Genetic Parameters and Selection Indices of Grain Yield trait and Its Components for Genotypes of Rice

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Abstract

This study was conducted at rice research station in Al-Mashkhab/Najaf, Iraq, to determine the best rice genotypes based on grain yield and selection index. Seven genotypes were planted using a three-replicates in randomized complete block design (RCBD) in 2021 and 2022. Mean squares of genotypes were significant for all traits at 1% probability in both seasons. FA1 and Furat1 outperformed the other seven genotypes in tiller number and grain yield. Heritability broad sense (H^2_{BS}) and predicted genetic improvement were high for most traits except plant height and panicle length, which were low. FA1 and AF2 genotypes had the greatest selection indices in both seasons. The genetic and phenotypic path coefficient analyses demonstrated a substantial direct influence of tillers on grain yield owing to the genetic and phenotypic link between grain production and its components. Furat genotype had the lowest grain yield and tiller coefficient of variation. m^{-2}, although genotype (FA1) had somewhat higher coefficient of variation than Furat. Thus, rice breeding programmers should use tillers and grains as selection indicators. Future experiments might assess the effectiveness of these improved genotypes under diverse conditions.

Keywords: Heritability, Path coefficient analysis, Selection index, Coefficient of variability, Rice genotypes.

Introduction

Most of the world's population relies on rice, which is produced at 502.98 million tonnes (14). After wheat and barley, Iraq produces 442.5 thousand tons of rice on 96.2 thousand hectares at 275 kg per hectare (10). Despite favorable conditions for growing, rice has a major problem with grain output and quality. The genetic factor (varieties) and environmental factors (temperature, humidity, photoperiod, seasons and locations) affect rice grain production, components and quality (25). The high values of heritability and selection indicators of important traits, in addition to high direct effect of them by genetic path coefficient on grain yield, gives a great opportunity to adopt more efficient breeding programs and the possibility of rapid selection of superior genotypes. Any program to develop rice varieties to obtain high yield is the main goal to be achieved by plant breeders all over the world, as these programs may generate distinct germplasm that may promote the replication of high yielding genotypes (12). The average productivity per unit area can be increased by achieving an appropriate adaptation between the genotype and the environmental conditions, which are the outcome of the contribution of a number of traits or components. This is dependent on a number of physiological processes and the extent of interaction and overlap between them during the plant life cycle (29). Selecting the most efficient components may increase grain yield. However, these relationships will guide this. Thus, the best genotypes with desirable features may be identified for future breeding programs. Some researchers found a high positive correlation between grain yield and important yield components, such as the weight of 1000 grains, the length of the panicle (23), the number of tillers.m^{-2} and the number of grains.panicle^{-1} (2). These positive correlation values between the yield and its key components might help choose a selection index. Thus, effective crop breeding programs can produce current genotypes (19). Selection index is needed since genetic worth cannot be assessed directly. A linear function of comfortable phenotypic values can estimate this. If genetic value and frequency correlate, selection index will be most effective. Plant breeders save time and effort by selecting multiple traits at once to improve grain yield (8). Thus, correlation coefficient and path coefficient analysis between grain yield and its components are advised to analyze variances and uncover correlations between features. Breeding approaches succeed by breaking the negative correlation between grain yield components. Plant breeders employ path coefficient analysis to find features that can be selection indices for crop grain production (22) and (16). Additionally, the genotypes that are superior and stable in a variety of environments could be successfully utilized as essential components in the breeding plans of the future. The selection index and path coefficient analysis of rice genotypes across two agricultural seasons will determine the direct and indirect impacts of yield component traits on grain yield.

Materials and Methods

Breeding materials and procedure

Five pure rice lines (FA1, FA2, AF1, AF2 and AF3) were chosen for 6 years of self-pollination after crossing two varieties (Furat and Anber33), planted the five lines and parents on June 25 for the 2021 and 2022 seasons (Al-Mishkhab rice research station in Najaf, Iraq). The seedlings were germinated in tries in a greenhouse for one week, then transferred to the field to acclimatize for 20 days, then placed one seedling in each hole in eight lines for each genotype and replicate with a unit experiment area of 2×3 m^2 and a distance of 25 cm between holes and lines. Irrigation began immediately after planting. At planting, 400 $kg.ha^{-1}$ of NPK (18-18-0) fertilizer was added to the soil and 300 $kg.ha^{-1}$ of urea (46%N) was added in two equal batches after one week of seedlings in the field and 30 days after the first batch (25). Field measurements were obtained at plant maturity for ten plants randomly selected from the middle lines of the following traits: days to heading (day), plant height (cm), panicle length (cm), No. $tillers.m^{-2}$, No. $grain.panicle^{-1}$, infertility %, 1000 grain weight (g) and grain yield $kg.ha^{-1}$.

Statistical Analysis

The data of traits taken for the seven genotypes used in the current study were analyzed statistically according to the randomized complete block design (RCBD) with three replicates. Means of genotypes were compared with Duncan's multiple range test at a probability level of 5% (20).

Genetic analysis

Singh and Chaudhary (27) and (13) methods used to find genetic parameters such as phenotypic, genetic and environmental variances, heritability broad sense (%), expected genetic advance (%), selection indices and path coefficient analysis. Selection index (In) between genotypes traits was estimated by equation: $In = b_1x_1 + b_2x_2 + \ldots + bnxn$, where, **bi** was calculated by matrices as the equation: $bi = P^{-1}$ g, where, $\mathbf{P^{-1}}$ represents the matrix inverse of phenotypic variances, **g** represents the genetic variances for other traits with the grain yield. Path coefficient model included four independent traits (Panicle length, No. $tillers.m^{-2}$, No. grain. $Panicle^{-1}$ and 1000 grain weight (g) were examined against the dependent trait (grain yield- named by Y) by the following equation: $P = R^{-1}$ r, where, **P** is the path coefficient value for the cause (Xn) to the effector (Y), while, $\mathbf{R^{-1}}$ is the inverse of the matrix of correlation genetic or phenotypic among all possible traits pairs were measured, while **r** represents the correlation of genetic or phenotypic between the grain yield and other traits. The direct and indirect impact were adopted according to following: neglect; value less than 0.1, low (0.1 to 0.19), medium (0.2 to 0.29), high (0.3 to 0.9) and very high is greater than 1.0 according to Al-Zubaidy and Al-Juboury (7). The coefficient of variability (CV%) for each genotype via their different environments was used as a stability parameter. According to this parameter, the genotype is more stable at a lower value of the coefficient of variance. The method suggested by Lin et al. (24) as follows: CV%= (S/ў) × 100, (as; **S** represents the standard deviation of variance ($\mathbf{S^2}$) and **ў** represents the grand mean. Whereas, variance value found by the equation:

$S^2= [\sum yij^2 - (\sum yij)^2/s]/(s-1)$, where **yij** represents the environment mean and **s** represents the number of environments.

Results and Discussion

Table (1) provided pooled variance analysis for seven genotypes across two seasons. Environment showed strong meaningful variations at 1% for all traits except 1000 grain weight. At 1000 grain weight, genotypes × environments showed strong significant differences at 1% for all studied traits. All traits exhibited 1% genetic differences. This suggests that genotype performance is unpredictable across seasons and that genotypes with high yield. components traits impact grain production. Musa et al. (25) found that the two varieties employed in this investigation had varying yield and component attributes in different seasons and places. Zaid et al. (30) indicated that

G×E interactions affect rice yield components traits impact grain production.

Table 1. Variance analysis results of selected seven rice genotypes traits over two seasons (2021 and 2022)

S.O.V	d.f	Mean square							
		Days to heading (day)	Plant height (cm)	Panicle length (cm)	No. tillers. m^{-2}	No. grain. $panicle^{-1}$	Infertility %	1000 grain weight (g)	Grain yield $kg.ha^{-1}$
Envi.	1	6.09**	106.24**	10.20**	39744.38**	676.81**	8.78**	0.004	4.61**
Geno.	6	507.41**	1589.05**	14.77**	39067.3**	1823.66**	150.85**	28.74**	10.65**
G × E	6	20.43**	111.08**	3.93**	3609.05**	218.05**	20.72**	0.22	0.87**
Error	28	1.26	1.99	0.09	87.14	0.79	0.37	0.26	0.01

** is significant probability level at the 1%, Envi. is environments and Geno. is genotypes.

Table (2) shows the averages of eight traits for the seven chosen rice genotypes in 2021 and 2022. FA1 had the maximum grain yield (7,735 $kg.ha^{-1}$) in this study. The genotype with the most tillers has good traits.m^{-2} (573.33 tillers), the longest panicle (25.70 cm) and the lowest infertility (17.53%). Grain yield and tillers were second for Furat genotype. Its infertility percentage (15.77%) was lowest. AF1 had the lowest grain yield (3,801 $kg.ha^{-1}$) and maximum infertility (29.43%). The second season (2022) genotype performance was similar to the first (2021), but the values were low, especially in the FA1 genotype's grain yield, which decreased by 20%, abundances by 18%, and tillers by 20%.m^{-2}. FA1 20% and 13% savings. AF1 had a 21% grain output and 9% higher infertility than 2021's first season. The genotype with the most tillers has good traits. m^{-2} (573.33 tillers), the longest panicle (25.70 cm) and the lowest infertility (17.53%). Furat had the second-highest grain yield (7,254 $kg.ha^{-1}$) and second lowest infertility percentage (15.77%). AF1 had the lowest grain output (3,801 $kg.ha^{-1}$) and greatest infertility percentage (29.43%). The genotypes performed similarly in the second season (2022), notably FA1 and Furat, which had the highest averages in both seasons, but the values were lower than in the first season (2021).

Table 2. Means of traits of selected seven rice genotypes in two seasons (2021 and 2022) and the averages of seasons.

Genotypes	Traits mean 2021							
	Days to heading (day)	Plant height (cm)	Panicle length (cm)	No. tillers. m^{-2}	No. grain. $panicle^{-1}$	Infertility %	1000 grain weight (g)	Grain yield $kg.ha^{-1}$
Furat	94.67c	79.67g	21.70d	520.33b	100.07d	15.77f	23.67b	7.254b
Anber33	106.33b	134.67a	24.93b	309.67f	131.83b	18.83cd	19.67e	4.529e
FA1	87.33d	95.67f	25.70a	573.33a	126.67c	17.53e	23.83b	7.736a
FA2	107.67b	118.00c	21.80d	361.33d	100.43d	19.63bc	20.67d	3.901f
AF1	111.67a	127.33b	23.87c	482.33c	93.40e	29.43a	19.67e	3.801f
AF2	106.00b	99.00e	24.57b	493.00c	137.23a	20.73b	25.77a	5.884c
AF3	106.33b	110.20d	25.60a	346.67e	136.70a	17.87de	21.67c	4.886d

Mean	102.86	109.22	24.02	440.95	118.01	19.51	22.13	5.427
	Traits mean 2022							
Genotypes	Days to heading (day)	Plant height (cm)	Panicle length (cm)	No. tillers. m^{-2}	No. grain. $panicle^{-1}$	Infertility %	1000 grain weight (g)	Grain yield $kg.ha^{-1}$
Furat	91.67d	84.20g	20.07f	453.33a	89.23e	15.20f	23.90b	5.963b
Anber33	103.67c	124.83a	24.70b	326.67d	115.37c	22.70c	20.40c	4.864d
FA1	85.33e	95.53f	21.57e	463.00a	104.30d	15.93ef	23.77b	6.232a
FA2	108.33b	118.67b	22.80d	319.33d	114.40c	19.60d	20.77c	4.316e
AF1	110.00b	107.50d	22.83d	415.67b	88.43e	32.30a	19.83d	2.993g
AF2	113.00a	99.33e	23.77c	363.67c	136.27a	16.33e	25.23a	5.200c
AF3	102.67c	112.20c	25.53a	314.33d	122.97b	24.03b	21.60c	3.785f
Mean	102.09	106.04	23.04	379.43	110.14	20.87	22.21429	4.765

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

Table (3) displays genetic parameters for seven rice genotypes. Genetic variation and phenotypic variance were higher than environmental variation of grain yield traits and their components. Heritability in the broad sense (H^2_{BS}) was high for all parameters except plant height (71%). Due to high heritability, grain yield (72%) and infertility (65%) had the highest expected genetic progression as a percentage of the average, while panicle length (16%) had the lowest. The genetic variation coefficients were high compared to the phenotypic and environmental variation coefficients and similar to the expected genetic improvement, with high values for grain yield (39.16%) and infertility (38.13%) and the lowest value for panicle length (11.14%). The better traits CVG% and CVP% values converge, indicating that they are less impacted by the environment. Some researchers found high values for grain yield and its components in the heritability% for traits: plant height, number of tillers, filled grain and 1000-grain weight (17) in 36 rice lines, the expected genetic improvement (15) for the most traits in 20 rice genotypes, and the coefficient of genetic variation by Abebe et al. (2) in 36 rice genotypes for plant height and grain yield traits.

Table 3. Variances and some genetic parameters in seven rice genotypes traits over two seasons (2021 and 2022).

Parameters	Traits							
	Days to heading (day)	Plant height (cm)	Panicle length (cm)	No. $tillers.m^{-2}$	No. grain. $panicle^{-1}$	Infertility %	1000 grain weight (g)	Grain yield $kg.ha^{-1}$
σ^2_P	179.14 ±43.45	584.89 ±141.86	6.873 ±1.67	14812.43 ±3592.54	716.78 ±173.84	60.58 ±14.69	9.65 ±2.34	3.98 ±0.97
σ^2_G	168.72 ±84.53	529.02 ±264.71	4.89 ±2.46	12993.39 ±6507.97	607.62± 303.79	50.16 ±25.13	9.49 ±4.789	3.55 ±1.77
σ^2_E	1.26	1.99±	0.09	87.14	0.79	0.37	0.26	0.006

	±0.34	0.53	±0.02	±23.29	±0.21	±0.09	±0.07	±0.002
GA	25.97	45.06	3.85	219.93	46.75	13.28	6.29	3.66
GA %	0.25	0.42	0.16	0.54	0.41	0.65	0.28	0.72
C.V.P.%	12.68	21.37	9.40	27.79	21.59	34.69	13.88	36.96
C.V.G.%	13.06	22.47	11.14	29.67	23.45	38.13	13.99	39.16
C.V.E. %	0.06	0.09	0.02	1.06	0.04	0.09	0.06	0.01
H^2_{BS}	0.94	0.904	0.71	0.88	0.85	0.83	0.98	0.89
Grand mean	102.48	107.63	23.53	410.19	114.08	20.19	22.17	5.096

Where: σ^2_P , σ^2_G and σ^2_E represent phenotypic, genetic and environmental variances , GA and GA% represent genetic advance and genetic advance of mean and P.C.V, G.C.V and E.C.V % represent coefficient variances of phenotypic, genotypic and environmental respectively, H^2_{BS} represent heritability broad sense.

Table (4) displays the genetic correlation coefficients between grain yield and its measured components and between attributes during the 2021 and 2022 research seasons. Grain yield was positively and significantly genetically and phenotypically correlated with tiller number.m^{-2} and 0.507. The panicle grains for the two seasons and genetic and phenotypic correlations were 0.779 and 0.762 and 0.753 and 0.741, respectively. The length of the panicle was genetically and phenotypically unrelated to grain yield, however a positive correlation (0.116 and 0.118) in the 2021 season and a negative correlation (-0.060 and -0.155) in the 2022 season were found. The genetic-phenotypic correlations of 1000 grains were modest and positive over the two growth seasons (0.118 and 0.218) and (0.019 and 0.018). It cannot be disregarded. Even though my characteristic (number of days heading to days to heading and infertility) had negative and extremely significant correlation coefficients with grain yield, the route coefficient analysis did not evaluate it. Saleh et al. (26) found a high and substantial link between grain yield, number of grains per panicle and 1000 grain weight in 22 rice genotypes over two seasons. Days to heading was negatively correlated. Unlike other variables, panicle length had a high genetic correlation with panicle grains and a negative genetic correlation with tillers.m^{-2} non-significant in 2021 and high significant in 2022 and the panicle length with 1000 grains weight was connected with a positive and non-significant genetic correlation in 2021 and a moral negative in 2022. It was linked to tillers in both seasons.m^{-2} adversely genetically with grain number.panicle^{-1} and definitely 1000 grains. Al-Wardi et al. (6) and Hossain et al. (18) found a high genetic correlation values in their study among grain yield and some yield components such as panicle length and numbers of grains in panicles and number of tiller.m^{-2}.

Table 4. Genetic and phenotypic correlations between grain yield and some components in two seasons (2021 and 2022).

Traits	Seasons	Panicle length (cm)	No. tillers.m^{-2}	No. grain. panicle^{-1}	1000 grain weight (g)	Days to heading (day)	Plant height (cm)	Infertility %	Grain yield kg.ha^{-1}
Panicle	2021	1	-0.189	0.789**	0.084	-0.099	0.221	-0.099	0.116

length (cm)	2022	1	-0.845**	0.691**	-0.379	0.576**	0.765**	0.441*	-0.060
No. tillers. m^{-2}	2021	-0.178	1	-0.288	0.646**	-0.726**	-0.804**	-0.239	0.732**
	2022	-0.825**	1	-0.687**	0.434*	-0.662**	-0.836**	-0.247	0.507*
No. grain. $panicle^{-1}$	2021	0.774**	-0.287	1	0.373	-0.114	-0.004	-0.426	0.779**
	2022	0.683**	-0.676**	1	0.293	0.447*	0.369	-0.273	0.762**
1000 grain weight (g)	2021	0.078	0.623**	0.367	1	-0.553**	-0.843**	-0.481*	0.219
	2022	-0.387	0.424	0.279	1	-0.337	-0.770**	-0.823**	0.019
Days to heading (day)	2021	-0.106	-0.719**	-0.109	-0.545**	1	0.724	0.789	-0.938**
	2022	0.571**	-0.646**	0.439*	-0.322	1	0.537	0.486	-0.706**
Plant height (cm)	2021	0.222	-0.798**	-0.005	-0.826**	0.716**	1	0.586	-0.859**
	2022	0.749**	-0.818**	0.365	-0.742**	0.525*	1	0.509	-0.583**
Infertility %	2021	-0.096	-0.230	-0.424	-0.462*	0.769**	0.580**	1	-0.722**
	2022	0.433*	-0.238	-0.273	-0.792**	0.485*	0.503*	1	-0.911**
Grain yield $kg.ha^{-1}$	2021	0.118	0.732**	0.753**	0.218	-0.927**	-0.855**	-0.717**	1
	2022	-0.155**	0.503*	0.741**	0.018	-0.699**	-0.578**	-0.907**	1

(**) and (*) are significant at probability levels 1% and 5%, respectively, Normal numbers are genetic correlation and **Bold** numbers are phenotypic correlation.

Path coefficient analysis was used to segment genetic and phenotypic correlation coefficients to better understand the relationship between grain yield and some key yield components, especially those that correlated well with the yield trait. Path coefficient analysis divides the genetic and phenotypic correlation coefficient into a direct and indirect influence between grain yield (the dependent variable) and the traits of the yield components (four attributes). Table (5) displays the genetic and phenotypic path coefficient analyses of grain yield and its components, including tillers.m^{-2} had the strongest direct influence on genetic path and phenotypic coefficients on grain yield in the 2021 and 2022 seasons (0.997 and 0.954, respectively). The genetic route coefficient was low (0.189) and the phenotypic path coefficient medium (0.297). Indirect impacts of tiller number.m^{-2}, they were negative through the rest of the yield components in the grain yield, except for the indirect effect via the panicle length, which was highly positive in the season 2022 (0.546 and 0.542) and not significant in the season 2021 (0.064 and 0.049) to analysis the genetic and phenotypic path parameters, respectively. Grain count. $panicle^{-1}$ had the highest direct effects on grain yield for the genetic path coefficient (0.831 and 0.513) and phenotypes (0.742 and 0.615) for 2021 and 2022, while its indirect effects were negative and not significant for the rest of the yield components. Some researchers found high direct effects of the length of panicles and low values of 1000 grain weight on the grain yield (6) and (21). The number of grains per plant had a high direct effects, with low direct effects of the number of tillers per square meter on grain yield in study of the genetic path analysis of 22 of (3). Whereas, According to Streck et al. (28), the length of the panicle may be used in indirect selection for grain yield.

Table 5. Genetic and phenotypic path analysis of grain yield and its components in two seasons (2021 and 2022).

Effect type	Symbol	Genetic effect value		Phenotypic effect value	
		2021	2022	2021	2022
Panicle length effect on grain yield					
- Direct effect	p_1y	-0.337	-0.646	-0.279	-0.657
- Indirect effect					
- By No. tillers. m^{-2}	$r_{12}p_2y$	-0.189	-0.160	-0.170	-0.245
- By No. grains. panicle^{-1}	$r_{13}p_3y$	0.656	0.354	0.575	0.420
- By 1000 grain weight	$r_{14}p_4y$	-0.013	-0.108	-0.007	-0.073
Sum of total effect of panicle length on grain yield	r_1y	0.116	-0.560	0.118	-0.555
No. tillers.m^{-2} effect on grain yield					
- Direct effect	p_2y	0.997	0.189	0.954	0.297
- Indirect effect					
- Panicle length	$r_{12}p_1y$	0.064	0.546	0.049	0.542
- By No. grains. panicle^{-1}	$r_{23}p_3y$	-0.239	-0.352	-0.214	-0.416
- By 1000 grain weight	$r_{24}p_4y$	-0.099	0.123	-0.058	0.080
Sum of total effect of No. tillers.m^{-2} on grain yield	r_2y	0.732	0.507	0.732	0.503
No. grains. Panicle^{-1} effect on grain yield					
- Direct effect	p_3y	0.831	0.513	0.742	0.615
- Indirect effect					
- Panicle length	$r_{13}p_1y$	-0.266	-0.447	-0.216	-0.449
- By No. tillers. m^{-2}	$r_{23}p_2y$	-0.290	-0.130	-0.275	-0.201
- By 1000 grain weight	$r_{34}p_4y$	-0.057	0.083	-0.034	0.053
Sum of total effect of No. grains. panicle^{-1} on grain yield	r_3y	0.219	0.019	0.218	0.018
1000 grain weight effect on grain yield					
- Direct effect	p_4y	-0.153	0.284	-0.092	0.189
- Indirect effect					
- Panicle length	$r_{14}p_1y$	-0.028	0.245	-0.022	0.254
- By No. tillers. m^{-2}	$r_{24}p_2y$	0.649	0.082	0.595	0.126
- By No. grains. panicle^{-1}	$r_{34}p_3y$	0.309	0.150	0.273	0.171
Sum of total effect of 1000 grain weight on grain yield	r_4y	0.779	0.762	0.753	0.741
Sum of residual effects		0.489	0.562	0.492	0.579

Table (7) presents selection indices for seven rice genotypes in two growing seasons (2021 and 2022). The genotypes FA1 and AF2 had the greatest selection index values in both seasons. In 2021, the genotype (FA1) had the greatest selection index, 136.961, but in 2022, it was second with 116.892. This genotype had the highest mean grain yield (6.984), lowest infertility (15.40%) and most tillers (518.17). The genetic genotype (AF2) ranked second in 2021 (134.116) and first in 2022 with the greatest selection index (118.590), outperforming all other genotypes. This genotype produced the number of grains (136.75) and grain yield (5.542 $kg.ha^{-1}$). Furat and AF1 had selection index ranks 4 and 6 over the two growth seasons. The genotype (FA2) had the lowest grain yield (4.109 $kg.\ ha^{-1}$) due to the lowest selection index (7) and selection index (109.727 and 109.135) for 2021 and 2022, respectively. The number of tillers increased the selection index in 42 and 56 rice lines, respectively, according to Anshori et al. (8); (9) and Alsabah et al. (4) chose 28 black rice lines from 54 based on a favorable selection index for additional yield testing. Also, Al-Wardi et al. (5) selected 13 genotypes by screening 22 rice genotypes.

Table 7. Selection indices of seven rice genotypes over two seasons (2021 and 2022).

Genotypes	Season 2021		Season 2022	
	Selection index	Trade-off sequence	Selection index	Trade-off sequence
Furat	115.139	6	111.342	4
Anber33	125.479	3	113.276	3
FA1	136.961	1	116.892	2
FA2	109.727	7	109.135	7
AF1	121.417	4	110.252	6
AF2	134.116	2	118.590	1
AF3	117.572	5	110.400	5

Table (8) displays the coefficient of variation and averages of seven selected rice genotypes during two seasons (2021 and 2022). The genotype's lower coefficient of variation indicates stability across nvironments. Furat has the lowest coefficient of variation for two major traits: grain yield (7.089%) and $tillers.m^{-2}$ (7.187%). Furat's qualities are more constant. The Furat cultivar had the second-highest average grain yield (6.608 $kg.ha^{-1}$) and number of tillers (486.83) after the genotype (FA1), which had the greatest $averages.m^{-2}$ (518.17) and its coefficient of variation (10.107 and 11.243) for the two variables was slightly higher than the genotype (Furat). The genotype (FA2) had modest coefficients of variation for the number of days to heading (0.467), infertility (0.629%), and 1000-grain weight (0.149). Thus, its grain production (4.109 $kg.ha^{-1}$) is among the most stable genotypes. Grain yield genotypes are fewer. AF1 has the lowest grain yield (3.397 $kg.\ ha^{-1}$) and greatest infertility rate (30.87%). Accordingly, the genotype with the highest grain yield need not be stable or vice versa. Abbas (1) and Debsharma et al. (11) indicated that the stability of the genotypes in four and seven environments was highly variable and could identified stable genotypes adapted across the environments for grain yield.

Table 8. The coefficient of variance (CV%) parameter and means of selected seven rice genotype traits over two seasons (2021 and 2022).

Genotypes	Parameters	Traits							
		Days to heading (day)	Plant height (cm)	Panicle length (cm)	No. tillers. m^{-2}	No. grain. $panicle^{-1}$	Infertility %	1000 grain weight (g)	Grain yield $kg.ha^{-1}$
Furat	CV%	0.959	3.048	1.366	7.187	6.692	6.402	0.376	7.089
	Mean	93.17d	81.93f	20.88f	486.83b	94.65f	16.48e	23.78b	6.608b
Anber33	CV%	0.719	4.783	3.056	10.086	4.911	3.709	0.202	15.224
	Mean	105.00c	129.75a	24.82b	318.17f	123.60c	20.77b	20.30de	4.697d
FA1	CV%	1.011	0.482	6.039	11.243	8.190	5.563	0.106	10.107
	Mean	86.33e	95.60e	23.63d	518.17a	107.67d	15.40f	23.80b	6.984a
FA2	CV%	0.467	0.870	3.148	10.562	6.971	0.629	0.149	9.021
	Mean	108.00b	118.33b	22.30e	340.33e	107.42d	19.62c	20.72d	4.109f
AF1	CV%	1.147	3.277	4.296	9.325	6.967	2.993	0.198	9.897
	Mean	110.83a	117.42b	23.35d	449.00c	98.82e	30.87a	19.75e	3.397g
AF2	CV%	1.491	0.734	2.598	14.726	1.441	7.652	0.279	8.5891
	Mean	109.50a	99.17d	24.17c	428.33d	136.75a	18.53d	25.50a	5.542c
AF3	CV%	1.131	1.604	0.709	9.542	5.768	8.294	0.271	13.925
	Mean	104.50c	111.20c	25.57a	330.50e	130.33b	20.85b	21.63c	4.336e
Grand mean		102.48	107.63	23.53	410.19	114.08	20.19	22.17	5.096

The value followed by the different letters for each trait are significantly different from each other (Duncan test, 0.05

Conclusion

The substantial genetic variation, heritability, and predicted genetic progress may help pick the best genotypes with desirable values and quick trait development in early generations. The genotype (Furat), one of Iraq's most cultivated, productive, and stable varieties had the highest selection index and grain yield, tillers and grains. The genetic and phenotypic path coefficient analysis showed high selection indicators for the number of tillers and grains due to their high positive correlations with grain yield. Thus, the quantity of tillers and grains are good selection indicators for future rice crop breeding programs. The genotype (Furat) has the lowest coefficient of variation for critical variables including tillers and grain yield, making it the most stable combination. Although, the genotype (FA1) had higher average traits for the number of tillers and grain yield, its coefficients of variation were higher than those of the genotype (Furat), so the stable genotype may not be superior in grain yield or its components.

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Conflict of interest

The authors have no conflict of interest.

References

1. **Abbas, S. H. 2023.** Effect of Planting Dates on Stability of New Rice Genotypes Traits Grown in Iraqi Conditions. *Basrah Journal of Agricultural Sciences,* 36(2):1–16. https://doi.org/10.37077/25200860.2023.36.2.01
2. **Abebe, T.; S. Alamerew and Tulu, L. 2017.** Genetic variability, heritability and genetic advance for yield and its related traits in rainfed lowland rice (*Oryza sativa* L.) genotype at Fogera and Pawe, Ethiopia. *Advances in Crop Science and Technology,* 5 (272):10-4172. https://doi.org/10.4172/2329-8863.1000272
3. **Al-Musawi, B. and M. Al- Anbari. 2022.** Estimation of path coefficient analysis for some quantitative traits in rice (*Oryza sativa* L.) genotypes. *Bionatura*, 7(4): 1–5. Available at: https://doi.org/10.21931/rb/2022.07.04.39
4. **Alsabah, R.; B.S. Purwoko; I.S. Dewi and Wahyu, Y. 2019.** Selection index for selecting promising doubled haploid lines of black rice. *SABRAO J. Breed. Genet*. 51(4): 430-441. https://doi.org/10.1016/j.rsci.2021.05.007
5. **Al-Wardi, M.E.Z.; S.H. Abbas and Musa, A.K.J. 2023a.** Estimation of Selection Indexes and some Genetic Parameters in the Genotypes of the Rice Crop Oryza sativa L. In *IOP Conference Series: Earth and Environmental Science* 1213(1):012002. https://doi.org/10.1088/1755-1315/1213/1/012001
6. **Al-Wardi, M.E.Z.; S.H. Abbas and Musa, A.K.J. 2023b**. Genetic Path Coefficient Analysis of Genotypes of Rice (Oryza sativa L.) Grown in Iraqi Conditions. In *IOP Conference Series: Earth and Environmental Science*, 1213 (1): 012002. https://doi.org/10.1088/1755-1315/1213/1/012002
7. **Al-Zubaidy, Kh.M.D. and Kh.Kh.A. Al-Juboury. 2016.** *Design and analysis of genetical experiments*. Dar Al Wadah Publishing House, Jordan - Amman, Dijla Library for Printing, Publishing and Distribution, Republic of Iraq – Baghdad, p.777 (In Arabic). https://books.google.iq/books?id=AN03zgEACAAJ
8. **Anshori, M.F.; B.S. Purwoko; I.S Dewi; S.W. Ardie and Suwarno, W.B. 2019.** Selection index based on multivariate analysis for selecting doubled-haploid rice lines in lowland saline prone area. *SABRAO J. Breed. Genet*. 51(2):161-174. http://sabraojournal.org/wp-content/uploads/2019/07/SABRAO-J-Breed-Genet-512-161-174-Anshori.pdf
9. **Anshori, M.F.; B.S. Purwoko; I.S. Dewi; W.B. Suwarno and Ardie, S.W. 2022.** Salinity tolerance selection of doubled-haploid rice lines based on selection index and factor analysis. *AIMS Agric Food*, 7(3): 520-535.

https://doi.org/10.3934/agrfood.2022032

10. **Central Statistical Organization. 2021.** *Production of crops and vegetables. Directorate of Agriculture Statistical,* The Ministry of Planning, Iraq- Baghdad, (in Arabic). https://cosit.gov.iq/ar/agri-stat/veg-prod
11. **Debsharma S.K.; P.R. Roy; R.A. Begumand and Iftekharuddaula K.M. 2020.** Elucidation of genotype× environment interaction for identification of stable genotypes to grain yield of rice (*Oryza sativa* L.) varieties in Bangladesh rainfed condition. *Bangladesh Rice Journal*, 24(1): 59-71. https://doi.org/10.3329/brj.v24i1.53240
12. **Duvallet, M.; P. Dumas; D. Makowski; J. Boé; P.M. del Villar and Ben-Ari, T. 2021**. Rice yield stability compared to major food crops in West Africa. *Environmental Research Letters*, 16(12): 124005. https://iopscience.iop.org/article/10.1088/1748-9326/ac343a
13. **Falconer, D.S. 2017.** *Introduction to quantitative genetics*. S. l.: CreateSpace Independent Publishing Platform. https://vulms.vu.edu.pk/Courses/GEN733/Downloads/Introduction%20to%20Quantitative%20Genetic-DS%20Falconer.pdf
14. **FAOSTAT. 2022.** *Grain production Worldwide by type., Food and Agricultural Organization of the United Nations*. (Accessed: 27/03/2023). Available at: https://www.statista.com/statistics/263977/World - grain- production-by-type/
15. **Faysal, A.S.; L. Ali; M.G. Azam; U. Sarker; S. Ercisli; K.S. Golokhvast and Marc, R.A. 2022.** Genetic variability, Character Association, and path coefficient analysis in transplant aman rice genotypes. *Plants*, 11(21): 2952. https://doi.org/10.3390/plants11212952
16. **Gayathri, N. and M. Subbara. 2020.** Studies on Character Association and Path Analysis in Slender Grain Rice (*Oryza sativa* L.) Varieties. Research and amp; Reviews: *Journal of Agricultural Science and Technology*, 9(1):30-33. https://doi.org/10.37591/rrjoast.v9i1.2623
17. **Hasan, N.A.; M.Y. Rafii,; A.R. Harun; N.S. Alı; N. Mazlan and Abdullah, S. 2022.** Genetic analysis of yield and yield contributing traits in rice (Oryza sativa L.) BC2F3 population derived from MR264× PS2. *Biotechnology & Biotechnological Equipment*, *36*(1):184-192 https://doi.org/10.1080/13102818.2022.2060760
18. **Hossain, M.S.; N.A. Ivy; M.S. Raihan; E. Kayesh, and Maniruzzaman, S. 2021.** Genetic Variability, Correlation and Path Analysis of Floral, Yield and its Component Traits of Maintainer Lines of Rice (*Oryza sativa* L.). *Bangladesh Rice Journal*, 24(1):1-9.

https://doi.org/10.3329/brj.v24i1.53235

19. **Htwe, N.M.; M. Aye and Thu, C.N. 2020.** Selection Index for Yield and Yield Contributing Traits in Improved Rice Genotypes. *International Journal of Environmental and Rural Development*, 11(2): 86-91. https://doi.org/10.32115/ijerd.11.2_86
20. **Ireland, C.R. 2010.** *Experimental statistics for agriculture and horticulture*. CABI. British Library, London, UK. https://www.sandbarbookstore.com/book/9781845935375
21. **Jeke, E.; T. Mzengeza; K. Kyung-Ho and Imani, C. 2021.** Correlation and path coefficient analysis of yield and component traits of KAFACI doubled haploid Rice (*Oryza sativa* L) Genotypes in Malawi. *Int J Agriculture Technology*, 1(2): 1-9. https://doi.org/10.33425/2770-2928.1005
22. **Kalyan, B.; K.V. Krishna and Rao, L.V. 2017.** Path coefficient analysis for yield and yield contributing traits in rice (*Oryza sativa* L.) genotypes. *International Journal of Current Microbiology and Applied Sciences*, 6(7): 2680-2687. https://doi.org/10.20546/ijcmas.2017.607.377
23. **Kumar, S.; M.P. Chauhan; A. Tomar; R.K. Kasana and Kumar, N. 2018.** Correlation and path coefficient analysis in rice (*Oryza sativa* L.). *The Pharma Innovation Journal*, 7(6): 20-26. https://www.thepharmajournal.com/archives/?year=2018&vol=7&issue=6&ArticleId=2115
24. **Lin, C.S.; M.R. Binns; and Lefkovitch, L.P. 1986.** Stability analysis: Where do we stand? 1. *Crop. Sci.* 26: 894–900 https://doi.org/10.2135/cropsci1986.0011183X002600050012x.
25. **Musa, A.J.; S.H. Abbas and Hameed, K.A. 2021.** Performance of Two Rice (*Oryza sativa* L.) Genotypes Under SRI and Conventional Farming Methods in Three Locations in Iraq. *Fourth International Conference for Agricultural and Sustainability Sciences*, 910(1):1315-1755 https://doi.org/10.1088/1755-1315/910/1/012138
26. **Saleh, M.M.; K.F.M. Salem and Elabd, A.B. 2020.** Definition of selection criterion using correlation and path coefficient analysis in rice (*Oryza sativa* L.) genotypes. *Bull Natl Res Cent.*,44(1):1-6. https://doi.org/10.1186/s42269-020-00403-y
27. **Singh, R.K. and B.D. Chaudhary. 2010.** *Biometrical methods in quantitative genetic Analysis*. Kalyani Publishers, New Delhi, p.304. https://www.cabdirect.org/cabdirect/abstract/19801689021
28. **Streck, E.A.; G.A. Aguiar; P.H.K. Facchinello; L. Perin; T.K. Krüger and de Magalhães Júnior, A.M. 2018.** Correlations and path analysis for yield components in irrigated rice. *Comunicata Scientiae*, 9(2): 154-161. https://doi.org/10.14295/cs.v9i2.2017

29. **Wening, R.H.; I.A. Rumanti; B.S. Purwoko; W.B. Suwarno and Khumaida, N. 2019.** Screening of submergence tolerant rice under artificial condition based on multiple selection indices. *Plant breeding and biotechnology*, *7*(4):.360-374. https://doi.org/10.9787/PBB.2019.7.4.360

30. **Zaid, I.U.; N. Zahra; M. Habib; M.K. Naeem; U. Asghar; M. Uzair; A. Latif; A. Rehman; G.M. Ali and Khan, M.R. 2022.** Estimation of Genetic Variances and Stability Components of Yield-Related Traits of Green Super Rice at Multi-Environmental Conditions in Pakistan. *Agronomy*, 12(5),1157**.** https://doi.org/10.3390/agronomy12051157