RESEARCH ARTICLE

SABRAO Journal of Breeding and Genetics
55 (1) 131-145, 2023
http://doi.org/10.54910/sabrao2023.55.1.13
http://sabraojournal.org/
pISSN 1029-7073; eISSN 2224-8978

PATH COEFFICIENT, EIGENVALUES, AND GENETIC PARAMETERS IN EGYPTIAN RICE (*ORYZA SATIVA* L.) UNDER AEROBIC CONDITIONS

B. ZAYED, S. BASSIOUNI, A. OKASHA, M. ABDELHAMED, S. SOLTAN, and M. NEGM*

Rice Research Department, Field Crops Research Institute, Agricultural Research Center, Egypt
*Corresponding author's email: mahrousnegm9@gmail.com
Email addresses of co-authors: bas.zayed@gmail.com, Sherif_maher2002@yahoo.com, dramira74@yahoo.com, mohamed.abdelhamed0018@gmail.com, drsasoltan@gmail.com

SUMMARY

The genetic parameters, eigenvalues in principal components, correlation, and path coefficient in Egyptian rice (*Oryza sativa* L.) proceeded to understand the interrelationship among studied traits, which helps develop selection strategies in genetic breeding programs under aerobic conditions. Twelve rice genotypes planted under the aerobic condition in a randomized complete block design included three replications during the 2020 and 2021 seasons. The analysis of variance revealed significant differences among studied genotypes, indicating a broad genetic diversity among its genotypes. Eigenvalues used helped to understand the data structure and trait relations and divided the 21 traits into two components. The highly positive phenotypic and genotypic correlations appeared in 16 characteristics, i.e., leaf area index, total chlorophyll, and antioxidant traits, indicating that any improvement of these traits will improve rice grain yield under aerobic conditions. The path structure showed that panicle weight, the number of panicles hill^{-1}, catalase, superoxide dismutase, root length, and flag leaf area had increased grain yield. The current results indicated that Egyptian hybrid1, GZ9399, and Giza179 could recommend for cultivation under aerobic conditions and serve as donors in breeding programs to improve tolerance to drought under aerobic conditions.

Keywords: aerobic rice, path coefficient, correlation, eigenvalue, genetic advance, heritability

Key findings: Aerobic rice in the furrow saved water, with less water required. The high differences found among studied genotypes under aerobic conditions revealed the best rice genotypes as donor in the breeding program that will help improve drought tolerance under aerobic conditions. The path analysis diagram showed that the most traits affecting grain yield were panicle weight, the number of panicles, superoxide dismutase and catalase activities, and leaf area index. These traits could benefit selection in breeding programs under aerobic conditions.

Communicating Editor: Dr. Akshaya K. Biswal

Manuscript received: August 25, 2022; Accepted: January 12, 2023.

INTRODUCTION

Rice (*Oryza sativa* L.) is the most relevant food crop and energy source for about half of the world's population and ranks second in production after wheat (Manjappa and Shailaja, 2014). It is also a leading cereal staple food, together with wheat and maize (Saikia and Deka, 2011). Effective strategies need the implementation to increase grain

Citation: Zayed B, Bassiouni S, Okasha A, Abdelhamed M, Soltan S, Negm M (2023). Path coefficient, eigenvalues, and genetic parameters in Egyptian rice (*Oryza sativa* L.) under aerobic conditions. *SABRAO J. Breed. Genet.* 55(1): 131-145. http://doi.org/10.54910/sabrao2023.55.1.13.

production to meet the food requirement of the ever-increasing population (Zhang, 2007; Kahani *et al*., 2018; Chakrobarty *et al*., 2021). Since the water resources in Egypt are limited and its population has increased, intensified production needs action; finding ways to save more irrigation water and managing it well becomes essential (Badawi and Ghanem, 2007; Kahani and Hittalmani, 2016; Vanitha *et al*., 2016). Rice is a semi-aquatic plant, highly affected by water shortage. Aerobic rice is a production system grown in well-drained, non-puddled, and non-saturated soils. Water savings result from land preparation, with no transplanting costs, seed costs, and labor costs from sowing to harvest (Parthasarathi *et al.,* 2012). Egypt's agriculture sector and food security are at risk. The Egyptian Government wants to reduce the area of rice fields due to a complete lack of freshwater budget (Al-Waqa'a Al-Masryah, 2020). It is crucial to improve water productivity, specifically when growing rice in regions with limited water. Aerobic rice indicates that growing rice under non-puddled, non-saturation, and well-drained, without ponded water, uses external irrigation and fertilizers. It is a potential rice cultivation system as water scarcity is increasing worldwide (Xie *et al.,* 2008). Aerobic rice technology is a better remedy for future climate change under drought conditions with less greenhouse gas emission (Lal *et al.,* 2013). Aerobic rice varieties can produce yields up to 4–6 t/ha with a proper application of fertilizers and preserves growth in soils with moisture content at lower field capacity (Parthasarathi et *al.,* 2012). The dominant root traits (root length, volume, thickness, and depth of root) in some adapted aerobic rice varieties can produce a high yield (Shashidhar *et al.,* 2013; Sachesh *et al.,* 2020). Gour *et al.* (2017) reported that principal component analysis helped examine the variation and estimate the relative contribution of various traits for total variability. Measurement of the correlation coefficient helps identify component traits' relative contribution toward yield (Dilruba *et al.,* 2014). Correlation analysis provides information on the nature and magnitude of the association of different components responsible for yields. With their mutual association, the development of a dependent variable and their indirect effect exerted through other traits is inevitably an integral part of growth and development. Under such a complex situation, the total correlation would be insufficient to explain the association for effectively manipulating the traits (Dewey and Lu, 1959). Path analysis divides the correlation into direct and indirect effects and measures the relative importance of the factors involved. The knowledge of interrelationships among various traits is necessary when selection for their simultaneous improvement is the target of the plant breeder. If two desirable characteristics are associated, selection for one will automatically be good enough to make meaningful improvements to the other. The objective of this study is to know the nature of the relationships among studied traits. The results could help develop selection strategies in breeding programs aimed at improving tolerance to drought under aerobic conditions.

MATERIALS AND METHODS

The experiments of aerobic rice cultivation proceeded at the Rice Research and Training Center at Sakha Agriculture Station in the two growing seasons of 2020 and 2021 under aerobic conditions. The conducted experiments had a randomized complete block design with three replications. Table 1 shows the origin, parentage, and genotype group of the studied

Table 1. Origin, parentage, and genotype group of the studied genotypes.

Genotypes	Parentage	Type
Giza177	Giza 171 / Yomji No.1 // Pi No.4	Japonica
Giza178	Giza 175/Milyang 49	Indica/Japonica
Giza179	GZ6296-12-1-2-1-1/GZ1368-S-5-4	Indica/Japonica
Sakha103	Giza 177 / Suweon 349	Japonica
Sakha104	GZ 4096-8-1 / GZ 4100-9-1	Japonica
Sakha105	GZ 5581-46-3 / GZ 4316-7-1-1	Japonica
Sakha108	Sakha101/ HR5824-B-3-2-3 //Sakha101	Japonica
GZ9399-4-1-1-3-2-2	Giza178/IR65844-29-13-12	Indica/Japonica
GZ6296-12-1-2-1-1	AC 1225 × Hua lien 202	Indica/Japonica
IET1444	T(N)1/CO29	Indica
Egyptian hybrid1	IR69625A / Giza178	Indica/Japonica
Egyptian Jasmine	IR262-43-8-1/NAHNG SARN	Indica

12 genotypes. The dry seed use progressed in dry land on furrows. The furrow meter wide measured 70 cm from the mid-bottom of the furrow, with 15 cm between every two hills. Watering during rice growth began in the first 25 days, as in drill seeded rice, then watering continued every eight days up to maturity. The recommended dose of nitrogen fertilizer (165 kg N/ha) application ensued in three equal splits (as basal and topdressing at panicle initiation). During the land preparation for the permanent field, basal application of phosphorus fertilizer at the rate of 35.5 kg, P2O5 ha^{-1} took place on the soil, with potassium fertilizer added, at the rate of 57 kg K2O ha^{-1} as a basal dose, incorporated into dry ground. Zinc application (Zn So4) 24 kg/ha^{-1} advanced before continuous flooding.

Studied traits

At heading, randomly taking plant samples ensued and transferred to the lab to determine leaf area index and flag leaf area (cm^2), using Portable Area Meter (Model LI– 3000A), chlorophyll content (SPAD value), and leaf rolling. Also, morphological traits and some antioxidants underwent estimations for electrolyte leakage, relative water content, and stomatal conductance. Other estimates used the following: the Bergmeyer method (1970) for catalase activity, Bradford (1976) for peroxidase activity, Bates *et al.* (1973) for proline content, and Beauchamp and Fridovich (1971) for superoxide dismutase activity. Counting a total number of panicles of 10 random hills took place. Ten random panicles collected from each plot gained measurement for panicle length, the total number of filled grains panicle^{-1}, the number of unfilled grain panicle^{-1}, panicle weight, and 1000-grain weight. Randomly measuring grain yield from an area had its moisture content adjusted to 14%.

Statistical analysis

Analysis of variance (ANOVA) estimated in a complete randomized block design tested their significance level, with genotypic and phenotypic correlation estimates using R studio (version 3.1.1.). Also, the genotypic coefficient of variability, phenotypic coefficient of variability, and genetic advance calculation used R studio (version 3.1.1.) (Jat *et al.,* 2017). The principal component analysis (PCA) technique used SPSS statistical package version 22.0 (SPSS Inc., Chicago, IL, USA) (Doran and Parkin, 1994). Performing path coefficients using IBM SPSS AMOS statistical software (version 24) continued (Amene, 2017; Bhutta *et al.,* 2019). Phenotypic diversity analysis of studied traits of 12 genotypes using the Gower-paired method employed the help of PAST (Paleontological Statistics) by Hammer *et al.* (2004).

RESULTS AND DISCUSSION

Mean performance

The genotypes' mean values for all studied traits appear in Tables 2 and 3. Giza179 showed the best genotype for the following characteristics, i.e., flag leaf area, total chlorophyll, peroxidase, stomatal conductance, proline content, root volume, and panicle weight, followed by Egyptian hybrid rice1 (EHR1) and GZ9399. Based on leaf area index, superoxide dismutase, the number of panicle hill^{-1}, filled grains panicle^{-1}, and filled grains panicle^{-1}, the genotype Giza179 gave the highest mean value under aerobic conditions, followed by GZ9399.

Concerning the root length, the variety Giza179 gave the highest mean value in both seasons, followed by GZ9399 and EHR1 in the first season, with the variety HER1 as the second-highest mean value in the second growing seasons. Furthermore, the highest mean value for relative water content came from Giza179, followed by Giza178 in the 2020 growing seasons, while the best genotype in the 2021 growing seasons resulted in Giza179, followed by EHR1. In the case of catalase, genotypes among EHR1 ranked the best genotypes, followed by GZ9399 and Giza179 in the first season. In the second season, the best genotypes emerged for HER1, followed by Giza179 and GZ9399. Zayed *et al.* (2017) reported similar findings for Giza179 and EHR1, giving the highest values of the most studied traits, with Giza178 coming in as third, whereas Giza177 provided the lowest values of the evaluated attribute.

Regarding leaf rolling, data in Tables 2 and 3 indicated that among genotypes, Giza179 followed by EHR1, ranked best, with GZ9399 scoring the lowest and the desirable mean value under aerobic conditions. Concerning electrolyte leakage among the genotypes, GZ9399 revealed the best genotype in the first year, while Giza179 scored the highest mean value in the second growing seasons. Moreover, the variety Egyptian Jasmine exhibited the longest panicle among the other studied genotypes in both seasons

Table 2. Mean performance of 12 rice genotypes for flag leaf area, leaf area index, leaf rolling, catalase, peroxidase, superoxide dismutase, total chlorophyll, electrolyte leakage, and stomatal conductance under aerobic conditions.

Genotypes	Flag leaf area		Leaf area index		Leaf rolling	
	2020	2021	2020	2021	2020	2021
Giza177	15.43e	14.87i	3.27h	3.37g	6.67a	6.33a
Giza178	21.83d	23.67d	4.60d	5.03c	2.67de	2.67cde
Giza179	32.73a	33.67a	5.90a	5.87a	2.00e	2.33de
Sakha103	14.90e	14.17ij	3.07i	3.13h	7.00a	6.67a
Sakha104	20.67d	18.53h	3.97f	4.30e	4.33bc	4.67b
Sakha105	14.00e	13.00j	3.03i	3.03h	7.33a	7.00a
Sakha108	21.00d	19.50gh	3.63g	3.87f	5.00b	4.67b
GZ9399	26.13c	25.27c	5.70b	5.50b	2.33de	3.00cd
GZ6296	21.33d	20.83fg	4.17e	3.87f	4.67b	4.33b
IET1444	20.50d	21.23ef	5.23c	4.53d	3.33cd	3.33c
EHR1	28.60b	28.10b	5.10c	5.00c	2.67de	2.00e
E. Jasmine	20.83d	22.50de	5.63b	5.07c	4.67b	4.67b
Genotypes	Catalase		Peroxidase		Superoxide Dismutase	
	2020	2021	2020	2021	2020	2021
Giza177	0.0853ef	0.0960f	1.207h	1.220j	0.2137h	0.2177g
Giza178	0.1160b	0.1187c	2.487c	2.563c	0.4200d	0.4050d
Giza179	0.1310a	0.1357b	2.927a	2.883a	0.5980a	0.5900a
Sakha103	0.0787f	0.0823g	1.173h	1.293i	0.2183h	0.2253g
Sakha104	0.1017cd	0.1027ef	1.473g	1.490h	0.3167f	0.3367e
Sakha105	0.0590g	0.0600h	1.203h	1.237ij	0.1617i	0.1493h
Sakha108	0.0933de	0.1007ef	1.533fg	1.580g	0.2860g	0.2850f
GZ9399	0.1420a	0.1373ab	1.797d	1.923d	0.5453b	0.4967b
GZ6296	0.1133bc	0.0967f	1.603ef	1.673f	0.3203f	0.2917f
IET1444	0.1157b	0.1077de	1.633e	1.753e	0.3980e	0.4500c
EHR1	0.1403a	0.1440a	2.650b	2.677b	0.5100c	0.4950b
E. Jasmine	0.1137bc	0.1107d	1.550f	1.583g	0.4047de	0.4160d
Genotypes	Total chlorophyll		Electrolyte leakage		Stomatal conductance	
	2020	2021	2020	2021	2020	2021
Giza177	26.67e	25.27e	21.33a	23.33a	581.7h	557.3g
Giza178	33.00c	32.67c	7.43f	9.67fg	811.7b	816.7c
Giza179	38.67a	37.87a	7.33f	7.33h	830.0a	853.3a
Sakha103	23.80f	23.70e	21.17a	21.43b	566.7i	553.3g
Sakha104	30.23d	27.63d	13.33c	14.00d	770.0d	753.3e
Sakha105	23.33	23.77e	21.67a	24.67a	640.0g	533.3h
Sakha108	29.67d	27.80d	18.53b	17.93c	690.0f	707.3f
GZ9399	37.00ab	35.20b	7.00f	8.50gh	823.3ab	816.7c
GZ6296	31.00cd	28.00d	17.00b	17.43c	733.3e	740.0e
IET1444	29.00d	29.47d	10.20de	11.33ef	790.0c	790.0d
EHR1	35.33b	36.00b	8.33ef	7.67h	836.7a	836.7b
E. Jasmine	29.33d	28.59d	11.00d	12.67de	695.0f	696.7f

Where, mean values followed by the different letters on the same column indicate statistical significance, according to Duncan's Multiple Range Test at the level ɑ = 5%.

under aerobic conditions, followed by Giza179 and EHR1. The tallest plant was EHR1. The breeder prefers the shortest plants because they are suitable for mechanical harvesting and tolerant to the wind; yet under stress, the shortest plant may mean dwarfism and sensitivity, so in this research, the tallest plant gains preference.

The highest mean value for 1000-grain weight was Sakha104; this trait may depend more on types of rice variety than tolerance or sensitivity to stress. Grain yield is a vital trait and the first aim for rice breeders. Among the studied genotypes, the three following genotypes are Giza179, followed by GZ9399, and EHR1 since these have the highest values for grain yield, with the best genotypes for easy cultivation under aerobic conditions. Also, these genotypes can benefit the breeding program by improving drought tolerance under aerobic conditions.

Table 3. Mean performance of 12 rice genotypes for proline content, root length, root volume, relative water content, no. of panicle hill^{-1}, panicle length, filled grains panicle^{-1}, unfilled grains panicle^{-1}, plant height, panicle weight, 1000-grain weight, and grain yield under aerobic conditions.

Genotypes	Proline content		Root length		Root volume		Relative water con.	
	2020	2021	2020	2021	2020	2021	2020	2021
Giza177	14.37e	11.53g	14.19g	14.83g	25.20h	28.70g	52.80f	49.20g
Giza178	24.43b	26.17bc	26.83b	25.90c	52.07c	53.33c	80.40b	76.83bc
Giza179	26.83a	27.73a	30.21a	30.77a	61.93a	65.40a	89.00a	82.70a
Sakha103	11.70f	14.45f	14.33g	14.80g	34.00g	34.33f	66.44d	41.60h
Sakha104	19.04d	20.30d	22.31d	21.60e	45.60d	45.80d	74.26c	66.67e
Sakha105	11.03f	11.30g	15.60f	13.87g	28.47h	28.70g	60.28e	34.47i
Sakha108	14.61e	14.50f	19.10e	19.67f	41.67e	40.93e	73.55c	63.00f
GZ9399	25.10ab	25.27c	27.51b	25.73c	58.44b	61.00b	76.77c	75.00c
GZ6296	15.30e	13.37f	19.67e	21.17e	37.67f	40.00e	67.86d	65.33ef
IET1444	22.10c	21.13d	23.87c	24.13d	54.60c	58.33b	76.54c	75.77bc
EHR1	25.50ab	27.20ab	27.10b	28.77b	65.17a	65.70a	76.14c	78.32b
E. Jasmine	18.57d	17.83e	19.10e	21.53e	42.08e	44.00d	73.30c	70.67d
Genotypes	No. of panicle hill^{-1}		Panicle length		Filled grains		Unfilled grains	
	2020	2021	2020	2021	2020	2021	2020	2021
Giza177	13.67f	13.00f	15.70d	15.90gh	70.00h	69.00h	32.00b	33.33d
Giza178	19.00d	22.33c	19.53bc	21.33bc	108.0d	114.7c	13.33g	12.33e
Giza179	24.00ab	24.67ab	20.00b	22.33ab	127.3a	122.3a	10.33h	11.00e
Sakha103	12.17g	12.67f	13.41e	14.50hi	60.67i	63.00i	37.33a	36.33a
Sakha104	15.43e	16.00e	18.17c	19.30de	78.33g	76.67g	25.33c	25.00c
Sakha105	9.67h	10.00f	13.33e	13.97i	53.33j	59.67j	33.00b	35.00a
Sakha108	14.33ef	15.67e	15.33d	17.00fg	68.00h	77.67g	16.33f	20.50d
GZ9399	24.50a	25.67a	20.23b	21.00bc	120.0b	124.0a	9.67h	11.67e
GZ6296	17.67d	18.50d	18.33c	18.33ef	95.33e	96.33e	21.00e	24.00c
IET1444	22.33c	23.33bc	20.37b	20.37cd	105.0d	101.0d	21.67e	19.67d
EHR1	23.00bc	24.33ab	20.83b	21.80bc	115.0c	118.3b	24.33cd	25.00c
E. Jasmine	14.67ef	15.00e	23.07a	23.40a	82.67f	81.67f	22.33de	21.33d
Genotypes	Plant height		Panicle weight		1000-grain weight		Grain yield	
	2020	2021	2020	2021	2020	2021	2020	2021
Giza177	77.33e	77.83de	1.477f	1.487g	25.47bc	25.67ab	6.33f	6.13g
Giza178	84.33c	86.53b	1.990c	2.020d	20.87g	20.93e	9.03b	9.33bc
Giza179	87.33b	89.00a	2.700a	2.797a	26.20ab	24.50c	9.43a	9.77a
Sakha103	71.00f	69.33f	1.433f	1.377h	24.83cd	26.37ab	5.80g	6.20g
Sakha104	81.33d	80.33c	1.667e	1.693f	27.00a	26.60a	7.43de	7.40e
Sakha105	68.33g	66.67g	1.227g	1.303h	25.27c	25.73ab	5.17h	5.33h
Sakha108	76.33e	76.00e	1.850d	1.800e	25.50bc	25.57b	7.73d	7.60e
GZ9399	87.33b	86.00b	2.483b	2.483c	24.07de	24.33c	9.37a	9.23c
GZ6296	79.67d	79.50cd	1.887d	1.683f	23.50ef	22.83d	7.40e	6.60f
IET1444	87.33b	88.33ab	2.033c	2.090d	19.83h	20.90e	8.60c	8.83d
EHR1	90.67a	90.67a	2.500b	2.707b	22.77f	22.73d	9.40a	9.47b
E. Jasmine	89.67a	88.33ab	1.850d	1.847e	20.13gh	20.83e	7.70de	7.60e

Where, mean values followed by the different letters on the same column indicate statistical significance, according to Duncan's Multiple Range Test at the level α = 5%.

Analyses of variance and genetic performance of rice genotypes under aerobic conditions

Table 4 showed a highly significant mean square for genotypes for all studied traits in both seasons. Broader genetic variation with greater diversity contained in the rice gene pool is necessary for utilization in rice breeding programs (Sivaranjani *et al.,* 2010). These results indicated high differences among genotypes under aerobic conditions and could select the best genotypes for planting and breeding programs under aerobic conditions.

Data in Table 5 indicated that most of the studied traits had the highest estimate of phenotypic (PCV) and genotypic (GCV) coefficient of variability, i.e., several panicles hill^{-1}, filled grain panicle^{-1}, unfilled grain panicle^{-1}, panicle weight, antioxidant activities, and other traits, which scored more than 20%. The lowest PCV and GCV emerged in plant height in both seasons, which was less than 10%. Meanwhile, 1000- grain weight differed from low to moderate GCV and PCV in the two growing seasons.

Furthermore, panicle length, stomatal conductance, total chlorophyll, and grain yield exhibited moderate PCV and GCV under both studied seasons. The PCV and GCV received classification, as suggested by Sivasubramanian and Menon (1973), where when less than 10% = Low, 10%–20% = Moderate, and more than 20% = High.

The relative availability of phenotypic coefficients of variation was higher than genotypic coefficients of variation for all the traits under study, indicating the environmental influence on the traits. In the same pattern, the effect of the environmental coefficient of variability (ECV) is low in all studied attributes except leaf rolling, which moderately indicated the high heritability of these traits, thus, can be beneficial in the breeding program to improve tolerance to aerobic conditions. An understanding of genetic variability is essential for the success of any plant breeding program. The parameters, such as genotypic and phenotypic coefficients of variation (GCV and PCV), help detect the variability in a given trait. Obtaining extensive genetic diversity will become flexible in the process of selection of superior genotypes or the improvement of traits (Lestari *et al.,* 2019). The high value of GCV also indicates the existence of high genetic variation, and selection using those features to improve the genotypes could be effective under aerobic conditions (Sabri *et al.,* 2020).

Heritability for all studied traits was high, ranging from 85.71% to 99.61%, indicating that precise selection can effectively improve yield in the genotypes under study. The heritability of a trait is essential in determining its response to selection. Plant genetic improvement for quantitative traits requires reliable heritability estimates to plan an efficient breeding program (Perera *et al.,* 2014). Heritability, with high genetic gain, could be more effective in predicting the resultant effect in selecting the best genotypes for yield and its attributing traits. Plant breeder uses selection to improve features of crops of interest by managing available genetic variability, with landraces known to have a wider range of variability (Abdala *et al.,* 2016). The observed highest value of genetic advance in mean percent emerged in most studied traits to ensure the possible gain from selection and the generation to another dependent of these attributes in a hybridization breeding program. The traits with high genetic advance percentages came from the control of the additive gene action, and the selection effectively improves those traits under aerobic conditions.

Table 4. Analysis of variance for studied traits of rice under aerobic conditions.

Source of variation	2020			2021		
	Replication (df=2)	Genotypes (df=11)	Error (df=22)	Replication (df=2)	Genotypes (df=11)	Error (df=22)
Leaf area index	0.01	3.39**	0.011	0.034	2.65**	0.011
Total chlorophyll	1.38	69.28**	1.81	0.495	67.73**	1.07
Flag leaf area	1.31	91.97**	1.07	0.20	107.52**	0.66
Leaf rolling	0.09	10.42**	0.469	0.028	8.69**	0.27
Catalase	0.0001	0.0019**	0.0001	0.00003	0.0017**	0.00002
Peroxidase	0.0011	1.053**	0.0017	0.00002	0.996**	0.0013
Superoxide dismutase	0.00005	0.057**	0.0001	0.00003	0.054**	0.0002
Proline content	0.441	95.82**	0.994	0.317	116.94**	0.66
Electrolyte leakage	0.06	104.98**	1.45	0.485	114.7**	1.12
Root length	0.759	90.58**	0.462	0.068	90.59**	0.713
Root volume	4.04	510.62**	3.78	0.241	539.69**	2.53
R. water content	1.51	267.94**	4.33	0.902	713.19**	2.16
Stomatal conductance	205.69	27701**	74.94	13.44	39889.1**	94.17
Plant height	0.194	161.26**	1.41	1.05	189.91**	1.812
No. of panicle hill^{-1}	0.90	74.71**	0.658	0.965	88.49**	1.06
Filled grains	0.44	1847.4**	4.79	1.03	1694.7**	3.33
Unfilled grains	1.86	236.93**	1.92	0.465	230.14**	0.935
Panicle length	0.279	28.79**	0.69	0.625	29.78**	0.78
Panicle weight	0.0018	0.619**	0.0035	0.002	0.744**	0.002
1000-grain weight	0.054	17.42**	0.231	0.73	14.42**	0.268
Grain yield	0.053	6.34**	0.032	0.018	6.88**	0.015

Where, *, ** Significant at 5% and 1% levels, respectively.

Table 5. Estimates of genetic parameters for all studied traits under aerobic conditions.

Traits	Grand Mean ± SEM		ECV%		GCV%		PCV%		h^2b%		GA%	
	2020	2021	2020	2021	2020	2021	2020	2021	2020	2021	2020	2021
Leaf area index	4.44±0.087	4.38±0.048	2.36	2.40	23.90	21.41	24.02	21.55	99.03	98.76	41.87	37.45
Total chlorophyll	30.59± 1.098	29.66±0.845	4.40	3.49	15.50	15.89	16.11	16.27	92.55	95.41	26.25	27.32
Flag leaf area	21.50±0.846	21.28±0.662	4.81	3.89	25.60	28.05	26.05	28.30	96.59	98.18	44.29	48.91
Leaf rolling	4.39±0.559	4.31±0.424	15.60	12.06	41.49	38.87	44.32	40.70	87.61	91.22	68.34	65.34
Catalase	0.110±0.006	0.108±0.003	9.09	4.14	22.27	21.91	24.05	22.30	85.71	96.55	36.28	37.89
Peroxidase	1.77±0.034	1.82± 0.030	2.33	1.98	33.44	31.64	33.53	31.70	99.52	99.61	58.72	55.57
Superoxide dismutase	0.366±0.009	0.363±0.010	2.73	3.90	37.63	36.89	37.73	37.10	99.48	98.90	66.05	64.57
Proline content	19.05±0.814	19.23±0.663	5.23	4.23	29.51	32.38	29.97	32.65	96.95	98.33	51.14	56.50
Electrolyte leakage	13.69±0.984	14.66±0.864	8.80	7.22	42.91	41.97	43.80	42.59	95.97	97.13	73.99	72.80
Root length	21.65±0.555	21.90±0.689	3.14	3.86	25.32	24.99	25.51	25.29	98.49	97.68	44.22	43.47
Root volume	45.57±1.558	47.19± 1.279	4.27	3.37	28.52	28.36	28.84	28.56	97.81	98.61	49.65	49.56
Relative water content	72.28±1.669	64.96±1.199	2.88	2.26	12.97	23.70	13.28	23.81	95.30	99.10	22.28	41.52
Stomatal conductance	730.7± 7.068	721.2±7.923	1.19	1.35	13.13	15.97	13.19	16.03	99.19	99.30	23.02	28.01
Plant height	81.72± 0.968	81.54± 1.099	1.45	1.65	8.93	9.71	9.05	9.85	97.42	97.19	15.52	16.85
Number of panicle hill^{-1}	17.54±0.662	18.43± 0.839	4.63	5.59	28.33	29.29	28.70	29.82	97.40	96.49	49.20	50.64
Filled grains panicle^{-1}	90.31±1.787	92.03±1.490	2.42	1.98	27.44	25.80	27.55	25.88	99.23	99.41	48.11	45.28
Unfilled grains panicle^{-1}	22.22±1.132	22.93±0.790	6.24	4.22	39.83	38.12	40.32	38.35	97.61	98.79	69.26	66.68
Panicle length	18.19±0.678	19.10±0.722	4.57	4.62	16.83	16.28	17.43	16.92	93.14	92.53	28.58	27.56
Panicle weight	1.92±0.048	1.94±0.036	3.08	2.31	23.59	25.64	23.79	25.74	98.32	99.20	41.17	44.94
1000-grain weight	23.79± 0.393	23.92±0.423	2.02	2.16	10.06	9.08	10.26	9.33	96.12	94.62	17.36	15.55
Grain yield	7.78±0.148	7.79±0.100	2.30	1.57	18.64	19.42	18.78	19.48	98.50	99.35	32.56	34.07

Where, PCV%: Phenotypic coefficient of variation, GCV%: Genotypic coefficient of variation, h^2b%: broad sense heritability, and GA%: genetic advance as a percent of the mean.

On the other hand, the values of the genetic advance for plant height (15.52% and 16.85%) and 1000-grain weight (17.36 and 15.55) were moderately genetic advance in the two growing seasons, respectively. The genetic advance as percent over mean was categorized, as suggested by Johnson *et al.* (1955), cited in GCV and PCV. High genetic advance, coupled with high heritability estimates, offers the most suitable condition for selection. It also indicates the presence of additive genes in the trait and the possibility of improvement by selecting such characteristics.

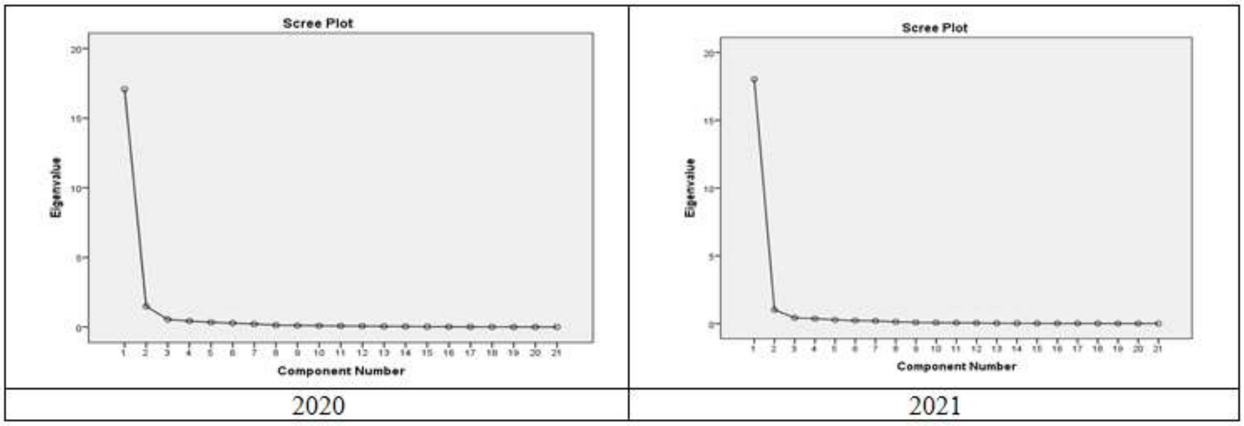
Principal component analysis (PCA)

Principal components analysis (PCA) is a mathematical procedure that transforms several possible correlated variables into a smaller number of uncorrelated variables (PC). The objective of PCA is to reduce the dimensionality of the parameter dataset and to identify new meaningful underlying variables (Gour *et al.,* 2017). The first PC accounts for as much of the variability in the data as possible, and each succeeding component accounts for as much of the remaining variability as possible. The PCA is a powerful tool in modern data analysis because this is a well-known multivariate statistical technique used to identify the minimum number of components, which can explain the maximum variability out of the total variability (Morrison, 1978). Data in Table 6 and Figures 1 and 2 showed the eigenvalue, the percent of the variance, and the percent of cumulative variance for the two PCs and the rotated component factor among PCs and studied traits.

The results showed that all the studied traits produced two PCs, with the eigenvalue value at more than one and a cumulative variability of 88.37 and 90.70 in two growing seasons, respectively. The eigenvalues in PC1 had the highest variance (81.32 and 85.87), yet, in PC2 these scored 7.05 and 4.83 in two seasons, respectively. These results agree with Venkata *et al.* (2019). Also, the results in Table 6 showed that the studied traits were divided into two groups based on the rotated component matrix. The PC1 traits, leaf area index, flag leaf area, total chlorophyll, peroxidase, catalase, superoxide dismutase, proline content, root length, root volume, relative water content, stomatal conductance, number of panicles hill^{-1}, filled grain panicle^{-1}, panicle weight and grain yield, exhibited with a positive value, whereas unfilled grain panicle^{-1}, leaf rolling, and electrolyte leakage with a negative value.

Table 6. Eigenvalues, % variance, cumulative eigenvalues, and rotated component matrix for 21 variables of rice genotypes in two growing seasons.

Principal components	2020		2021	
	PC1	PC2	PC1	PC2
Eigenvalue	17.08	1.48	18.03	1.01
Variance%	81.32	7.05	85.87	4.83
Cumulative%	81.32	88.37	85.87	90.70
Traits	Rotated Component Matrix		Rotated Component Matrix	
Leaf area index	0.735	0.595	0.817	0.494
Total chlorophyll	0.938		0.937	
Flag leaf area	0.951		0.894	0.333
Leaf rolling	-0.884	-0.343	-0.842	-0.446
Catalase	0.813	0.456	0.869	0.350
Peroxidase	0.874		0.874	
Superoxide dismutase	0.910	0.361	0.866	0.436
Proline content	0.880	0.392	0.897	0.302
Electrolyte leakage	-0.809	-0.523	-0.841	-0.492
Root length	0.942		0.894	0.408
Root volume	0.892	0.318	0.902	0.353
Relative water content	0.832		0.768	0.595
Stomatal conductance	0.879	0.315	0.838	0.459
Plant height	0.673	0.675	0.672	0.676
Number of panicle hill^{-1}	0.865	0.344	0.862	0.369
Filled grains panicle^{-1}	0.885	0.376	0.876	0.378
Unfilled grains panicle^{-1}	-0.811		-0.725	-0.481
Panicle length	0.551	0.762	0.625	0.701
Panicle weight	0.932		0.940	
1000-grain weight		-0.926		-0.934
Grain yield	0.886	0.401	0.882	0.411



2020

2021

Figures 1, 2: Scree plot of principal component analysis of rice genotypes among eigenvalue and principal components in two seasons.

Furthermore, the traits of PC2 were plant height, panicle length, and one thousand-grain weight in both seasons. Noteworthy to mention that total chlorophyll and panicle weight in both seasons besides flag leaf area, superoxide dismutase, root length, and root volume in only one season, had a high positive value for the rotated component matrix equal to 0.90, and more than that providing their great contribution portion in their variance. Likewise, the value of the rotated component matrix for cell electrolyte leakage, unfilled grain panicle^{-1}, leaf rolling, and 1000-grain weight had negative charge, indicating their negative role or undesirable effect on rice grain yield under aerobic conditions. As for 1000-grain weight in the current study, it revealed that the nominated sensitive rice genotypes for drought had a high value of 1000-grain weight compared with tolerant ones, which probably attributed to their undesirable role. Moreover, the negative value of cell electrolyte leakage confirmed the importance of keeping a healthy cell membrane without damage that happens with water deficit under aerobic cultivation. A similar result came from Chunthaburee *et al.* (2015).

Thus, the results of the principal component analysis used in the study have revealed the traits contributing to the variation. These scores can propose accurate selection indices whose intensity could result from variability explained by each principal component (Maji and Shaibu, 2012) to identify and classify maximum variability into total variability for grouping the accessions by considering several traits and relationships among them.

Phenotypic and genotypic correlations coefficient

The degree of correlation among the traits is significant in plant breeding as a tool for indirect selection. Correlation studies help the plant breeder during selection and provide an understanding of yield components (Konate *et al.,* 2016). Knowing the correlation between grain yield and other traits is crucial to the breeder for improving complex quantitative traits like grain yield, for which straight selection is much more effective in increasing production under aerobic conditions. The assessed phenotypic and genotypic correlation coefficients among the studied traits and grain yield appear in Table 7. Grain yield was highly significant and positive in both phenotypic and genotypic correlations with leaf area index, chlorophyll content, flag leaf area, catalase activity, peroxidase activity, proline content, superoxide dismutase activity, stomatal conductance, root length, root volume, relative water content, plant height, number of panicles hill^{-1}, filled grain panicle^{-1}, panicle length, and panicle weight. Indications that these traits showed the strongest associates of grain yield agree with the current findings of Wattoo *et al.* (2010) and Dilruba *et al.* (2014) who cited that those traits could benefit selection in breeding programs to obtain rice genotypes tolerant to drought under aerobic conditions. On the contrary, the grain yield exhibited a strong negative association with leaf rolling, electrolyte leakage, and unfilled grain panicle^{-1} by phenotypic and genotypic correlation in both seasons, consistent with Paul and Sarmah (1997) and Dilruba *et al.* (2014) who reported

Table 7. Estimates of correlation coefficient among studied traits and grain yield.

Grain yield (t/ha^{-1})	With traits	Leaf area index (LAI)		Total chlorophyll (CHL)		Flag leaf area (FLA)		Leaf rolling (LR)	
		2020	2021	2020	2021	2020	2021	2020	2021
	RP	0.85**	0.81**	0.89**	0.91**	0.88**	0.89**	-0.94 **	-0.93**
	RG	0.87**	0.92**	0.95**	0.94**	0.89**	0.90**	-0.96**	-0.96**
	With traits	Catalase (CAT)		Peroxidase (POX)		Proline content (PRO)		Superoxide dismutase(SOD)	
		2020	2021	2020	2021	2020	2021	2020	2021
	RP	0.91**	0.91**	0.82**	0.87**	0.94**	0.95**	0.93**	0.94**
	RG	0.97**	0.92**	0.83**	0.88**	0.96**	0.96**	0.94**	0.95**
	With traits	Electrolyte leakage (EL)		Root length (RL)		Root volume (RV)		Relative water content (RWC)	
		2020	2021	2020	2021	2020	2021	2020	2021
	RP	-0.92**	-0.94**	0.93**	0.94**	0.92**	0.96**	0.83**	0.91**
	RG	-0.94**	-0.96**	0.94**	0.96**	0.94**	0.97**	0.84**	0.93**
	With traits	Stomatal conductance(STC)		Plant height (PH)		No. of panicle hill^{-1} (PN)		Filled grains panicle^{-1} (FG)	
		2020	2021	2020	2021	2020	2021	2020	2021
	RP	0.89**	0.92**	0.87**	0.86**	0.92**	0.92**	0.93**	0.91**
	RG	0.91**	0.93**	0.89**	0.88**	0.94**	0.94**	0.94**	0.92**
	With traits	Unfilled grain panicles^{-1}(UFG)		Panicle length (PL)		Panicle weight (PW)		1000-Grain weight (TWG)	
		2020	2021	2020	2021	2020	2021	2020	2021
	RP	-0.83**	-0.86**	0.77**	0.81**	0.93**	0.92**	-0.34*	-0.51**
	RG	-0.85**	-0.88**	0.81**	0.85**	0.95**	0.93**	-0.35	-0.52

Where RG=genotypic correlation and RP = phenotypic correlation.

similar types of observations. The weight of 1000-grain was negatively significant in the first year and highly negatively significant in the second year, with grain yield in phenotypic correlation only.

Path analysis

The structure path analysis employed the use of AMOS software to understand the effect of the studied traits on grain yield under aerobic conditions, based from the suggestion the model gave. According to the model, the direct traits affecting grain yield are panicle weight, the number of panicles, and relative water content, as an endogenous variable for grain yield. In contrast, the rest of the traits grouped as exogenous ones indicated an indirect effect on grain yield. These results agree with Kiani and Agahi (2016) and Zarbafi *et al.* (2019). Figures 3 and 4 and Table 8 illustrate the results of path analysis diagrams in both studied years. The trait with the most direct positive effect on grain yield from endogenous variables appeared from the group of panicle weight (1.006 and 1.104), followed by the number of panicles (0.126 and 0.067) and relative water content (0.040 and 0.039) in the two growing seasons, respectively. These results indicated the importance of traits grouped by panicle weight for increasing grain yield. The highest indirect positive effects on grain yield resulted in catalase (7.509 and 3.593), superoxide dismutase (2.485 and 0.828), leaf area index (0.086 and 0.147), and root length (0.048 and 0.024), indicating the big role of these traits to improve the grain yield under aerobic condition. Catalase and superoxide dismutase serve as reactive oxygen species scavengers that help the plant survive under aerobic conditions. Meanwhile, the root length is a vital trait enabling the plants to absorb water from the depths, and the leaf area index provides evidence concerning the health of plants (Bhutta *et al.,* 2019; Kiani and Agahi, 2016).

On the same pattern, the leaf area index (0.086 and 0.132), flag leaf area (0.034 and 0.027), and total chlorophyll (0.029 and 0.045) had immense effects on panicle weight in both seasons, respectively. Based on directed positive traits on relative water content, the best trait was root length (1.211 and 0.610).

Catalase (59.76 and 53.83) is the most directed and desirable trait on the number of panicles hill^{-1}, followed by superoxide dismutase (19.78 and 12.41) and proline content (0.492 and 0.98) in both seasons, respectively, indicating the importance of these traits for increasing panicle number under aerobic conditions and thus, improving the

Table 8: Direct and indirect effects for the predictor variables in path analysis.

Direct effect			Traits	Indirect effect with Grain Yield	
Direct with	2020	2021		2020	2021
Direct with Grain yield	1.006	1.104	Panicle weight		
	0.040	0.039	Relative water content		
	0.126	0.067	No. of panicles hill^{-1}		
Direct with Panicle weight	0.004	0.005	Filled grains panicle^{-1}	0.005	0.006
	0.002	0.014	Unfilled grains panicle^{-1}	0.002	0.015
	-0.024	-0.004	Panicle length	-0.024	-0.004
	-0.015	0.011	1000-grain weight	-0.015	0.012
	0.034	0.027	Flag leaf area	0.034	0.029
	0.086	0.132	Leaf area index	0.086	0.146
	0.029	0.045	Total chlorophyll	0.029	0.050
Direct with Relative water content	-0.017	0.103	Stomatal conductance	-0.001	0.004
	0.291	-0.125	Root volume	0.012	-0.005
	1.211	0.610	Root length	0.048	0.024
	0.188	-0.778	Leaf rolling	0.007	-0.031
Direct with Number of panicles hill^{-1}	0.495	0.098	Proline content	0.062	0.007
	19.78	12.41	Superoxide dismutase	2.485	0.828
	-1.384	1.217	Peroxidase	-0.174	0.081
	59.76	53.83	Catalase	7.509	3.593
	-0.119	-0.019	Plant height	-0.015	-0.001
	0.138	-0.177	Electrolyte Leakage	0.017	-0.012

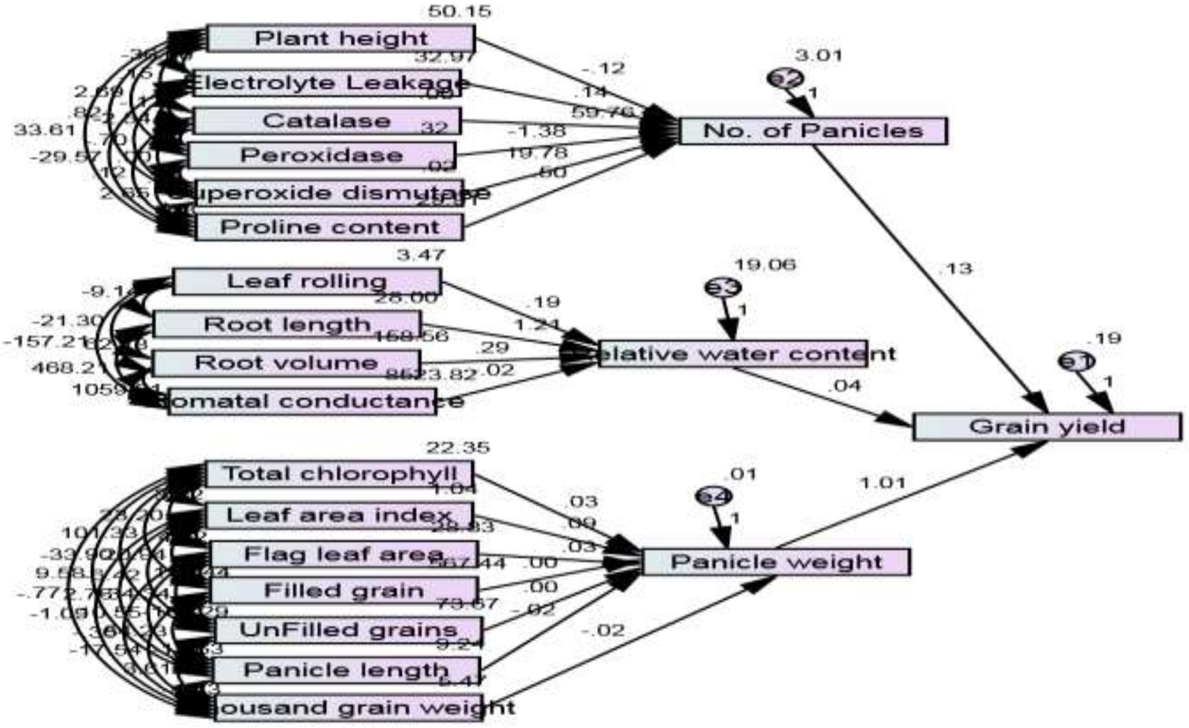


Figure 3. A path analysis diagram for grain yield under aerobic conditions in 2020. Chi-square = 744.32 and Degrees of freedom = 148.

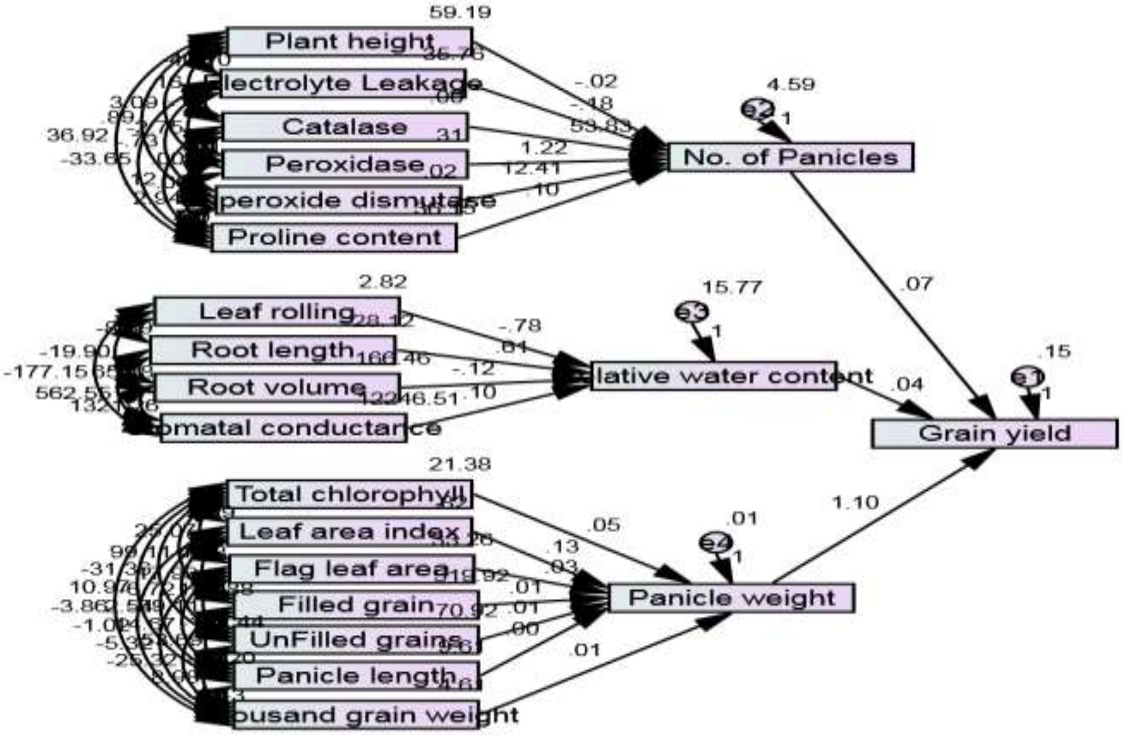


Figure 4. A path analysis diagram for grain yield under aerobic conditions in 2021. Chi-square = 782.281 and Degrees of freedom = 148.

grain yield (Kiani and Agahi, 2016; Bhutta *et al.,* 2019).

Cluster analysis

The phenotypic diversity analysis helped search for classifiers (Figures 5 and 6). The dendrogram presented genetic relationships among rice genotypes based on the results under aerobic conditions. Data showed that the rice genotypes grouped into two major clusters in the 2020 growing seasons. The first cluster divides into two sub-clusters. The first sub-cluster has three genotypes: Sakha103 and Sakha105 in the first group and Giza177 in the second group, with near similarity, meaning these three rice genotypes are closely genetically related and have the same behavior sensitivity under aerobic conditions. The second sub-cluster contains two groups—the first group has Egyptian Jasmine, and the second group has Sakha104, Sakha108, and GZ6296. These genotypes are considered moderately tolerant under aerobic conditions.

On the other hand, the second cluster divided the rest of the rice genotypes into two sub-clusters: the first sub-cluster includes Giza178 and IET1444, with the same similarity. The second sub-cluster includes more tolerant genotypes under aerobic conditions, i.e., Egyptian hybrid1, Giza179 in the same group, and the same similarity while listed in a separate group with the nearest likeness with Giza179 and EHR1. The results indicated the light differences between groups from growing seasons to others, with the same genotypes listed in the same cluster and sub-cluster. The current results showed that Egyptian hybrid1 GZ9399 and Giza179 could recommend for cultivation under aerobic conditions and in breeding programs as a donor to improve tolerance to drought under aerobic conditions. Venkata *et al.* (2019) also reported these findings. The clustering pattern showed significant genetic variability among the rice genotypes tested, indicating an excellent opportunity to improve by hybridizing genotypes from different clusters.

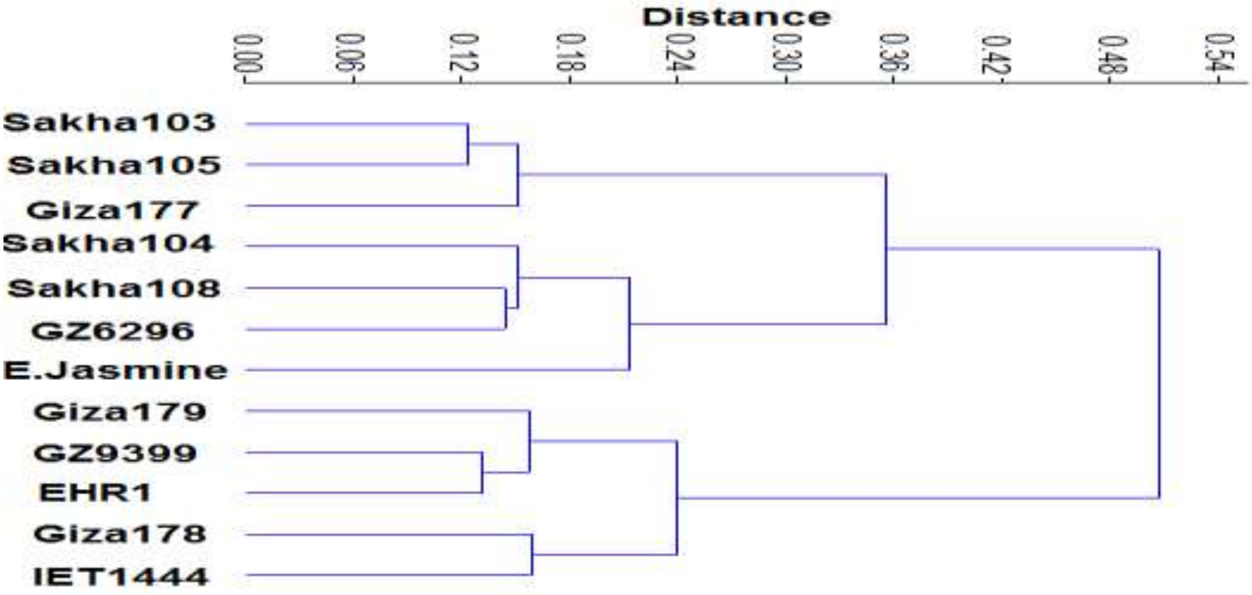


Figure 5. Dendrogram obtained by hierarchical cluster analysis using the mean performance of studied traits among rice genotypes in 2020.

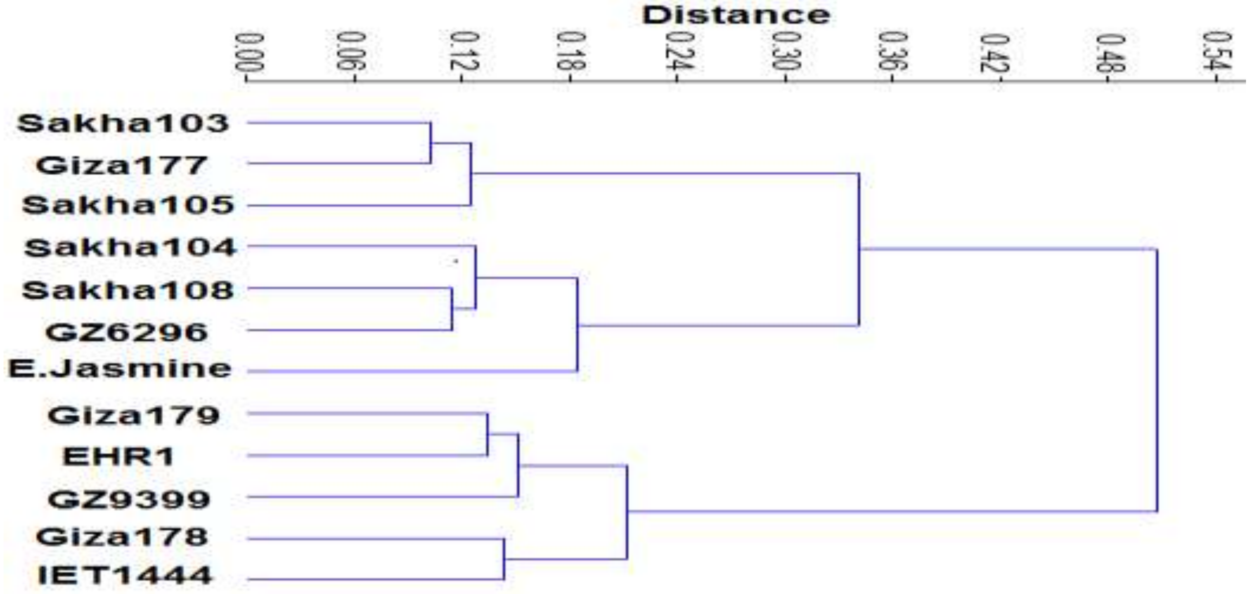


Figure 6. Dendrogram obtained by hierarchical cluster analysis using the mean performance of studied traits among rice genotypes in 2021.

CONCLUSIONS

Appropriate rice grain yields can result from the ability of the rice genotype to produce the superior growth and yield component traits alongside root and antioxidant traits under aerobic conditions. Most of the attributes governed by additive gene action had a relationship, indicating that user selection based on these traits may improve tolerance to aerobic cultivation. Significant differences were among studied genotypes, signifying a broad genetic diversity among its genotypes. Egyptian hybrid1 GZ9399 and Giza179 could recommend for cultivation under aerobic conditions and in breeding programs as a donor to improve tolerance to drought under aerobic conditions.

ACKNOWLEDGMENTS

The authors would like to express their deep appreciation to the Academy of Science Research and Technology, Egypt, for supporting this work during the initiative of rice improvement under climate changes and salinity stresses.

REFERENCES

Abdala AJ, Bokosi JM, Mwangwela AM, Mzengeza TR (2016). Correlation and path co-efficient analysis for grain quality traits in F_1 generation of rice (*Oryza sativa* L.). *J. Plant Breed. Crop Sci.* 8: 109-116.

Al-Waqa'a Al-Masryah (2020). Published an appendix to the Official Gazette in its 22nd issue (continued), the decision of Dr. Mohamed Abdel-Aty, Minister of Water Resources and Irrigation, No. 305 of 2020, dated 12/28/2020.

Amene TB (2017). Assessment of factors affecting the performance of agricultural cooperatives in the wheat market: The case of Gedeb Hasasa District, Ethiopia. *Afr. J. Bus. Manage.* 11: 393-414.

Badawi AT, Ghanem SA (2007). Integrated Water Management in Rice Fields. 4th INWEPF Steering Meeting and Symposium, Bangkok, Thailand.

Bates LS, Waldren RP, Teare ID (1973). Rapid determination of free proline for water stress studies. *Plant and Soil* 39: 205-207.

Beauchamp C, Fridovich I (1971). Superoxide dismutase: Improved assays and an assay applicable to acrylamide gels. *Anal. Biochem.* 44: 276-287.

Bergmeyer HU (1970). Methoden der enzymatischen, analyse (Berlin: Akademie Verlag). 1: 636-47.

Bhutta MA, Munir S, Qureshi MK, Shahzad AN, Aslam K, Manzoor H, Shabir G (2019). Correlation and path analysis of morphological parameters contributing to yield in rice (*Oryza sativa*) under drought stress. *Pak. J. Bot*. 51: 73-80.

Bradford MA (1976). A rapid and sensitive method for the quantitation of microgram quantities of protein utilizing the principle of protein-dye binding. *Anal. Biochem*. 72:248-254.

Chakrobarty T, Al-Galib MA, Islam MZ, Rahman MA (2021). Adoption and adaptability of modern Aman rice cultivars in Faridpur Region – Bangladesh. *SABRAO J. Breed. Genet.* 53(4): 659-672. https://doi.org/10.54910/sabrao2021.53.4.9.

Chunthaburee S, Dongsansuk A, Sanitchon J, Pattanagul W, Theerakulpisut P (2015). Physiological and biochemical parameters for evaluation and clustering of rice genotypes differing in salt tolerance at the seedling stage. *Saudi J. Biol. Sci.* 23: 467-477.

Dewey RD, Lu KH (1959). A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agron. J.* 51: 515-18.

Dilruba K, Siddique MN, Sarkar U, Hasnat MZ, Sultana J (2014). Phenotypic and genotypic correlation coefficient of quantitative traits and trait association of aromatic rice. *J. Biosci. Agric. Res.* 1: 34-46.

Doran JW, Parkin TB (1994). Defining and assessing soil quality. In 'Defining soil quality for a sustainable environment'. (Soil Science Society of America, Inc., Madison, WI). pp. 3-21.

Gour l, Maurya SB, Koutu GK, Singh SK, Shukla SS, Mishra DK (2017). Traitization of rice (*Oryza sativa* L.) genotypes using principal component analysis including scree plot & rotated component matrix. *Int. J. Chem. Stud.* 5: 975-983.

Hammer Q, Harper DAT, Ryan PD (2004). PAST: Paleontological statistics software package for education and data analysis. Palaeontol. Electron. 4.

Jat ML, Jat RK, Singh P, Jat SL, Sidhu HS, Jat HS, Bijarniya D, Parihar CM, Gupta R (2017). Predicting yield and stability analysis of wheat under different crop management systems across agro-ecosystems in India. *Am. J. Plant Sci.* 8: 1977-2012.

Johnson HW, Robinson HF, Comstock RE (1955). Genotypic and phenotypic correlations in soybeans and their implications in selection 1. *Agron. J.* 47: 477-483.

Kahani F, Hittalmani S (2016). Identification of F_2 and F_3 segregants of fifteen rice crosses suitable for cultivation under aerobic situation. *SABRAO J. Breed. Genet*. 48(2): 219-229.

Kahani F, Hittalmani S, Erfani R, Haradari C (2018). Heterotic effects and combining ability for yield traits in rice developed for semi-dry aerobic cultivation. *SABRAO J. Breed. Genet*. 50(1): 46-61.

Kiani S, Agahi K (2016). Correlation and path coefficient analysis of morphological traits affecting grain shape in rice genotypes (*Oryza Sativa* L.). *Agric. For.* 62: 227-237.

Konate AK, Zongo A, Kam H, Sanni A, Audebert A (2016). Genetic variability and correlation analysis of rice (*Oryza sativa* L.) inbred lines based on agro-morphological traits. *Afr. J. Agric. Res.* 11: 3340-3346.

Lal B, Nayak AK, Gautam P, Tripathi R, Singh T, Katara JL (2013). Aerobic rice: A water saving approach for rice production. *Pop. Kheti*. 1:1-4.

Lestari AP, Hairmansis A, Hermanasari R, Yullianida Y, Suwarno S (2019). Early yield testing and selection of upland rice on the observational study in Kebumen, Central Java. *Zuriat* 30: 1-5.

Maji AT, Shaibu AA (2012). Application of principal component analysis for rice germplasm traitization and evaluation. *J. Plant Breed. Crop Sci.* 4: 87-93.

Manjappa U, Shailaja GH (2014). Association analysis of drought and yield-related traits in F2 population of Moroberekan/IR64 rice cross under aerobic condition. *Int. J. Agric. Sci. Res.* 4: 79-88.

Morrison DE (1978). Multivariate Statistical Methods (2nd ed.) 4th Print, McGraw Hill Kogakusta Ltd.

Parthasarathi T, Vanitha K, Lakshamanakumar P, Kalaiyarasi D (2012). Aerobic rice-mitigating water stress for the future climate change. *Int. J. Agron. Plant Prod*. 3: 241-254.

Paul SK, Sarmah AK (1997). Interrelationship of yield and yield contributing traits in upland ahu rice. *J. Agric. Sci. Soc. North-East India* 10: 164-167.

Perera U, Ratnasekera D, Senanayake S, Abeysiriwardena DS (2014). Genetic parameters and correlations of yield attributing characteristics of weedy rice in Sri Lanka. *J. Natl. Sci. Found. Sri Lanka* 42: 299-306.

Sabri RS, Rafii MY, Ismail MR, Yusuff O, Chukwu SC, Hasan N (2020). Assessment of agro-morphologic performance, genetic parameters and clustering pattern of newly developed blast resistant rice lines tested in four environments. *Agron.* 1098: 1-17.

Sachesh S, Surya P, Bhattarai M, David J, Midmore (2020). Aerobic rice with or without strategic irrigation in the subtropics. *Agron.* 10: 1-23.

Saikia D, Deka SC (2011). Cereals: From staple food to nutraceuticals. *Int. Food Res. J.*18: 21-30.

Shashidhar HE, Adnan K, Mahmoud T, Raveendra GM, Pavan K, Vimarsha HS, Soman R, Kumar NG, Bekele BD, Bhavani P (2013). Breeding for drought resistance using whole plant architecture—conventional and molecular approach. in Plant Breeding from Laboratories to Fields.

Sivaranjani AKP, Pandey MK, Sudharshan I, Kumar GR, Madhav MS, Sundaram RM (2010). Assessment of genetic diversity among basmati and non-basmati aromatic rice of India using SSR markers. *Curr. Sci.* 99: 221-226.

Sivasubramanian S, Menon PM (1973). Genotypic and phenotypic variability in rice. *Madras Agric. J.* 60: 1093-1096.

Vanitha J, Amudha K, Mahendran R, Srinivasan J, Robin S, Usha Kumari R (2016). Genetic variability studies for zinc efficiency in aerobic rice. *SABRAO J. Breed. Genet*. 48(4): 425–433.

Venkata R, Reddy P, Vemireddy LR, Srividhya A, Reddy KH, Siddiq EA (2019). Genetic analysis of culm strength and its related traits in rice (*Oryza sativa* L.). *Appl. Biol. Res.*21: 166-175.

Wattoo JI, Khan AS, Ali Z, Babar M, Naeem M, Amanullah M, Hussain N (2010). Study of correlation among yield-related traits and path coefficient analysis in rice (*Oryza sativa* L.). *Afr. J. Biotechnol.* 9: 7853-7856.

Xie G, Jun Y, Huaqi W, Bouman BAM (2008). Progress and yield bottleneck of aerobic rice in the North China Plain: A case study of varieties Handao 297 and Handao 502. *Agric. Sci. China* 7: 641-646.

Zarbafi SS, Rabiei B, Ebadi AA, Ham JH (2019). Statistical analysis of phenotypic traits of rice (*Oryza sativa* L.) related to grain yield under neck blast disease. *J. Plant Dis. Prot.* 126: 293-306.

Zayed BA, Khedr RA, Hadifa AA, Okasha AM (2017). Some anti-oxidants, physio-morphological, and yield of varying rice varieties affected by salinity levels. *J. Plant Prod. Mans.Univ*.8: 747-754.

Zhang QF (2007). Strategies for developing green super rice. *Proc. Natl. Acad. Sci. U.S.A*.104:16402-16409.