

GENETIC VARIABILITY AND ASSOCIATION STUDY OF DIFFERENT AGRONOMIC TRAITS WITH YIELD IN RICE

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ABSTRACT

This study was performed to evaluate the diversity of various morphological characters and their relationship with yield in rice. At the time of maturity different traits were recorded under normal field conditions in Randomized Complete Block Design (RCBD) experiment. Significant variation was observed in all genotypes with respect to their desired traits. Plant yield, number grains per panicle, unfilled grains per panicle and plant height showed highest genetic variability. Highly significant association of 1000 grain weight was observed positive with panicle length, grains per panicle, seed setting% and yield per plot/hectare showed positive association with seed setting and 1000 grain weight ($r=0.31^{**}$, $r=0.34^{**}$, $r=0.45^{**}$, $r=0.66^{*}$, $r=0.48^{*}$, $r=0.58^{**}$, $r=0.56^{**}$). Biplot analysis (PCA) was also conducted for both qualitative and quantitative traits. Days to flowering (34.2 %) showed highest variability followed by days to maturity, plant height, panicle length, tillers per plant and grains per panicle (18.7%, 12.4%, 7.90%, 6.80%, 5.90% respectively). The scree plot, score plot and loading plot showed greatest genetic variability among the genotypes and the desirable traits. This study will hopefully, be beneficial in selection of parents to produce desirable recombinants for rice breeding program.

Keywords: Agronomic traits, Association, *Oryza sativa*, Variability, Yield.

INTRODUCTION

Rice (*Oryza sativa* L.) crop accounts for major food of the world and more than 3.5 billion people dependent on it (Yang and Zhang, 2010; Hu *et al.*, 2015). Rice species cultivated in diverse climatic conditions in more than 100 countries worldwide (Muthayya *et al.*, 2014). Genetic diversity and any crop improvement program depend upon the availability of genetic resources by the application of different breeding and molecular approaches that may fulfill the world's rice requirements through development and improvement of new high yield rice varieties (Kush, 2005). Genetic variability among the germplasm is a key characteristic of crop plants along with other desirable traits that are helpful for the enhancement of production and having resistance against biotic and abiotic stresses (Pratap *et al.*, 2014).

Rice grain yield and other yield related traits can be improved by the utilization of modern techniques i.e. genetic recombination, mutation and molecular breeding for increasing the selection efficiency of plants based on qualitative and quantitative traits (Akinwale *et al.*, 2011; Oladosu *et al.*, 2014). This can also be useful for maintaining, refreshing and enhancement of germplasm under changing climatic conditions.

Rice adaptation and adopting intensified cropping system can also be helpful for the enhancement yield and improved agricultural traits depending upon the selection criteria and genetic variability (Yu *et al.*, 2003; Wang *et al.*, 2003). Rice grain yield and other genotypic and phenotypic traits are influenced by environment and also associated with each other. On the other hand, extent of genetic variation among germplasm and significant association of yield and yield related traits should be considered for the selection and improvement of new plant population (Habib *et al.*, 2005; Pandey *et al.*, 2009; Dutta *et al.*, 2013). The success of conventional and molecular breeding also associated with the presence of genetic variability in the population and ability of the traits to transfer from one generation to another. This will enhance the selection process of the new plant population and their various agricultural traits that associated with the yield and selection of the varieties (Yang *et al.*, 2007; Yang and Hwa, 2008; Shahidullah *et al.*, 2009). Thousands of rice varieties are evolved through the processes of hybridization, mutation and natural selection from wild species. Phenotypic and genotypic variability in germplasm is an important step to the plant breeders for the best plant population selection for further enhancement of yield potential of the crop (Singh *et al.*, 2000; (Ogunbayo *et al.*, 2014; Moosavi *et al.*, 2015).

The objectives of this study were the (1) evaluation of rice based on morphological traits and (2) Screening of

rice genotypes on the basis of yield and other related characters. All the genotypes used in this study had significant genetic divergence.

MATERIALS AND METHODS

The experiment was conducted in the year 2019 at the University of the Punjab, Lahore in the experimental field area under RCBD design with three replications. Various desirable traits were measured at the maturity stage of each genotype.

Plant material

Seeds of one hundred rice germplasm lines were collected from world renowned institutes i.e. Rice Research Institute (RRI) Kala Shah Kaku, Lahore, Pakistan and United States Department of Agriculture (USDA), USA. The germplasm lines comprised of land races, approved varieties, advanced breeding lines and cultivars.

Field evaluation

Seeds of 100 germplasm lines were used for field evaluation at research area of department. Seeds were soaked and sown in puddled field conditions using broadcasting method. Nursery was transferred to field after 25 days in RCBD design with three replications used for each sample. Fertilizer was applied in between 25-40 days of transplant of seedlings with a ratio of 120:60:60 kg/ha NPK.

Morphological Traits

All the germplasm lines were evaluated on the basis of various qualitative and quantitative traits i.e. days to 50% flowering, days to maturity, plant height, tiller per plant, panicle length, grains per panicle, unfilled grains/panicle, seed setting percentage, 1000 grains weight, yield/plot and yield/hectare. All the data were recorded at the time of maturity of each genotype. On the basis of studied traits all the genotypes showed greatest genetic diversity.

Statistical analysis

Variance analysis was used for analyzing the data of recorded traits of all genotypes. Desirable traits of all the genotypes were also analyzed by using Principal Component Analysis (PCA) to determine the genetic variability for these traits. Mean values of all the recorded traits of genotypes used for PCA analysis. For this purpose SAS version 9.2 (SAS Institute, 2008) was used for analyzing of each genotype.

RESULTS AND DISCUSSION

There is significant difference between genotypes yields and its related traits as shown by ANOVA (Table 1). There is a significant phenotypic difference among observed accessions. Documentation of genotypic variation will be useful for further studies as the phenotypic data exhibited a wide difference. For effective breeding scheme some knowledge about genetic variation of germplasm is very necessary for screening and selection in breeding process. The variation in germplasm is very helpful to identify these variations either due to genetic or environment (Dutta *et al.*, 2013). For widening the gene pool of rice germplasm genetic variation of the yield and dependent factors are crucial for breeding scheme (Konate *et al.*, 2019). Crop improvement is followed by genetic diversity by which various characteristics are screened. A positive significant genetic differences and correlation studies among the genotypes along with desired traits provides the information to the researcher for better selection of genotypes (Ogunbayo *et al.*, 2014; Paswan *et al.*, 2019; Srivastava *et al.*, 2017).

All the growing genotypes were different from each other by its characters that also been determined by (Girma *et al.*, 2018; Paswan *et al.*, 2019). The information regarding the growing of genotypes for crop improvement is utmost crucial. There is valuable information obtained by phenotypic & genotypic factors. For breeding desirable traits heritability, variation and correlation played an important role in this aspect (Bekele *et al.*, 2013; Kamana *et al.*, 2019). For selection and other breeding applications genetic variation of traits is important (Tiwari *et al.*, 2019). Hence the grown genotypes shown variation in different traits. Due to significant difference, the genetic improvement is absolute.

CORRELATION ANALYSIS

Correlation analysis enabled us to get information of the relationship between variables (Khatun *et al.*, 2015). The positive association was observed in days to 50% flowering with unfilled grains per panicle and plant height ($r=$

0.57**; $r=0.59^{**}$). The results are presented in the Table 2. Plant height and panicle length was positively correlated with days to maturity ($r=0.45^{**}$; $r=0.43^{**}$). The highly significant positive correlation observed by plant height along with panicle length, number of grains per panicle, seed setting percentage and 1000 grain weight ($r=0.41^{**}$; $r=0.63^{**}$; $r=0.59^{**}$; $r=0.62^{**}$). Tillers per plant has highly positive association with seed setting percentage ($r=0.05^{**}$). Panicle length has significant positive relationship with 1000 grain weight and yield per hectare ($r=0.31^{**}$; $r=0.51^{**}$). Grains per panicle has positive association with 1000 grain weight, yield per plot and yield per hectare ($r=0.34^{**}$; $r=0.29^{*}$; $r=0.36^{*}$). A positive association was observed between unfilled grains per panicle and seed setting percentage ($r=0.63^{**}$). Seed setting percentage positively correlated with 1000 grain weight ($r=0.45^{**}$), yield per plot ($r=0.66^{**}$), yield per hectare ($r=0.58^{**}$), while 1000 grain weight has positive relationship with yield per plot and yield per hectare ($r=0.48^{**}$; $r=0.56^{**}$). Yield per plot has positive association with yield per hectare ($r=0.51^{**}$). Thus, all related traits will be utilized for increasing the yield potential of the crop (Nor *et al.*, 2014; Hossain *et al.*, 2015; Islam *et al.*, 2016).

Knowledge about correlation coefficients is very essential because the grain yield and other quantitative traits are influenced by many factors (Hossain *et al.*, 2015; Girma *et al.*, 2018). So, correlation is one of the best methods to find out the relation among various traits (Sravan *et al.*, 2012). Plant height has not significantly associated with yield described by (Golam *et al.*, 2011; Nor *et al.*, 2014; Kamana *et al.*, (2019) and positive association of days to 50 % flowerings with number of grains per panicle and plant height investigated by (Khan *et al.*, 2014; Girma *et al.*, 2018) for numbers of panicles. The best correlation had been displayed between the. Similarly observations were supported by Aris *et al.* (2010), Kohnaki *et al.* (2013) and Paswan *et al.* (2019).

Hence, the correlation studies are, therefore necessary to lead the way of frequency of traits and the screening compulsory to be measured in improving traits for instance grain yield. The outcomes of the current experiment showed that there was presence of significantly high correlation among grains yield along with other agronomic characters. Alike results were previous stated by Gulzar and Subhasl (2012), Khatun *et al.*, (2015) and Moosavi *et al.*, (2015).

Principal component and cluster analysis

The results of PCA expressed in Table 3, 4 and Fig 1. Principal components having more than more than one eigen value that showed more variability among the traits studied for each genotype. Three components showed collective variability is 65.3%. The PC1 had 34.2%, PC2 showed 18.7% and PC3 exhibited 12.4% variability between the genotypes and their various traits under study. The variance and eigen value associated with principal components that decreased gradually and stopped at 0.70%. The first PC was more related to days to maturity, plant height, tillers per plant, grains per panicle, seed setting %, 1000 grain weight, yield per plot and yield per hectare were the most related traits for the consideration. In second principal component the days to 50% flowering, days to maturity, plant height, tillers per plant, panicle length, grains per panicle, unfilled grains per panicle and seed setting % were the most related traits. The third principal component exhibited positive effects for days to 50% flowering, plant height, tillers per plant, grains per panicle, 1000 grain weight that showed maximum variation for these characters. It was also cleared that all the principal components showed maximum variation for days to 50% flowering; number of tillers per plant and 1000 grain weight. On the basis of similar morphological characters rice genotypes classified in to different clusters as mentioned in Fig. 4. The grouping or clustering of genotypes were done on the basis of various morphological characters. The genotypes with similar traits/characters were classified in the same group.

Based on the eigen value principal components variation considered to be very important in screening and selection of the genotypes (Sharma *et al.*, 2006). Principal components and eigen values that showed genetic differences among genotypes as shown in the Fig. 1. Higher number eigen values showed more variability and also helpful for selection of parents and improvements of varieties through breeding (Shahidullah *et al.*, 2009).

In biplot principal component analysis almost all traits showed positive effect on their respective genotypes except two traits number of grains per panicle and unfilled grains per panicle. This showed the diversity of the genotypes along with the desired characteristics. This type of information will be very useful for further screening of genotypes for the development of new plant population and start up a new breeding program (Fig 2). In loading plot component traits association showed positive effects with each other along with their principal components (Fig 3).

In the current study the genotypes divided into four main clusters and fourteen sub clusters with respect to their same genotypic and phenotypic traits that can be utilized for in breeding program for screening and development of new plant population (Sanni *et al.*, 2008; Seetharam *et al.*, 2009). The study is equally beneficial for breeders and researchers to utilize in their research to the best interest of the community and economy of the country.

Table 1. Mean squares values of genetic variability of studied traits.

S.O.V	D.F	DF	DM	PH	TP	PL	G/P	UG/P	SS	TGW	Y/P	Y/H
Replications	2	1.85	3.61	315.46	4.68	3.17	140.28	213.20	102.10	1.13	1.33	133022
Genotypes	99	8.93*	6.63*	448.61**	32.14**	10.06**	1715.02**	333.83**	98.33**	38.30**	1.02**	2501472**
Error	198	6.48	3.68	28.00	4.22	2.14	548.94	104.83	20.13	4.1	0.31	122303

DF= Days to 50% Flowering, DM= Days to Maturity, PH= Plant Height (cm), TP= Tiller per Plant, PL= Panicle Length (cm), G/P= Grains per Panicle, UG/P= Unfilled grains/Panicle, SS= Seed Setting percentage, TGW= 1000 Grains weight (g), Y/P= Yield/plot (kg), Y/H= Yield/hectare (Kg)

Table 2. Correlation analysis among studied traits in 100 rice genotypes during (2018-19).

Traits	DF	DM	PH	TP	PL	G/P	UG/P	SS	TGW	Y/P	Y/H
DF50%	1.00										
DM	-0.35*	1.00									
PH	0.57**	0.45**	1.00								
TP	-0.41**	0.13NS	0.25*	1.00							
PL	0.31*	0.43**	0.41**	-0.05NS	1.00						
G/P	-0.51**	0.13NS	0.63**	0.36*	0.11NS	1.00					
UG/P	0.59**	0.12NS	-0.11NS	-0.09	0.39*	0.13NS	1.00				
SS%	0.23*	0.38*	0.59**	0.05**	0.36*	-0.12NS	0.63**	1.00			
TGW	-0.58**	0.15NS	0.62**	0.35*	0.31**	0.34**	-0.22NS	0.45**	1.00		
Y/plot	-0.36*	0.06NS	0.23*	0.14*	0.36*	0.29*	0.08NS	0.66**	0.48**	1.00	

Table 3. PCA analysis of 100 rice genotypes on the basis of phenotypic traits.

Variable	Eigen Vectors										
	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11
DF50%	-0.147	0.469	0.119	0.534	-0.225	0.104	0.301	0.370	0.340	0.227	-0.060
DM	0.224	0.065	-0.483	0.649	0.144	-0.146	0.034	-0.300	-0.395	-0.027	-0.037
PH	0.170	0.472	0.336	-0.108	0.132	0.396	-0.129	-0.444	-0.224	0.419	0.103
T/P	0.440	0.150	0.019	0.067	0.034	0.367	-0.100	0.303	-0.009	-0.541	0.499
PL	-0.099	0.494	-0.279	-0.157	0.218	-0.287	-0.625	0.331	-0.005	0.051	-0.104
G/P	0.265	0.355	0.048	-0.339	0.125	-0.512	0.601	0.070	-0.179	-0.049	0.092
U/G/P	-0.257	0.076	-0.444	-0.196	0.543	0.482	0.348	0.025	0.135	-0.059	-0.151
SS%	0.420	0.102	-0.183	-0.056	-0.044	-0.117	-0.068	-0.423	0.747	-0.070	-0.118
TGW	0.327	-0.373	0.048	0.115	0.471	-0.098	-0.026	0.305	0.165	0.561	0.267
Y/plot	0.236	-0.034	-0.535	-0.289	-0.571	0.216	0.060	0.168	-0.134	0.383	0.063
Y/H	0.468	-0.065	0.200	0.000	0.052	0.173	-0.013	0.263	-0.158	-0.075	-0.777

Table 4. Traits variability of 100 rice genotypes with respect to Eigen value, variation% and cumulative%.

Traits	PC	Eigen Value	% Variation	Cumulative Value	Cumulative %
DF50%	PC1	3.7605	34.2	0.342	34.2
DM	PC2	2.0564	18.7	0.529	52.9
PH	PC3	1.3604	12.4	0.652	65.2
T/P	PC4	0.8689	7.90	0.731	73.1
PL	PC5	0.7436	6.80	0.799	79.9
G/P	PC6	0.6528	5.90	0.858	85.8
U/G/P	PC7	0.4906	4.50	0.903	90.3
SS%	PC8	0.4702	4.30	0.946	94.6
TGW	PC9	0.2986	2.70	0.973	97.3
Y/plot	PC10	0.2157	1.90	0.993	99.3
Y/H	PC11	0.0824	0.70	1.000	100

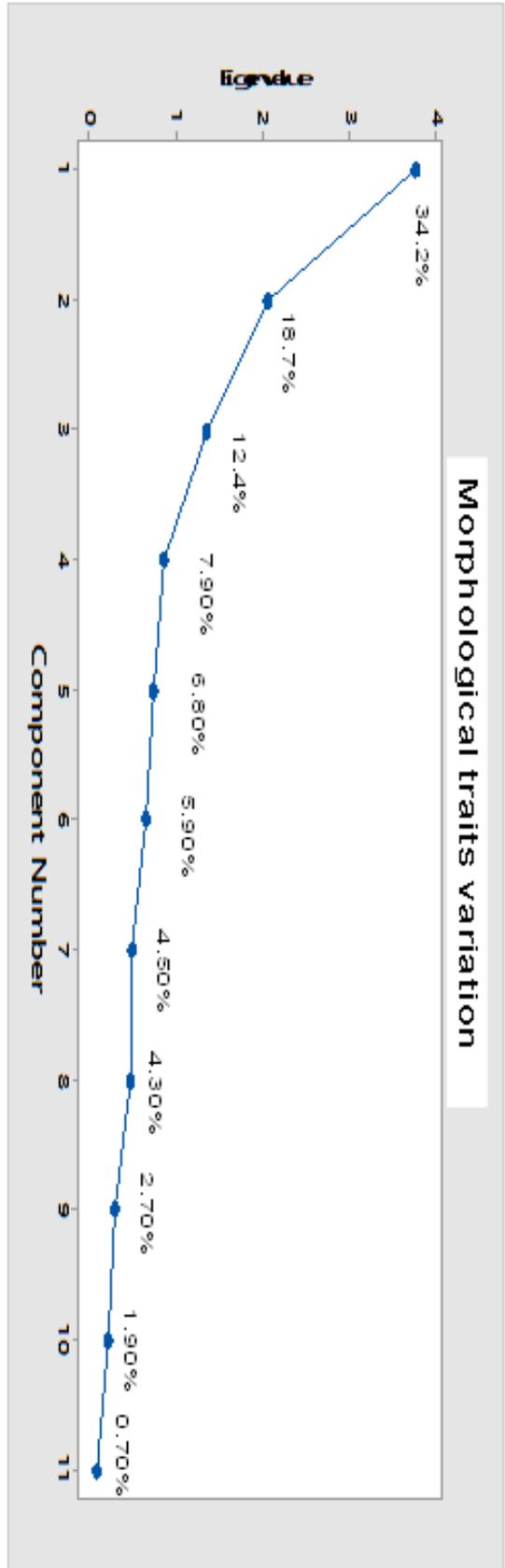


Fig. 1. Scree plot showed relationship between Eigen values and the number of principal components of 100 rice genotypes on the basis of morphological traits.

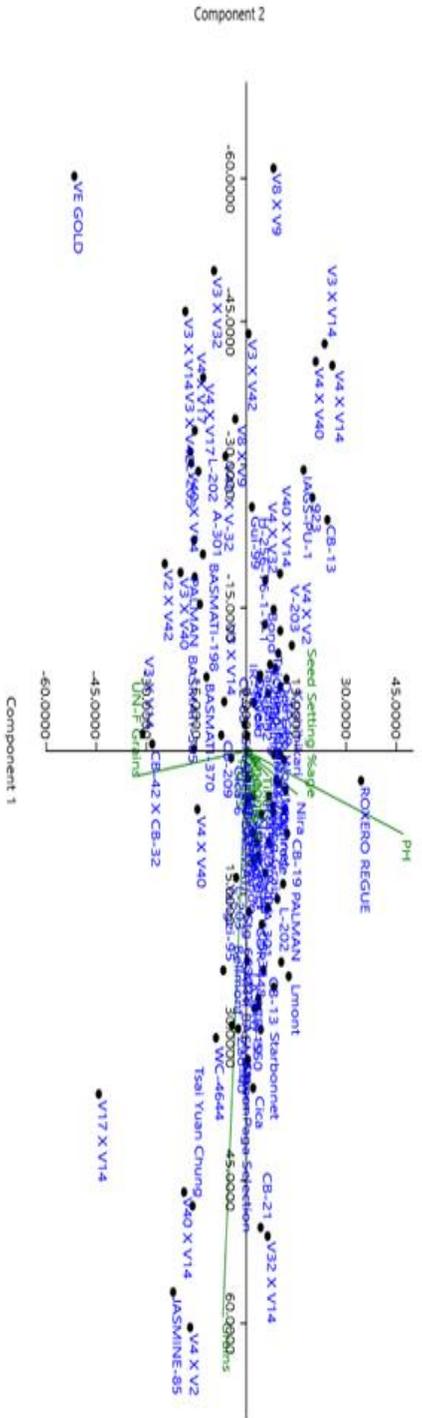


Fig. 2. Biplot PCA analysis of 100 genotypes of rice between their traits and the principal components numbers.

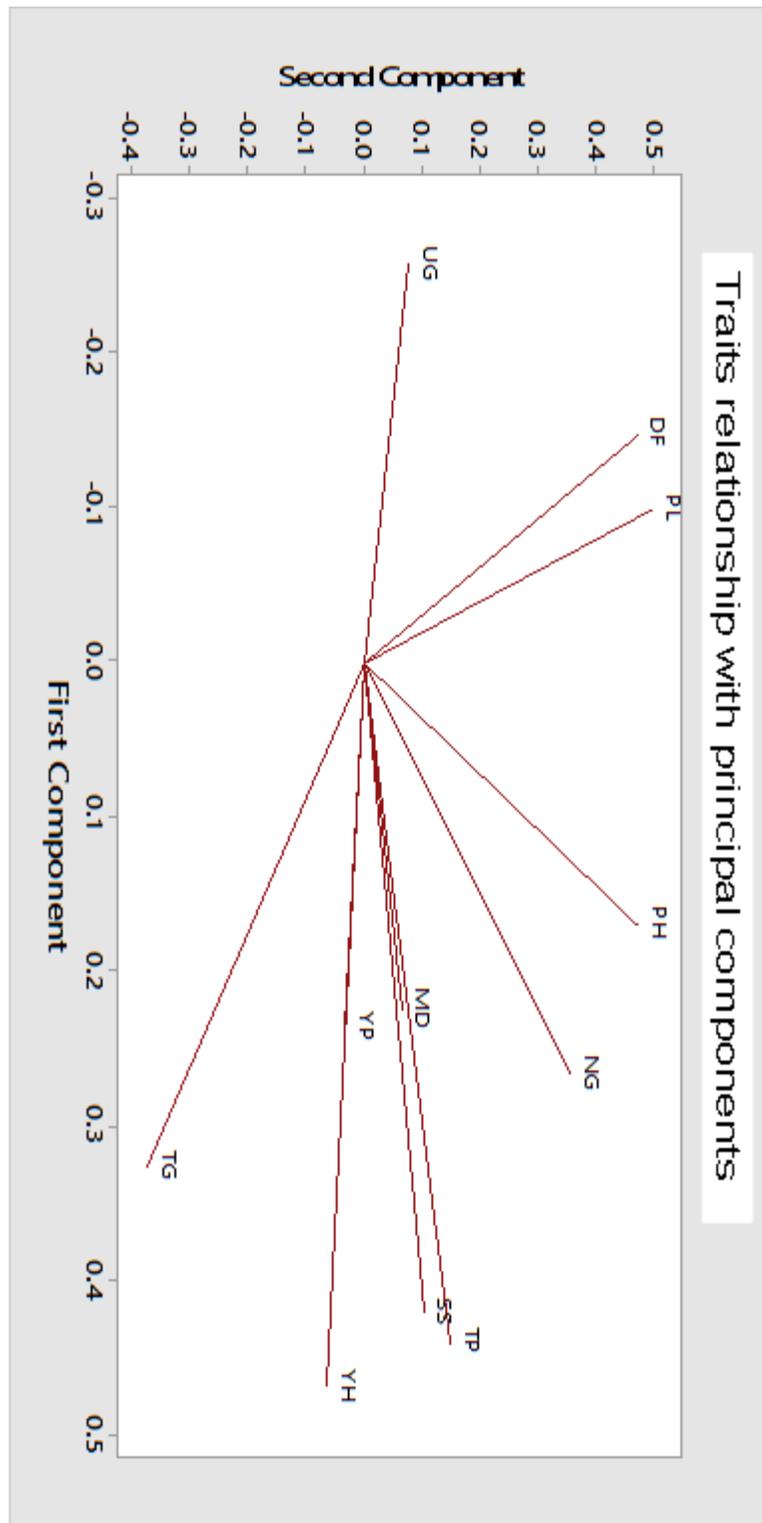


Fig. 3. Loading plot 100 genotypes PCA analysis of rice between desirable traits and the number of principal components.

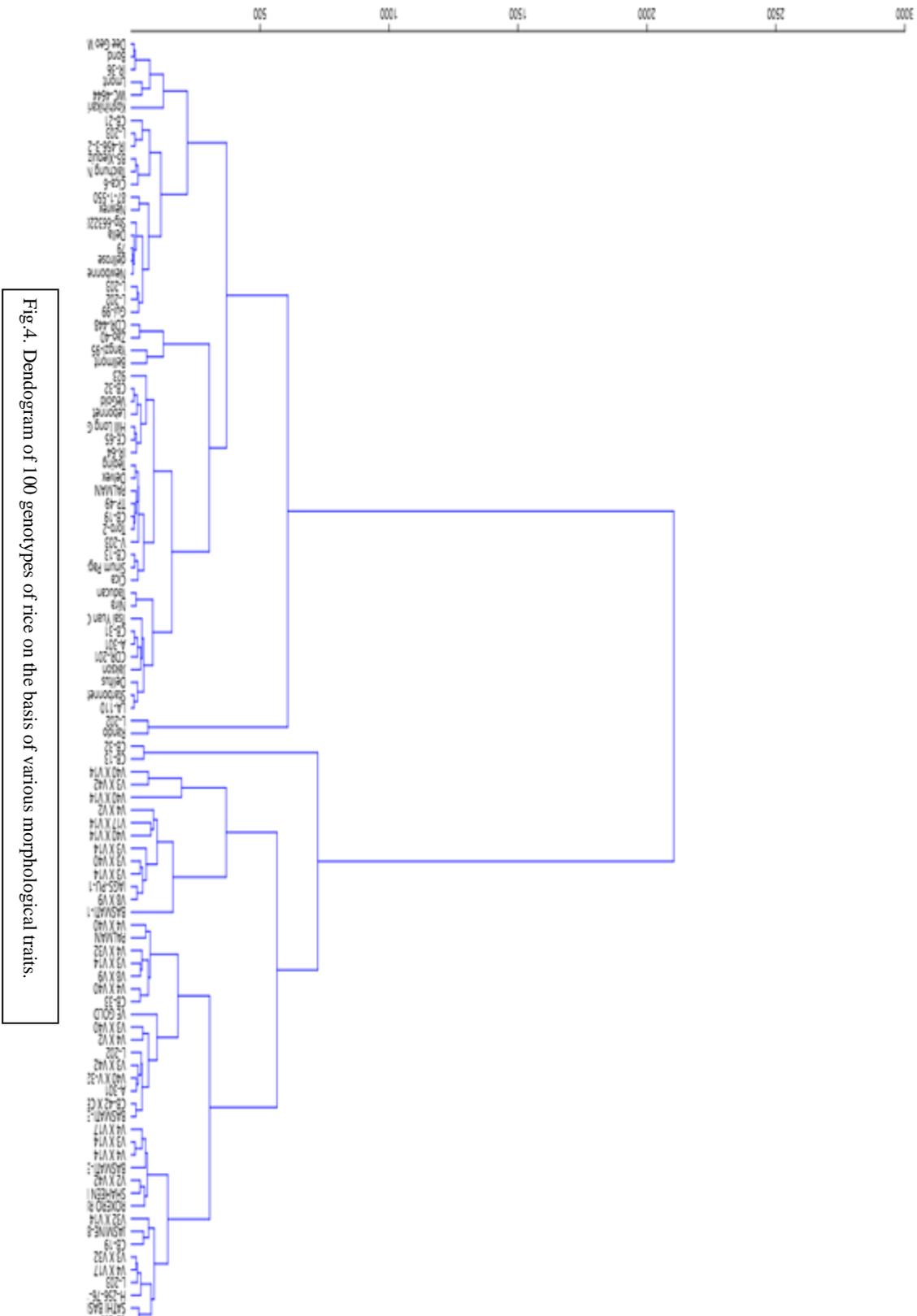


Fig.4. Dendrogram of 100 genotypes of rice on the basis of various morphological traits.

CONCLUSION

Number of genotypes have been identified based on various yield and related traits. The following genotypes (CB-13, CB-19, CB-21, L-202 and Palman) with better yield and yield related traits will be very useful in future breeding program for the improvement and development of new plant population with high genetic potential in climatic changing environment. Such types of genotypes would also be very useful for the production significant transgressive segregants. For indirect selection, quantitative traits seeds per panicle, panicle length, 1000 grain weight, yield per plot and yield per hectare could be used for the screening of high yielding rice genotypes.

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