

## Genetic Variability Study of some Rice Genotypes (*Oryza sativa* L.) for Morphological, Yield and Grain Quality Traits

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### ABSTRACT

The present investigation aimed to study the genetic diversity among some genotypes of rice in two successive seasons 2014 and 2015 at the experimental farm of Sakha research station. Thus, genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), heritability in broad sense ( $h^2$ ) and genetic advance (GA) were determined for all the studied traits. In addition, the nature and magnitude of genetic divergence estimated in 24 rice genotypes using Mahalanobis  $D^2$  – statistics by considering 17 quantitative traits. High estimates of GCV and PCV were recorded for panicle exertion%, gelatinization temperature, grain elongation% and amylose content%. Heritability in broad sense was high for all characters under study. High heritability coupled with high genetic advance were recorded for number of filled grains/panicle and plant height traits. Based on genetic distance, the 24 studied genotypes were grouped into 11 clusters. Cluster III was the largest and consisted of five genotypes, followed by cluster X with four genotypes, while clusters VI and XI contained two genotypes for each one. However, clusters I, V, VII, VIII and IX included one genotype for each one. The highest inter clusters distance (102.605) was between cluster V and XI while, the lowest one was found between cluster II and X (22.017). Principal component analysis revealed that seven quantitative traits (grain length, grain shape, plant height, amylose content%, 1000-grain weight, number of panicles/plant and panicle length) were significantly influenced the variation in these genotypes. Therefore, the present investigation determined the genetic variability in some genotypes that could be used to improve the rice breeding programme with respect studied traits.

**Keywords:** Rice, genetic diversity, morphological traits, multivariate analysis.

### INTRODUCTION

Rice is a major food crop, and it comes after wheat among all the cultivated cereals (Abodolereza and Racionzer 2009). To meet the constantly extension requires of varietal developments, the assessment and characterization of all the present germplasm are required. Genetic improvement essentially depends on the amount of presence for genetic variability in the studied population (Adebisi *et al.*, 2001).

The evaluation of genetic diversity among the different genotypes is the first and initial process in any plant breeding programme. Genetic divergence is the useful tool for an efficient choice of parental lines for crossing to improve high yield potential varieties. A detailed understanding about the extent structure of genetic diversity in different cultivars of the same type is important for the development of appropriate and efficient strategies for collection, conservation, and preservation of cultivar relatives (Ogunbayo *et al.*, 2005).

The genetic development of any plant is highly dependent on the amount of several genetic parameters, such as, genotypic and phenotypic variances, genotypic and phenotypic coefficient of variation (GCV and PCV), broad sense heritability and genetic advance on which the breeding methods are used for its further amendment. The magnitude of variability is determined by genotypic and phenotypic coefficient of variances which help the botanical descriptors by knowledge about proportional amount of variability in different traits (Chakravorty *et al.*, 2013).

With the improvement of advanced biometric techniques like multivariate analysis depend on Mahalanobis Statistic, estimate of amount of variation in the population and determining of related contribution of different components to the total divergence intra and inter cluster levels have now become available. The use of Mahalanobis  $D^2$  statistic for determining genetic divergence has been proved by Eswaran (2012) and Ovung *et al.*, (2012).

To have convenient characterization and assessment of the rice genotypes, the above mentions are found to be good for utilization of the traits and such kind of these genotypes in breeding program for the future. So, this study aimed to evaluate 24 rice genotypes to assess the nature and magnitude of genetic diversity among the genotypes for further utilization in rice breeding programmes.

### MATERIALS AND METHODS

#### Plant materials:

The present study comprised 24 genotypes of tropical japonica rice, collected from the Genetic Stock of Rice Research and Training Center (RRTC), Sakha, Kafr El-Sheikh, Egypt. The origin of these genotypes as presented in Table 1.

#### Methods:

This investigation was conducted at the experimental farm of Sakha research station during two successive rice growing seasons of 2014 and 2015. The experiment was designed in a Randomized Complete Block Design with three replications, the date of sowing was May first, and the seedlings were transplanted after 30 days old. All agricultural practices were applied according to the procedures recommended for rice crop in Research and Training Center (RRTC), Sakha, Kafr El-Sheikh, Egypt. Each plot contained 4 rows; the seedlings were planted at spacing of 20 x 20 cm row to row and plant to plant. Ten competitive random plants from the middle rows of the experimental plots were taken for recording the data on the following traits: days to 50% heading, plant height (cm), panicle exertion (%), panicle length (cm), number of panicles/plant, No. of filled grains/panicle, 1000-grain weight (g), grain yield/plant(g), spikelets fertility (%), hulling (%), milling (%), head rice (%), grain length (mm), grain shape (L/W ratio), grain elongation (%) amylose content (%) and Gelatinization temperature.

**Table 1. List of 24 rice genotypes and their origin with their salient features of grain shape.**

No.	Entry	Origin	Grain shape
1	IR 65600-77-4-2-1	IRRI	medium
2	IR 65600-127-6-2	IRRI	medium
3	IR 65600-129-1-1-2	IRRI	bold
4	IR 69093-41-2-3-2	IRRI	bold
5	IR 69853-70-3-1-1	IRRI	bold
6	IR 68011-15-1-1	IRRI	medium
7	IR 65603-57-4-2	IRRI	bold
8	IR 65598-27-3-1	IRRI	bold
9	IR 65564-44-2-3	IRRI	bold
10	IR 65597-29-3-2-3	IRRI	bold
11	IR 68167-28-3-2-2	IRRI	bold
12	IR 66158-38-3-2	IRRI	bold
13	IR 66159-189-5-5-3 (NPT)	IRRI	bold
14	IR 66160-121-4-5-3 (NPT)	IRRI	bold
15	IR 67962-40-6-3-3 (NPT)	IRRI	bold
16	IR 67966-188-2-2-1 (NPT)	IRRI	bold
17	IR 68544-29-2-1-3-1-2 (NPT)	IRRI	bold
18	IR 68552-55-3-2 (NPT)	IRRI	bold
19	IR 69116-67-3-2-3 (NPT)	IRRI	bold
20	IR 69432-54-1-1-2-2 (NPT)	IRRI	bold
21	IR 67954-46-1-3-2	IRRI	bold
22	IR 67964-46-1-3-2	IRRI	medium
23	MOROBEREKAN	West Africa	medium
24	KATY	IRRI	medium

IRRI: International Rice Research Institute.

**Statistical analysis:**

The obtained data were subjected to statistical analyses using SPSS (version 13.0) software. Subsequently, the genotypic and phenotypic coefficients of variation were measured using the formulae suggested by Burton (1952). Broad sense heritability was calculated as outlined by Hanson *et al.*, (1956). Genetic advance was estimated by the method suggested by Johnson *et al.*, (1955). Genetic diversity was estimated following the Mohalanobis's distance (D2) method according to Rao (1952). Clustering of genotypes was measured according to Tocher's Method (Rao, 1952) and principle component analysis studied according to Jager *et al.*, (1983).

**RESULTS AND DISCUSSION**

**Analysis of variance**

Significant differences were exhibited among the 24 rice genotypes for the studied traits as shown in Table 2. Data illustrate the presence of high amount of genetic variability among these genotypes.

**Genetic Parameters**

Considerable improvement and success breeding programs for any crop largely depends on the amount of genetic variability among genotypes, which selected for further manipulation to achieve the breeding target. A survey of genetic variability with the help of suitable parameters such as genotypic ( $\sigma^2_g$ ) and phenotypic ( $\sigma^2_p$ ) variance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability ( $h^2_{b.s}$ ) in broad sense and genetic advance (GA) are necessary to start an efficient breeding program.

A wide range of variations in seventeen studied traits were observed among 24 rice genotypes with respect to vegetative, yield and its components and grain quality traits (Table 3).

**Table 2. Analysis of variance and mean squares of combined data for morphological traits in rice genotypes.**

Traits	S.O. V.	Years	Reps. / years	Genotypes	Genotypes / years	Error
Df		1	4	23	23	92
Days to 50% heading	36.50**	0.38	252.95**	0.70	0.52	
Plant height	26.84	5.76	1671.09**	0.51	0.88	
Panicle exertion%	6.52*	0.46	361.14**	0.27	0.63	
Panicle length.	46.46**	0.95	25.04**	0.90	0.59	
No. of panicles / plant	3.89	4.37	14.89**	0.18	0.51	
No. of filled grains/panicle	904.11*	95.51	3886.61**	20.56	37.15	
1000 grain weight	0.19	0.04	80.17**	0.71	0.53	
Grain yield/plant	41.93**	1.39	146.77**	0.23	0.92	
Spiklets fertility%	23.93	1.12	137.67**	0.39	0.95	
Hulling%	5.90	1.67	45.48**	0.41	0.77	
Milling%	1.77	2.08	48.10**	0.12	0.63	
Head rice%	2.33	1.14	192.64**	0.12	1.81	
Grain length.	0.01	0.01	1.58**	0.01	0.01	
Grain shape	0.02	0.01	0.28**	0.01	0.01	
Elongation%	0.01	1.22	533.72**	0.01	1.60	
Amylose content%	0.09	0.01	77.08**	0.01	0.05	
Gelatinization temperature	0.02	0.04	15.53**	0.00	0.03	

\*\* : significant at 0.01 probability level.

**Vegetative traits**

Table 3 presents estimates of genotypic ( $\sigma^2_g$ ) and phenotypic ( $\sigma^2_p$ ) variance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability ( $h^2_{b.s}$ ) in broad sense and genetic advance (GA) over two years combined data. Expectedly, phenotypic variance was generally higher than the genotypic variance in all the studied traits. High genotypic and phenotypic variances were observed in plant height (278.43 and 279.19), respectively. The highest estimated values of genotypic (GCV) and phenotypic coefficients of variation (PCV) were recorded for panicle exertion%, followed by plant height, panicle length, and days to 50% heading, with estimated values of (88.79 and 89.17), (16.57 and 16.59), (8.20 and 8.88) and (6.05 and 6.10), respectively. Moreover, the phenotypic coefficient of variation (PCV) was close to genotypic coefficient of variation (GCV) for all studied vegetative traits. Furthermore, high estimates of broad sense heritability ( $h^2_{b.s}$ ) were exhibited for all vegetative traits; it was ranged from 85.17% for panicle length to 99.73% for plant height. These findings indicated to the studied vegetative traits mainly controlled by genetic factors. Thus, the simple selection methods could be efficient in order to improving these traits. These results in conformity with findings by Cruz *et al.*, (2008), Mamunur Rahman *et al.* (2012), Dutta *et al.* (2013), Vanisree *et al.* (2013) and Dhurai *et al.* (2014).

In addition, the results revealed that the genetic advance was high for plant height (34.33) followed by panicle exertion% (15.91) and days to 50% heading (13.27), while, the lowest value was detected for panicle length (3.82). The genetic advance is an efficient evidence of the progress that predicted as result of choice the related population. Heritability in conjunction with genetic advance would give a more reliable index of better selection, high heritability compared with high genetic advance were recorded for plant height, panicle exertion%

and days to 50% heading, suggesting the effectiveness of selection in early generation to improve these vegetative traits. These results are in agreement with that recorded earlier by Hasan *et al.* (2013) and Shahriar *et al.* (2014).

**Yield and its component traits**

The results shown in Table 3 demonstrated that the phenotypic variance was higher than genotypic variance in all studied traits and the highest value was recorded in number of filled grains/panicle (687.80 and 631.20), respectively. Estimates of phenotypic coefficient of variability (PCV %) was higher than genotypic coefficient of variability (GCV %) for yield and its components, which indicates the apparent variation not only cause to genotypes but also cause to the environment's influence. The highest genotypic coefficient of variation (GCV %) estimates was found in number of filled grains/panicle (14.75), grain yield/plant (12.44), 1000-grain weight (11.48), and number of panicles per plant (10.02). On the contrary, the lowest estimated value of genotypic coefficient of variability (GCV) was determined for spikelet fertility%. Close values for the variation of genotypic and phenotypic coefficients indicated to insignificant effect of environment in the explanation of these traits and the selection in early generation which played an important role for improvement of these traits. These results are in agreement with the earlier results by Hossain *et al.* (2015) and Vanisree *et al.* (2013). These results confirmed by the estimates of heritability for yield and its components, which ranged from 85.96% for number of panicles per plant to 97.25 % for grain yield per plant. However, high estimates of broad sense heritability ( $h^2_{bs}$ ) also recorded for spikelets fertility% (96.79), 1000-grain weight (95.74) and number of filled grains per panicle (91.77). In addition, high estimates of heritability coupled with moderate and/or high estimates of genetic advance for most of studied yield and its components. This

suggested that the lead of both additive and non-additive gene actions in its inheritance, indicating again that the selection in early generation could be played an important role in improving number of these traits. These findings were in agreement with that recorded previously by Prajapati *et al.* (2011), Hasan *et al.* (2013) and Singh *et al.* (2013).

**Grain quality traits**

In general, the results presented in Table 3 concerning grain quality traits exhibited that phenotypic variance was higher than genotypic variance in all studied traits and the highest value was observed in grain elongation% (88.95 and 90.02), respectively. The phenotypic (PCV) and genotypic coefficients of variation (GCV) estimates were close in magnitudes. The highest estimated values of phenotypic (PCV) and genotypic coefficients of variation (GCV) were detected for gelatinization temperature followed by grain elongation% with estimated values (29.03 and 29.13) and (25.67 and 25.82), respectively. On the contrary, the lowest estimated values were recorded for hulling%, milling% and grain length and their estimated values were ranged between 3.49 and 3.64 for hulling%, 9.12 and 9.17 for grain length, respectively. The traits with high estimates of PCV and GCV were influenced mainly by additive and non-additive gene actions, while, traits that affected by low PCV and GCV were high influenced by environmental factors in addition to genetic factors. While, moderate GCV and PCV were recorded for amylose content (19.41% and 19.44%) and grain shape (11.13% and 11.21%), respectively. This illustrates the presence of comparatively moderate variation for these traits that could be utilized for development through selection in advanced generations. The same results were illustrated previously by Umadevi *et al.* (2010), Subbaiah *et al.* (2011) and Gangashetty *et al.* (2013).

**Table 3. Estimation of genetic parameters for 17 studied traits in 24 rice genotypes over combined.**

Traits	$\sigma^2_g$	$\sigma^2_p$	$\sigma^2_e$	GCV	PCV	$h^2_{(bs\%)}$	GA
<b>Vegetative traits</b>							
Days to 50% heading	42.04	42.62	0.52	6.05	6.10	98.64	13.27
Plant height (cm)	278.43	279.19	0.88	16.57	16.59	99.73	34.33
Panicle exertion%	60.15	60.66	0.63	88.79	89.17	99.16	15.91
Panicle length (cm)	4.02	4.72	0.59	8.20	8.88	85.17	3.82
<b>Yield and its components</b>							
No. of panicles / plant	2.45	2.85	0.51	10.02	10.81	85.96	2.99
No. of filled grains / panicle	631.20	687.80	62.38	14.75	15.40	91.77	49.58
1000- grain weight	13.24	13.83	0.53	11.48	11.74	95.74	7.34
Grain yield / plant	24.42	25.11	0.92	12.44	12.61	97.25	10.04
Spiklets fertility%	22.88	23.64	0.95	5.25	5.33	96.79	9.69
<b>Grain quality</b>							
Hulling%	7.51	8.16	0.77	3.49	3.64	92.02	5.42
Milling%	8.00	8.46	0.63	4.07	4.18	94.55	5.66
Head rice%	32.09	33.33	1.81	9.97	10.16	96.26	11.45
Grain length (mm)	0.26	0.27	0.01	9.12	9.17	98.87	1.05
Grain shape	0.05	0.06	0.01	11.13	11.21	98.60	0.44
Grain elongation%	88.95	90.02	1.60	25.67	25.82	98.81	19.31
Amylose content %	12.85	12.88	0.05	19.41	19.44	99.70	7.37
Gelatinization temperature	2.59	2.61	0.03	29.03	29.13	99.31	3.30

$\sigma^2_g$ : genotypic variance,  $\sigma^2_p$ : phenotypic variance,  $\sigma^2_e$ : environmental variance, GCV: genotypic coefficient of variation, PCV: phenotypic coefficient of variation,  $h^2_{(bs\%)}$ : heritability in broad sense, GA: genetic advance.

High estimates of broad sense heritability ( $h^2_{bs}$ ) values were found for all grain quality traits. These values were ranged from 92.02% for hulling% to 99.70% for

amylose content%. Regarding genetic advance, different estimated values were observed, it was low for grain shape (0.44), grain length (1.05), gelatinization temperature

(3.30), hulling % (5.42), milling% (5.66) and amylose content % (7.37). Moreover, moderate estimated values of genetic advance were observed for head rice % (11.45). On the other side, such estimates were high for grain elongation% (19.31). High estimated values of heritability in related to moderate genetic advance were recorded for grain elongation% and head rice% proposed the lead of both additive and non-additive gene actions in its inheritance, hence adoption of breeding methods which could exploit both the gene actions would be a prospective approach. High heritability coupled with low genetic advance was recorded for grain shape, grain length, gelatinization temperature, hulling%, milling% and amylose content%, which indicated limited scope for selection. These results are in harmony with thus findings earlier by Chakraborty *et al.*, (2009 and 2010) and Nirmaladevi *et al.*, (2015).

**Genotypic and phenotypic correlation**

The efficiency of selection for yield mainly based on direction and magnitude of relatedness between yield and its components, as well as, among yield component traits. However, the correlation analysis provides useful information on the type and magnitude of relatedness of different components with grain yield in addition to the nature of interrelation ships among the component traits themselves (Vanisree *et al.*, 2013). Therefore, the covariance analysis was made between all pairs of studied the yield and yield component traits, subsequently the

correlation values were determined for each pair of traits with respect to each rice group under study.

Obviously, results in Table 4, demonstrated that both genotypic and phenotypic correlation coefficients were significant or highly significant in positive direction between grain yield/plant and each of panicle length, number of panicles/plant, number of filled grains/panicle, 1000-grain weight and fertility%, these results illustrated that the selection of these traits will be important in improving the grain yield in these rice genotypes. On the other hand, it was non-significant positively correlated with each of days to 50% heading, panicle length, panicle exertion%, hulling%, milling%, head rice%, grain length, grain shape, grain elongation%, amylose content% and gelatinization temperature. This finding implied that selection for these traits not effective in improving grain yield in these rice genotypes.

The genotypic and phenotypic correlation coefficients found to be significant in positive direction between days to 50% heading and number of filled grains /panicle. In addition, significant negative estimates of genotypic correlation coefficients observed between plant height and number of panicles/plant. Moreover, it was significant or highly significant phenotypically associated with panicle exertion%, panicle length, grain length, grain shape, grain elongation% and amylose content% in positive direction.

**Table 4. Genotypic and phenotypic correlation coefficients in 17 traits for 24 rice genotypes.**

Traits		P.H.	P.EX. %	P.L.	N.P/P	N.F.G.	1000 - G.W.	F %	Hull %	Mill %	H.R. %	G.L.	G.Sh	E. %	A.C. %	G.T.	G.Y/P
DH 50%	G	-0.233	-0.038	0.096	0.205	0.498*	0.041	0.001	-0.386	-0.253	0.263	-0.186	-0.293	-0.158	-0.021	0.218	0.037
	P	-0.233	-0.037	0.094	0.200	0.495*	0.041	0.003	-0.375	-0.250	0.260	-0.185	-0.292	-0.157	-0.021	0.217	0.035
P.H.	G		0.490*	0.522**	-0.401*	0.177	0.313	0.173	0.146	0.301	-0.122	0.686**	0.710**	0.493*	0.519**	-0.078	0.340
	P		0.485*	0.510**	-0.389*	0.171	0.312	0.166	0.140	0.300	-0.120	0.684**	0.706**	0.491*	0.518**	-0.067	0.334
P.EX.%	G			0.429*	0.122	0.411*	0.200	0.442*	-0.045	0.088	-0.234	0.291	0.321	0.099	0.131	0.523**	0.262
	P			0.414*	0.120	0.407*	0.199	0.426*	-0.044	0.088	-0.231	0.288	0.318	0.097	0.129	0.519**	0.252
P.L.	G				-0.359	0.620**	0.318	0.164	-0.140	0.000	0.066	0.336	0.343	0.290	0.112	0.066	0.556**
	P				-0.350	0.599**	0.307	0.160	-0.132	-0.000	0.065	0.327	0.333	0.285	0.109	0.064	0.543**
N.P./P.	G					-0.289	-0.527**	0.283	0.041	-0.164	-0.282	-0.497*	-0.338	-0.016	-0.541**	0.26	0.558**
	P					-0.284	-0.513**	0.270	0.033	-0.154	-0.271	-0.481*	-0.326	-0.016	-0.525**	0.25	0.549**
N.F.G.	G						0.079	0.419*	0.094	0.002	0.199	-0.062	-0.085	0.196	-0.091	-0.339	0.583**
	P						0.077	0.425*	0.087	0.002	0.199	-0.062	-0.080	0.194	-0.090	-0.331	0.573**
1000 - G.W.	G							0.208	0.176	0.130	0.196	0.665**	0.405*	0.109	0.323	-0.010	0.408*
	P							0.211	0.175	0.132	0.194	0.660**	0.399*	0.107	0.322	-0.010	0.401*
F%	G								0.162	0.243	0.152	0.420*	0.371	-0.045	0.469*	-0.588**	0.458*
	P								0.168	0.236	0.151	0.412*	0.362	-0.041	0.461*	-0.578**	0.452*
Hull%	G									0.818**	0.203	0.128	0.019	0.033	0.198	-0.262	0.238
	P									0.792**	0.199	0.128	0.018	0.031	0.194	-0.258	0.233
Mill%	G										0.443*	0.335	0.281	-0.148	0.409*	-0.014	0.364
	P										0.433*	0.330	0.273	-0.146	0.403*	-0.015	0.356
H.R.%	G											0.094	-0.028	-0.176	0.273	0.087	0.280
	P											0.092	-0.027	-0.171	0.270	0.086	0.274
G.L.	G												0.935**	0.126	0.711**	-0.016	0.331
	P												0.932**	0.124	0.710**	-0.016	0.327
G.Sh.	G													0.127	0.671**	0.037	0.266
	P													0.125	0.669**	0.037	0.263
E.%	G														0.052	-0.071	0.184
	P														0.052	-0.071	0.182
A.C. %	G															-0.006	0.167
	P															-0.006	0.164
G.T.	G																0.357
	P																0.351

Days to 50% heading ( DH 50% ), Plant height (P.H.), Panicle exertion% (P.EX%), Panicle length (P.L), No. of panicles/plant (N.P/P.), No. of filled grains/panicle (N.F.G), 1000-grain weight (1000- G.W), Grain yield/plant (G.Y/P), Spiklets fertility % ( F%), Hulling%( Hull%), Milling%( Mill%), Head rice%( H.R.%), Grain length (G.L.), Grain shape (G.Sh.), Grain elongation% (E.%), Amylose Content% (A.C. %), Gelatinization temperature (G.T).

High and highly significant positive estimates of genotypic and phenotypic correlation coefficients were observed between panicle exertion% and each of panicle length, number of filled grains/ panicle, fertility% and gelatinization temperature traits, respectively. Furthermore, highly significant positive estimates of genotypic and phenotypic correlation coefficients were exhibited between panicle length and number of filled grains/panicle, with coefficient values of 0.620 and 0.599 for genotypic and phenotypic correlation coefficients, respectively.

It is clear that the number of panicles/plant was negatively either significant or highly significant with 1000-grain weight (-0.527 and -0.513), grain length (-0.497 and -0.481) and amylose content% (-0.541 and -0.525) for genotypic and phenotypic correlation coefficients, respectively. Significant and positive estimates of genotypic and phenotypic correlation coefficient were observed between number of filled grains/panicle and fertility% with genotypic and phenotypic coefficients values; 0.419 and 0.425, respectively.

Clearly, 1000-grain weight was positively and highly significant or significantly associated with grain length and grain shape. Apparently, genotypic correlation coefficients were significant in positive direction between fertility% and grain length and amylose content% traits. On the other side, it was negatively and highly significant correlated with gelatinization temperature, their genotypic and phenotypic correlation coefficient was -0.588 and -0.578, respectively.

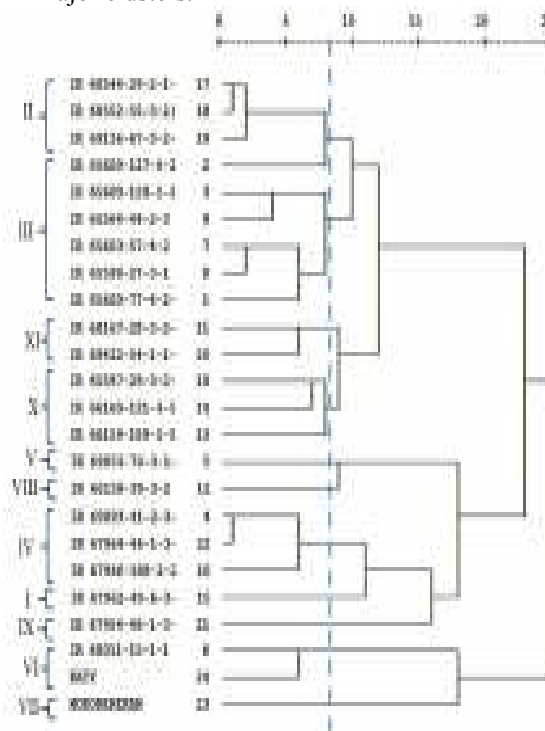
Manifestly, hulling% was positively and highly significantly associated with milling%. Moreover, milling % was strongly correlated with head rice% and amylose content% with respect to genotypic and phenotypic correlation coefficients. In addition, estimates of phenotypic and genotypic correlation coefficients were positive highly significant between grain length and each of grain shape and amylose content%, respectively. While, grain shape was high positive significant associated with amylose content%.

Furthermore, the results cleared that the genotypic correlation coefficient was close or little higher than the related values of phenotypic correlation coefficient for most trait pairs of the rice genotypes. This indicated that these traits were mainly controlled by genetic factors, while the environmental factors play minor role in the explanation of these traits. Similar results were recorded

previously by Cruz *et al.* (2008), Hairmansis *et al.*, (2010), Abarshahr *et al.*, (2011), Sohrabi *et al.*, (2012), Vanisree *et al.*, (2013) and Premkumar *et al.*, (2016).

**Cluster analysis**

Cluster analysis depend on 17 traits was conducted using Ward method using Euclidian distance as shown in Figure 1. If the same cutting is done on the distance seven, the 24 rice genotypes were divided into 11 major clusters.



**Figure 1. Dendrogram of 24 rice genotypes using ward method based on Euclidian distance for all 17 studied traits.**

**Distribution of genotypes**

The results shown in Table 5 indicated that 24 rice genotypes were distributed to 11 clusters including different number of genotypes. Cluster III contained the highest number of genotypes (five genotypes) while, cluster X, cluster II, cluster IV, cluster VI and cluster XI contained 4, 3, 3, 2 and 2 genotypes, respectively. The lowest clusters were I, V, VII, VIII and IX that included the same number of genotype only one for each one (Eswaran 2012 and Ovung *et al.*, 2012).

**Table 5. Distribution of 24 rice genotypes within each cluster.**

Cluster	Number of genotypes	Name of genotypes included
I	1	IR 67962-40-6-3-3 (NPT)
II	3	IR 68544-29-2-1-3-1-2 (NPT), IR 68552-55-3-2 (NPT), IR 69116-67-3-2-3 (NPT)
III	5	IR 65600-77-4-2-1, IR 65600-129-1-1-2, IR 65603-57-4-2, IR 65598-27-3-1, IR 65564-44-2-3
IV	3	IR 69093-41-2-3-2, IR 67966-188-2-2-1 (NPT), IR 67964-46-1-3-2
V	1	IR 69853-70-3-1-1
VI	2	IR 68011-15-1-1, KATY
VII	1	MOROBEREKAN
VIII	1	IR 66158-38-3-2
IX	1	IR 67954-46-1-3-2
X	4	IR 65597-29-3-2-3, IR 66159-189-5-5-3 (NPT), IR 66160-121-4-5-3 (NPT), IR 65600-127-6-2
XI	2	IR 68167-28-3-2-2, IR 69432-54-1-1-2-2 (NPT)

**Intra and inter cluster analysis**

Intra and inter clusters distance of 24 genotypes of rice are presented in Table 6. The highest intra clusters distance were recorded for cluster III (13.268), while the intra clusters distance were disappeared within the clusters I, V, VII, VIII and IX (zero distance) cause each cluster contain only one genotype. In respect of inter clusters distance, the lowest was found between cluster II and X (22.017) while, the highest distance was found between cluster V and IX (102.605). On the other hand, the genotypes grouped into the same cluster, as well as, the lowest values of inter cluster distance indicating a close relationship between them and exhibited the lowest divergence's degree from one another. Therefore, the hybridization made between genotypes belonging to the

same cluster or between genotypes of closed related clusters; no transgressive segregants are predicted from these combinations. In addition, the highest values inter cluster distance suggesting the maximum variability among them. Thus, hybridization programmes could be designed in such a way that the parental genotypes relating to different clusters with high amount of divergence could be used to get appropriate transgressive segregants. These results are in agreement with those obtained by Chaturvedi and Maurya (2005), Yadav *et al.*, (2011), Eswaran (2012) and Kumar *et al.*, (2013). So, it is proposed that hybridization should be attempted between the genotypes relating to cluster separated by large inter cluster distances.

**Table 6. Intra cluster distances (Bold) and inter cluster distances (D<sup>2</sup>) for 24 rice genotypes.**

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	0.00	41.751	35.058	28.660	59.963	57.288	73.301	45.216	47.635	49.888	59.923
II		6.343	24.195	34.441	76.058	53.329	73.563	59.620	57.218	22.017	37.786
III			13.268	29.913	75.449	37.789	62.776	60.750	54.192	24.262	31.100
IV				10.179	49.767	52.906	62.137	33.957	36.834	47.210	58.273
V					0.00	82.124	79.755	26.135	41.564	92.026	102.605
VI						10.426	42.836	76.360	63.952	53.741	51.861
VII							0.00	78.487	60.903	80.400	82.774
VIII								0.00	41.238	75.833	87.771
IX									0.00	69.827	79.728
X										15.145	19.350
XI											11.406

**Principal component analysis**

Principal component analysis (PCA) explained the genetic diversity of the different genotypes of rice. PCA measure the importance and contribution of each component to total variance. Also, it could be used for measurement of independent impact of a particular trait to the total variance. Whereas, each coefficient of proper vectors indicates the degree of contribution of every original variable with each principal component is associated. Therefore, PCA help researchers to distinguish significant relationship among the traits. The eigenvalues are often used to determine how many factors involved in the present variation.

The results presented in Table 7 revealed that, the traits are associated, so to understand their distinct impact, principal component analysis was studied. The first five components in PCA analysis with eigenvalues >1, which contributed 76.376% of the variation for the 24 rice genotypes were estimated for 17 agro-morphological traits. The other PCs (6-17) had values less than one. The first PC, with eigenvalue of 4.753, contributed 27.959% of the total variation, while the second PC with eigenvalue of 2.579 accounted for 15.173% of total variation for 24 genotypes of rice. PC3 had eigenvalues of 2.026 and contributed 11.916% for total variation. PC4 and PC5 had eigenvalues of 1.904 and 1.722, respectively and contributed 11.20% and 10.129% for the total variability.

The first principal component accounted for more than 27% of the total variance. The variables that had moderately to highly values and positively correlated were grain length with loading of 0.910, grain shape (0.828), plant height (0.811), amylose content% (0.747), 1000-grain weight (0.633) and panicle length (0.521).

First component identified number of panicles/plant that presenting negative contributions. As a result, the first component differentiated those accessions that had grain length, grain shape, plant height, amylose content%, 1000-grain weight, panicle length variation and low number of panicles/plant. The second principal component PC2 accounted for more than 15% variation and was associated with spikelets fertility% (-0.709), panicle exertion% (0.695), gelatinization temperature (0.657) and panicle length (0.556). PC3 was more related to number of filled grains/panicle (0.771) and days to 50% heading (0.611). In PC4, the variables moderately and positively correlated were milling% with loading of 0.643, head rice% (0.582), grain yield/plant (0.552) and hulling% (0.548). PC5 was related to grain elongation % (0.548) and days to 50% heading (-0.530).

Therefore, the distinguished traits that coupled in different principal components and sharing towards explaining the variance has the trend to remain together that to be considering during exploitation of these traits in rice breeding program. Four traits, viz., grain length, grain shape, plant height and amylose content% contributed highly positively to PC1. In PC1, grain length showed the heaviest positive weight. The traits with positive weight in PC2 were panicle exertion% followed by gelatinization temperature and panicle length; therefor, this component measured by vegetative traits. The traits with highly positive weight in PC3 were number of filled grains/panicle (0.771) which is one of yield contributes in nature and followed by days to 50% heading (0.611) which is vegetative in nature. The traits with positive weight in PC4 were milling% followed by head rice%, grain yield/plant and hulling%. The above results suggested that such as in PC1, PC2, PC3 and PC4,

each of the genotype contributes both vegetative and yield component traits and, in other cases, each genotype contributes only in one-side, either yield components or vegetative, as vegetative in PC2 and yield components in PC4.

The tool of PCA has an efficient application in choice of parental genotypes for different breeding objectives. The cumulative variance of 76.376% by the first five axes with eigenvalue of > 1.0 shows that the related traits which belong to the axes displayed great impact on the morphology of these genotypes, and could efficiently be used for choice among them. In general, the results are in agreement with those reported by Chakravorty et al., (2013), Gana et al., (2013) and Sarwar et al., (2015).

**Table 7. Principal component analysis (PC) of 17 agro-morphological traits for rice genotypes.**

Traits	Component				
	PC1	PC2	PC3	PC4	PC5
Days to 50% heading	-0.162	0.175	0.611	0.072	-0.530
Plant height	0.811	0.233	-0.121	-0.205	0.272
Panicle exerssion%	0.361	0.695	-0.313	0.096	-0.079
Panicle length	0.521	0.556	0.455	0.034	0.240
No. of panicles/plant	-0.589	0.119	-0.444	0.218	0.263
No. of filled grains/panicle	0.181	0.085	0.771	0.094	0.453
1000-grain weight	0.633	0.017	0.166	-0.015	-0.196
Grain yield/plant	0.481	0.339	0.119	0.552	0.146
Spiklets fertility%	0.374	-0.709	0.124	-0.296	-0.075
Hulling%	0.292	-0.481	-0.224	0.548	0.435
Milling%	0.497	-0.404	-0.229	0.643	0.112
Head rice%	0.215	-0.297	0.408	0.582	-0.313
Grain length	0.910	-0.037	-0.170	-0.183	-0.195
Grain shape	0.828	0.040	-0.291	-0.255	-0.129
Grain elongation%	0.252	0.289	0.049	-0.255	0.548
Amylose content%	0.747	-0.249	-0.105	-0.066	-0.324
Gelatinization temperature	-0.053	0.657	-0.297	0.420	-0.453
Eigenvalue	4.753	2.579	2.026	1.904	1.722
% variance contribution	27.959	15.173	11.916	11.200	10.129
Cumulative variance contribution	27.959	43.131	55.048	66.248	76.376

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## دراسة التنوع الوراثي في بعض التراكيب الوراثية للأرز لبعض الصفات المورفولوجية والمحصولية وصفات الجودة

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أجريت هذه الدراسة لتقدير التنوع الوراثي لبعض التراكيب الوراثية للأرز في موسمين زراعيين متتاليين ٢٠١٤، ٢٠١٥. تم إجراء هذه التجربة في المزرعة البحثية لمحطة بحوث سخا. وكذلك تقدير بعض الصفات الوراثية مثل معامل التباين الوراثي والمورفولوجي ودرجة التوريث والتحسين الوراثي لكل الصفات المدروسة كما تم تقدير طبيعية وأهمية التنوع الوراثي باستخدام تحليل Mahalanobis D<sup>2</sup> لسبعة عشر صفة تحت الدراسة وكانت أهم النتائج :- سجلت صفة طرد السنبل ودرجة الجلنتة و نسبة استطالة الحبوب ونسبة الأميلوز تقديرات عالية لمعامل التباين الوراثي والمورفولوجي . كما كانت نسبة معامل التوريث بالمعنى الواسع عليه لكل الصفات المدروسة، حيث ارتبطت القيم العالية لكلا من معامل التوريث في المدى الواسع والتحسين الوراثي لصفات عدد الحبوب الممتلئة لكل دالية ، ارتفاع النبات، نسبة استطالة الحبوب وطرد السنبل. وقد قسمت التراكيب الوراثية الأربعة وعشرون المستخدمة على أساس التباين الوراثي إلى إحدى عشر مجموعة. وكانت المجموعة الثالثة أكبر المجاميع التي احتوت على خمسة تراكيب وراثية وتلاها المجموعة الخامسة بأربع تراكيب وراثية، بينما احتوت المجاميع السادسة والحادية عشر على تركيبين وراثيين لكل مجموعة. على أي حال اشتملت المجاميع الأولى والخامسة والسابعة والثامنة والتاسعة كل منها على تركيب وراثي واحد. وكان أعلى تباين وراثي (١٠٢,٦٠٥) بين المجموعة الخامسة والحادية عشر بينما كان أقل تباين وراثي (٢٢,٠١٧) بين المجموعة الثانية والثالثة. أوضح تحليل المكونات الرئيسية (PCA) لسبعة صفات كمية وهي طول الحبة وشكل الحبة وارتفاع النبات ونسبة الأميلوز ووزن الألف حبة و عدد الفروع المثمرة لكل نبات وطول الدالية اختلافات عالية المعنوية بين التراكيب الوراثية المستخدمة لذلك تهدف هذه الدراسة الى تحديد مدى اتساع التباين الوراثي للتراكيب الوراثية والتي يمكن استخدامها في تطوير برامج تربية وتحسين الأرز في برامج التربية المستقبلية.