, F. N. (2012). Correlation and Path Coefficient Analysis in Wheat Genotypes under Irrigated and Non-Irrigated Conditions. *Asian Journal of Agricultural Sciences*, 4(5): 346-351.
- Kumar, D. and Kerkhi, S. A. (2015). Genetic Variability, Heritability And Genetic Advance For Yield Component And Quality Trait In Spring Wheat (*Triticum Aestivum* L.). *The Bioscan* 10(4): 2125-2129.
- Subhashchandra, B., Lohithaswa, H. C., S. A. Desai, R. R. Hanchinal, I. K. Kalappanavar, K. K. Math and P. M. Salimath. (2015). Assessment of genetic variability and relationship between genetic diversity and transgressive segregation in tetraploid wheat, Karnataka. *J. Agric. Sci.*, 22 (1): (36-38) 2009.
- Tabassum Ahmad, Anil Kumar, Deepanker Pandey, Birendra Prasad. 2013. Correlation and path coefficient analysis for yield and its attributing traits in bread wheat (*Triticum aestivum* L. *em Thell*) <https://doi.org/10.31018/jans.v10i4.1867>.
- Verma, P. N., Singh, B. N. and Yadav, R. K. (2013) Genetic variability and divergence analysis of yield and its contributing traits under sodic soil condition in wheat (*T. aestivum* L.). *International Journal of Agricultural Sciences*, 3(2): 395-399.
- Zaeifizadeh, K. M., Ghasemi, M., Azimi, M. and Vahabzadeh, J. M. (2011). Path analysis of yield and yield components in synthetic bread wheat (*Triticum aestivum* L.) genotypes. *Advances in Environmental Biology*. 5 (1): 98-103. 20.

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