



Dijlah Journal of Agricultural Sciences

Journal homepage: <https://djas.uowasit.edu.iq/index.php/djas/en>



Research article

Genetic Variability, Heritability, and Trait Association Analysis of Physiological and Morphological Traits in Iraqi Rice (*Oryza sativa* L.) Genotypes

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ARTICLE INFO

Keywords:

Oryza sativa L.;
Iraqi rice;
genetic variability;
broad-sense heritability;
genetic advance; trait
association;
phenotypic selection.

Article history:

Received: 20th Jan 2026
Accepted: 1st Mar 2026
Online: 30 Jun 2026

ABSTRACT

Assessing genetic diversity and trait relationships is essential for identifying useful selection criteria in rice breeding. In this study we looked at genetic variability, broad sense heritability, genetic advance, and also how traits relate to each other, focusing on some selected physiological and morphological characteristics across five Iraqi rice, *Oryza sativa* L. genotypes. A field trial was carried out under a randomized complete block design with three replications, during the 2025 summer season in Wasit Governorate, Iraq. Chlorophyll content, flag leaf length, flag leaf width, leaf area, plant height, and number of tillers were noted at heading to flowering stage, 113 days after sowing. The variance analysis, showed significant to very significant differences among genotypes for every trait we measured, which suggests there was a clear and measurable phenotypic variation inside the materials that were tested. Analysis of variance showed significant to highly significant differences among genotypes for all traits examined, so it looks like there is clear phenotypic variation across the materials that were tested. The Local Amber genotype managed to record the highest mean values for chlorophyll SPAD, flag leaf dimensions, leaf area, plant height, and number of tillers, all within this particular environment. Broad-sense heritability was from 71.93% for flag leaf length up to 96.32% for number of tillers, but genetic advance as a percentage of the mean was top for number of tillers and leaf area. Overall, these outcomes point that number of tillers and leaf area may be more responsive to selection in the tested genotypes. Pearson correlation analysis then indicated positive relationships among essentially all measured traits, and especially strong links were observed between leaf area and flag leaf width, plant height, and number of tillers. Overall, the findings provide preliminary evidence of useful variability among Iraqi Amber-type rice genotypes and suggest that leaf area and tiller number may serve as potential indirect selection indicators. Further multi-location and multi-season studies including grain yield are recommended to confirm their breeding value.

1. Introduction

Addressing the pressing issue of global food security amidst swiftly evolving climate conditions poses a significant challenge, necessitating the creation of innovative, climate-resilient crop strains through

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the effective use of crop genetic diversity (Maxted et al., 2024). The extensive genetic variation found in key cereals such as rice (*Oryza sativa* L.) stems from thousands of years of domestication, adaptation, and cross-border dispersal, including the historical movement of japonica rice from China to India, which eventually led to the emergence of the indica type (Stevens et al., 2016). In West Asia, a vital global center for crop diversity, the preservation and study of indigenous plant genetic resources are crucial for avoiding genetic loss and providing traits necessary for contemporary crop enhancement (Maxted et al., 2024).

This specific demand for durable crops is especially apparent in Iraq, where farmers have more and more stressed that acquiring viable seeds depends largely on choosing rice plants that exhibit strong performance and resilience under the unique local climate characteristics of the area (Hassan & Hama-Ali, 2022). This need for robust crops to be accomplished locally is most apparent in Iraq, where farmers have become more insistent that access to viable seeds is dependent on choosing rice plants that perform well and are strong and hardy in the region's particular local climate (Hassan & Hama-Ali, 2022).

The differentiation in genetic background among the local crops is the key first step for application in breeding. A recent genetic differentiation study on short- and long-grain rice accessions grown in the Kurdistan region of Iraq based on simple sequence repeat (SSR) markers revealed the existence of separate japonica and indica subpopulations (Hassan & Hama-Ali, 2022). Though all these molecular studies suggest that 72% of genetic variation is contributed by differences among populations, they also demonstrate that there is virtually no gene flow throughout the region (Hassan & Hama-Ali, 2022). This highlights the necessity of an intensive breeding program for studying and ameliorating the local genotypes (Hassan & Hama-Ali, 2022). On the basis of this basic molecular information the present investigation was carried out to study genetic diversity, heritability and association of traits of physiological and morphological characters among the Iraqi rice genotypes with the view of utilizing the information for further selection and breeding to climate resilience.

This experiment was performed with the aim of determining the degree of genetic diversity, the heritability, and the correlation of traits among some important physiological and morphological traits in five Iraqi rice (*Oryza sativa*) genotypes. Quantitative traits including chlorophyll contents, flag leaf length and width, leaf area, plant height and tiller number were evaluated at the summer heading stage. The study also focused on the identification of the best genotype especially the Local Amber Genotype and reliable efficient indirect selection criteria in term of gain under selection along with correlation of the important traits that would be the crucial instrument for the improvement of rice varieties suited to the Iraqi environment of agriculture.

2. Materials and Methods

2.1 Study Site and Experimental Season

The study was executed in the farmland, which lies in Al-kut (southern part of Wasit Governorate, Iraq), a prime rice cultivation area in central and southern Iraq during the summer rice growing season of 2025. The crop was planted on 25 May 2025, physiological and morphological observations were made on 15 September 2025 (113 days after sowing, DAS) at heading to flowering stage. To reduce soil environmental differences between treatments, normal agronomic measures for rice production, such as land preparation, irrigation, fertilization, weed control, and disease and insect management were identical applied to all the plots during the study period.

2.2 Plant Materials

Evaluations were carried out on five genotypes of Amber-type rice materials (*Oryza sativa* L.) from Iraq; these represent the local cultigens. The genotypes G1-G5 represented the following rice types: G1 = Amber 33, G2 = Amber Abu Khasslah, G3 = Amber Al-Fuhud, G4 = Amber Al-Najaf and G5 = Local Amber Genotype. The aim was to investigate the degree of variability and relationships between the traits in these genotypes for many physiological and morphological traits of interest.

2.3 Experimental Design and Crop Management

The experiment was conducted in a randomized complete block design (RCBD) with three replications. Each replication had five plots, representing the five rice genotypes, making a total of 15 experimental units. Genotypes within the blocks were randomized to account for field variability. Five randomly selected representative plants from each plot were tagged for observations. The mean of the sampled plants in each plot was considered as an experimental unit for statistical analyses. The field preparation and crop management practices were according to the normal recommendations for rice in the area. To ensure that the differences observed among genotypes were a result of genetic and not environmental factors, irrigation and fertilizer treatments were applied evenly to all experimental plots.

2.4 Measurement of Physiological and Morphological Traits

The morphophenological analyses were carried out at 113 days after sowing (DAS), when the crop was at the heading to flowering stage of development. The chlorophyll content was measured with a portable SPAD chlorophyll meter and reported as SPAD units using the values obtained from the flag leaf that was fully expanded. Flag leaf length (cm) was the distance from the base of the next-to-last leaf lamina to its apex and flag leaf width (cm) was the maximum width of the leaf lamina. Leaf area (cm²) was calculated by the following standard relationship for rice leaves: $LAR = FLL \times FLW \times 0.75$ where 0.75 is the correction factor used for estimating rice leaf area. Plant height (cm) was recorded from the soil surface to the apex of the highest panicle or leaf and the number of tillers per plant was obtained by counting the number of all tillers produced by each plant under test. These parameters were applied to determine the physiological and morphological variations between all the rice genotypes under study.

2.5 Statistical Analysis

The data were analyzed following the randomized complete block design (RCBD) by using Python statistical packages. The analysis of variance (ANOVA) was conducted for each trait individually under the linear model as follows:

$$Y_{ij} = \mu + G_i + R_j + e_{ij}$$

where Y_{ij} is the observation of the i th genotype in the j th replication, μ is the overall mean, G_i is the effect of the i th genotype, R_j is the effect of the j th replication, and e_{ij} is the random experimental error. The effect of genotype was tested for significance against the residual error. When significant differences among genotypes were observed, mean separation is done using Tukey's HSD ($p = 0.05$)

(Table 1). Also, the Least Significant Difference (LSD) at 5% level of significance was worked out from the residual mean square for making pairwise comparison among the genotypes means.

Table 1. Formulae used for the estimation of genetic parameters in rice genotypes

Genetic Parameter	Formula
Environmental variance (VE)	$VE = MSE$
Genotypic variance (VG)	$VG = (MSG - MSE) / r$
Phenotypic variance (VP)	$VP = VG + VE$
Genotypic coefficient of variation (GCV, %)	$GCV (\%) = [\sqrt{VG} / \bar{X}] \times 100$
Phenotypic coefficient of variation (PCV, %)	$PCV (\%) = [\sqrt{VP} / \bar{X}] \times 100$
Broad-sense heritability (H^2 , %)	$H^2 (\%) = (VG / VP) \times 100$
Genetic advance (GA)	$GA = k \times \sqrt{VP} \times H^2$
Genetic advance as percent of mean (GAM, %)	$GAM (\%) = (GA / \bar{X}) \times 100$

Where:

MSG = Mean square due to genotypes obtained from ANOVA.

MSE = Error mean square (residual mean square).

r = Number of replications.

$\bar{X}$ = Grand mean of the trait.

k = Selection differential constant (2.06 at 5% selection intensity).

H^2 = Broad-sense heritability expressed as a decimal in the calculation of genetic advance.

Traits with high heritability and high genetic advance as percent of mean (GAM) were probably controlled by additive gene effect and hence selection may be effective for such traits in rice breeding.

2.7 Correlation Analysis

Pearson's Correlation Among various physiological and morphological traits, the Pearson's Correlation (r) is calculated at plot level to estimate the strength and direction of association between different traits. The significance of correlation coefficients was tested, correlation matrices and scatter plots were constructed to depict the relationships between the traits. Positively correlated traits with high magnitude were also potential indirect selection criteria for rice breeding.

3. Results and Discussion

3.1 Mean Performance and Analysis of Variance

The average values of the five rice genotypes for physiological and morphological traits are shown in Table 2. There was a wide range of variation among genotypes for all traits. The Local Amber Genotype gave the highest mean for most of the traits i.e. chlorophyll SPAD (44.89), flag leaf length (30.03 cm), flag leaf width (1.88 cm), leaf area (42.38 cm²), plant height (99.71 cm), and number of

tillers (19.93). In contrast, a minimum value was obtained for Amber Al-Fuhud in most of parameters studied. Means were separated by the LSD test at 5 % level of probability and shown that genotypes were different for traits. For chlorophyll SPAD, Local Amber Genotype had the maximum mean and was on par with Amber Abu Khasslah, whereas Amber Al-Fuhud had the minimum value. Flag leaf length, Local Amber Genotype and Amber Abu Khasslah were in the best statistical group, Amber 33, Amber Al-Najaf and Amber Al-Fuhud were in the following statistical group. For flag leaf width, leaf area, plant height, and number of tillers, a more distinct separation for genotypes was observed. These results demonstrate that significant phenotypic variation existed among the tested rice genotypes.

The analysis of variance under the randomized complete block design is summarized in Table 3. The results revealed significant to highly significant genotypic differences for all studied traits. The genotype effect was significant at $P < 0.01$ for flag leaf length and $P < 0.001$ for chlorophyll SPAD, flag leaf width, leaf area, plant height, and number of tillers. Replication effects were not significant for all studied traits, indicating limited block-to-block variation under the experimental conditions. The mean performance of the genotypes for major traits is illustrated in Figure 1.

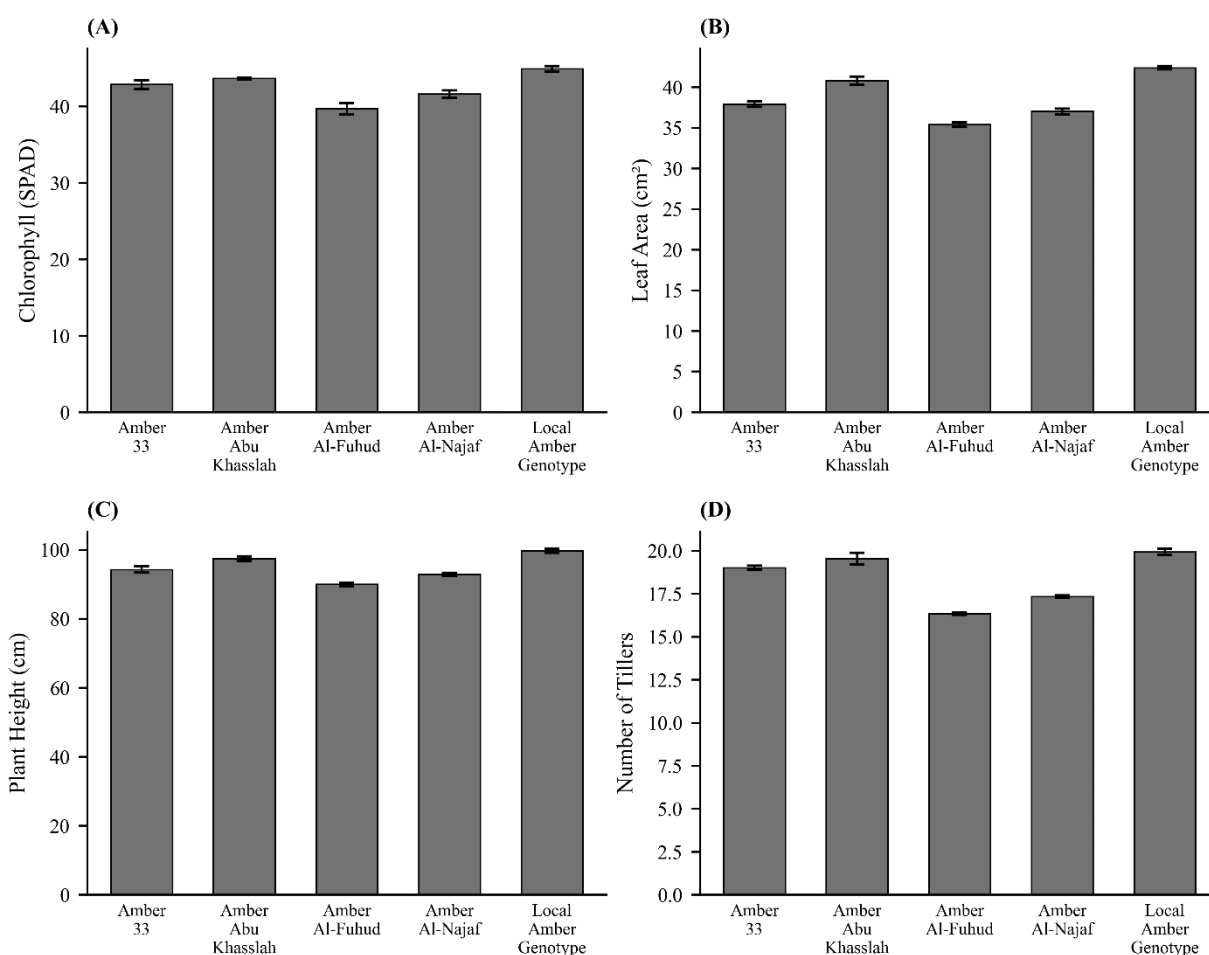


Figure 1. Mean performance of rice genotypes for: (A) chlorophyll SPAD, (B) leaf area, (C) plant height, and (D) number of tillers.

Table 2. Mean performance of rice genotypes for physiological and morphological traits

Trait	Genotype	Mean	SE	Rank	CLD	LSD _{0.05}
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Chlorophyll SPAD	Local Amber Genotype	44.8933	0.5249	1	a	1.7119
Chlorophyll SPAD	Amber Abu Khasslah	43.6333	0.5249	2	ab	1.7119
Chlorophyll SPAD	Amber 33	42.8533	0.5249	3	bc	1.7119
Chlorophyll SPAD	Amber Al-Najaf	41.5933	0.5249	4	c	1.7119
Chlorophyll SPAD	Amber Al-Fuhud	39.6867	0.5249	5	d	1.7119
Flag leaf length (cm)	Local Amber Genotype	30.0327	0.2296	1	a	0.7487
Flag leaf length (cm)	Amber Abu Khasslah	29.6927	0.2296	2	a	0.7487
Flag leaf length (cm)	Amber 33	28.8567	0.2296	3	b	0.7487
Flag leaf length (cm)	Amber Al-Najaf	28.7367	0.2296	4	b	0.7487
Flag leaf length (cm)	Amber Al-Fuhud	28.4420	0.2296	5	b	0.7487
Flag leaf width (cm)	Local Amber Genotype	1.8818	0.0107	1	a	0.0349
Flag leaf width (cm)	Amber Abu Khasslah	1.8317	0.0107	2	b	0.0349
Flag leaf width (cm)	Amber 33	1.7524	0.0107	3	c	0.0349
Flag leaf width (cm)	Amber Al-Najaf	1.7172	0.0107	4	d	0.0349
Flag leaf width (cm)	Amber Al-Fuhud	1.6593	0.0107	5	e	0.0349
Leaf area (cm ²)	Local Amber Genotype	42.3847	0.3638	1	a	1.1863
Leaf area (cm ²)	Amber Abu Khasslah	40.8000	0.3638	2	b	1.1863
Leaf area (cm ²)	Amber 33	37.9220	0.3638	3	c	1.1863
Leaf area (cm ²)	Amber Al-Najaf	37.0127	0.3638	4	c	1.1863
Leaf area (cm ²)	Amber Al-Fuhud	35.3920	0.3638	5	d	1.1863
Plant height (cm)	Local Amber Genotype	99.7067	0.6360	1	a	2.0740
Plant height (cm)	Amber Abu Khasslah	97.3600	0.6360	2	b	2.0740
Plant height (cm)	Amber 33	94.2800	0.6360	3	c	2.0740
Plant height (cm)	Amber Al-Najaf	92.8333	0.6360	4	c	2.0740
Plant height (cm)	Amber Al-Fuhud	89.9400	0.6360	5	d	2.0740
Number of tillers	Local Amber Genotype	19.9333	0.1719	1	a	0.5607
Number of tillers	Amber Abu Khasslah	19.5333	0.1719	2	ab	0.5607
Number of tillers	Amber 33	19.0000	0.1719	3	b	0.5607
Number of tillers	Amber Al-Najaf	17.3333	0.1719	4	c	0.5607
Number of tillers	Amber Al-Fuhud	16.3333	0.1719	5	d	0.5607

Note: Means followed by the same letter within each trait are not significantly different according to the LSD test at $P \leq 0.05$.

Table 3. Analysis of variance for physiological and morphological traits under RCBD

Trait	Source	SS	df	MS	F	P	Significance
Chlorophyll SPAD	Genotype	47.60731	4	11.90183	14.39737	0.000999	***
Chlorophyll SPAD	Replication	0.98800	2	0.49400	0.59758	0.572958	ns
Chlorophyll SPAD	Error	6.61333	8	0.82667			
Chlorophyll SPAD	Total	55.20864	14				
Flag leaf length	Genotype	5.49515	4	1.37379	8.68715	0.005214	**
Flag leaf length	Replication	0.05650	2	0.02825	0.17863	0.839663	ns
Flag leaf length	Error	1.26512	8	0.15814			
Flag leaf length	Total	6.81677	14				
Flag leaf width	Genotype	0.09490	4	0.02373	69.07779	0.000003	***
Flag leaf width	Replication	0.00088	2	0.00044	1.28625	0.327831	ns
Flag leaf width	Error	0.00275	8	0.00034			
Flag leaf width	Total	0.09853	14				
Leaf area	Genotype	97.14595	4	24.28649	61.17889	0.000005	***
Leaf area	Replication	0.55025	2	0.27513	0.69306	0.527736	ns
Leaf area	Error	3.17580	8	0.39698			
Leaf area	Total	100.87200	14				
Plant height	Genotype	175.15160	4	43.78791	36.08675	0.000036	***
Plant height	Replication	2.72848	2	1.36424	1.12431	0.371279	ns
Plant height	Error	9.70725	8	1.21341			
Plant height	Total	187.58740	14				
Number of tillers	Genotype	28.20267	4	7.05067	79.51880	0.000002	***
Number of tillers	Replication	0.27733	2	0.13867	1.56391	0.267128	ns

Number of tillers	Error	0.70933	8	0.08867
Number of tillers	Total	29.18933	14	

Note: ns = not significant; ** = significant at $P \leq 0.01$; *** = significant at $P \leq 0.001$.

3.2 Genetic Variability, Heritability, and Genetic Advance

The magnitude of variability and the expected response to selection for all examined traits was investigated through estimation of the genetic parameters. As presented in Table 4 and Figure 2A, the GCV and PCV were quite similar for most parameters, indicating that the genetic factors had a significant effect on the phenotypic expressions.

Among these parameters of traits, number of tillers had the maximum GCV and PCV i.e. 8.27% and 8.42% respectively. This was followed by leaf area (GCV and PCV were 7.29 and 7.47). These results show relatively higher variation in number of tillers and leaf area as compared to other traits. Conversely, flag leaf length had the minimum GCV and PCV of 2.18 and 2.57% respectively, indicating a relative low degree of variation in respect of this character among the considered genotypes.

Broad-sense heritability values ranged from 71.93% for flag leaf length to 96.32% for number of tillers. Similarly, the heritability ranges for flag leaf width, leaf area, and plant height were 95.78%, 95.25%, and 92.12%, respectively. Genetic progress as a percentage of the average or mean was significantly different among the traits. The maximum value was attained in the case of number of tillers (16.71%), followed by leaf area (14.66%) and flag leaf width (10.06%). These results indicate that number of tillers and leaf area might have better selection response among the tested genotypes compared to other traits with lower GAMs, like flag leaf length, plant height and chlorophyll SPAD.

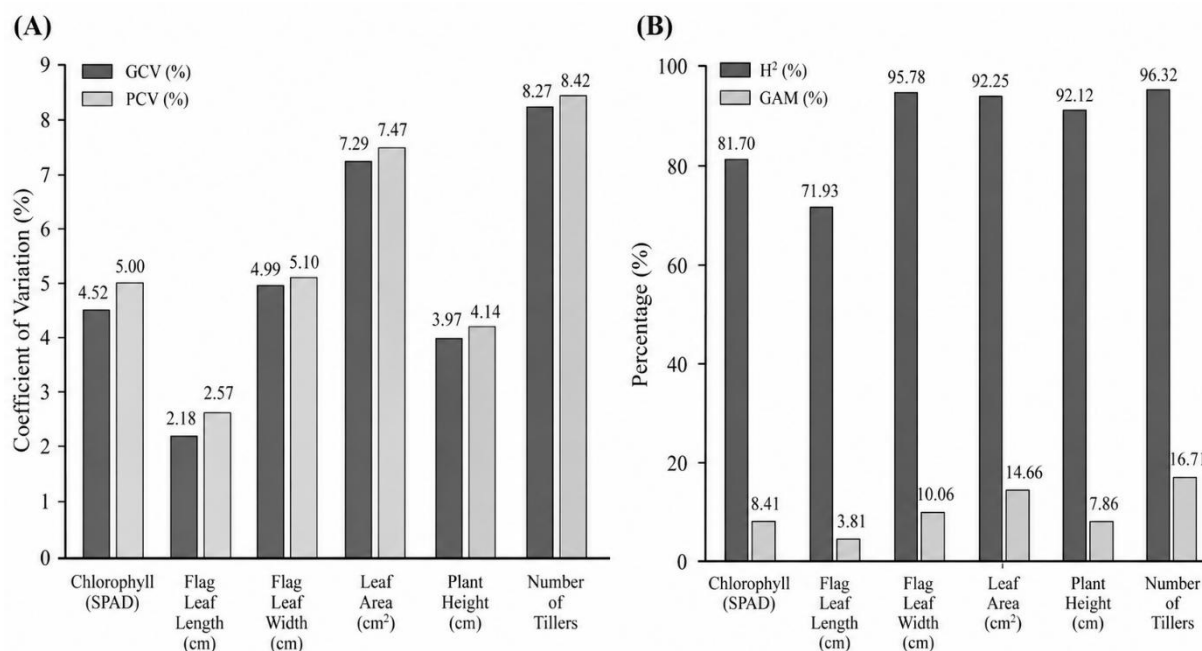


Figure 2. Genetic variability parameters of the measured traits: (A) genotypic and phenotypic coefficients of variation and (B) broad-sense heritability and genetic advance as percentage of the mean.

Table 4. Genetic variability and heritability parameters of the studied rice traits

Trait	Grand mean	VG	VP	VE	GCV (%)	PCV (%)	H ² (%)	GA	GAM (%)
Chlorophyll SPAD	42.5320	3.6917	4.5184	0.8267	4.52	5.00	81.70	3.5777	8.41
Flag leaf length (cm)	29.1521	0.4052	0.5634	0.1581	2.18	2.57	71.93	1.1121	3.81
Flag leaf width (cm)	1.7685	0.0078	0.0081	0.0003	4.99	5.10	95.78	0.1780	10.06
Leaf area (cm ²)	38.7023	7.9632	8.3601	0.3970	7.29	7.47	95.25	5.6734	14.66
Plant height (cm)	94.8240	14.1915	15.4049	1.2134	3.97	4.14	92.12	7.4485	7.86
Number of tillers	18.4267	2.3207	2.4093	0.0887	8.27	8.42	96.32	3.0799	16.71

Abbreviations: VG = genotypic variance; VP = phenotypic variance; VE = environmental variance; GCV = genotypic coefficient of variation; PCV = phenotypic coefficient of variation; H² = broad-sense heritability; GA = genetic advance; GAM = genetic advance as percentage of the mean.

3.3 Trait Association and Correlation Analysis

The physiological and morphological traits were subjected to Pearson's correlation analysis for pairwise associations (Table 5). A positive association was found in all the traits under measurement, though the magnitude of association between trait pairs was not uniform. These positive associations suggest that when certain traits are improving others may be improving too at the tested environment. The Chlorophyll SPAD was found positively related with flag leaf width ($r = 0.9068$), number of tillers ($r = 0.8822$), leaf area ($r = 0.8655$), plant height ($r = 0.8129$) and flag leaf length ($r = 0.7083$). Leaf area was highly correlated with flag leaf width ($r = 0.9837$), plant height ($r = 0.9421$), flag leaf length ($r = 0.9385$) and number of tillers ($r = 0.9011$), suggesting that leaf growth-related traits were significantly associated with overall plant growth.

Number of tillers was positively correlated with all the other traits. The highest correlations were with the flag leaf width ($r = 0.9179$), plant height ($r = 0.9107$), leaf area ($r = 0.9011$), and chlorophyll SPAD ($r = 0.8822$). The result is that genotypes exhibiting more robust vegetative growth and larger leaf traits produced more tillers.

Scatterplots for selected trait associations are displayed in Fig. 3. Positive trends were also noted in the relationships between chlorophyll SPAD and leaf area ($r = 0.8655$), leaf area and tiller number ($r = 0.9011$), and plant height and tiller number ($r = 0.9107$). These results indicate that these traits may be useful for indirectly selecting in the tested genotypes. Nonetheless, since grain yield was not evaluated in the current study, these traits should be considered only as tentative selection indicators and not as validated criteria for yield enhancement.

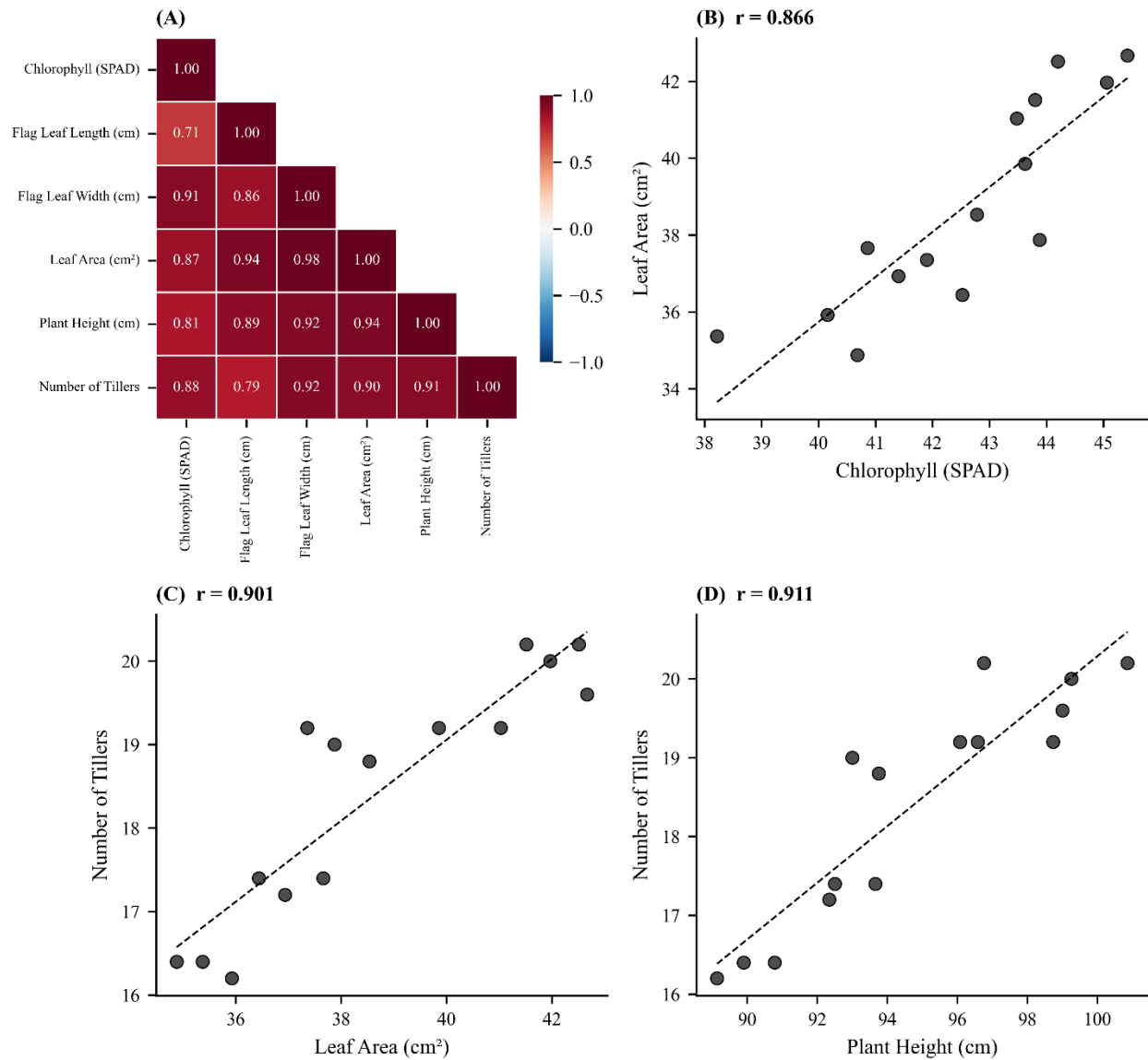


Figure 3. Correlation heatmap and scatter plots showing relationships among selected traits: (A) correlation heatmap, (B) chlorophyll SPAD and leaf area, (C) leaf area and number of tillers, and (D) plant height and number of tillers.

Table 5. Pearson correlation matrix among physiological and morphological traits

Trait	Chlorophyll SPAD	Flag leaf length	Flag leaf width	Leaf area	Plant height	Number of tillers
Chlorophyll SPAD	1.0000	0.7083	0.9068	0.8655	0.8129	0.8822
Flag leaf length	0.7083	1.0000	0.8614	0.9385	0.8948	0.7912
Flag leaf width	0.9068	0.8614	1.0000	0.9837	0.9221	0.9179
Leaf area	0.8655	0.9385	0.9837	1.0000	0.9421	0.9011
Plant height	0.8129	0.8948	0.9221	0.9421	1.0000	0.9107
Number of tillers	0.8822	0.7912	0.9179	0.9011	0.9107	1.0000

In this study, five genotypes of Iraqi Amber-type rice were grown under field conditions to investigate the genetic variation, broad-sense heritability and genetic advance, as well as the associations of the traits. These revealed significant genotypic variation for the entire measured physiological and morphological attributes, indicating that measurable variability existed among the studied genotypes. The Local Amber Genotype displayed the highest average values for the chlorophyll content, flag leaf traits, leaf area, plant height and tillers number in the environment tested. These observations indicate that exotic (local) Amber-type rice materials have the potential to harbor agronomically relevant phenotypic variation and therefore can be considered in rice enhancement programmes.

The highly significant genotype effect detected by the analysis of variance shows that the genotypes under study were not similar in their physiological and morphological attributes. Such variation is a necessary precondition for selection as breeding improvement relies upon existence of distinguishable different genotypes (Meena et al., 2025). Nonetheless, as this study is limited to five genotypes, the detected variation should be regarded as indicative rather than as representative of a large genetic pool. The better performance of the Local Amber Genotype could be due to its adaptation to the local growing condition but further testing at other sites, seasons and involving a larger germplasm set is required before much recommendation can be made either for breeding or for farmers' utilization.

The genetic variation the estimates of genetic variabilities revealed that PCV and GCV values were close to each other for most of the characters indicating that the genetic factors are mainly involved in phenotypic expression and stability in the characters, however, the environmental variance was also involved in the expression of characters. Highest GCV and PCV values were observed for total number of tillers, leaf area, which reveals comparatively higher degree of variation and higher chance of getting selection. Whereas lowest GCV and PCV were recorded for flag leaf length means little variation among genotypes for this trait. These findings are overall in good agreement with reports indicating that vegetative and yield associated attributes can be a source of useful variability for rice enhancement (Roy and Shil, 2025).

The broad-sense heritability was 69.93% for flag leaf length and 96.32% for number of tillers with moderate to high genetic influence on the expression of the traits under the study conditions. The broad-sense heritability should be considered with genetic gain as high heritability does not necessarily indicate high gain from selection. The present study number of tillers and leaf area showed higher genetic advance as percentage of mean, this is indicative that, these characters were liable to effective selection as related to other traits lower GAM, such as flag leaf length, plant height, and chlorophyll SPAD. However, the results of broad-sense heritability are not to be taken alone as evidence for additive gene action, since broad-sense heritability captures both additive and non-additive effect. Additional multi-environment and progeny study are required for confirmation of the inheritance pattern of these traits.

Correlation analysis indicated positive correlations among all traits, but the magnitude of correlations varied between trait pairs. Leaf area correlated positively with flag leaf width, plant height and number of tillers, indicating that within the examined genotypes leaf development and vegetative growth were correlated. Chlorophyll SPAD exhibited positive correlations with leaf area, flag leaf

width, plant height, and number of tillers, implying that increased chlorophyll content could be associated with enhanced vegetative growth. These are biologically reasonable relationships, since larger leaf size and higher chlorophyll concentration would potentially contribute to higher photosynthetic capacity and greater plant vigor (Simkin et al., 2019; Pan et al., 2023). However, given that grain yield was not evaluated in the present study, these traits are to be considered as potential indirect selection criteria rather than as validated yield-improving traits.

Although this study has provided useful insights, several limitations need to be taken into account. First, only five Amber-type genotypes (a fairly limited genetic base) were tested. Second, the study was performed in one location for one summer season, and thus, the genotype-by-environment interactions were not evaluated. These three limitations, as well as a focus on physiological and morphological characters at the heading to flowering stage that excluded grain yield or yield-component information is discussed. Hence, it is necessary that further investigations be carried out in more and diverse germplasm, at multi-locations and multi-seasons including final yield to ascertain the breeding value and stability of the identified traits.

4. Conclusion

The current investigation showed that significant differences existing among five Iraqi rice genotypes for physiological and anatomical attributes at heading to flowering stage. The Local Amber Genotype was found best in mean under tested environment for chlorophyll content, flag leaf traits, leaf area, plant height and tiller production. All traits were found to have significant to highly significant genotypic effect as revealed by the analysis of variance. Broad-sense heritability (H^2) for flag leaf length and number of tillers was 71.93 and 96.32%, respectively, indicated moderate-high broad-sense heritability. Number of tillers and leaf area also had relatively high genetic advance as percent of mean and high heritability indicating these are the best traits for selection within evaluated genotypes. Pearson correlation analysis indicated positive correlation among all studied traits, particularly between leaf area, flag leaf width, plant height, and number of tillers. However, since the research was conducted on only five genotypes in a single location and season, and without grain yield data, the results must be viewed as preliminary. Further multi-location multi-season investigations involving larger germplasm and including yield as a parameter are needed to validate the breeding utility of these traits.

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