BREEDING POTENTIAL OF RICE GENOTYPES IN TWO AGROCLIMATIC CONDITIONS OF SULAIMANI - KURDISTAN REGION - IRAQ

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ABSTRACT

This study was aimed to investigate the genetic variability of 26 rice genotypes and evaluation at two locations in Sulaimani governorate, Gaba and Chawtan which were completely different in their environmental condition during the season of 2019. The performances of the genotypes were analyzed at both locations as well as the average of both. Simple coefficients of correlation were used to assess the grain yield components and their relationships. Path analysis was used to determine the direct and indirect effects of such components on grain yield plant^{-1}. The genotypes were grouped based on the agro-morphological features using cluster analysis. Almost all of the traits at both locations and the average of both locations showed highly significant differences; Chawtan outperformed Gaba location for the traits no. of tillers plant^{-1}, no. of panicle plant^{-1}, 1000-grain weight, and plant^{-1} grain yield, whereas higher values were found for plant height and no. of grains panicle^{-1} for Gaba location. At both locations, there was a highly significant and positive association between the number of tillers and panicles in plant^{-1} and grain yield plant^{-1}. The number of panicle plants^{-1} had the most favorable direct effects on grain yield at both locations. At both locations, the highest positive indirect effect on grain output was provided by the number of tillers plant^{-1} *via* the number of panicle plant^{-1}. Based on the agro-morphological features, the rice genotypes were grouped into 5 clusters at both locations. At both locations, Cluster V gave better values regarding grain yield.

Keywords: Rice genotypes, genetic diversity, association analysis, path analysis, cluster analysis.

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إمكانية التربية لتراكيب وراثية من الرز في بيئتين زراعيتين في السليمانية – إقليم كوردستان – العراق

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المستخلص

تهدف هذه الدراسة الى تقييم التباين الوراثي لـ 26 نوعاً وراثياً من الرز في موقعين مختلفين في محافظة السليمانية، هما موقعي كةبة وجوتان اللذان يختلفان كلياً من حيث الظروف المناخية خلال موسم النمو للعام 2019. تم إجراء تحليل لأداء الأنماط الجينية في كلا الموقعين وكذلك متوسط الموقعين. وأيضاً تم تحليل مكونات حاصل الحبوب وعلاقاتها المتبادلة باستخدام معاملات الارتباط البسيطة. كما تم تقدير التأثيرات المباشرة وغير المباشرة لهذه الصفات على حاصل الحبوب النبات$^{-1}$ باستخدام تحليل المسار. وتم إجراء تحليل الكتلة من أجل تجميع الأنماط الجينية إعتماداً على الصفات الزراعية المظهرية. تقريباً تم تسجيل فروقات معنوية جداً لجميع الصفات في كلا الموقعين ومتوسط كلا الموقعين؛ تجاوز موقع جوتان موقع كةبة للصفات عدد الأشطاء نبات$^{-1}$، عدد الداليات نبات$^{-1}$، وزن 1000 حبة، حاصل الحبوب نبات$^{-1}$ ، بينما سُجلت قيم أعلى لطول النبات و عدد الحبوب دالية$^{-1}$ في وقع كةبة. عدد الأشطاء نبات$^{-1}$، عدد الداليات نبات$^{-1}$ سجلت علاقة ارتباط موجبة ومعنوية جداً مع حاصل الحبوب نبات$^{-1}$ في كلا الموقعين. و في كلا الموقعين أيضاً، عدد الداليات نبات$^{-1}$ سجلت أعلى تأثير إيجابي ومباشر على حاصل الحبوب. عدد الأشطاء نبات$^{-1}$ عبر عدد الداليات نبات$^{-1}$ قد أعطت أعلى تأثير إيجابي غير مباشر على حاصل الحبوب في كلا الموقعين. تم تجميع الأنماط الجينية للرز في 5 مجموعات في كلا الموقعين بناءً على الصفات الزراعية المظهرية. في كلا الموقعين، أعطت المجموعة V قيم أفضل فيما يتعلق بحاصل الحبوب.

الكلمات المفتاحية: الأنماط الجينية للأرز، التنوع الجيني، تحليل الارتباط، تحليل المسار، تحليل الكتلة.

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INTRODUCTION

The development of rice genotypes with greater production potential is the goal of Iraqi breeders of the *Oryza sativa* L. plant. Numerous varieties of rice have been developed and adapted because to the country's different agro-ecosystems (28). The average production per unit area in Iraq is too low comparing the other countries due to the decreasing in soil fertility as results of cultivating of wheat after the rice and also due to the high water consumption during the growing season which is not available in all of the cultivation area especially in summer (2,11,12). Increasing yield per unit area is one method for increasing rice production; another is to cultivate additional land. To increase grain production, the genetic improvement of rice must be strengthened. In order to create an effective selection method, it was essential to comprehend the relationship between yield and the characteristics that contribute to it. Multivariate analysis is one of the approaches that is most commonly used to assess genetic variability by breeders when determining improved rice varieties. For high production levels to be sustained, genetic diversity is essential (28). The most important decision a plant breeder makes is which parents to use in a hybridization strategy. Utilizing genetic divergence to choose parents for an effective hybridization and breeding program makes sense (29). According to (24), identifying the elements crucial for population-level genetic diversity may help in the selection of diverse parents for hybridization programs. In order to identify and measure diversity in a variety of rice using agro-morphological traits, several researchers have used multivariate analysis (16, 21). A plant breeder must have a thorough awareness of the phenotypic and genotypic interactions of multiple economic aspects in order to choose and breed different varieties and lines of rice with increased yield potential (3, 18). The strength and direction of the relationship between yield and its component traits are revealed through correlation analysis of yield and those traits. Twenty different varieties of rice were examined by Yong-xiang *et al.* (31) using 9 different traits. It was discovered that rice grain yield plant^{-1} and the number of grain panicles^{-1} were positively connected. Sabesan *et al.* (22) investigated 54 rice varieties and found that plant height and the number of plant^{-1} tillers were positively correlated with grain yield plant^{-1}. According to Hairmansis *et al.* (8), plant height had a negative effect on grain yield plant^{-1}, while 1000-grain weight had less of an effect (8). Florence *et al.* (7) examined 32 genotypes originating from various geographical areas. 32 genotypes were grouped into four groups *via* cluster analysis. 75 genotypes were examined by Pervaiz *et al.* (17). Using cluster analysis, 75 genotypes were divided into four main groups that distinguished between tall, late-maturing, thin aromatic types, and early non-aromatic genotypes. It is challenging to study rice genotypes in the Iraqi Kurdistan region due to a lack of available information and previous research on rice production in the area. Currently, rice yields at the Kurdistan region are low and not profitable due to a lack of improved varieties, poor agronomic practices, and the presence of pests and diseases. Improving rice productivity in Iraq, which is distinguished by extremely different agro-climates and various growing conditions, depends significantly on the presence of genetic diversity. The objectives of this study were to determine the degree of diversity and identify potential genotypes for rice hybridization based on agro-morphological traits and also to identify rice genotypes that have both high mean grain yield and stable yield performance across different environments for the region. Additionally, determine the degree of association of the yield and the other traits in each environment through the correlation analysis and partitioning of the correlation coefficient to determine direct and indirect effects through alternate pathways of various traits and grain yield through path analysis. Another goal of the current investigation is to group the genotypes into distinct clusters to use in further study.

MATERIALS AND METHOD

Plant Materials

Twenty-six different rice genotypes were collected throughout Iraq for this study, these genotypes were named according to the region from which they were originally sourced as well as the local name (Table 1).

Table 1. The description and details of the studied genotypes

Genotypes	Locations	Local Names
G_1	Belula	Nagaza
G_2	Hawasan	Nagaza
G_3	Psakan	Nagaza
G_4	Bani Khelan	Nagaza
G_5	Gulah Jaw	Sarda
G_6	Qarabolakh	Sarda
G_7	Ban Snwq	Sarda
G_8	Setapan	Sarda
G_9	Kokz	Sarda
G_{10}	Garmk	Sarda
G_{11}	Qzilja	Sarda
G_{12}	Mughagh	Sarda
G_{13}	Kalabash	Sarda
G_{14}	Chalagh	Sarda
G_{15}	Klbashi	Sarda
G_{16}	Tapa Tolaka	Sarda
G_{17}	Grdi Go	Sarda
G_{18}	Bjeel	Shashmay
G_{19}	Surchi Qalat	Shashmay
G_{20}	Nwava	Sadry
G_{21}	Surchi Qalat	Ambar
G_{22}	Grd Bdaw	Shashmay
G_{23}	Al-Mishkhab Najaf	Ambar-Muaazra
G_{24}	Grdi Tle	Shashmay
G_{25}	Qarany Agha	Shashmay
G_{26}	Kfradol	Garma

Experimental sites

The study was conducted at two locations in Sulaimani governorate, Gaba Village / Peramagroon Township (Lat. 35^{o} 71' 94"; N, Long. 45^{o} 07' 60"; E, 937 MASL, 30 Km Northwest of Sulaimani city) in a clay soil and Chawtan Village / Penjwen Township (Lat. 35^{o} 49' 92"; N, Long. 45^{o} 89' 35"; E, 870 MASL, 45 Km East of Sulaimani city) in a silty-clay soil during the growing season of 2019. The climatic data during the experimental periods are given in Table 2 and the water analyses are given in Table 3.

Experimental design

Twenty-six rice cultivars were planted in the second week of May 2019 at Gaba location and in the third week of May 2019 at Chawtan location. At both locations, Rice was planted at a spacing of 20 cm. The area of the plot was 6 m^2. The fertilizers at a rate of 100; 40; 40 of N; P; K [nitrogen (N), phosphorus (P), and potassium (K)] Kg ha^{-1} were applied *via* NPK Fertilizer 18; 18; 18. As a base dose, the full dosages of phosphorus and potassium, as well as half of the dose of N, were utilized, and the remaining 50% nitrogenous fertilizer was divided into two halves. The first was applied during the tillering stage, and the second was during the booting step. Other cultural operations were accomplished according to the normal field practices.

Studied data

At maturity, five plants $plot^{-1}$ were sampled randomly for recording the agronomic characters, plant height (cm), number of tillers $plant^{-1}$, number of panicles $plant^{-1}$, number of grains $panicle^{-1}$, panicle length (cm), grain length (mm), grain width (mm), 1000-grain weight (g), and grain yield $plant^{-1}$ (g).

Table 2. The meteorological data during the growing season 2019 at Gaba and Chawtan locations

Months	Gaba Location				Chawtan Location			
	Air temp. (^{o}C)			Prec.	Air temp. (^{o}C)			Prec.
	Avg.	Max.	Min.	Depth (mm)	Avg.	Max.	Min.	Depth (mm)
January	4.2	9.0	0.0	147.8	1.9	3.6	0.2	172.5
February	5.7	8.0	4.0	114.4	2.7	4.9	0.6	127.5
March	7.2	11.0	4.0	183.4	4.4	6.6	2.2	214.5
April	10.6	14.0	7.0	141.6	9.6	11.0	10.5	139.0
May	18.9	27.0	11.0	19.8	14.9	18.6	11.2	51.5
June	25.6	30.0	23.0	0.0	26.3	28.2	24.6	0.0
July	26.3	21.0	24.0	0.0	28.0	33.1	23.0	0.0
August	28.4	33.0	24.0	0.0	27.24	32.1	22.4	0.0
September	23.7	28.0	19.0	0.0	24.0	26.7	21.3	0.0
October	19.1	24.0	12.0	57.6	16.7	19.9	13.6	68.5
November	11.4	16.0	7.0	24.4	6.3	9.0	3.7	29.0
December	7.9	11.0	6.0	67.6	1.5	2.7	0.3	240.0
Total				756.6				1042.5

Table 3. Water Analysis at Gaba and Chawtan locations

Parameter	Gaba Location	Chawtan Location
Total Hardness	304.8	207.2
Ca^{+2} ppm in 1000 ml	99.39	72.78
Mg^{+2} ppm in 1000 ml	13.80	6.22
pH	7.39	7.43

Statistical analysis

The data were statistically analyzed according to the methods of analysis of variance as a general test using Randomized Complete Block Design (RCBD) with three replicates; a combined analysis of variance across locations was also conducted for the studied characters. All possible comparisons among the means were carried out by using the Least Significant Difference (L.S.D) test at significant levels of 0.05 and 0.01.

The correlation coefficients were calculated to determine the degree of association of characters with yield and also among the yield components themselves in each environment. Phenotypic correlations were computed by using the formula given by (24).

The path coefficient analysis was carried out through the solution of the following equations as suggested by (24) through Analysis of Moment Structures (AMOS) Ver. 18 Software. The hierarchical cluster analysis based on Euclidean Distance and Unweighted Pair-group Linkage (UPGMA) was also performed to cluster the rice genotype's relatedness based on agro-morphological traits using the IBM SPSS program, Ver. 19 (26).

RESULTS AND DISCUSSION

Performance of the genotypes: Highly significant differences were detected among the genotypes for all of the studied traits at Gaba and Chawtan locations, according to the mean squares of the variance analysis which indicates the presence of huge differences among the studied genotypes (Table 4). This demonstrates the genotypes' significant potential for utilization as a genetic source for breeding reasons (14). The mean squares of the combined analysis of the variances were presented in Table 5, which indicated the presence of highly significant mean squares due to the locations for the traits plant height, no. of tillers plant^{-1}, no. of panicles plant^{-1}, no. of grains panicle^{-1}, 1000-grain weight, and grain yield plant^{-1}, while the mean squares due to the genotypes were highly significant for all of the studied traits. Concerning the (Genotypes×Environments) interaction they were indicated to be highly significant for all of the traits except for grain width which was significant only. These findings emphasize the importance of the genotypes, the environment, and the interaction effect of Genotypes×Environments. The interaction effects have significant impacts and cannot be ignored when studying rice growth in multi-locations experiments.

Table 4. Mean squares of the variance analysis of the studied traits across locations

S.O.V	d.f	Plant height (cm)	No. of tillers plant^{-1}	No. of panicles plant^{-1}	No. of grains panicle^{-1}	Panicle length (cm)	Grain length (mm)	Grain width (mm)	1000-grain weight (g)	Grain yield plant^{-1} (g)
Gaba Location										
Replicates	2	3.962	0.051	0.090	306.515	3.500	0.481	0.052	0.00005	46.654
Genotypes	25	121.482 **	15.172 **	11.412 **	18291.209 **	12.726 **	1.622 **	0.257 **	20.090 **	31658.132 **
Exp. Error	50	4.540	0.267	0.227	655.644	3.058	0.370	0.019	0.001	20.065
Chawtan Location										
Replicates	2	3.500	2.577	1.885	45.521	1.705	0.080	0.317	0.00046	228.167
Genotypes	25	657.360 **	71.282 **	65.200 **	4134.782 **	15.795 **	1.651 **	0.310 **	13.35065 **	315423.399 **
Exp. Error	50	5.635	2.773	2.235	79.535	2.934	0.097	0.119	0.00041	120.917

Table 5. Mean squares of the Combined Analysis of Variance of the studied traits

S.O.V	d.f	Plant height (cm)	No. of tillers plant^{-1}	No. of panicles plant^{-1}	No. of grains panicle^{-1}	Panicle length (cm)	Grain length (mm)	Grain width (mm)	1000-grain weight (g)	Grain yield plant^{-1} (g)
Locations	1	10716.981 **	2700.006 **	2633.853 **	712981.736 **	0.410 n.s	0.535 n.s	0.004 n.s	1.107 **	3583581.641 **
Error (a)	4	3.731	1.314	0.987	176.018	2.603	0.281	0.184	0.0003	137.410
Genotypes	25	389.661 **	37.061 **	32.666 **	13372.464 **	22.137 **	2.470 **	0.442 **	29.393 **	163675.224 **
Genotypes × Location	25	389.181 **	49.393 **	43.946 **	9053.528 **	6.384 **	0.803 **	0.124 *	4.048 **	183406.308 **
Error (b)	100	5.291	1.581	1.281	382.293	3.116	0.243	0.072	0.001	73.310

The mean performance of the genotypes at Gaba location was presented in Table 6, indicating that the mean values for plant height, no. of tillers plant^{-1}, no. of panicles plant^{-1}, no. of grains panicle^{-1}, panicle length, grain length, grain width, 1000-grain weight, grain yield plant^{-1} ranged from 97.000 to 120.000 cm, 3.000 to 11.000, 2.667 to 10.333, 102.778 to 391.333, 14.000 to 23.333 cm, 5.727 to 9.377 mm, 2.470 to 3.633 mm, 18.434 to 28.332 g and 53.000 to 471.667 g respectively. G$_{17}$ showed the highest value for plant height with 120.000 cm, while G$_{21}$ recorded the maximum values for no. of tillers plant^{-1}, no. of panicles plant^{-1}, grain length, grain yield plant^{-1} with 11.000, 10.333, 9.377 mm, and 471.667 g respectively. G$_{16}$ showed the maximum value for no. of grains plant^{-1} reached 391.333 grains, while G$_{3}$ and G$_{6}$ with 3.663 mm were superior to the other genotypes in grain width. The highest value for 1000-grain weight was 28.332 g recorded by G$_{4}$. The data disclosed an enormous extent of improvement in rice grain yield in the Kurdistan region.

Table 6. Performance of the genotypes at Gaba location

Genotypes	Plant height (cm)	No. of tillers plant^{-1}	No. of panicles plant^{-1}	No. of grains panicle^{-1}	Panicle length (cm)	Grain length (mm)	Grain width (mm)	1000-grain weight (g)	Grain yield plant^{-1} (g)
G$_{1}$	110.000	6.667	6.333	163.532	16.000	7.713	3.217	23.689	165.000
G$_{2}$	115.000	4.333	4.000	157.500	15.667	7.437	3.183	25.962	71.000
G$_{3}$	112.000	3.333	3.000	190.000	20.000	7.637	3.663	27.726	49.000
G$_{4}$	110.000	5.333	5.333	116.111	20.000	7.377	3.447	28.332	91.333
G$_{5}$	107.000	3.333	3.000	233.333	17.333	7.380	3.263	24.532	53.333
G$_{6}$	112.000	3.667	3.333	222.778	15.000	7.637	3.633	25.333	57.333
G$_{7}$	103.000	4.333	4.000	330.000	17.667	7.157	3.523	26.150	144.333
G$_{8}$	113.000	4.667	4.333	222.500	19.000	7.680	3.503	24.500	103.667
G$_{9}$	100.000	6.667	6.333	102.778	20.667	5.727	3.517	27.794	113.000
G$_{10}$	100.000	3.333	3.000	335.333	17.667	7.063	3.157	23.286	75.667
G$_{11}$	98.000	4.333	4.000	278.000	20.000	7.573	3.317	24.892	114.000
G$_{12}$	98.000	4.000	3.667	183.333	18.333	7.243	3.277	23.804	60.000
G$_{13}$	103.000	3.000	2.667	310.556	16.333	7.027	3.250	22.842	53.000
G$_{14}$	103.000	3.667	3.333	297.194	18.333	6.913	3.053	22.004	80.333
G$_{15}$	97.000	4.333	4.000	286.750	18.000	6.527	3.177	20.686	101.333
G$_{16}$	108.000	3.333	3.000	391.333	17.333	6.653	3.230	22.820	65.000
G$_{17}$	120.000	3.667	3.333	340.056	20.333	7.110	3.270	23.658	100.667
G$_{18}$	107.000	4.667	4.333	153.833	17.000	6.867	3.153	20.602	62.667
G$_{19}$	97.000	6.000	5.667	129.244	19.667	7.057	3.023	19.656	97.667
G$_{20}$	105.000	9.000	8.333	141.991	18.000	9.013	2.863	21.460	229.333
G$_{21}$	100.000	11.000	10.333	214.012	19.000	9.377	2.470	19.474	471.667
G$_{22}$	106.000	11.000	8.000	214.444	19.333	7.013	3.187	23.594	335.333
G$_{23}$	103.000	3.000	3.000	297.333	23.333	8.500	2.510	18.434	59.000
G$_{24}$	98.000	6.667	6.333	270.786	18.667	7.707	3.597	24.192	286.667
G$_{25}$	105.000	6.333	6.000	230.667	15.333	7.427	3.323	25.533	225.000
G$_{26}$	115.000	6.000	5.667	294.578	14.000	7.163	3.383	25.320	189.667
LSD $_{(p\leq0.05)}$	3.494	0.848	0.782	41.993	2.868	0.997	0.228	0.039	7.346
LSD $_{(p\leq0.01)}$	4.659	1.130	1.042	55.984	3.823	1.330	0.304	0.052	9.794

Table 7 shows the mean performance of the genotypes at Chawtan location, indicating that the mean values for plant height, no. of tillers plant^{-1}, no. of panicles plant^{-1}, no. of grains panicle^{-1}, panicle length, grain length, grain width, 1000-grain weight, grain yield plant^{-1} ranged from 52.000 to 106.000 cm, 5.667 to 25.000, 5.000 to 24.000, 35.414 to 219.625, 14.000 to 23.333 cm, 5.170 to 8.813 mm, 2.433 to 3.663 mm, 19.342 to 28.118 g and 48.667 to 1357.333 g respectively. G_{10} gave the highest values for plant height, no. of tillers plant^{-1}, and no. of panicles plant^{-1} reached 106.000 cm, 25.000 tillers, and 24.000 panicles respectively. G_{24} with 219.625 grains recorded the highest value for no. of grains panicle^{-1}, G_{23} gave the maximum panicle length with 23.333 cm, G_{21} with 8.813 mm gave the maximum value for grain length and it is closely followed by G_{23} with 8.700 mm. G_{20} recorded the maximum grain width of 3.663 mm. G_6 recorded the maximum 1000-grain weight with 28.118 g and G_{12} was superior to the other genotype concerning the grain yield plant^{-1} with 1357.333 g.

Table 7. Performance of the genotypes at Chawtan location

Genotypes	Plant height (cm)	No. of tillers plant^{-1}	No. of panicles plant^{-1}	No. of grains panicle^{-1}	Panicle length (cm)	Grain length (mm)	Grain width (mm)	1000-grain weight (g)	Grain yield plant^{-1} (g)
G_1	**82.000**	**5.667**	**5.000**	**60.800**	**15.333**	**7.600**	**3.313**	**23.884**	**48.667**
G_2	**81.000**	**8.333**	**7.000**	**99.000**	**14.000**	**7.490**	**3.653**	**24.984**	**120.333**
G_3	**84.000**	**8.667**	**8.333**	**105.194**	**19.000**	**7.313**	**3.490**	**25.680**	**186.667**
G_4	**91.000**	**15.667**	**15.333**	**81.030**	**19.000**	**7.403**	**3.350**	**26.235**	**616.667**
G_5	**89.000**	**14.667**	**13.000**	**125.184**	**19.667**	**6.893**	**3.550**	**25.018**	**544.333**
G_6	**102.000**	**14.667**	**14.333**	**117.262**	**17.667**	**6.800**	**3.310**	**28.118**	**630.667**
G_7	**99.000**	**11.000**	**10.333**	**98.726**	**19.667**	**7.090**	**3.610**	**27.446**	**286.667**
G_8	**99.000**	**12.333**	**11.000**	**99.545**	**22.667**	**6.917**	**3.317**	**24.886**	**306.000**
G_9	**85.000**	**12.667**	**12.667**	**68.739**	**19.667**	**7.060**	**3.337**	**22.872**	**293.333**
G_{10}	**106.000**	**25.000**	**24.000**	**100.490**	**18.667**	**7.029**	**3.053**	**23.204**	**1340.000**
G_{11}	**97.000**	**23.667**	**20.667**	**64.000**	**15.000**	**7.310**	**3.033**	**26.774**	**815.333**
G_{12}	**97.000**	**22.667**	**21.333**	**115.994**	**22.333**	**6.657**	**3.270**	**23.954**	**1357.333**
G_{13}	**73.000**	**7.667**	**10.667**	**91.591**	**16.667**	**6.520**	**3.297**	**23.056**	**178.000**
G_{14}	**79.000**	**14.333**	**13.667**	**123.307**	**18.667**	**7.020**	**3.407**	**22.832**	**554.667**
G_{15}	**99.000**	**16.333**	**15.667**	**56.186**	**17.333**	**7.133**	**3.287**	**23.124**	**324.000**
G_{16}	**103.000**	**11.333**	**9.667**	**96.230**	**16.667**	**7.000**	**3.267**	**23.800**	**235.333**
G_{17}	**99.000**	**10.333**	**9.667**	**152.426**	**18.333**	**6.770**	**3.290**	**23.204**	**354.333**
G_{18}	**99.000**	**10.667**	**9.667**	**96.859**	**18.000**	**7.517**	**3.340**	**23.036**	**216.667**
G_{19}	**100.000**	**11.667**	**11.333**	**68.763**	**16.333**	**8.300**	**2.433**	**20.933**	**265.667**
G_{20}	**52.000**	**11.667**	**10.667**	**62.470**	**17.000**	**8.540**	**3.663**	**22.686**	**156.667**
G_{21}	**55.000**	**11.333**	**11.000**	**140.455**	**19.667**	**8.813**	**2.523**	**19.372**	**370.667**
G_{22}	**97.000**	**15.667**	**15.000**	**104.113**	**20.000**	**7.233**	**3.233**	**23.667**	**605.000**
G_{23}	**63.000**	**20.000**	**19.667**	**35.414**	**23.333**	**8.700**	**2.517**	**19.342**	**285.000**
G_{24}	**103.000**	**8.667**	**8.000**	**219.625**	**17.333**	**5.170**	**3.073**	**22.733**	**345.000**
G_{25}	**97.000**	**13.667**	**17.667**	**80.031**	**16.000**	**7.467**	**3.427**	**24.467**	**501.333**
G_{26}	**83.000**	**13.667**	**12.667**	**129.098**	**16.667**	**7.185**	**3.395**	**25.349**	**398.000**
LSD $_{(p\leq0.05)}$	**3.893**	**2.731**	**2.452**	**14.626**	**2.809**	**0.511**	**0.566**	**0.033**	**18.034**
LSD $_{(p\leq0.01)}$	**5.190**	**3.641**	**3.269**	**19.499**	**3.745**	**0.681**	**0.755**	**0.044**	**24.042**

As the average for both locations, the performances of the genotypes were illustrated in Table 8. Genotype 17 produced the maximum values for plant height and no. of grains panicle^{-1} reached 109.500 cm and 246.241 grains respectively, whilst G_{10} gave the highest values for no. of tillers plant^{-1} and no. of panicles plant^{-1} with 14.167 and 13.500 respectively. The highest values for panicle length and grain length were 23.333 mm and 9.095 mm recorded by G_{23} and G_{21} respectively. G_7 gave the maximum values for grain width and 1000-grain weight reached 3.567 mm and 26.798 g respectively. The highest value for grain yield plant^{-1} was 708.667 shown by G_{12}.

Table 8. Performance of the genotypes at the average of both locations

Genotypes	Plant height (cm)	No. of tillers plant^{-1}	No. of panicles plant^{-1}	No. of grains panicle^{-1}	Panicle length (cm)	Grain length (mm)	Grain width (mm)	1000-grain weight (g)	Grain yield plant^{-1} (g)
G_1	96.000	6.167	5.667	112.166	15.667	7.657	3.265	23.787	106.833
G_2	98.000	6.333	5.500	128.250	14.833	7.463	3.418	25.473	95.667
G_3	98.000	6.000	5.667	147.597	19.500	7.475	3.577	26.703	117.833
G_4	100.500	10.500	10.333	98.570	19.500	7.390	3.398	27.284	354.000
G_5	98.000	9.000	8.000	179.259	18.500	7.137	3.407	24.775	298.833
G_6	107.000	9.167	8.833	170.020	16.333	7.218	3.472	26.726	344.000
G_7	101.000	7.667	7.167	214.363	18.667	7.123	3.567	26.798	215.500
G_8	106.000	8.500	7.667	161.023	20.833	7.298	3.410	24.693	204.833
G_9	92.500	9.667	9.500	85.759	20.167	6.393	3.427	25.333	203.167
G_{10}	103.000	14.167	13.500	217.911	18.167	7.046	3.105	23.245	707.833
G_{11}	97.500	14.000	12.333	171.000	17.500	7.442	3.175	25.833	464.667
G_{12}	97.500	13.333	12.500	149.664	20.333	6.950	3.273	23.879	708.667
G_{13}	88.000	5.333	6.667	201.073	16.500	6.773	3.273	22.949	115.500
G_{14}	91.000	9.000	8.500	210.251	18.500	6.967	3.230	22.418	317.500
G_{15}	98.000	10.333	9.833	171.468	17.667	6.830	3.232	21.905	212.667
G_{16}	105.500	7.333	6.333	243.781	17.000	6.827	3.249	23.310	150.167
G_{17}	109.500	7.000	6.500	246.241	19.333	6.940	3.280	23.431	227.500
G_{18}	103.000	7.667	7.000	125.346	17.500	7.192	3.247	21.819	139.667
G_{19}	98.500	8.833	8.500	99.004	18.000	7.678	2.728	20.295	181.667
G_{20}	78.500	10.333	9.500	102.230	17.500	8.777	3.263	22.073	193.000
G_{21}	77.500	11.167	10.667	177.233	19.333	9.095	2.497	19.423	421.167
G_{22}	101.500	13.333	11.500	159.278	19.667	7.123	3.210	23.631	470.167
G_{23}	83.000	11.500	11.333	166.374	23.333	8.600	2.513	18.888	172.000
G_{24}	100.500	7.667	7.167	245.205	18.000	6.438	3.335	23.463	315.833
G_{25}	101.000	10.000	11.833	155.349	15.667	7.447	3.375	25.000	363.167
G_{26}	99.000	9.833	9.167	211.838	15.333	7.174	3.389	25.335	293.833
LSD $_{(p\leq0.05)}$	10.351	3.814	3.580	52.569	2.218	0.681	0.328	1.028	219.019
LSD $_{(p\leq0.01)}$	13.681	5.041	4.731	69.478	2.932	0.900	0.434	1.359	289.469

The effect of locations on the studied traits were presented in Table 9, and it was revealed that Gaba location exceeded Chawtan location in plant height and no. of grains plant^{-1} by 18.626% and 135.89% respectively, whilst Chawtan location predominated Gaba location in the traits no. of tillers plant^{-1}, no. of panicles plant^{-1}, 1000-grain weight, and grain yield plant^{-1} by 159.44, 171.85, 0.70, and 228.11% respectively.

Table 9. Effect of locations on the studied traits

Locations	Plant height (cm)	No. of tillers plant^{-1}	No. of panicles plant^{-1}	No. of grains panicle^{-1}	Panicle length (cm)	Grain length (mm)	Grain width (mm)	1000-grain weight (g)	Grain yield plant^{-1} (g)
Gaba	105.577	5.218	4.782	234.922	18.154	7.384	3.238	23.703	132.885
Chawtan	89.000	13.538	13.000	99.713	18.256	7.267	3.248	23.871	436.013
LSD $_{(p\leq0.05)}$	0.859	0.510	0.442	5.898	n.s	n.s	n.s	0.007	13.394
LSD $_{(p\leq0.01)}$	1.424	0.845	0.733	9.781	n.s	n.s	n.s	0.012	17.703

Correlation analysis

The correlation analysis among the studied traits at Gaba location was presented in Table (10). No. of tillers plant^{-1} recorded highly significant and positive correlations with no. of panicles plant^{-1} and grain yield plant^{-1} with (0.977**) and (0.903**) respectively, whilst it correlated significant and negatively (-0.414*) with no. of grains panicle^{-1}. A highly significant and positive correlation was detected between no. of panicles plant^{-1} and grain yield plant^{-1} (0.897**), while it correlated significantly and negatively with no. of grains plant^{-1} (-0.458*), but correlated significantly and positively with grain length (0.432*). A significant and positive association was detected between grain length and grain yield plant^{-1} (0.486*) and the association between grain width with 1000-grain weight was highly significant and positive (0.820**). Concerning the grain yield plant^{-1}, as noticed in the results selection genotypes with high values due to the traits no. of tillers plant^{-1}, no. of panicles plant^{-1} and grain length have a great impact on increasing the grain yield plant^{-1} in rice genotypes at Gaba location. Madhavilatha *et al.* (13) reported that no. of grains panicle^{-1} and 1000-grain weights were positively associated with grain yield plant^{-1}. Khan *et al.* (10) found correlation of plant height and no. of tillers plant^{-1} was positive. Grain yield plant^{-1} had positive correlation with no. of grains panicle^{-1}. Sabesan *et al.* (22) observed that grain yield plant^{-1} was positively associated with plant height. Hairmansis *et al.* (8) reported that plant height had negative effect on grain yield plant^{-1} while 1000-grain weight had negligible effect on grain yield.

Table 10. Correlation coefficient analysis at Gaba location

Traits	Plant height (cm)	No. of tillers plant^{-1}	No. of panicles plant^{-1}	No. of grains panicle^{-1}	Panicle length (cm)	Grain length (mm)	Grain width (mm)	1000-grain weight (g)
Plant height (cm)	1.000							
No. of tillers plant^{-1}	-0.160	1.000						
No. of panicles plant^{-1}	-0.180	0.977**	1.000					
No. of grains panicle^{-1}	0.012	-0.414*	-0.458*	1.000				
Panicle length (cm)	-0.281	0.024	0.018	-0.076	1.000			
Grain length (mm)	0.041	0.371	0.432*	-0.104	0.107	1.000		
Grain width (mm)	0.278	-0.306	-0.329	-0.030	-0.280	-0.524	1.000	
1000-grain weight (g)	0.382	-0.142	-0.146	-0.189	-0.193	-0.337	0.820**	1.000
Grain yield plant^{-1} (g)	-0.187	0.903**	0.897**	-0.091	-0.015	0.486*	-0.321	-0.183

*** .Correlation is significant at the 0.05 level (2-tailed), $t_{0.05}(24)=2.064$**

****. Correlation is significant at the 0.01 level (2-tailed), $t_{0.01}(24)=2.797$**

Table 11 shows the correlation analysis among the studied traits at Chawtan location. Plant height recorded a highly significant and negative correlation with grain length (-0.617**), whilst showing a significant and positive correlation with 1000-grain weight (0.467*). The association between no. of tillers plant^{-1} and no. of panicles plant^{-1} as well as grain yield plant^{-1} were positive and highly significant with (0.961**) and (0.844**) respectively. No. of panicles plant^{-1} recorded highly significant and positive correlation with grain yield plant^{-1} reached (0.828**). The correlation between no. of grains panicle^{-1} and grain length was highly significant and negative (-0.616**). Grain length recorded a significant and positive correlation with 1000-grain weight (-0.429*). The correlation between grain width and 1000-grain weight was highly significant and positive (0.660**). Breeding rice genotypes have high values for the traits no. of tillers plant^{-1}, and no. of panicles plant^{-1} resulting in an increase in the weight of grain produced by the plant at Chawtan location. Rashid *et al.* (20) found that plant height showed significant positive correlation with panicle length, highly significant positive correlation with no. of tillers plant^{-1}, highly significant negatively correlation with no. of grains panicle^{-1}, significant and negative correlation with 1000-grain weight and highly significant negative correlation with grain yield plant^{-1}, also they recorded that No. of tillers plant^{-1} showed non-significant positive correlation with no. of grains panicle^{-1}, non-significant negative correlation with 1000-seed weight and non-significant positive correlation with grain yield plant^{-1}. Iftekharuddaula *et al.* (9) were found that panicle length and 1000-grain weight were positively associated with rice grain yield plant^{-1} and plant height. Rasheed *et al.* (19) revealed by correlation that no. of tillers plant^{-1} was positively associated with grain yield plant^{-1}. Surek and Beser (27) reported grain yield plant^{-1} significantly correlated with no. grains panicle^{-1}. Borbora *et al.* (5) found that 1000-grain weight were highly associated with grain yield plant^{-1}.

Table 11. Correlation coefficient analysis at Chawtan location

Traits	Plant height (cm)	No. of tillers plant^{-1}	No. of panicles plant^{-1}	No. of grains panicle^{-1}	Panicle length (cm)	Grain length (mm)	Grain width (mm)	1000-grain weight (g)
Plant height (cm)	1.000							
No. of tillers plant^{-1}	0.212	1.000						
No. of panicles plant^{-1}	0.180	0.961**	1.000					
No. of grains panicle^{-1}	0.220	-0.230	-0.265	1.000				
Panicle length (cm)	-0.075	0.348	0.335	0.035	1.000			
Grain length (mm)	-0.617**	0.061	0.063	-0.616**	0.049	1.000		
Grain width (mm)	0.102	-0.267	-0.276	0.069	-0.212	-0.379	1.000	
1000-grain weight (g)	0.467*	0.038	-0.005	0.057	-0.225	-0.429*	0.660**	1.000
Grain yield plant^{-1} (g)	0.370	0.844**	0.828**	0.134	0.291	-0.234	-0.111	0.170

*** .Correlation is significant at the 0.05 level (2-tailed), $t_{0.05}(24)=2.064$**

****. Correlation is significant at the 0.01 level (2-tailed), $t_{0.01}(24)=2.797$**

Path coefficient analysis

The path coefficient analysis for grain yield plant^{-1} was presented in Table 12 at Gaba location, which indicated that, the maximum positive direct effect on grain yield recorded by no. of panicles plant^{-1} (0.537) followed by no. of tillers plant^{-1} and no. of grains panicle^{-1} with 0.497 and 0.392 respectively, while the highest positive indirect effect was 0.525 recorded by no. of tillers plant^{-1} *via* no. of panicles plant^{-1} and followed by 0.232 for grain length *via* no. of panicles plant^{-1}. The results of residual effect (R=0.019) revealed that 98% of the grain yield plant^{-1} was contributed by the traits studied in this experiment. The role of other independent variables which had not been included in this experiment was expected to influence grain yield only by 2%. This result indicates the adequacy of the traits that were included in this study.

Table 12. Path coefficient analysis confirming direct (diagonal values) and indirect effects on Seed weight plant^{-1} at Gaba location

Traits	Plant height (cm)	No. of tillers plant^{-1}	No. of panicles plant^{-1}	No. of grains panicle^{-1}	Panicle length (cm)	Grain length (mm)	Grain width (mm)	1000-grain weight (g)
Plant height (cm)	-0.070	0.011	0.013	-0.001	0.020	-0.003	-0.019	-0.027
No. of tillers plant^{-1}	-0.080	0.497	0.486	-0.206	0.012	0.184	-0.152	-0.070
No. of panicles plant^{-1}	-0.097	0.525	0.537	-0.246	0.009	0.232	-0.177	-0.078
No. of grains panicle^{-1}	0.005	-0.162	-0.179	0.392	-0.030	-0.041	-0.012	-0.074
Panicle length (cm)	0.003	0.0003	0.0002	0.001	-0.011	-0.001	0.003	0.002
Grain length (mm)	0.007	0.065	0.076	-0.018	0.019	0.175	-0.092	-0.059
Grain width (mm)	0.022	-0.025	-0.026	-0.002	-0.022	-0.042	0.080	0.066
1000-grain weight (g)	0.022	-0.008	-0.008	-0.011	-0.011	-0.020	0.048	0.058
Grain yield plant^{-1} Correlation	-0.187	0.903**	0.897**	-0.091	-0.015	0.485*	-0.321	-0.182

Residual = 0.019

Table 13 illustrates the path coefficient analysis for grain yield plant^{-1} at Chawtan location, the highest positive direct effect showed by no. of panicles plant^{-1} with 0.517 and followed by no. of tillers plant^{-1} and no. of grains panicle^{-1} with 0.439 and 0.382 respectively. The direct effects of other traits were too low to be considered of any consequence. These results are in conformity to that of (15, 25).The highest positive indirect effect was 0.497 recorded by no. of tillers plant^{-1} *via* no. of panicles plant^{-1} and followed by 0.422 which recorded by no. of panicles plant^{-1} *via* no. of tillers plant^{-1}. The experiment's traits accounted for 93% of the variance in grain yield plant^{-1}, as determined by the residual effect (R=0.069). Only a 7 % change in grain yield was predicted to result from the effect of other independent factors that were not part of this experiment. This finding validates the importance of the characteristics used in this research.

Table 13. Path coefficient analysis confirming direct (diagonal values) and indirect effects on Seed weight plant^{-1} at Chawtan location

Traits	Plant height (cm)	No. of tillers plant^{-1}	No. of panicles plant^{-1}	No. of grains panicle^{-1}	Panicle length (cm)	Grain length (mm)	Grain width (mm)	1000- grain weight (g)
Plant height (cm)	0.116	0.025	0.021	0.026	-0.009	-0.072	0.012	0.054
No. of tillers plant^{-1}	0.093	0.439	0.422	-0.101	0.153	0.027	-0.117	0.017
No. of panicles plant^{-1}	0.093	0.497	0.517	-0.137	0.173	0.032	-0.143	-0.002
No. of grains panicle^{-1}	0.084	-0.088	-0.101	0.382	0.013	-0.235	0.026	0.022
Panicle length (cm)	0.001	-0.004	-0.004	0.000	-0.012	-0.001	0.003	0.003
Grain length (mm)	-0.044	0.004	0.004	-0.044	0.004	0.071	-0.027	-0.031
Grain width (mm)	0.012	-0.031	-0.031	0.008	-0.024	-0.043	0.114	0.075
1000-grain weight (g)	0.015	0.001	0.0002	0.002	-0.007	-0.014	0.021	0.032
Grain yield plant^{-1} Correlation	0.370	0.844**	0.828**	0.134	0.291	-0.234	-0.111	0.170

Residual = 0.069

Cluster analysis

Dendrogram of the cluster analysis based of the agro-morphological data at Gaba location was presented in Figure1, The cluster analysis clusters 26 rice genotypes into five clusters. According to the dendogram Cluster I included 10 Genotypes *viz.* G_5, G_6, G_8, G_2, G_{18}, G_3, G_{12}, G_4, G_{19}, and G_9. Cluster II also included 10 Genotypes *viz.* G_7, G_{26}, G_{11}, G_{15}, G_{13}, G_{23}, G_{14}, G_{10}, G_{17}, and G_{16}. Cluster III included included 2 Genotypes *viz.* G_1 and G_{20}. Cluster IV included 3 Genotypes *viz.* G_{24}, G_{25}, and G_{22}. Cluster V included only G_{21}. The dendogram revealed that Clusters III and Cluster V have the greatest genetic distance between them, indicating that their genetic material was varied. Despite the fact that they are of the same species, the parents involved in the cross may have come from different origins. Table 14 represents the Agglomeration schedule of the average linkage (Between Groups) at both locations, within cluster I, G_2 and G_4 had the greatest diversity with a distance coefficient of 90.028, which was likely due to the participation of different parents in their crosses or might have been the result of a mutation; whereas G_5 was most similar to G_6 (12.607) and the variation between them may be the result of their different origins. Within cluster II, G_7 and G_{10} had most distance (95.504), while G_{11} has a slight difference from G_{15} (16.150). Concerning Gaba location, Table 15 shows that Cluster II includes genotypes recorded better values for panicle length, grain width, and 1000-grain weight. Cluster III included genotypes which were superior for plant height; Cluster V includes genotypes which were superior for no. of tillers plant^{-1}, no. of panicle plant^{-1}, no. of grain panicle^{-1}, and grain yield plant^{-1}. Cluster I and IV dose not record any superiority in any of the traits.

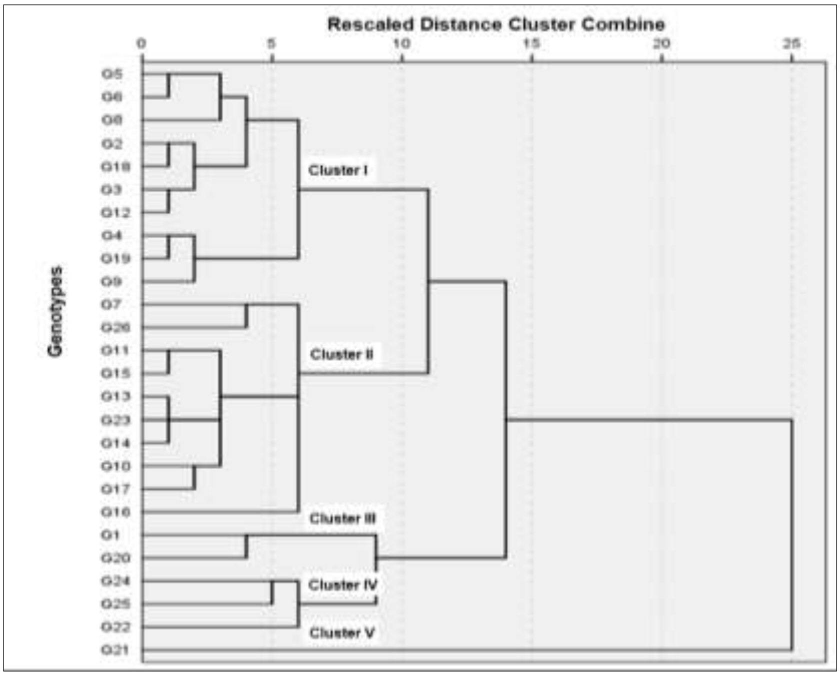

Figure1. Dendrogram of 26 rice genotypes using average linkage (Between Groups) at Gaba location

Table 14. Agglomeration schedule of the average linkage (Between Groups) at both locations

Stages	Gaba Location			Chawtan Location		
	Cluster Combined		Distance Coefficients	Cluster Combined		Distance Coefficients
	Cluster 1	Cluster 2		Cluster 1	Cluster 2	
1	G_5	G_6	12.607	G_5	G_{14}	14.720
2	G_2	G_{18}	13.340	G_{16}	G_{18}	19.181
3	G_{11}	G_{15}	16.150	G_7	G_8	19.808
4	G_{13}	G_{23}	16.795	G_3	G_{13}	20.015
5	G_3	G_{12}	19.514	G_{10}	G_{12}	25.467
6	G_4	G_{19}	21.397	G_4	G_{22}	26.696
7	G_{13}	G_{14}	26.397	G_9	G_{19}	31.788
8	G_4	G_9	29.652	G_4	G_6	35.095
9	G_{10}	G_{17}	32.477	G_7	G_9	39.813
10	G_2	G_3	35.910	G_{21}	G_{26}	41.430
11	G_{10}	G_{13}	47.695	G_3	G_{16}	49.989
12	G_5	G_8	49.222	G_7	G_{15}	50.359
13	G_{10}	G_{11}	54.038	G_{17}	G_{21}	50.489
14	G_7	G_{26}	58.937	G_2	G_{20}	59.460
15	G_2	G_5	61.997	G_7	G_{23}	61.483
16	G_1	G_{20}	68.176	G_5	G_{25}	67.172
17	G_{24}	G_{25}	73.991	G_2	G_3	78.501
18	G_{10}	G_{16}	89.781	G_4	G_5	89.672
19	G_2	G_4	90.028	G_{17}	G_{24}	90.470
20	G_{22}	G_{24}	93.381	G_2	G_7	119.350
21	G_7	G_{10}	95.504	G_2	G_{17}	164.029
22	G_1	G_{22}	131.576	G_1	G_2	228.990
23	G_2	G_7	155.375	G_4	G_{11}	244.642
24	G_1	G_2	194.067	G_1	G_4	357.347
25	G_1	G_{21}	361.437	G_1	G_{10}	989.845

Table 15. The average performance of the genotypes for the studied traits according to the distinct clusters at both locations

Clusters	Plant height (cm)	No. of tillers plant^{-1}	No. of panicles plant^{-1}	No. of grains panicle^{-1}	Panicle length (cm)	Grain length (mm)	Grain width (mm)	1000-grain weight (g)	Grain yield plant^{-1} (g)
					Gaba Locations				
Cluster I	107.100	4.600	4.300	171.141	18.267	7.204	3.366	24.824	75.900
Cluster II	105.000	3.333	3.000	190.000	20.000	7.637	3.663	27.726	49.000
Cluster III	107.500	7.833	7.333	152.761	17.000	8.363	3.040	22.575	197.167
Cluster IV	107.100	4.600	4.300	171.141	18.267	7.204	3.366	24.824	75.900
Cluster V	100.000	11.000	10.333	214.012	19.000	9.377	2.470	19.474	471.667
					Chawtan Locations				
Cluster I	92.500	14.778	14.833	105.154	18.500	7.136	3.379	25.056	575.444
Cluster II	97.000	23.667	20.667	64.000	15.000	7.310	3.033	26.774	815.333
Cluster III	86.063	11.646	11.125	101.270	18.271	7.345	3.218	23.281	270.146
Cluster IV	82.000	5.667	5.000	60.800	15.333	7.600	3.313	23.884	48.667
Cluster V	101.500	23.833	22.667	108.242	20.500	6.843	3.162	23.579	1348.667

The Dendrogram of the cluster analysis at Chawtan location was illustrated in Figure2. The cluster analysis clusters 26 rice genotypes also into five clusters. According to the dendogram Cluster I included 6 Genotypes *viz.* G_5, G_{14}, G_{25}, G_4, G_{22}, and G_6. Cluster II included G_{11} only. Cluster III included include 16 Genotypes *viz.* G_{21}, G_{26}, G_{17}, G_{24}, G_7, G_8, G_9, G_{19}, G_{15}, G_{23}, G_{16}, G_{18}, G_3, G_{13}, G_2, and G_{20}. Cluster IV included G_1 only. Cluster V included 2 Genotypes *viz.* G_{10} and G_{12}.

The distance coefficient in Table 14 at Chawtan location presented that Clusters IV and Cluster V have the greatest genetic distance between them, indicating that their genetic material was varied. Despite the fact that they are of the same species, the parents involved in the cross may have come from different origins. Within cluster I, G_4 and G_5 had the greatest diversity with a distance coefficient of 89.672 which was likely due to the participation of different parents in their crosses or might have been the result of a mutation; whereas G_5 was most similar to G_{14} (14.720) and the variation between them may be the result of their different origins. Within cluster III, G_2 and G_{17} had most distance (164.029), while G_{16} has a slight difference from G_{18} (19.181). At Chawtan location, Table 15 shows that Cluster I included genotypes recorded better grain width. Cluster II included genotypes which were superior for 1000-grain weight; Cluster IV included genotypes which were superior for grain width. Cluster V includes genotypes which were superior in Plant height, no. of tillers plant^{-1}, no. of panicle plant^{-1}, no. of grain panicle^{-1}, Panicle length, and grain yield plant^{-1}. Cluster III dose not record any superiority in any of the traits. Cluster analysis provided with a complete view of the variation present among the 26 rice genotypes and it might be use for the plant breeders for the genetic improvement of rice. According to many researchers results, there is genetic variation among rice genotypes, which could be grouped into a variety of unique clusters. Alamir (1) demonstrated the presence of genetic diversity among the investigated genotypes by grouping 36 low land rice genotypes with 12 morphological features into 7 clusters. Twenty irrigated lowland rice genotypes with 11 morphological characters were separated into 4 clusters by (4), who also demonstrated significant genetic variation within the studied genotypes. Twenty-four accessions of irrigated rice were divided into five clusters by (21). Worede *et al.* (30) divided Twenty-four upland rice varieties into 2 clusters based on 17 morpho-agronomic parameters. Thirty-two early maturing rice genotypes were divided into 3 clusters by (23). Thirty-nine genotypes of rice grown under irrigation were divided into 6 separate clusters by (6).

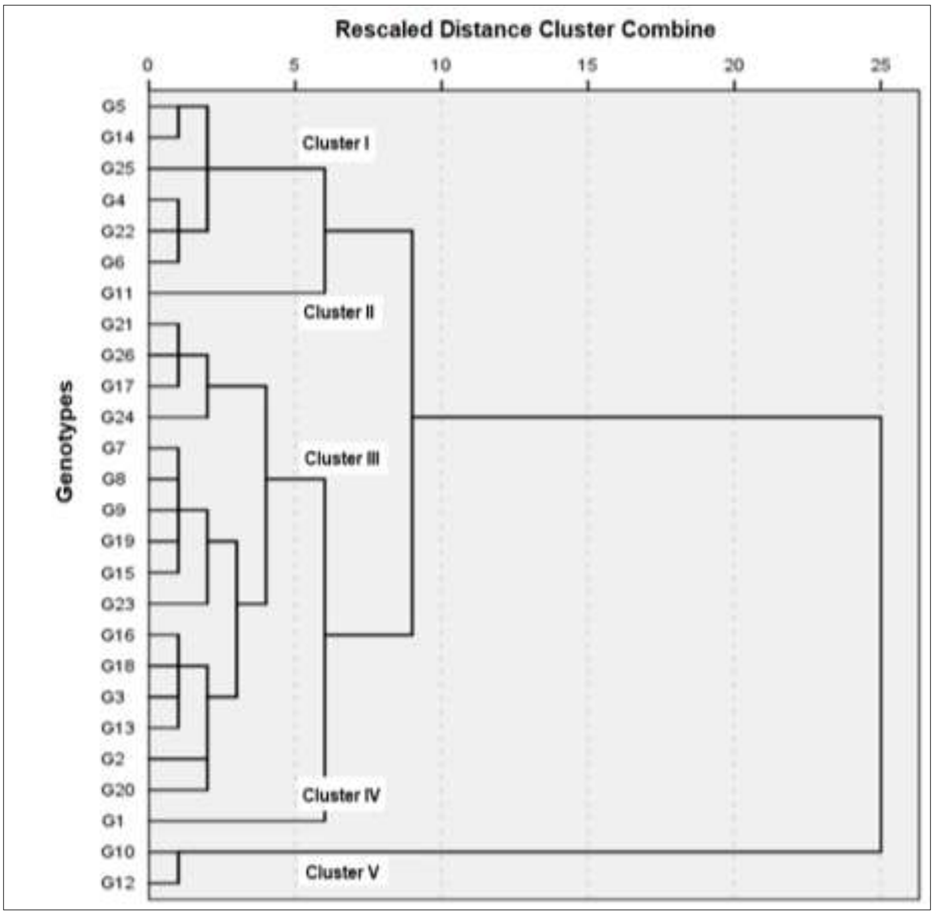

Figure2. Dendrogram of 26 rice genotypes using average linkage (Between Groups) at Chawtan location

CONCLUSIONS

To generate information about the genetic variability of the genotypes a total of 26 local rice genotypes were evaluated at two locations in Sulaimani governorate *viz.* Gaba and Chawtan during the growing season 2019. The analysis of variance showed highly significant differences among the tested genotypes for all of the studied traits, which indicates the presence of considerable genetic variability between the genotypes. Combined Analysis of variance revealed highly significant differences due to the locations and Genotypes×locations interaction. G_{21} (Surchi Qalat–Ambar) with (471.667g) and G_{12} (Mughagh–Sarda) with (1357.333g) recorded the maximum grain yield at Gaba and Chawtan locations respectively. At both locations, no. of tillers plant^{-1}, and no. of panicle plant^{-1} produced a highly significant and positive correlation with grain yield. Additionally, the maximum positive direct effects on grain yield effect were recorded by no. of panicle plant^{-1}. No. of tillers plant^{-1} *via* no. of panicle plant^{-1} obtained the maximum positive indirect effect on grain yield at both locations. Five distinct clusters of the genotypes were noticed at both locations. Cluster V recorded higher grain yield at both locations.

REFERENCES

1. Alamir, A., 2018. Genetic Variability of Grain Yield and Yield Related Traits for Newly Introduced Low Land Rice (*Oryza sativa* L.) Genotypes at Fogera, North Western Ethiopia. M.Sc. Thesis, School of Graduate Studies of Bahir Dar University, College of Agriculture and Environmental Sciences, Ethiopia. pp.102.

2. Al-Hasanie, L. N. H. and A. D. Al-Maadhedi 2017. Influence of irrigation periods and organic fertilizer on tow rice varieties grown under The System of Rice Intensification (SRI)", Iraqi Journal of Agricultural Sciences (IJAS) 48(3): 823-840. https://doi.org/10.36103/ijas.v48i3.396

3. Amin, E. A., 1979. Correlation and path-coefficient analysis in some short-stature rice cultivars and strains. Inter. Rice Commission Newsletter, 28:19-21.

4. Baloch A., M. Baloch, R. Baloch, M. Kandhro, I. Odhano, H. Bughio and A. Rajput 2016. Evaluation of genetic diversity in rice (*Oryza sativa* L.) genotypes. Sindh University Research. Journal-SURJ (Science Series). 48pp.

5. Borbora, T. K., G. N. Hazarika and A. K. Medhi 2005. Correlation and path analysis for plant and panicle characters in rice (*Oryza sativa*). Agric. Biotechnology, Jorhat. 30 (20): 215-220.

6. Chakma S. P., H. Huq, F. Mahmud, and A. Husna 2012. Genetic diversity analysis in rice (*Oryza sativa* L.). Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Sher-e-Bangla Nagar, Dhaka-1207. Bangladesh J. Pl. Breed. Genet. 25(1): 31-39.

7. Florence, C., L. Zapico1, J. A. Namocatcat and J. L. Cariño-Turner 2010. Genetic diversity analysis of traditional upland rice cultivars in Kihan, Malapatan, Sarangani Province, Philippines using morphometric markers. Philppine J. Sci. 139(2): 177-180.

8. Hairmansis, A., B. Kustianto, Supartopo and Suwarno 2010. Correlation analysis of agronomic characters and grain yield of rice for tidal swamp areas. Indonessian J. Agric. Sci. 11(1): 11-15.

9. Iftekharuddaula, K. M., Khalida Akhtar, M.S. Hassan, K. Fatima. And A. Badshah 2002. Character association and selection criteria in irrigated rice. J. Biol. Sci. 2(4):243-246.

10. Khan, A. S., M. Imran and M. Ashfaq 2009. Estimation of genetic variability and correlation for grain yield components in rice (*Oryza sativa*). Amercian-Eurasian J. Agric. Environ. Sci., 6(5): 585-590.

11. Lateef, M.A., A.D. Kasar and A.A. Mudhi 2017a. Policy analysis matrix for the essential cereal crops varieties (rice Buhooth1, and corn synthetic genotype Baghdad3) (study case) in Iraq for the year 2012. Iraqi Journal of Agricultural Sciences (IJAS) 48(3):812-822. https://doi.org/10.36103/ijas.v48i3.395

12. Lateef, M.A., A.D. Kasar and A.A. Mudhi 2017b. Investment priorities in the agricultural scientific research in Iraq using policy analysis matrix approach cereals crops (rice Amber, Al-Baraka Buhooth2, corn synthetic genotype Fajer1, and wheat Buhooth158) study case", Iraqi Journal of Agricultural Sciences (IJAS) 48(3):797-811. https://doi.org/10.36103/ijas.v48i3.394

13. Madhavilatha, L., M. R. Sekhar, Y. Suneetha and T. Srinivas 2005. Genetic variability, correlation and path analysis for yield and quality traits in rice (*Oryza sativa*). Res. Crops. 6(3): 527-534.

14. Manifesto, M.M., A.R. Schlatter, H.E. Hopp, E.Y. Suarez and J. Dubcovsky 2001. Quantitative Evaluation of Genetic Diversity in Wheat Germplasm Using Molecular Markers. Crop Breeding Genetics and Cytology, 41: 682-690.

15. Mishra, L.K., and R.K. Verma 2002. Correlation and path analysis for morphological and quality traits in rice (*O. sativa* L.). Plant Archives. 2002; 2(2):275-284.

16. Nachimmuthu, V.V., S. Robin, D. Sudhakar, M. Raveendran, S. Rajeswari, S. Manonmani 2014. Evaluation of rice genetic diversity and variability in a population panel by principal component analysis. Indian J. Sci. Technol. 7(10):1555–1562.

17. Pervaiz, A. H., M. A. Rabbani, I. Khaliq, S. R. Pearce and S. A. Malik 2010. Genetic diversity associated with agronomic traits using microsatellite markers in Pakistani rice landraces. Elect. J. Biotechnol. 13(3): 1-12.

18. Ragarathinam, S. and V. D. G. Raja 1992. Correlation and path analysis in some rice varieties under alkaline stress. Madras Agric. Res. J. 79: 374-378.

19. Rasheed, M. S., H. A. Sadaqat and M. Babar 2002. Correlation and path analysis for yield and its components in Rice. Asian J. PI. Sci. 1(3): 241-244.

20. Rashid, K., I. Khaliq, M. O. Farooq, M. Z. Ahsan 2013. Correlation and Cluster Analysis of Some Yield and Yield Related Traits in Rice (*Oryza sativa*), International Journal of Agricultural Science and Research (IJASR) 3(4): 25-30.

21. Ravikumar, B., N. Satyanarayana, K. Chamundeswari, M. Bharathalakshmi and A. Vishnuvardhan 2015. Principal component analysis and character association for yield components in rice (*Oryza sativa* L.) cultivars suitable for irrigated ecosystem. Andhra Pradesh Rice Research Institute and Regional Agricultural Research Station, Maruteru, India. Current Biotica. 9(1): 25-35.

22. Sabesan, T., R. Suresh and K. Saravanan 2009. Genetic variability and correlation for yield and grain quality characters of rice grown in costal saline low land of Tamilnadu. Elect J. Plant Breeding. 1: 56-59.

23. Sarker, M., L. Hassan, M. Rashid and S. Seraj 2013. Molecular characterization and morphological clustering of exotic early maturing rice (*Oryza sativa* L.) lines. Journal Bangladesh Agril. Univ. 11(2): 233–240.

24. Singh R.K., B.D. Chaudhary 1985. Biometrical Methods in Quantitative Genetic Analysis; Kalyani Publishers; New Delhi: pp. 215–218.

25. Singh, R., V. Yadav, D.N. Mishra and A. Yadav 2018. Correlation and path analysis studies in Rice (*Oryza sativa* L.). Journal of Pharmacognosy and Phytochemistry (SP1)2084-2090.

26. STATISTIC, I. S. 2011. IBM SPSS STATISTIC program, Version 19 statistical software packages". IBM Corporation, New York.

27. Surek, H., N. Beser 2003. Correlation and path coefficient analysis for some yield related traits in rice (*Oryza sativa*) under thrace conditions. Turk. J. Agric. For. 27: 77-83.

28. Tripathi, A., R.Bisen, R.P.Ahirwal, S. Paroha, R. Sahu, A.R.G. Ranganatha 2013. Study on genetic divergence in sesame (*sesamum indicum* L.) Germplasm based on morphological and quality traits. Bioscan. 2013;8(4):1387–1391.

29. Vivekananda, P., S. Subramanian 2014. Genetic divergence in rainfed rice Oryza. 30: 60–62.

30. Worede, F., T. Sreewongchai, C. Phumichai and P. Sripichitt 2014. Multivariate analysis of genetic diversity among some rice genotypes using morpho-agronomic traits. Journal of Plant Sciences 9: 14-24.

31. Yong-xiang, F. 2008. Correlation and cluster analysis for yield properties of early-japonica rice in cold area. J. Anhui. Agric. Sci. 23(49): 150-186.