

Path Coefficient Analysis and Selection Index in Different Rice (*Oryza sativa* L.) Genotypes

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DOI: <https://doi.org/10.36077/kjas/2024/v16i1.10965>

Received date: 6/1/2023

Accepted date: 26/2/2023

Abstract

Improving the grain yield in rice can be done more efficiently by selecting the yield components than selecting the grain yield itself, provided that these traits have a desirable genetic correlation with the grain yield trait. A field experiment was carried out in the rice research station in Al-Mashkhab/ Najaf/ IRAQ to determine the traits correlated with grain yield and to select the superior genotypes with their selection index among the sixteen genotypes planted during the growing season of 2021. During the 2022 season six genotypes were selected to evaluate the path coefficient analysis for the grain yield and its components according to randomized complete block design (RCBD) with three replicates. The results showed that the mean squares of the genotypes were significant for all studied traits ($P < 0.1$). The superiority of the genotypes Furat1, Jasmine and K2 over the rest of six genotypes that were selected for having a high selection index, especially in the trait of grain yield, number of tillers.m⁻² and number of grains.panicle⁻¹. The genetic and phenotypic path coefficient analysis revealed that there was a high direct effect of the yield components on the grain yield due to the high positive and desirable values of the genetic and phenotypic correlation between the grain yield and its components including the number of tillers.m⁻², the number of grains.panicle⁻¹ and the panicle length, which are selective indicators for improving grain yield. Furthermore, the aforementioned traits showed high values of heritability in the broad sense and good stability during the two study seasons. Thus, the characteristics of the number of tillers.m⁻² and the number of grains per panicle can be considered as one of the best criteria to be adopted as a selection index in the breeding programs for the rice crop. Moreover, further investigations are required for these criteria at different experimental conditions in order to testing their efficiency.

Keywords: Genetic correlation, Path coefficient analysis, Selection index, Heritability, Rice genotypes



Introduction

Rice is one of the main cereal crops used in food and comes third in position regarding its productivity after maize and wheat, with a global production estimated at 505 million tons (14). In Iraq, rice is ranked third after wheat and barley in the cultivated and productive areas. Rice cultivated areas was estimated in 2021 at 97 thousand hectares that produced approximately 155 thousand tons (9). The rice crop suffers from low productivity and quality of the grain, despite the availability of favorable factors for its cultivation. The genetic factor represented by the varieties and the environmental factors represented by temperature, humidity and photoperiod, which play a major role in influencing the characteristics of the rice yield, its components and in qualitative traits (10).

Therefore, the programs of high-yielding rice varieties are the main objective of most plant breeders worldwide, as these programs may generate new high-yielding genotypes. Improving grain yield by selecting the components may be more efficient than selecting the grain yield itself, provided that these traits have a desirable genetic correlation with the grain yield. To identify the best genotypes with desirable traits for their subsequent use in breeding programs and to select an appropriate selection index that can aid in successful breeding programs. A group of researchers has indicated a high positive correlation of grain yield with the number of panicles per plant and the number of grains per plant (2) and weight of 1000-grain and panicle length (23) and (16).

The necessity of using a selection index is important because the genetic value cannot be directly evaluated, while it is better estimated by a linear function of the observable phenotypic values. The maximum response to the selection index will be achieved if the correlation between genetic value and index is maximized (18). Hence, conducting studies to analyze the

variances and find the relationships between the different traits by analyzing the correlation coefficient and also analyzing the path coefficient between the grain yield and its components is highly recommended. Therefore, the success of breeding methods depends on breaking the negative correlation among the components of the grain yield. Path coefficient analysis has been used by plant breeders to help identify traits that can be useful as selection indices for improving crop grain yield (21).

To achieve the desired goal of the breeding programs, it is essential to study the relationship between the yield and its components. Therefore, path coefficient analysis has been suggested as the most common statistical method and it is used to quantify the direct and indirect effects of different traits on a responsive trait (usually the grain yield). In a study by Al-Musawi and Al-Anbari (3) and Faysal et al. (15) there was a significant positive correlation between grain yield with the characteristics of the number of grains plant⁻¹ and the weight of 1000 grains, and the number of panicles, in addition to the highest direct effects on grain yield by the number of grains by genetic path coefficient analysis method. Therefore, the research aimed to study the selection index and the path coefficient analysis to find out the direct and indirect effects of the studied traits on grain yield, and this may allow to improve yield and contribute to the success of breeding programs.

Materials and Methods

Sixteen rice genotypes were used in the current study in the first season (2021) as shown in Table (1), while, in the second season (2022) six genotypes were selected from the first season. The two experiments were carried out at the rice research station in Al-Mishkhab /Najaf city /Iraq, according to (RCBD) with three replicates. The field was prepared in terms of plowing, smoothing, amending, dividing

and planting at the beginning of the third week of June for the seasons 2021 and 2022. Then the seedlings were transferred to the main field at 20 days old by placing one seedling in each hole in line with three meters in length. The distance between the

holes (25 cm) and between the lines (25 cm). After seedlings being transplanted the field was directly irrigated by the traditional irrigation method (continuous watering).

Table 1. Pedigree the studied genotypes included in the study

Ser.	Genotypes	Pedigree	Ser.	Genotypes	Pedigree
1	T33	Line *	9	T34	Line *
2	K1	Line *	10	T92	Line *
3	T93	Line *	11	T58	Line *
4	T94	Line *	12	Anber33	Iraqi variety
5	T65	Line *	13	Khader	Research International Rice Institute
6	T45	Line *	14	Furat1	Research International Rice Institute
7	T32	Line *	15	Baraka	India
8	K2	Line *	16	Jasmine	Vietnam

*Lines resulting from crosses among local varieties were used in the study

The fertilizer NPK (18-18-0) was applied with an amount of 400 kg.ha⁻¹ mixed with the soil, while urea fertilizer (46%N) was added in two equal batches at an amount of 140 kg.ha⁻¹. The first batch was added after 10 days of seedlings transplanted, while the second batch was added a month after the first batch (25). The measured traits were estimated as an average of ten plants chosen randomly from each experimental unit including: number of days to 50% flowering, plant height (cm), panicle length (cm) number of tillers.m⁻², number of grain panicle⁻¹, number of days' physiological maturity, 1000 grain weight (gm) and grain yield (kg.ha⁻¹). A statistical analysis of data for all studied traits was carried out using statistical programs in the Excel and Genstat, and the averages of genotypes were compared according to Duncun's polynomial test at a probability level of 0.05 (19). Table (2) shows temperature data in the experiment area during the growing seasons (2021 and 2022).

Table 2. Agro-meteorological data in the experiment area during the growing seasons (2021 and 2022)

Month	Season	Air temperature °C		
		Max	Min	Average
July	2021	41.23	28.33	34.78
	2022	42.04	28.11	35.58
August	2021	43.41	28.12	35.77
	2022	44.13	28.03	36.08
September	2021	38.90	22.67	30.78
	2022	38.67	23.03	30.99
October	2021	32.79	20.11	26.45
	2022	31.02	20.65	25.84
November	2021	26.78	12.34	19.56
	2022	25.68	13.34	19.84

Source: Center Agricultural Meteorology, Ministry of Agriculture - Republic of Iraq

The genetic parameters, path coefficient and selection index were estimated as reported by Al-Zubaidy and Al-Jaboury (5) and Falconer (13), such as phenotypic, genetic and environmental variances, values of phenotypic and genetic variation coefficients, less than 10% is low, 10-30% is medium and more than 30% is high, as selection takes place in populations with a

large genetic and phenotypic variation coefficient. Heritability in the broad sense, the ranges are estimated, less than 40% are low, 40-60% are medium, and more than 60% are high. The expected genetic advance was estimated and the ranges were used for the expected genetic advance as follows: less than 10% are low, between 10%-30% are medium, and more than 30% are high. The correlations between the studied traits were estimated using the Microsoft Excel 2016 and the correlation was tested based on the equations:

$$t=r/SEr, \text{ where } SEr = \sqrt{\frac{1-r^2}{N-2}}.$$

The correlation coefficient values were classified into (low, medium, high) if they fall within the ranges (0-0.39), (0.40-0.69), (0.70-1.00), respectively. Selection index (In) was created with all possibilities from the equation: $In = b_1x_1 + b_2x_2 + \dots + b_nx_n$, where, b_i was calculated by matrices from the equation $bi = P^{-1}g$, as P^{-1} represents the inverse of the matrix of phenotypic variances and covariances, g

represents the common genetic variances for each trait with the grain yield.

The path coefficient was calculated with the model that included four independent traits (x_1, x_2, x_3, x_4) that were tested with the dependent trait (Y or grain yield) as shown in **Figure (1)** that represented the path coefficient using correlation matrices and as follows: $P = R^{-1}r$, as: P represents the path coefficient from the cause (X_n) to the effector (Y), whereas, R^{-1} represents the inverse of the matrix of correlation coefficients (genetic or phenotypic) between all possible pairs for the measured traits, while (r) represents the factor of correlation coefficients (genetic or phenotypic) between the yield and the measured traits. A measure of direct and indirect influence was adopted according to the following gradation: the value greater than 1 is very high, (0.3 to 0.9) is a high value, (0.2 to 0.29) is a medium value, (0.1 to 0.19) is a low value, and the value less than 0.1 is a neglected value according to (5).

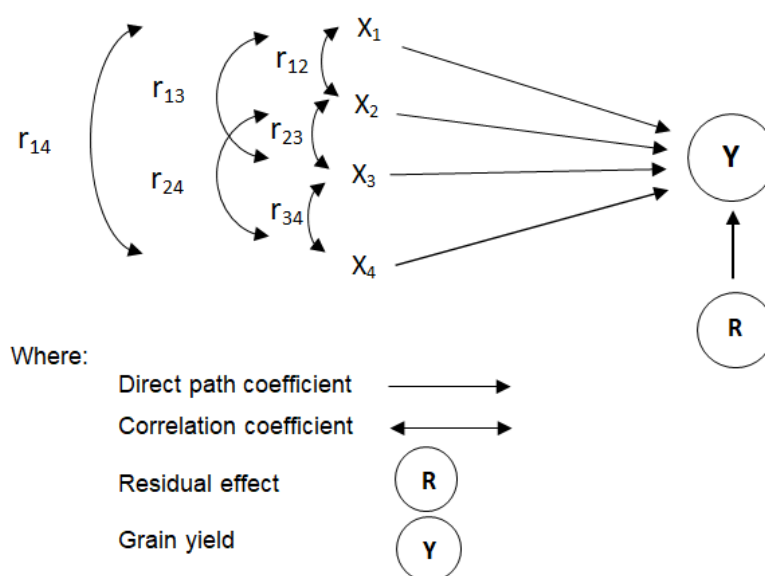


Figure 1. The path relationship diagram of the measured traits affecting the grain yield. where r_{14} correlation between x_1 and x_4 trait

Stability parameters (Genotypic resultant-GR) for each genotype according to Elsahookie adopted by Al-Zubaidy and Al-

Jubory (5) measured according to the following formula: $GR = (PS)(y_i./y..)$, where, phenotypic stability $PS = 1 - (S/y_i.)$,

where S represent standard division, y_i is genotype mean over environments (seasons) and $y_{..}$ is general mean of trait. According to this method, the genotype stability increases when the value of phenotypic stability is close to 85%.

Results and Discussion

Table 3. Variance analysis results of sixteen rice genotypes traits in the 2021 season

Source of variances	d.f	Mean square							
		50% Flowering (day)	Plant height (cm)	No. grain. panicle ₁	No. tillers. m ⁻²	Panicle length (cm)	Physiological maturity (day)	1000 grain weight (g)	Grain yield (kg.ha ⁻¹)
Replicates	2	4.77	1.89	0.15	101.27	1.161	1.27	0.003	32170.33
Genotypes	15	38.87**	392.18**	9.37**	4840.5**	1897.62**	34.19**	20.067**	891711.3**
Error	30	1.28	2.81	0.26	190.98	10.113	2.47	0.009	27650.16

(**) Significant at probability level 1%, d.f is the degree of freedom.

Table (4) shows the values of some genetic parameters for sixteen rice genotypes. It is noted that the values of genetic and phenotypic variances are high compared to the environmental variance of the traits of the grain yield and its components. This gives evidence that genetics play a crucial role in displaying the trait and thus effective selection, therefore, allowing the plant breeder to directly select the genetic material that desired in the breeding program for efficient genotypes that are slightly affected by the environment. Estimation of heritability may be more useful in selecting the best genotype along with estimating the expected genetic advance. The values of heritability in the broad sense (h^2_{BS}) were high for all the studied traits, and this in turn led to a rise in the values of the expected genetic advance as a percentage of the average. The highest means were for the trait of the number of grains in the panicle (0.361 grains), the average for the rest of the traits, including the number of tillers m⁻² (0.268), while, the lowest mean was for the length of the panicle (0.137 cm).

The results of the analysis of mean variance showing a significant difference for all studied traits at the probability level of 1% for the mean of squares of the genotypes (table 3) This indicates that the genotypes are different in their gene pool for all traits. Thus, it shows that there is a sufficient amount of variance between the genotypes selected in this study (10).

Therefore, the selection of genotypes based on these traits will be more effective to be successful in the selection of the elite cultivar. This result was accompanied by an increase in the values of the phenotypic variation coefficients for the above two traits (number of grains and number of tillers). This indicated that there was a large amount of phenotypic variation (V_P) for these two traits between the genotypes that was due to the environment merely, and this means that the random environmental fluctuations caused greater changes in these traits. Approximately equal amounts of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for a 1000-grain weight trait indicate that these traits are less affected by the environment. These results are consistent with what were mentioned by Abebe et al. (2) in their studies on 36 rice genotypes, Hossain et al. (17) in a study included five genotypes and the study of Niharika et al. (26) on 40 rice genotypes. The high values of variance, heritability, expected genetic advance and important traits such as yield component



traits allow plant breeders to benefit from them as a selection index in the early generations for different traits.

Table 4. Variances and some genetic parameters in sixteen rice genotypes traits in the 2021 season

Parameters	Traits				
	Panicle length (cm)	No. tillers. m ⁻²	No. grain. panicle ⁻¹	1000 grain weight (g)	Grain yield (kg.ha ⁻¹)
V _E	0.256 ±0.064	190.982 ±47.745	10.113 ±2.528	0.009 ±0.002	27650.16 ±6912.54
V _G	3.039 ±1.071	1549.839 ±553.378	629.169 ±216.853	6.686 ±2.293	288020.38 ±101926.52
V _P	3.295 ±0.788	1740.821 ±416.136	639.282 ±152.818	6.695 ±1.600	315670.53 ±75459.69
h ² _{BS}	0.922	0.890	0.984	0.999	0.912
GA	3.449	76.520	51.261	5.323	1056.02
GA %	0.137	0.268	0.361	0.223	0.168
E.C.V %	2.016	4.842	2.237	0.401	2.651
G.C.V %	6.949	13.794	17.647	10.833	8.558
P.C.V %	7.235	14.619	17.788	10.840	8.959
Mean	25.09	285.39	142.14	23.87	6271.33

Where: V_G, V_E and V_P are genetic, environmental and phenotypic variances respectively, h²_{BS} is Heritability in broad sense, GA is genetic advance, GA% is the genetic advance of mean and E.C.V, G.C.V and P.C.V % are coefficient variances of environmental, genotypic and phenotypic respectively.

Table (5) shows the values of genetic correlation coefficients between grain yield and other measured traits, and among traits. It is noticed that the grain yield had a positive and significant genetic correlation with panicle length, number of tillers m⁻² and number of grain.panicle⁻¹ (0.054, 0.592 and 0.573) respectively. Whereas, a negative and non-significant relationship with an important trait of the components of the yield, which is the weight of 1000 grains by (-0.309). The weight of 1000 grains is one of the essential traits of the yield components that cannot be neglected. While the correlation coefficients for the rest of the traits (number of days to 50% flowering, plant height and the number of

days to physiological maturity) with the grain yield were negative and significant, these traits were neglected in the subsequent study and were not one of the important components of the grain yield, furthermore it was less important through selection index method. The genetic and phenotypic correlations showed that they were in the same direction, this may indicate that the genetic effect in the association between the different traits is controlled by the genetic action in showing the trait at the expense of environmental effect. The results were similar to Kumar et al. (23) and Rani et al. (27) as they found positive and significant correlations between their selected traits.

Table 5. Genetic and phenotypic correlations between grain yield and some components in the 2021 season

Traits	Correlation	Panicle length (cm)	No. tillers. m ⁻²	No. grain. panicle ⁻¹	1000 grain weight (g)	50% Flowering (day)	Plant height (cm)	Physiologic al maturity (day)
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Grain yield (kg.ha ⁻¹)	r _G	0.354*	0.592**	0.573**	-0.309	-0.528**	-0.714**	-0.693**
	r _P	0.362*	0.556**	0.534**	-0.287	-0.488*	-0.674**	-0.591**
1000 grain weight (g)	r _G	-0.210	-0.333	-0.460*				
	r _P	-0.203	-0.311	-0.458*				
No. grain. panicle ⁻¹	r _G	0.180	0.085**					
	r _P	0.187	0.046					
No. tillers. m ⁻²	r _G	-0.482*						
	r _P	-0.469*						

(**) and (*) are significant at probability levels 1% and 5%, respectively, r_G is genetic correlation and r_P is phenotypic correlation.

To obtain more information about the nature and importance of the relationship between grain yield and the measured traits, the genetic and phenotypic correlation coefficients were segmented using path coefficient analysis according to the pathway relationship in Figure (1). Path coefficient analysis is used to divide the genetic and phenotypic correlation coefficient into its direct and indirect effects between the dependent variable (grain yield) and the independent used variables (four traits). Depending on the direct and indirect effects, it is possible to infer from it and obtain a selection index for the benefit of plant breeders in the selection programs (1).

Table (6) analysis of the genetic path coefficient between the grain yield and some of its components showed the direct effect of the number of tillers.m⁻² was the highest and most positive on the grain yield (0.867), whereas, the second and third ranks were for the two traits of the number of grains.panicle⁻¹ with a direct effect (0.575) and panicle length (0.439). However, the least impact was for the weight of 1000 grains on the grain yield (0.336). Generally, all the traits of the yield components showed an indirect, low and negligible effect on the grain yield. The sum of the total effects of the yield traits on the grain yield was positive and high,

except for the total effects of the weight of 1000 grains on the grain yield, which was negative and negligible (8) and (20) who obtained a high direct effect of the number of effective tillers per plant and the number of grains in a panicle.

The high values of the direct effect of the number of tillers.m⁻² and the number of grains.panicle⁻¹ on the grain yield is positive and high, which represents the largest part of the correlation between these two traits and the grain yield, and it is accompanied by the sum of the total effects of the two positive traits, which are also high (0.592 and 0.573), respectively. It is clear from the above results that the number of tillers.m⁻² and the number of grains.panicle⁻¹ have a direct, high positive impact on the grain yield and can contribute to increasing the yield. Thus, they can be considered among the best criteria for adoption as a selection index in rice breeding programs. Similar results have been observed by Streck et al. (28) and Sucharitha et al. (29)

The results of the phenotypic path analysis in the same Table (6) showed results that were very similar to the results of the genetic path analysis for the traits of the components of the yield in their direct and indirect effects on the grain yield.

Table 6. Genetic and phenotypic path analysis of grain yield and its components in the 2021 season

Effect type	Symbol	Effect value		Classification
		Genetic	Phenotypic	
1- Panicle length effect on grain yield				
- Direct effect	p_{1y}	0.439	0.401	High
- Indirect effect				
- By No. tillers.m ⁻²	r_{12p2y}	-0.418	-0.383	Ignore
- By No. grains.panicle ⁻¹	r_{13p3y}	0.104	0.105	Ignore
- By 1000 grain weight	r_{14p4y}	-0.071	-0.062	Ignore
Sum of the total effect of Panicle length on grain yield	r_{1y}	0.054	0.062	
2- No. tillers.m ⁻² effect on grain yield				
- Direct effect	p_{2y}	0.867	0.814	High
- Indirect effect				
- Panicle length	r_{12p1y}	-0.212	-0.189	Ignore
- By No. grains.panicle ⁻¹	r_{23p3y}	0.049	0.026	Ignore
- By 1000 grain weight	r_{24p4y}	-0.112	-0.095	Ignore
Sum of the total effect of Panicle length on grain yield	r_{2y}	0.592	0.556	
3- No. grains.panicle ⁻¹ effect on grain yield				
- Direct effect	p_{3y}	0.575	0.561	High
- Indirect effect				
- Panicle length	r_{13p1y}	0.079	0.075	Ignore
- By No. tillers.m ⁻²	r_{23p2y}	0.074	0.037	Ignore
- By 1000 grain weight	r_{34p4y}	-0.155	-0.139	Ignore
Sum of the total effect of Panicle length on grain yield	r_{3y}	0.573	0.534	
4- 1000 grain weight effect on grain yield				
- Direct effect	p_{4y}	0.336	0.304	High
- Indirect effect				
- Panicle length	r_{14p1y}	-0.092	-0.081	Ignore
- By No. tillers.m ⁻²	r_{24p2y}	-0.289	-0.253	Ignore
- By No. grains.panicle ⁻¹	r_{34p3y}	-0.264	-0.257	Ignore
Sum of the total effect of 1000 grain weight on grain yield	r_{4y}	-0.309	-0.287	

Table No. (7) presents the mean traits for sixteen rice genotypes and their selection indices. The Furat1 genotype ranked the first order with the highest value of the selection index amounting to 9124.44. It was superior compared to all studied genotypes by giving high and significant average of the number of tillers.m⁻² (382.67) and a grain yield of 6885.33 kg ha⁻¹.

Whereas, the Jasmine genotype came in the second rank with a value of the selection index amounting to 8769.45, which was characterized by high values of its traits such as the number of tillers.m⁻² (358.33) and the number of grains in the panicle (172.27 grain) and the average grain yield (6598.67 kg.ha⁻¹), which differed slightly from the genotypes (T65, T92 and T93), which recorded values of the selection indices of 8619.89, 8553.77

and 8513.06, with an average grain yield (6784.00, 6184.00 and 6613.33 kg.ha⁻¹) for the three genotypes, respectively.

However, the Anber33 genotype showed the low value of the selection index by 6393.93 with the lowest grain yield (4920.0 kg.ha⁻¹), 1000 grain weight (21.23 g) and the number of tillers.m⁻² (233.00), despite having high values for the average traits such as the panicle length (25.43 cm) and the number of grains per panicle (117.37 grain). Based on the current results of the genetic and phenotypic correlation coefficients, the genetic and phenotypic path coefficients and the selection indices between the grain yield and other traits, indicate that the grain yield can be

improved by improving some of the traits of the yield component. Two traits came the most important according to the results of the current study, which included the number of tillers per square meter and the number of grains per panicle, therefore selection index values based on these two traits may be more effective and efficient in selecting highly productive genotypes. These results agree with studies in selection index methods in 50 improved rice genotypes (18), 28 black rice lines (4), 36 doubled-haploid rice lines (6), 56 doubled-haploid rice lines adaptive to saline environment (7) and 95 lines and four check rice varieties (30).

Table 7. Mean of six rice genotypes traits and its selection indices in 2021 season

Genotypes	Traits					Selection index	Trade-off sequence
	Panicle length (cm)	No. tillers. m ⁻¹	No. grain. panicle ⁻¹	1000 grain weight (g)	Grain yield (kg.ha ⁻¹)		
T33	24.57 df	260.67 f	139.30 ef	24.20 e	6045.33 f	7734.99	13
K1	23.83 eg	256.33 fg	164.03 b	28.23 a	6138.67 ef	7856.45	12
T93	25.30 d	297.33 d	155.90 c	23.23 f	6613.33 ac	8513.06	5
T94	26.40 c	255.33 fg	151.87 cd	24.13 e	6405.33 ce	8113.83	10
T65	27.40 b	281.33 df	150.87 cd	22.13 g	6784.00 ab	8619.89	3
T45	26.50 c	265.00 ef	152.27 cd	24.90 c	6634.67 ac	8398.19	7
T32	23.57 g	254.67 fg	119.03 h	27.90 b	5318.67 h	6914.01	15
K2	23.77 fg	277.67 df	142.73 e	24.63 d	6668.00 ac	8469.49	6
T34	24.73 de	266.67 ef	149.43 d	24.23 e	6184.00 df	7922.04	11
T92	24.70 de	332.67 c	126.43 g	22.13 g	6184.00 bc	8553.77	4
T58	26.50 c	277.67 df	148.20 d	22.00 g	6477.33 bd	8275.36	8
Anber33	25.43 d	233.00 g	117.37 h	21.23 i	4920.00 i	6393.93	16
Khader	28.87 a	277.00 df	176.87 a	21.53 h	6417.33 ce	8253.47	9
Furat1	22.37 h	382.67 a	135.53 f	24.20 e	6885.33 a	9124.44	1
Anber Braka	25.17 d	290.00 de	72.17 i	28.10 a	5694.67 g	7390.15	14
Jasmine	22.30 h	358.33 b	172.27 a	19.10 j	6598.67 ac	8769.45	2
Mean	25.09	285.39	142.14	23.87	6271.33	8081.41	

The values followed by the same letter for each trait are not significantly different from each other (Duncan test, 0.05)

From the results of the first season (2021), six genotypes were selected based on their superiority in the average traits of the grain

yield and some of its components, which led to an increase in the values of the selection indices for them. Table (8) shows



the results of the analysis of variance for the traits of six selected genotypes from the season 2021 the averages of genotype variance showed a highly significant difference and at a probability level of 1% for all studied traits, except for the trait of the number of days until physiological

maturity did not reveal the statistical significance. The significance of this source indicates that the gene pool of the six genotypes is different and that the possibility of selection among them is possible (1).

Table 8. Variance analysis results of selected six rice genotypes traits in 2022 season

Source of variance	d.f	Mean square							
		50% Flowering (day)	Plant height (cm)	Panicle length (cm)	No. tillers. m ⁻²	No. grain. panicle ⁻¹	Physiological maturity (day)	1000 grain weight (gm)	Grain yield (kg.ha ⁻¹)
Replicates	2	0.72	2.72	0.15	705.4	8831.4	5.06	0.12	4469.4
Genotypes	5	8.86**	63.39**	31.77**	10425.6**	42948.8**	7.82	10.40**	7933.4**
Error	10	0.79	1.26	0.68	174.2	2797.0	6.26	0.11	733.9

(**) and (*) are significant probability levels 1% and 5%, respectively

The results of Table (9) shows the averages of eight traits for the six selected genotypes in rice. The Furat1 genotype showed the highest grain yield of 6958.67 kg.ha⁻¹ and which is significantly differed from all genotypes except for the Jasmine genotype. The reason for the superiority of Furat1 genotype may be due to the high number of tillers.m⁻² (422.7) and the weight of 1000 grains (24.23 gm). It was followed by the Jasmine genotype with a high grain yield of 6844.00 kg.ha⁻¹, which was characterized by a high mean of the number of grains in the panicle (150.90) and the number of tillers.m⁻² (289.0). Regarding K2 genotype showed a significant difference in the trait of grain

yield (6722.67 kg.ha⁻¹) from the T93 and Khader genotypes, but it did not differ significantly from the T65 genotype. Moreover, K2 showed the highest average weight of 1000 grains (24.33 g) and differed significantly from the other genotypes except for the Furat1 genotype. While the Khader genotype showed the lowest average grain yield trait (6401.33 kg.ha⁻¹), despite having the longest panicle and number of tillers.m⁻². The percentage of infertility during the fertilization period and the grain filling stage are as a result of sensitivity to the light period and high temperatures. The results were similar to what has been recorded by Musa et al. (25).

Table 9. Means of selected six rice genotypes traits in the 2022 season

Genotypes	Traits							
	50% Flowering (day)	Plant height (cm)	Panicle length (cm)	No. tillers. m ⁻²	No. grain. panicle ⁻¹	Physiological maturity (day)	1000 grain weight (g)	Grain yield (kg.ha ⁻¹)
T93	99.00 b	89.00 c	28.00 b	262.0 d	153.17 bc	139.67	23.00 b	6513.33 cd
T65	98.33 b	93.33 b	28.73 b	284.7 bd	157.07 b	137.00	22.33 c	6678.67 bc
K2	101.67 a	92.00 b	24.90 c	273.3 cd	145.33 cd	138.33	24.33 a	6722.67 b

Khader	100.67 a	97.67 a	30.40 a	301.7 b	175.27 a	138.00	21.3 d	6401.33 d
Furat1	102.33 a	84.00 d	21.63 d	422.7 a	141.00 d	140.33	24.23 a	6958.67 a
Jasmine	102.33 a	89.67 c	24.40 c	289.0 bc	150.90 bd	141.33	19.43 e	6844.00 ab
Mean	100.72	90.94	26.34	305.56	153.79	139.11	22.43	6686.44

The values followed by the same letter for each trait are not significantly different from each other (Duncan test, 0.05)

The results of the analysis of variance are shown in Table (10) for the six genotypes selected from rice during two planting seasons in 2021 and 2022. It was noticed that the mean squares of the genotypes were significant for all the studied traits at the probability level of 1% except for the characteristic of the number of days to physiological maturity, which was significant at the probability of 5%. This indicates that there is a sufficient amount of variation between the genotypes selected for the study. While the environments showed highly significant differences in the mean of variances for the traits of the number of days to 50% flowering, plant height, panicle length and number of days to physiological maturity at probability level 1%. This can be explained by fluctuating due to the environmental difference (seasons). While the means of variance for the environmental and genetic interaction showed a significant difference at the

probability level of 1% for the traits of the number of days to 50% flowering, the height of the plant, the length of the panicle, the number of tillers m^{-2} , the number of grains per panicle, and the number of days to physiological maturity, while, the remaining traits were not significant. The significance of the source indicates that the genotypes differ in their performance from one environment to another (seasons) and the environmental role is greater in the traits when the trait shows a significant difference in both sources (environments and genetic \times environmental interaction) such as, the number of days to 50% flowering and plant height, the length of the panicle and less in the weight of 1000 grains and grain yield. Whereas, the number of tillers. m^{-2} and the number of grains per panicle showed a moderate effect by the environments. These results are in agreement with Debsharma et al. (11) and Duvallet et al. (12).

Table 10. Variance analysis results of selected six rice genotypes traits over two seasons (2021 and 2022)

Source of variances	d.f	Mean square							
		50% Flowering (day)	Plant height (cm)	Panicle length (cm)	No. tillers. m^{-2}	No. grain. panicle $^{-1}$	Physiological maturity (day)	1000 grain weight (g)	Grain yield (kg.ha $^{-1}$)
Environment	1	26.694*	215.11**	16.268**	420.2	326.78	200.69**	0.014	361.3
Genotypes	5	11.361*	200.778**	51.664**	14440.1*	10659.56**	12.25*	22.657**	11234.4**
G \times E	5	9.761**	40.044**	2.042**	2404.1**	1559.60**	7.09	0.109	1614.0
Error	24	1.083	1.972	0.449	225.0	236.39	4.39	0.057	1493.7

(**) and (*) are significant probability levels at 1% and 5%, respectively

Table (11) shows the phenotypic, genetic and environmental variances and the heritability in the broad sense (h^2_{BS}) for

eight traits and six genotypes of rice during both seasons (2021 and 2022). The values of genetic and phenotypic variance were



high and have their values very close compared to environmental variance for seven traits except for the trait of the number of days to physiological maturity, which did not reach statistical significance. This indicates the significance of the genotypes of interesting genes that can play an effective role in showing the trait and thus effective selection, allows plant breeders to select the desired genetic

material in the breeding program directly due to low impact by the environment. The values of heritability in the broad sense were high for all the studied traits except for the number of days to 50% flowering and the number of days to physiological maturity were reached 40.37 and 37.99, respectively. Hossain et al. (17) and Zaid et al. (31) reported similar results in their studies.

Table 11. Genetic parameters of selected six rice genotypes traits over two seasons (2021 and 2022)

Parameters	Traits							
	50% Flowering (day)	Plant height (cm)	Panicle length (cm)	No. tillers. m ⁻²	No. grain. panicle ⁻¹	Physiological maturity (day)	1000 grain weight (g)	Grain yield (kg.ha ⁻¹)
V _G	3.426 ±2.025	66.269 ±35.76	17.07 ±9.20	4738.4 ±2571.7	347.44 ±198.84	2.620 ±1.219	7.533 ±1.634	51946.6 ±32084.8
V _E	1.083 ±0.300	1.972 ±0.547	0.449 ±0.125	225.00 ±62.40	23.64 ±6.56	4.390 ±1.217	0.057 ±0.016	23898.7 ±6628.3
V _P	8.487 ±2.028	86.619 ±20.71	18.167 ±4.342	5977.9 ±1429.1	429.36 ±102.64	6.897 ±1.649	7.597 ±1.816	68837.9 ±16455.4
h ² _{BS}	40.37	76.51	93.97	79.26	80.92	37.99	99.16	75.46
Mean	99.86	93.39	25.67	308.97	154.74	136.75	22.45	6673.81

Where: V_G is genetic variance, V_E is environmental and V_P is phenotypic variances, h²_{BS} is Heritability in the broad sense and ± standard deviation.

The results of Table (12) show the stability parameters of eight traits for six genotypes during the 2021 and 2022 seasons according to Elsahookie adopted by Al-Zubaidy and Al-Jubory (5). According to this method, genotypic stability increases when the value of phenotypic stability is close to 85%. When the value is less than 85%, it is less stable under different conditions. The higher cultivars in the phenotypic stability and genotypic resultant values close to one can be relied upon in breeding programs to increase production and phenotypic stability together. The two genotypes, Jasmine and Furat1, showed stable values for more studied traits (three traits). The Jasmine

genotype exhibited high values of stability parameters for important traits such as the panicle length, the number of tillers.m⁻², and the weight of 1000 grains, and the Furat1 genotype showed high values of the stability parameters for the traits such as plant height, panicle length, and the number of grains per panicle. While the genotypes: T93, K2 and Khader showed high stability values for one trait (the number of tillers.m⁻²). While the T65 genotype did not display any stability values for all the studied traits. Duvallet et al. (12), Debsharma et al. (11), Lakew et al. (24), Kumar et al. (22), and Zaid et al. (31) have indicated similar results in their studies.

Table 12. Stability parameters of selected six rice genotypes traits over two seasons (2021 and 2022)

Genotypes	Traits							
	50% Flowering (day)	Plant height (cm)	Panicle length (cm)	No. tillers. m ⁻²	No. grain. panicle ⁻¹	Physiological maturity (day)	1000 grain weight (g)	Grain yield (kg.ha ⁻¹)
T93	0.989	0.931	0.963	0.824	0.986	1.003	1.022	0.972
T65	0.983	0.985	1.056	0.908	0.966	0.966	0.983	0.997
K2	1.002	0.959	0.916	0.882	0.918	0.988	1.079	0.997
Khader	0.939	1.042	1.112	0.879	1.130	0.959	0.946	0.958
Furat1	0.992	0.877	0.837	1.211	0.868	0.967	1.077	1.029
Jasmine	0.993	0.956	0.851	0.888	0.946	0.968	0.847	0.981
Mean	99.86	93.39	25.67	308.97	154.74	136.75	22.45	6673.8

Conclusion

The significant differences between the performance of genotypes as a result of their differences in their gene pool give a great incentive to proceed with the breeding program and the possibility of rapid selection of superior genotypes, which may be an alternative to the currently cultivated varieties. The encouraging results for Furat1 and K2 genotypes, especially the grain yield (6958.67 and 6401.33 kg.ha⁻¹), which displayed high selection indices, can be adopted and applied into future studies under the influence of different experimental conditions to test its efficiency. The promising results are shown by the analysis of the genetic and phenotypic path coefficient of the presence of a high direct effect of yield components on the grain yield as a result of the high positive and identifiable values of the genetic and phenotypic correlation between the yield of grains with some of its components included, the number of tillers.m⁻², the number of grains.panicle⁻¹ and the length of the panicle, which can be considered as selected indicators for improving grain yield. Thus, the traits of the number of tillers.m⁻² and the number of grains per panicle can be considered among the best criteria for adoption as a selection index in the breeding programs for the rice crop. In addition, the two traits exhibited high values for heritability in the broad

sense and high stability values during the two study seasons for high grain yield genotypes.

Conflict of Interest

The author have no conflict of interest.

Acknowledgments

The author extends his sincere thanks to the Ministry of Agriculture and the Agricultural Research Department in the Iraqi Ministry of Agriculture for carrying out the study at the rice research station in Al Mashkhab. I especially thank Dr. Abdul-Kadhim Jawad Musa and the work team for their great assistance in completing the current study during the implementation of the experimental research and data collection.

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