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## Multivariate Analysis of Genetic Diversity among some Rice Genotypes Using Morpho-agronomic Traits

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### ABSTRACT

The availability of access to diverse genetic material is important to be successful in any plant breeding effort. An investigation was undertaken to assess genetic diversity of 24 known rice genotypes based on 17 morpho-agronomic traits by using multivariate analyses: hierarchical cluster and Principal Component (PC) analyses. Cluster analysis separated the genotypes into two groups which are in contrast for flowering, plant types, biomass, grain yield, seed width, seed length and seed weight. The first three PCs explained 73.5% of the total variability. Days to flowering, plant height, culm length, panicle length, biomass, seed length and shape were the important traits in differentiating the genotypes. The hierarchical cluster and PC analyses were in agreement in grouping the genotypes. Parental combinations from the two clusters with higher value of Euclidean distance could be used for genetic improvement. Generally KOH1 is the most diverged genotype from others. Thus crossing of this genotype with Azucena, CH1, KDML105 and SPR1 may result in heterotic expression in the  $F_1$  and substantial variability in the subsequent segregating population.

**Key words:** Genetic diversity, multivariate analysis, morpho-agronomic traits, NERICA, rice

### INTRODUCTION

More than half of the population of the world depends on rice as the main source of food. Rice is one of the world's most important food crops in terms of its production and area coverage. About 11% of the world's cultivated land is devoted for its production. Among the continents of the world, Asia is the first both in production and consumption of rice. Most of the Asians get 35-75% of their calories from rice (Khush, 2005). In the year 2011 about 164.1 million ha of land was used for rice production worldwide. In the same year nearly equal amount of land was allocated for rice in the content of Africa and in Thailand (FAO, 2013).

Genetic diversity has a multitude of importance. It is considered as a means of survival and adaptation to changing environments (Gao, 2003; Rao and Hodgkin, 2002); it has a role in collection and conservation of germplasm and crop improvement (Duran *et al.*, 2009). Moreover, the information helps to study heterosis as genetic diversity between parents is generally related to the magnitude of heterosis (Virk *et al.*, 2003). This shows the necessity of divergent parents in any crossing program in order to be benefited from the hybrid vigor in the  $F_1$  and from the variability created in the subsequent segregating population. Whether the objective is hybrid or

pure-line variety development, the availability of and access to diverse genetic material is important to be successful in any plant breeding effort (Hoisington *et al.*, 1999; Naik *et al.*, 2006; Maxted *et al.*, 2002; Rohman *et al.*, 2004).

Evaluation of genetic resources for various agronomic traits and the assessment of the amount of genetic variation within them is useful to allow more efficient genetic improvement (Hausmann *et al.*, 2004). In order to further improve the already adapted crop varieties for traits of agronomic importance, crossing with other parents with proved agronomic superiority is necessary. This calls for the assessment of genetic diversity and identification of parental lines for hybridization or crossing. The present investigation was undertaken with the objective to assess genetic diversity of some known rice genotypes by using morpho-agronomic traits and to identify the most important character in differentiating the genotypes.

## MATERIALS AND METHODS

**Experimental materials and place of study:** In the genetic diversity study, a total of 24 rice genotypes were used. The materials include 13 *indica*, four *japonica*, four New Plant Types, one tropical japonica and two NERICA genotypes (Table 1). NERICA signifies New Rice for Africa; genotypes developed by interspecific hybridization of *O. glaberrima* and *O. sativa* (Samado *et al.*, 2008). The trial was conducted at Kasetsart University, Bangkhen Campus, Bangkok, Thailand during 2012 rainy season.

**Experimental design and data collection:** The treatments were arranged in a randomized complete block design with three replications. A spacing of 20 cm between genotypes and between

Table 1: Description of the 24 rice genotypes used for the diversity analysis using 17 morpho-agronomic traits

Name	Type	Origin
NERICA 3	Interspecific cross	Cote d'Ivoire
NERICA 4	Interspecific cross	Cote d'Ivoire
KOH1	japonica	Japan
TW1	japonica	Taiwan
TW2	japonica	Taiwan
NI	japonica	Japan
NPT4	New plant type	Philippines
NPT8	New plant type	Philippines
NPT13	New plant type	Philippines
NPT18	New plant type	Philippines
Azucena	Tropical japonica	Philippines
CH1	indica	China
CH2	indica	China
CH3	indica	China
PTT1	indica	Thailand
CNT1	indica	Thailand
SPR1	indica	Thailand
PSL60-2	indica	Thailand
KDML105	indica	Thailand
IR64	indica	Philippines
RD31	indica	Thailand
TDK1	indica	Laos
TDK5	indica	Laos
CO39	indica	India

plants was left. Fertilization and insecticide application were done uniformly to all plots. The plants were protected from the possible damage of birds and rats by wire mesh. Data for 17 morphological and agronomic traits were collected from each plot using the Standard Evaluation System for rice (IRRI, 2002). Paddy-rice seed width and length were measured as averages of 15 seeds by using digital Rice Grain Analyzer. The traits studied include days to flowering, No. of total tillers, number of productive tillers, plant height (cm), culm length (cm), flag-leaf length (cm), panicle length (cm), number of total spikelets, number of fertile spikelets, 100-seed weight (g), biomass (g), yield per plant, harvest index (%), seed width (mm), seed length (mm), seed shape (length, width ratio) and spikelet fertility (%).

**Data analyses:** Analysis of Variance (ANOVA) was computed by using CropStat7.2 and the mean values of traits were used for further analysis. The mean values were then standardized to a mean of zero and variance of unity before cluster analysis to remove the biases due to differences in the scale of measurement. PAST 1.93 (Palaeontological Statistics; Hammer *et al.*, 2001) computer software was used for phenotypic correlation, cluster and principal component analyses.

## RESULTS

**Analysis of variance:** The univariate ANOVA showed significant ( $p < 0.01$ ) variation among the rice genotypes for all the morpho-agronomic traits considered (Table 2). The significance signifies the possibility of using all traits for further analysis. From the result it was observed that CO39 was the earliest (75.3 days) while KDML105 was the latest (149.67 days) genotypes to flower. Similarly, CO39 and Azucena were the shortest (68.69 cm) and the tallest (167 cm) genotypes, respectively.

Table 2: Minimum and maximum mean values and overall means, standard errors and coefficients of variation of 17 morpho-agronomic traits of 24 rice genotypes

Traits	MS (df = 23)	Minimum		Maximum		Mean±SE	CV (%)
		Value	Cultivar	Value	Cultivar		
Days to flowering	1081.24**	75.33	CO39	149.67	KDML105	106.97±2.97	4.80
Total tillers	21.05**	3.33	NERICA3	14.89	CNT1	8.11±1.14	24.30
Productive tillers	16.64**	3.13	NERICA3	10.78	NPT8	6.73±1.15	29.60
Plant height (cm)	1940.85**	68.69	CO39	167.00	AZUCENA	111.43±5.72	8.90
Culm length (cm)	1596.25**	46.96	CO39	137.78	AZUCENA	85.01±4.74	9.70
Flag leaf length (cm)	144.79**	32.58	IR64	56.29	CH1	43.77±4.09	16.20
Panicle length (cm)	50.43**	17.56	KOH1	32.09	NPT8	26.42±1.73	11.40
Total spikelets	13726.00**	61.33	NI	342.56	CH1	205.12±17.67	14.90
Fertile spikelets	7820.19**	55.89	KOH1	277.22	CH1	151.00±16.22	18.60
100-seed weight (g)	0.39**	1.68	CH3	3.15	NERICA3	2.48±0.95	6.70
Biomass (g)	1699.46**	8.87	KOH1	90.45	TDK5	48.88±10.53	37.30
Yield per plant (g)	118.53**	5.04	KOH1	29.06	CH1	16.25±3.74	39.90
Harvest index (%)	524.16**	15.26	TDK1	66.10	CO39	37.89±5.24	23.90
Seed width (mm)	0.24**	2.04	NPT8	3.01	TW1	2.37±0.06	4.00
Seed length (mm)	5.71**	6.55	TW1	10.85	TDK5	9.22±0.13	2.40
Seed shape	2.31**	2.18	TW1	5.00	NPT8	3.99±0.09	3.80
Spikelet fertility (%)	289.47**	57.24	NPT18	95.18	NI	74.67±4.23	9.80

\*\* : Significant at 0.01 probability level

The analysis also showed that KOH1 was the lowest (5.04 g) whereas, CH1 was the highest (29.06 g) in yield among the genotypes. Also, NPT18 and NI were the least (57.24%) and the most (95.18%) fertile genotypes identified, respectively.

**Phenotypic correlation:** In order to assess traits association, phenotypic correlation analysis was done and the result is depicted in Table 3. Generally the result showed high order of correlation between most of the traits under study. Days to flowering was highly and significantly correlated with plant height (0.883), culm length (0.893), biomass (0.772) and harvest index (-0.732). Similarly, yield per plant was highly and significantly correlated with total tillers (0.541), plant height (0.525), panicle length (0.649), total spikelets (0.585), filled spikelets (0.539), biomass (0.716), seed length (0.606) and seed shape (0.622) towards the positive direction. Also, strong and significant association of harvest index was detected with days to flowering (-0.732), plant height (-0.603), culm length (-0.601), total spikelets (-0.455), biomass (-0.705) and spikelet fertility (0.710). Spikelet fertility was negatively correlated to all traits under study except harvest index.

**Euclidean distance:** Euclidean distance matrix was produced by assuming 276 total possible pairwise combinations of the 24 rice genotypes (Table 4). The distance coefficients ranged from 1.142 for NERICA3-NERICA4 to 10.267 for KOH1-Azucena pairwise cultivar combinations with a mean of 5.172. Also TW1-TW2 (1.743), CH2-CH3 (1.848) and NPT4-NPT18 (1.976) were the next smaller pairwise Euclidean distances. Similarly, the next higher distance values were that of KOH1 with CH1 (10.183), KDML105 (9.788) and SPR1 (9.368). KOH1 is generally the most diverged genotype from others with higher mean Euclidean distance of 7.426 while RD31 was the least with mean Euclidean distance of 4.41.

**Hierarchical cluster analysis:** Hierarchical clustering was attempted by using paired group algorithm with different distance measures like Gower, Euclidean, Mahalanobis and Manhattan. The result showed that Gower, Euclidean and Manhattan distance measures yielded similar dendrogram topology and similar cluster membership of the rice genotypes; however, Mahalanobis distance measure yielded different dendrogram topology which was characterized by chaining of genotypes. The dendrogram of the morpho-agronomic traits grouped the genotypes into two clusters with additional subgroups in each groups. Group I was composed of 17 genotypes and group II included 7 genotypes. Group I was made up of miscellaneous type of genotypes as it was composed of 10 *indica*, four NPT, one tropical japonica and two NERICA types. This group was further divided into four subgroups: Subgroup1 contained the two NERICAs; subgroup 2 was made up of the four NPTs and seven *indica* types; subgroup 3 contained a distinct cultivar CH1, this variety was characterized by longer flag-leaf, higher number of spikeletes and higher yield and subgroup 4 included KDML105, Azucena and TDK1. Members of this subgroup were late maturing and tall plant types. However, group II contained four *japonica* and three *indica* types. This group also further divided in to three subgroups: Subgroup 1 contained TW1 and TW2 (*japonica* types); subgroup 2 was made up of CH2, CH3 and CO39 (*indica* types) and subgroup 3 was composed of NI and KOH1, *japonica* types (Fig. 1). ANOVA was run to declare whether any of the mean differences of the traits between the two groups were significant. Accordingly, the result showed significant ( $p < 0.01$ ) differences for most of the traits under study except for traits related to tillers and spikeletes and harvest index. On average, the genotypes in cluster II were significantly earlier

Table 3: Phenotypic correlation coefficients between 17 morpho-agronomic traits in 24 rice genotypes

Parameters	DF	TNT	PT	PHT	CL	FLL	PNL	TSP	FSP	HSW	BM	YLD	HI	SW	SL	SSH
TNT	0.023															
PT	-0.164	0.910**														
PHT (cm)	0.883**	-0.001	-0.156													
CL (cm)	0.893**	-0.059	-0.216	0.990**												
FLL (cm)	0.362	-0.303	-0.261	0.579**	0.540**											
PNL (cm)	0.451*	0.325	0.248	0.631**	0.518**	0.554**										
TSP	0.511*	0.017	-0.146	0.561**	0.525**	0.533**	0.530**									
FSP	0.382	-0.082	-0.251	0.514*	0.492*	0.587**	0.422*	0.924**								
HSW (g)	0.077	-0.028	0.003	0.202	0.126	0.328	0.550**	0.039	-0.081							
BM (g)	0.772**	0.345	0.218	0.798**	0.770**	0.351	0.614**	0.614**	0.428*	0.231						
YLD (g)	0.376	0.541**	0.497*	0.525**	0.464*	0.431*	0.649**	0.585**	0.539**	0.166	0.716**					
HI (%)	-0.732**	-0.127	0.033	-0.603**	-0.601**	-0.139	-0.357	-0.455*	-0.211	-0.185	-0.705**	-0.152				
SW (mm)	-0.132	-0.302	-0.254	-0.375	-0.330	-0.178	-0.472*	-0.285	-0.379	0.219	-0.301	-0.431*	0.056			
SL (mm)	0.413	0.198	0.165	0.667**	0.597**	0.476*	0.780**	0.300	0.305	0.400	0.605**	0.606**	-0.252	-0.711**		
SSH	0.337	0.301	0.262	0.601**	0.537**	0.387	0.706**	0.334	0.373	0.147	0.550**	0.622**	-0.209	-0.888**	0.947**	
SFF	-0.428*	-0.194	-0.172	-0.257	-0.215	-0.020	-0.386	-0.387	-0.029	-0.252	-0.543**	-0.204	0.710**	-0.027	-0.138	-0.095

DF: Days to flowering, TNT: Total No. of tillers, PT: Productive tillers, PHT: Plant height, CL: Culm length, FLL: Flag-leaf length, PNL: Panicle length, TSP: Total spikelets, FSP: Filled spikelets, HSW: Hundred-seed weight, BM: Biomass, YLD: Yield per plant, HI: Harvest index, SW: Seed width, SL: Seed length, SSH: Seed shape, SFF: Spikelet fertility

\*\*, \*: Significant at 0.01 and 0.05 probability levels, respectively

Table 4. Pairwise Euclidean distance coefficients for all possible combinations of the 24 genotypes using 17 morpho-agronomic traits

Parameters	AZUCENA	CHI	CH2	CH3	CNT1	CO39	IR64	KDML105	KOHI	NERICA3	NERICA4	NI	NPT13	NPT18	NPT4	NPT8	PSL60-2	PTT1	RD31	SPR1	TDK1	TDK5	TW1	TW2	
CHI	5.666																								
CH2	7.283	6.102																							
CH3	7.230	7.028	1.848																						
CNT1	7.135	4.812	5.938	7.174																					
CO39	9.399	8.192	3.249	3.775	7.147																				
IR64	7.264	6.397	3.860	4.636	3.669	4.644																			
KDML105	3.045	5.338	7.093	7.239	6.174	8.744	6.365																		
KOHI	10.267	10.183	5.260	5.129	8.912	3.558	6.163	9.788																	
NERICA3	6.499	5.965	5.763	5.857	6.596	6.193	5.558	6.225	6.945																
NERICA4	6.751	6.055	5.434	5.652	6.467	5.829	5.369	6.394	6.337	1.142															
NI	10.222	9.194	5.089	6.041	6.993	3.958	5.205	9.613	3.639	7.571	6.888														
NPT13	6.563	6.980	4.821	4.852	5.415	5.111	3.100	6.072	5.962	4.331	4.435	6.346													
NPT18	5.472	4.834	5.819	6.262	4.353	7.002	4.628	4.777	8.672	5.600	5.954	8.145	4.021												
NPT4	6.278	5.636	5.880	6.265	4.546	6.781	4.522	5.596	8.130	5.550	5.802	7.624	4.050	1.976											
NPT8	6.461	4.457	5.575	6.624	2.627	6.888	3.987	5.699	9.061	6.428	6.503	7.685	4.780	3.314	4.445										
PSL60-2	5.122	4.686	5.389	5.873	3.599	7.315	3.820	4.186	8.901	6.340	6.468	8.021	4.866	3.215	3.725	3.459									
PTT1	6.119	4.026	4.980	6.061	2.220	6.240	3.167	4.961	8.009	5.118	4.995	6.730	4.269	3.676	4.347	2.142	3.285								
RD31	6.254	5.403	5.062	5.872	2.899	5.857	2.531	5.385	7.377	5.010	5.053	6.365	2.861	3.115	3.687	2.491	3.469	1.988							
SPR1	5.280	4.087	6.547	7.219	3.516	7.886	4.740	4.035	9.368	5.324	5.554	8.516	4.840	3.164	4.296	3.065	3.208	2.415	2.833						
TDK1	4.355	6.860	6.727	6.525	6.230	7.983	5.312	3.911	8.383	5.632	5.858	8.713	3.953	4.297	4.998	5.566	4.298	5.059	4.251	4.063					
TDK5	5.677	5.513	6.445	6.941	3.926	7.737	4.252	4.450	9.020	6.173	6.342	8.363	4.129	2.684	3.613	3.280	2.830	3.228	2.756	2.420	3.359				
TW1	7.513	8.012	5.572	5.462	7.397	5.528	5.851	7.214	5.516	6.152	6.116	6.272	4.430	5.007	4.524	7.034	6.640	6.594	5.600	6.927	5.845	6.229			
TW2	7.159	7.123	5.429	5.599	6.054	5.708	5.619	6.543	6.150	6.180	6.134	6.218	4.898	4.448	3.878	6.526	5.873	5.984	5.322	6.299	5.937	5.832	1.7434		

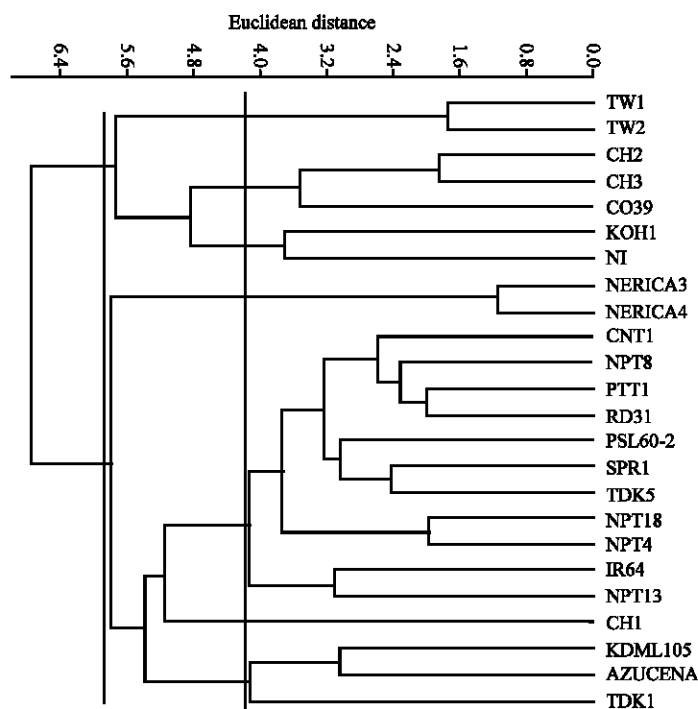


Fig. 1: Dendrogram of 24 rice genotypes based on 17 morpho-agronomic traits constructed by means of paired group algorithm and Euclidean distance

(91.8 vs. 113.2 days) and shorter (82.99 vs. 123.15 cm) than that of cluster I. Compared with cluster I, the genotypes in cluster II had significantly lower biomass (26.38 vs. 58.14 g) and grain yield (11 vs. 18.41 g) (Table 5).

**Principal component analysis:** The result of the principal component analysis (PCA) is depicted in Fig. 2 and Table 6. The objective of principal component analysis is reduction of dimensionality of a data set with a large number of correlated variables or traits (Jolliffe, 2002). PCA was carried out by using 24 genotypes and 17 traits. In the analysis a total of 17 PCs, equals to the number of traits, were extracted. However, the first five PCs with eigen values greater than 1 were retained. The result showed that 89.68% of the variability was explained by the first five Principal Component (PC) axes. Out of the five, the first and the second explained 44.52 and 16.64% of the variation, respectively. Days to flowering, plant height, culm length, panicle length, biomass, seed length and shape were the important traits contributing to the first PC. In the second PC, however, total and productive tillers were important. Similarly, flag-leaf length, harvest index, seed width and spikelet fertility were important in the third axis. While only 100-seed weight was important in the fourth axis. Total and filled spikelets and yield per plant were the important traits contributing to the fifth PC (Table 6). The first axis differentiated genotypes which were late flowering, tall, higher in biomass and grain yield, with slender (narrow and tall) seeds from genotypes which were early flowering, short, low biomass and grain yield with round (wide and short) seeds. The second axis however differentiated genotypes with higher total and productive tillers from those with low tillers. Generally the PC analysis broadly grouped the genotypes based



Table 5: Mean-squares and cluster means for 17 morpho-agronomic traits of the 24 rice genotypes

Traits	MS (df: 1)	Mean	
		Cluster 1 (n: 17)	Cluster 2 (n: 7)
Days to flowering	2272.02**	113.22	91.81
Total tillers	4.42	8.39	7.44
Productive tillers	0.83	6.85	6.44
Plant height (cm)	7998.04**	123.15	82.99
Culm length (cm)	5131.35**	94.40	62.23
Flag leaf length (cm)	295.70**	46.02	38.30
Panicle length (cm)	317.06**	28.76	20.76
Total spikelets	18337.86*	222.86	162.05
Fertile spikelets	7793.82	162.57	122.92
100-seed weight (g)	0.94**	2.60	2.17
Biomass (g)	5003.70**	58.14	26.38
Yield per plant (g)	272.46**	18.41	11.00
Harvest index (%)	605.14	34.67	45.71
Seed width (mm)	0.53**	2.27	2.60
Seed length (mm)	36.40**	10.01	7.30
Seed shape	11.66**	4.44	2.90
Spikelet fertility (%)	151.47	73.06	78.59

\*\* , \* : Significant at 0.01 and 0.05 probability levels

Table 6: Eigenvalues, total variance, cumulative variance and eigenvectors for 17 morpho-agronomic traits in the 24 rice genotypes

Traits	Axis 1	Axis 2	Axis 3	Axis 4	Axis 5
Days to flowering	<b>0.276</b>	-0.212	-0.225	-0.111	-0.235
Total tillers	0.083	<b>0.501</b>	-0.213	-0.173	0.082
Productive tillers	0.035	<b>0.543</b>	-0.176	-0.061	0.110
Plant height (cm)	<b>0.327</b>	-0.161	-0.007	0.009	-0.223
Culm length (cm)	<b>0.307</b>	-0.201	-0.013	-0.041	-0.277
Flag leaf length (cm)	0.219	-0.211	<b>0.271</b>	0.215	0.262
Panicle length (cm)	<b>0.299</b>	0.132	0.029	0.283	0.171
Total spikelets	0.262	-0.160	0.038	-0.290	<b>0.431</b>
Fertile spikelets	0.228	-0.172	0.266	-0.325	<b>0.375</b>
100-seed weight (g)	0.101	-0.009	-0.124	<b>0.709</b>	0.244
Biomass (g)	<b>0.321</b>	0.023	-0.230	-0.076	-0.014
Yield per plant (g)	0.272	0.239	0.065	-0.101	<b>0.299</b>
Harvest index (%)	-0.218	0.147	<b>0.439</b>	0.070	0.143
Seed width (mm)	-0.196	-0.258	<b>-0.334</b>	0.175	0.284
Seed length (mm)	<b>0.289</b>	0.162	0.197	0.278	-0.216
Seed shape	<b>0.278</b>	0.231	0.254	0.077	-0.244
Spikelet fertility (%)	-0.151	0.007	<b>0.496</b>	-0.023	-0.138
Eigenvalue	7.568	2.829	2.099	1.498	1.251
Variance (%)	44.517	16.643	12.349	8.815	7.362
Cumulative variance (%)	44.517	61.16	73.509	82.324	89.685

on zones of origin into temperate and tropical categories. The ones located to left of the two dimensional plane being temperate with the exception of CO39, while those to the right being tropical in zone of origin (Fig. 2).

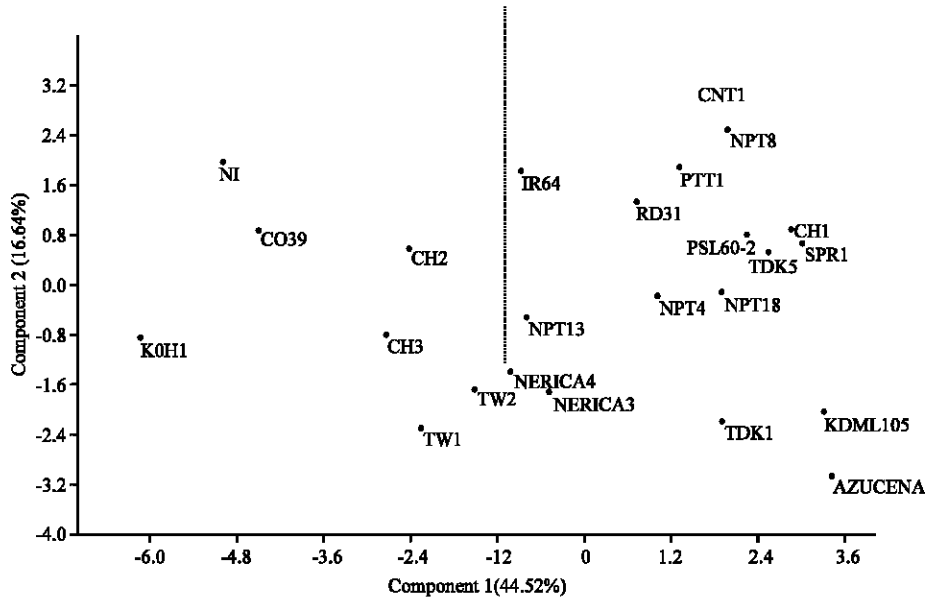


Fig. 2: Scattered distribution of the 24 rice genotypes by using 17 morpho-agronomic traits on the first two principal component axes

## DISCUSSION

The significant ( $p < 0.01$ ) variation among the rice genotypes for all the morpho-agronomic traits and the range of values obtained for most of the traits indicates a sizable variability in the genotypes studied for the 17 traits considered. The correlation study showed that late flowering is important in attaining tall plant types, higher biomass and lower harvest index. It also showed that more number of tillers, tall plant types (increased height and panicle length), higher number of spikelets, heavier above ground mass, seed length and shape were the important traits in attaining higher yield per plant in rice. However, early flowering, short plant types (lower height and culm length), lower number of total spikelets, light above ground-mass but higher level of spikelet fertility are important to improve harvest index. Significant correlations of yield and yield-related traits were reported by other workers in inbred lines, hybrids and landrace rice (Chakravorty *et al.*, 2013; Janwan *et al.*, 2013; Seesang *et al.*, 2013).

The pairwise Euclidean distance coefficients estimated in this study ranged from 1.142-10.267 with a mean of 5.172. However, Caldo *et al.* (1996a) estimated a range of Euclidean distance varying between 2.23 and 16.71 with a mean of 7.55 for 78 improved rice genotypes by using 33 qualitative and quantitative traits. In a separate study of 81 ancestral lines of Philippines modern rice genotypes, Caldo *et al.* (1996b) computed Euclidean distance estimates ranging from 3.97-17.389 with a mean of 8.80 using 41 traits. The output of hierarchical cluster analysis exhibited similar dendrogram topology and cluster membership of the rice genotypes for Gower, Euclidean and Manhattan distance measures. This confirms the stability of the dendrogram constructed. Generally, the first group was characterized by late flowering, tall plant types, higher biomass and grain yield, slender (narrow and long) and heavier seeds. Unlike the first group, the second group was characterized by early flowering, short plant types, lower biomass and grain yield, round (wide and short) and light weighted-seeds.

Principal Components (PCs) are orthogonal and independent of each other (Mohammadi and Prasanna, 2003); they explain the variability which was not explained by the others. In this study, the total variability was explained by five PCs. This may indicate the contribution of many traits with higher level of correlation to explain the gross diversity. In a study of Caldo *et al.* (1996b), 75% of the variability was accounted for by seven PCs. In their work, Chakravorty *et al.* (2013) explained the total variability by six PC axes; Caldo *et al.* (1996a, b) explained 67% of the variation by 10 PCs. Jolliffe (2002) stated that PCs are ordered so that the first few retain most of the variation present in all of the original variables. In this experiment, the first and the second PCs explained 61.16% of the variability, the first being the most important. Accordingly, the traits included in the first PC especially those with comparatively high loadings are important in separating the genotypes. Generally, the PC analysis showed high level of diversity of the rice genotypes as the entire variation cannot be explained by few principal components. High level of simple sequence repeat (SSR) DNA marker diversity was also reported for the same set of genotypes investigated (Worede *et al.*, 2013).

## CONCLUSION

The study showed the presence of considerable level of diversity in the genotypes analyzed and the importance morpho-agronomic traits to study genetic diversity. Days to flowering, plant height, culm length, panicle length, biomass, seed length and shape were the important traits in differentiating the genotypes under study. The hierarchical cluster analysis was in general agreement with the PC analysis in grouping the genotypes into two clusters. Parental combinations from the two clusters with higher value of Euclidean distance (dissimilarity) coefficient could be used for genetic improvement by crossing. Generally KOH1 is the most diverged genotype from others. Thus crossing of this genotype with the likes of Azucena, CH1, KDML105 and SPR1 may result in heterotic expression in the F<sub>1</sub> and substantial variability in the subsequent segregating population.

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