



**Full Length Article**

## Association of Various Morphological Traits with Yield and Genetic Divergence in Rice (*Oryza sativa*)

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### ABSTRACT

This study was carried out to assess the genetic diversity for various rice traits and their association with yield. The experiment was conducted in field condition with natural environmental and data on various plant parameters for each genotype were recorded at different stages of plant development. Forty rice genotypes were evaluated on the basis of various morphological traits in a field experiment. There was a significant variation for all the traits studied among the genotypes. The results indicated that the highest genetic variability was observed in plant height, spikelets per panicle, panicle length, days to heading and days to maturity. Significant correlation with yield was also noticed for Panicle length ( $r=0.265^{**}$ ), seeds per panicle ( $r=0.266^{**}$ ) and seed weight per panicle ( $r=0.339^{**}$ ) showed significant positive correlation with grain yield. All the traits were also studied through principal component analysis (PCA). The highest variability was observed in plant height, tillers per plant, panicle length and flag leaf area. The combined variation among these traits was 67.7%. The twenty selected genotypes on the basis of yield parameters were further evaluated for the seed traits measurements using vernier caliper. All the seed traits studied also showed significant variation amongst the genotypes. The seed length and seed width showed maximum variation (88%) with respect to other seed traits. The derived information would be very useful to select potentially breeding lines for future rice improvement program. © 2012 Friends Science Publishers

**Key Words:** Rice; *Oryza sativa*; Yield; Correlation; PCA; Morphological traits; Seed traits

### INTRODUCTION

Any crop improvement program depends on the utilization of germplasm stock available in different research organizations/institutes of the world. So to meet the world's rice requirements will also depend upon the development of high yielding varieties having resistance against biotic and abiotic stresses using conventional and biotechnological approaches (Khush, 2005).

Improvement of the rice grain yield per unit area is the only way to achieve increased rice production because of the reduction in area devoted to rice production (Cassman, 2003). Irrigated rice contributes >75% of total rice production, although it accounts for about 55% of total rice area (Fairhurst & Dobermann, 2002). Rice yield can also be increased by adopting the intensified cropping system (Wang *et al.*, 2003 and Yu *et al.*, 2003).

Rice grain yield is a quantitative polygenic character and highly influenced by environment. Extent and significance of association of yield with yield components should be considered, while determining the selection criteria of germplasm on the basis of available genetic variation (Habib *et al.*, 2005). The success of breeding program also depends upon the amount of genetic

variability present in the population and extent to which the desirable traits are heritable. Different morphological traits play very important role for more rice production with new plant type characteristics associated with the plant yield (Yang *et al.*, 2007; Yang & Hwa, 2008). Phonological properties of rice also associated with the yield potential of the different rice varieties for the selection of the best varieties that further involved in rice breeding program (Shahidullah *et al.*, 2009).

Thousands rice cultivars have been evolved through selection from the cultivated material many centuries ago, which are well adapted to the local environments. Many of those rice cultivars having good quality characteristics and higher yield potential under biotic and abiotic stress environments. Since the dawn of civilization, thousands of locally adapted genotypes of aromatic rice have evolved through human selection (Singh *et al.*, 2000).

Study of genetic divergence among the plant materials is an important tool to the plant breeders for an efficient selection of the diverse parents for their potential use in a rice breeding program for the improvement of the rice production. Parents identified on the basis of divergence for any breeding program would be more promising (Arunachalam, 1981; Kwon *et al.*, 2002).

The appearance of rice with bran (brown) and without bran (white) is important to the consumers. Thus, components of appearance traits are one of the first criteria for rice quality that breeders consider in developing new varieties for open release and commercial production (Dela & Khush, 2000). Grain shape is an important agronomic trait in cereal crops such as rice, wheat, and barley because it is directly or indirectly related to quality and quantity of grain products (Ayoub *et al.*, 2002; Bresseghello & Sorrels, 2006; Zheng *et al.*, 2007). Factors contributing to general grain appearance are grain size, shape and colour. Intensive work has been done by breeders to select for bright, clear, translucent grains with spindly shape (Graham, 2002; Sharifi *et al.*, 2009).

Rice seed length and width are the two important quantitative traits also closely related to the exterior quality of the rice (Shi *et al.*, 2000). Genetic analyses of length and width of rice kernels have been reported by some of the researchers and most of the studies have shown that rice grain shape is quantitatively inherited (He *et al.*, 1999; Zhang *et al.*, 2005). It has been shown that rice grain shape is controlled by triploid endosperm genes, cytoplasmic genes, and maternal genes (Shi *et al.*, 2005) and their genotype into environment interaction effects.

The length, width and seed thickness is one of the quantitative measures of grain shape. Grain morphology i.e. color, size and shape having unique position for the breeders during the selection and evaluation process (Kasem *et al.*, 2009; Bai *et al.*, 2010). It is thought to relate to the largest shape variation in small grain crops. On the other hand, length width ratio is the major genetic variation of rice grain shape and highly associated with the quantitative traits parameters and can be used in the breeding program for the improvement of the rice varieties (Iwata *et al.*, 2010).

In this study, first we measured the morphological traits of forty genotypes of rice under field condition at the reproductive stage of each genotype for the selection of best parents on yield parameter basis. Secondly the selected parents on yield basis were further evaluated on the basis of grain shape of each genotype i.e., length, width and thickness. All the genotypes used in this study were the basmati type genotypes except IRRI-6, KSK 282 and KSK-133. The objectives of this study were to (1) evaluate the phenotypic diversity of rice based on morphological traits and seed parameters and (2) Identification of the morphological traits responsible for the yield difference among the rice genotypes.

## MATERIALS AND METHODS

**Plant material:** This study comprised of 40 varieties/lines (31 advance lines & 9 improved varieties) i.e., CB-4, CB-5, CB-10, CB-11, CB-12, CB-13, CB-14, CB-15, CB-16, CB-17, CB-19, CB-20, CB-21, CB-22, CB-26, CB-27, CB-28, CB-29, CB-30, CB-31, CB-32, CB-33, CB-34, CB-36, CB-38, CB-39, CB-40, CB-41, CB-42, CB-43, CB-44, Basmati-

385, Basmati-Super, Basmati-198, Basmati-2000, IRRI-6, KSK-282, KSK-133, Basmati-Pak and Basmati-370. All the material was obtained from Rice Research Institute (RRI) Kala Shah Kaku Lahore.

**Nursery preparation:** Before sowing, seeds of all genotypes were treated with fungicide (2 g Benlate/kg) of rice seed. All the seeds were soaked in water at 30°C for two days. The soil was also well prepared for the growing of rice nursery. The sandy clay loam soil was used for this purpose. The seeds of each genotype were sown separately in different blocks through broadcasting method. Rice nursery was used for transplanting within 30 to 40 days after the date of sowing.

**Transplantation:** The nursery of all the rice genotypes was transplanted in the field using randomized complete block design (RCBD) with three replications. Nine inches row to row and plant to plant distance was maintained for each genotype in each replication. Each block consisted on 5 lines of each genotype with 10 transplanted plants. Herbicides were used for the controlling of weeds. Agrochemicals were also used for the controlling insect pest and diseases.

**Recording data:** Some morphological traits were measured at the physiological maturity stage taking 10 plants from each genotype. Plant height was measured in cm from the plant base to the tip of the highest leaf (or panicle, whichever was longer). Productive tillers of each plant were counted to determine the total number of panicles in each plant. The panicle length of the central tiller of the each plant was measured in cm. The leaf breadth and length was measured in centimeter of main tiller of each plant of the flag leaf with respect to the each genotype. The spikelet's per panicle of main tiller of each plant were counted at maturity stage, Seeds per panicle of main tiller of each plant was counted separately after harvesting, Seed weight per panicle of main tiller of each plant was measured in grams after harvesting, The 1000 seed weight of each genotype was measured after harvesting, The whole plant yield of each genotype was measured in grams after harvesting of each genotype, Days to heading of each genotype was determined when 50% plants of an entry have shown ear emergence starting from the date of sowing and days to maturity of each genotypes was determined at the maturity stage when 50% plants of an entry have matured starting from the date of sowing.

**Seed traits measurements:** On the basis of morphological traits 20 genotypes i.e., CB-13, CB-14, CB-15, CB-16, CB-17, CB-19, CB-21, CB-27, CB-32, CB-33, CB-36, CB-38, CB-39, CB-40, CB-42, Basmati-385, Basmati-Super, Basmati-198, Basmati-2000 and Basmati-Pak performing better with respect to yield and yield contributing traits were selected for further studies. Seed length and width of these genotypes were measured using vernier calipers. The seed length, width and thickness of these genotypes were measured with bran and without bran. The 10 seeds of each genotype were randomly selected for the seed size and

shape measurement. First we measured the seeds of each genotype with bran, and then after removing the husk manually measured the seeds of all genotypes without bran.

**Seed classification:** The seed size and shapes of each genotype were measured by using vernier calipers. Seed size was defined by the length of the seeds of each genotype in its longest dimension and was categorized as very long (>7.50 mm), long (6.61-7.50 mm), medium (5.51-6.60 mm) and short (< 5.50 mm). Seed shape was defined by the length: width (L/W) ratio and ranges from slender (3.0 or >3.0), medium (2.1-3.0), bold (2) and round (1 or < 1). Length and width ratio was calculated by the following formula.

$$\text{Seed length width ratio} = \frac{\text{Seed Length (mm)}}{\text{Seed Width (mm)}}$$

**Statistical analysis:** Data were analyzed by two-way analysis of variance (ANOVA). Principal Component analysis was also used to determine genetic variability for these traits. Genotypic means were used for the PCA with

respect to each trait. Each data analysis was conducted by using SAS (Statistical Analysis System) version 9.2 (SAS Institute, 2008).

## RESULTS

Two way ANOVA (Analysis of variance) indicated significant ( $P < 0.01$  &  $0.05$ ) effects of genotypes in almost all the traits studied. The analysis of variance of mean square values of all the morphological traits are presented in the Table I. All the genotypes showed highly significant variations for all the traits studied. Furthermore there was a significant effect of genotypic into environmental interaction on all the traits. The extent of variability for any character is very important for the improvement of crop through breeding. Significant variation in all the traits studied indicated the presence of high genetic diversity among all the genotypes of rice. Plant height, spikelets per panicle, seeds per panicle, and days to heading and maturity days showed highest variations among the genotypes.

**Table I: Mean square values of 12 morphological parameters of rice under field condition**

Source of Variation	D.F	PH (cm)	T/P (cm)	PL (cm <sup>2</sup> )	FLA	PB/P	S/P	Seed/p (g)	SW/P (g)	1000GW (g)	PY	HD	MD
Genotypes	39	667.52**	13.62**	17.75**	57.92**	3.44**	1445.26**	1228.97**	0.3**	18.23**	40.09**	402.91**	469**
Replication	2	135.70	5.47	6.95	177.62	9.00	430.17	25.52	0.380	31.82	98.30	8.72	178.53
Error	78	14.44	2.67	7.10	6.97	1.05	387.32	215.11	0.102	2.34	23.46	0.887	84.51

Level of significance  $p < 0.05 = *$  and  $P < 0.01 = **$

PH= plant height; T/P= tillers per plant; PL= panicle length; FLA= flag leaf area; PB/P= primary branches per panicle; S/P= number of spikelets per panicle; Seed/p=number of seeds per plant; SW/P=seed weight per plant; 1000GW=1000 grain weight; PY=plant yield; HD=heading days; MD=maturity days

**Table II: Simple correlations among different morphological traits of rice under field condition**

Traits	PH	T/P	PL	FLA	PB/P	S/P	Seed/P	SW/P	1000GW	PY	HD	MD
PH	1.00											
T/P	-0.030ns											
PL	0.662**	-0.086ns										
FLA	0.395**	-0.160ns	0.302**									
PB/P	0.431**	-0.213*	0.490**	0.372**								
S/P	0.453**	-0.135ns	0.608**	0.162ns	0.584**							
Seed/P	0.197*	-0.236**	0.365**	0.169ns	0.393**	0.552**						
SW/P	0.027ns	-0.193*	0.328**	0.099ns	0.231**	0.437**	0.770**					
1000GW	-0.082ns	-0.159ns	0.018ns	-0.127ns	0.079ns	0.076ns	-0.053ns	-0.112ns				
PY	0.141ns	0.095ns	0.265**	0.134ns	0.170ns	0.121ns	0.266**	0.339**	-0.042ns			
HD	0.416**	0.052ns	0.321**	0.208*	0.116ns	0.389**	0.293**	0.159ns	-0.118ns	0.165ns		
MD	0.418**	0.095ns	0.375**	0.175*	0.157ns	0.373**	0.148ns	0.077ns	-0.107ns	0.076ns	0.654**	1.00

Level of significance  $p < 0.05 = *$  and  $P < 0.01 = **$

**Table III: Eigen value, % variance and cumulative eigen values of 12 morphological traits under field condition**

Traits	PC	Eigen values	% Variation	Cumulative	Cumulative%
Plant height	PC1	3.9623	33.0	0.33	33.0
Tillers/plant	PC2	1.7113	14.3	0.473	47.3
Panicle length	PC3	1.3658	11.4	0.587	58.7
Flag leaf area	PC4	1.0780	9.0	0.676	67.6
Primary branches	PC5	0.9787	8.2	0.758	75.8
Spikelets/panicle	PC6	0.7857	6.5	0.823	82.3
Seeds/panicle	PC7	0.5803	4.8	0.872	87.2
Seed weight/panicle	PC8	0.4838	4.0	0.912	91.2
1000 grain weight	PC9	0.3744	3.1	0.943	94.3
Plant yield	PC10	0.2849	2.4	0.967	96.7
Heading days	PC11	0.2276	1.9	0.986	98.6
Maturity days	PC12	0.1672	1.4	1.00	100.0

**Table IV: Principal components (PCs) for 12 morphological traits of forty genotypes of rice under field condition**

Variable	Eigen Vectors											
	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12
Plant height	0.345	-0.0318	0.236	-0.139	-0.093	0.111	0.360	-0.222	-0.394	-0.400	0.339	0.274
Tillers/plant	-0.094	-0.373	-0.376	-0.002	-0.497	0.397	-0.482	-0.260	-0.035	-0.064	-0.064	0.012
Panicle length	0.396	-0.072	0.144	-0.010	-0.234	0.169	0.406	-0.320	0.313	0.220	-0.500	-0.264
Flag leaf area	0.230	-0.104	0.232	-0.602	0.173	-0.328	-0.462	-0.322	0.134	0.181	0.109	-0.054
Primary branches	0.333	0.134	0.350	-0.142	-0.147	0.243	-0.332	0.576	-0.017	-0.238	-0.345	0.172
Spikelets/panicle	0.401	0.083	0.083	0.287	-0.024	0.311	-0.120	0.126	-0.024	0.584	0.522	-0.035
Seeds/panicle	0.343	0.389	-0.249	0.081	0.154	0.042	-0.161	-0.157	0.268	-0.389	0.034	-0.602
Seed weight/panicle	0.280	0.452	-0.384	0.022	0.093	0.021	-0.021	-0.276	0.228	-0.063	-0.060	0.651
1000 grain weight	-0.034	0.179	0.440	0.532	-0.402	-0.418	-0.238	-0.284	-0.009	-0.112	0.008	0.069
Plant yield	0.181	0.106	-0.349	-0.271	-0.602	-0.462	0.195	0.325	-0.013	0.074	0.173	-0.075
Heading days	0.292	-0.357	-0.236	0.259	0.221	-0.341	-0.105	0.071	-0.486	0.258	-0.402	0.138
Maturity days	0.273	-0.440	-0.137	0.292	0.180	-0.180	-0.062	0.193	0.605	-0.343	0.182	-0.071

**Table V: Clusters of forty rice genotypes on the basis morphological traits**

Cluster Number	Genotypes
Cluster 1	CB4, CB5, CB28
Cluster 2	CB10, CB27, CB33, CB11
Cluster 3	CB13, CB16, CB15, CB41, CB19, CB44
Cluster 4	CB14, CB17, CB32, CB20, CB21, CB36, CB38, CB26, Bas Super
Cluster 5	CB42, IRRI-6, Bas-2000
Cluster 6	CB12, CB22, CB31, Bas-385
Cluster 7	CB40, KSK-282, KSK133, Bas-370, Bas-Pak
Cluster 8	CB39, Bas-198
Cluster 9	CB29, CB30
Cluster 10	CB34, CB43

On the basis of these traits the genotypes, which perform better with respect yield and yield contributing traits were selected for the further genetic analysis for the improvement of the rice crop. The quantitative traits i.e. number of spikelets per panicle, number of seeds per panicle, seed weight per panicle and thousand grain weight that directly contributed to the yield of the rice genotypes. Other traits i.e., plant height, number of tillers per plant, panicle length, flag leaf area, primary branches per panicle, heading days and maturity days were also important with respect to the yield of the plants.

Phenotypic correlations among all the morphological traits presented in the Table II. In this study, plant yield was positively and significantly correlated with panicle length ( $r=0.265^{**}$ ), number of seeds per panicle ( $r=0.266^{**}$ ) and seed weight per panicle ( $r=0.339^{**}$ ). On the other hand, panicle length was positively and significantly associated with flag leaf area ( $r=0.302^{**}$ ), number of primary branches per panicle ( $r=0.490^{**}$ ), number of spikelets per panicle ( $r=0.608^{**}$ ), number of seeds per panicle ( $r=0.365^{**}$ ), seed weight per panicle ( $r=0.328^{**}$ ) and heading days ( $r=0.321^{**}$ ). The number seeds per panicle were having positive and significant correlation with seed weight per panicle and days to heading ( $r=0.770^{**}$  &  $r=0.293$ ).

**Principal component and cluster analysis:** The PCA was performed for all the morphological traits of rice genotypes as indicated in the Table III and IV. Out of twelve, four principal components exhibited more than one eigen value

and showed about 67.7% variability among the traits studied for each genotypes. So, these four principal components were given due importance for the further explanation. The PC1 had 33%, PC2 showed 14.3%, PC3 exhibited 11.4% and PC4 showed 9% variability among the genotypes for the traits under study. Eigen value and variance associated with each principal, decreased gradually and stopped at 0.1672 and 1.4%, respectively.

The first PC was more related to plant height, panicle length, flag leaf area, primary branches per panicle, number of spikelets per panicle, number of seeds per panicle, seed weight per panicle, plant yield, heading days and maturity days so it must be considered. In second principal component the primary branches, seeds per panicle, seed weight per panicle, 1000 grain weight and plant yield were the more related traits. The third principal component exhibited positive effects for plant height, panicle length, flag leaf area, primary branches per panicle and 1000 grain weight. It showed maximum variation for these characters. The fourth principal component was more related to number of spikelets per panicle, 1000 grain weight, heading days and maturity days. Genotypes were poor for plant height, number of tillers per plant, flag leaf area, number of primary branches per panicle and plant yield. It had negative impact towards the overall yield. From first four PCs it was cleared that the 1000 grain weight, spikelets per panicle, primary branches per panicle, number of seeds per panicle and seed weight per panicle had high weight age value and number of tillers per plant had lowest value. Rice genotypes were also classified in to different clusters on the basis of various morphological traits as mentioned in Table V and Fig. 2. The similar genotypes were classified in to the same cluster based on their various morphological traits studied.

**Seed traits:** On the basis of above morphological traits twenty genotypes were selected for the seed traits measurements. The analysis of variance of mean square values of all the seed traits were presented in the Table VI. The genotypes studied for the seed parameters with bran and without bran showed highly significant variation for all the seed traits. The results indicated that the genetic variation occurred among the genotypes.

**Table VI: Mean squares of seed parameters of 20 rice genotypes with bran and without bran**

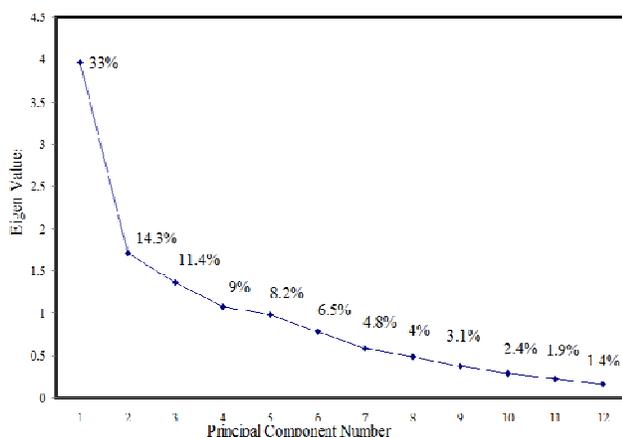
Source of Variation	D.F	Seed traits with bran				Seed traits without bran			
		SL (mm)	SW (mm)	ST (mm)	L/W	SL (mm)	SW (mm)	ST (mm)	L/W
Genotypes	19	1.18**	0.0562**	0.0435**	0.622**	0.7433**	0.0519**	0.0320**	0.476**
Replication	2	0.2508	0.00091	0.0082	0.1328	0.0515	0.0097	0.0102	0.088
Error	38	0.3322	0.0156	0.0142	0.212	0.2295	0.0067	0.0108	0.089

Level of significance  $p < 0.05 = *$  and  $P < 0.01 = **$

SL= Seed length; SW= Seed width; ST= Seed thickness; L/W= Seed length width ratio

**Table VII: Eigen value, % variance and cumulative eigen values of seed traits of 20 genotypes of rice**

Traits	PC	Eigenvalues	% Variation	Cumulative	Cumulative%
<b>Seed traits with bran</b>					
SL	PC1	2.053	51.35	0.5135	51.35
SW	PC2	1.522	38.06	0.8941	89.41
ST	PC3	0.417	10.43	0.9984	99.84
LWR	PC4	0.0065	0.16	1.00	100
<b>Seed traits without bran</b>					
SL	PC1	2.053	51.33	0.5133	51.33
SW	PC2	1.496	37.41	0.8874	88.74
ST	PC3	0.444	11.10	0.9984	99.84
LWR	PC4	0.0063	0.16	1.00	100

**Fig. 1: Scree plot of principal component analysis of 40 genotypes of rice between their Eigen values and the number of principal component**

The mean values of these traits (seed length, seed width, seed thickness & seed length width ratio) lead to the determination of seed size and shape of the each genotype (data was not shown).

Seed parameters were also analyzed through principal component analysis. The contribution of the first principal component was very high and accounted for more than 51% of the total variation, whereas the contribution of the fourth and later component was less than 0.2%. The total variation of the first two components was more than 88%, indicating that the shape and size variation of the seed of each genotype is explainable using those components.

The seed traits with bran and without bran, their eigen values, variation and cumulative values presented in the Table VII. Some principal components having positive values and some having negative values for all the seed

traits with bran and without bran. Principal components having positive values showed maximum variation for the specific trait and negative values showed less variation for the specific trait. Cluster analysis of the twenty rice genotypes is shown in Fig. 5, in which the genotypes were classified on the basis of seed parameters in to different clusters.

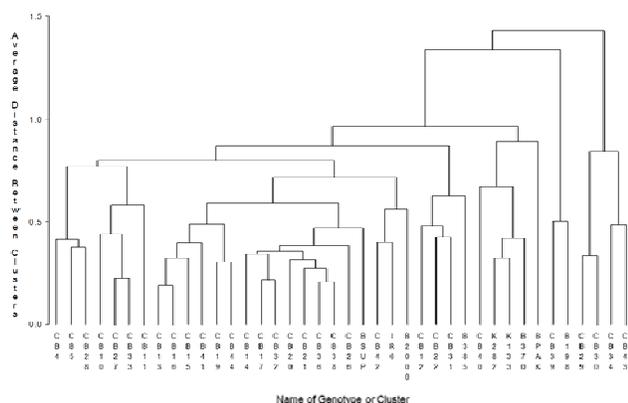
## DISCUSSION

This study consisted on two parts; first we studied the various morphological traits of the forty rice genotypes and secondly we studied the seed traits of the selected genotypes based on the yield and yield contributing traits. Some of the genotypes having more contribution in yield and yield related traits with respect to their great genetic potential. Phenotypic and genotypic divergence was present in all the genotypes under study with respect to their respective traits. These results are in good agreement with some earlier findings reported by other scientist (Cheema *et al.*, 2004; Bose & Pradhan, 2005; Shahidullah *et al.*, 2009).

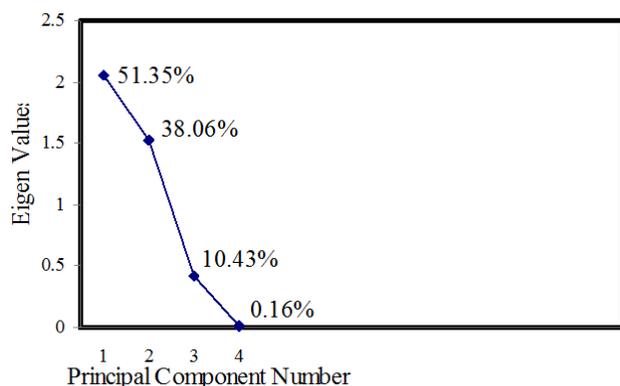
The genotypes, which having better yield and yield contributing traits and also having a great genetic diversity with respect to their mean values were selected (CB-13, CB-14, CB-15, CB-16, CB-17, CB-19, CB-21, CB-27, CB-32, CB-33, CB-36, CB-38, CB-39, CB-40, CB-42, Basmati-385, Basmati-Super, Basmati-198, Basmati-2000 & Basmati-Pak) for the further study of the seed parameters of these genotypes to screen out the diverse parents. Genetic diversity was present in the forty genotypes of rice due to differences in yield and other morphological traits. Genotypic differences of rice genotypes were evaluated on the basis of grain yield (Hayashi *et al.*, 2007; Hein *et al.*, 2007). Some morphological traits of rice were also studied by (Saleem *et al.*, 2009) for the development of high yielding varieties. Some traits having positive significant correlation and some having negative non significant correlation for all the rice genotypes. Similar results have been reported by (Khan *et al.*, 2009; Vange, 2009). A strong association was present between the plant yield and the other yield contributing traits i.e., panicle length ( $r=0.265**$ ), number of seeds per panicle ( $r= 0.266**$ ) and seed weight per panicle ( $r= 0.399**$ ).

The yield contributing traits also associated with other traits that have also a great contribution for the improvement of the yield. Panicle length associated with the other traits i.e., flag leaf area, number of primary branches per panicle, number of spikelets per panicle, number of seeds per panicle

**Fig. 2: Dendrogram of 40 genotypes of rice based on their morphological traits**



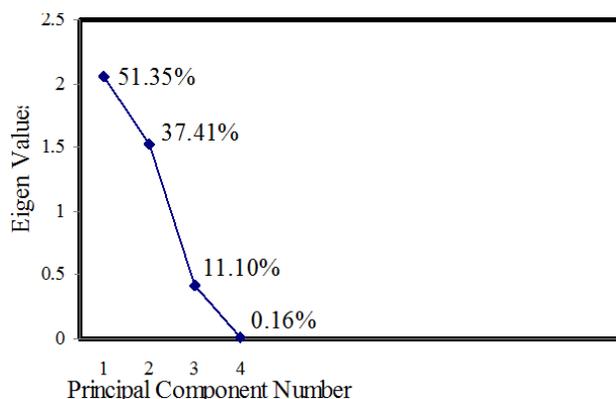
**Fig. 3: Scree plot of principal component analysis of rice genotypes between their Eigen values and the number of principal component with bran**



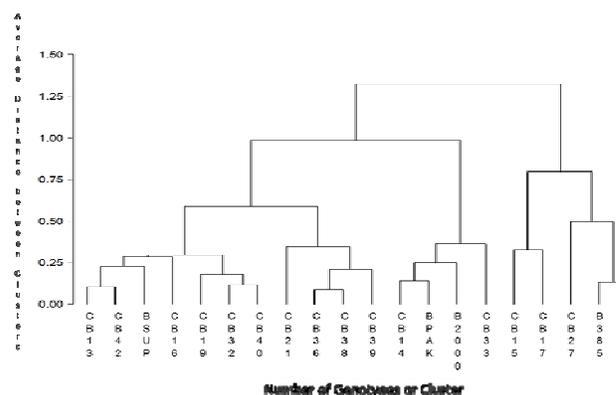
and grain weight per panicle that traits also directly or indirectly associated with the plant yield. Similar studies were also reported by (Ramkrishnan *et al.*, 2006). Panicle length highly associated with total number of spikelets per panicle and the number of seeds per panicle strongly correlated with grain weight per panicle ( $r=0.608^{**}$ ,  $r=0.770^{**}$ ). Association between panicle with yield and some other yield related traits were reported by (Liu *et al.*, 2007). On the other hand, number of seeds per panicle strongly associated with seed weight per panicle. Correlation between yield and other yield traits were reported by (Jeng *et al.*, 2006; Tao *et al.*, 2006).

In principal component analysis the first four principal components considered to be more important because they have more than one eigen value that showed total variation more than 67% for the rice genotypes under study. Variation was present in rice landraces that leads to the determination of genetic diversity (Sharma *et al.*, 2006). These principal components showed variation individually among the rice genotypes for the specific trait under study (first PC exhibited variation 33%, second PC14.3%, third PC 11.4% & fourth PC showed variation 9%) as shown in the Table IV. The variation among the rice genotypes based on

**Fig. 4: Scree plot of principal component analysis of rice genotypes between their Eigen values and the number of principal component without bran**



**Fig. 5: Cluster diagram of 20 genotypes of rice based on their seed traits**



their eigen values and their principal component as shown in the Fig. 1. Those principal components having more than one eigen value that showed more variation among the rice genotypes for the selection of the diverse parents. Shahidullah *et al.* (2009) reported the genetic divergence among the rice genotypes on the basis of their phenological traits that take part in the selection of the diverse genotypes for the further improvements of the rice varieties through breeding.

Each principal component described separately for the various morphological traits of the rice genotypes in Table IV. The PC1 showed positive effect for the specific traits under study i.e., plant height, panicle length, flag leaf area, number of primary branches per panicle, number of spikelets per panicle, number of grains per panicle, grain weight per panicle, plant yield, heading days and maturity days. PC2 was more related to number of grains per panicle, grain weight per panicle, number of primary branches per panicle, 1000 grain weight and plant yield. PC3 exhibited positive effect for the plant height, panicle length, flag leaf area, number of primary branches per panicle and 1000 grain weight. PC4 was more and showed positive effect for number of spikelets per panicle, 1000 grain weight, heading

days and maturity days. It was cleared that 1000 grain weight had highest values among all the 12 variables except one and number of tillers per plant having lowest values. Mostly the yield contributing traits were poor in PC3 and PC4 in comparison with PC1 and PC2. From this study it is cleared that a good hybridization breeding program can be initiated by the selection of genotypes from the PC1 and PC2. Agro-morphological diversity and variation among the rice accessions play a very important role for the crop improvement (Sanni *et al.*, 2008; Seetharam *et al.*, 2009).

Rice genotypes were also classified in to different clusters based on their various morphological traits. Genotypes having the same characteristics were classified into the same cluster. Most of the important genotypes were selected from Cluster 3, cluster 4, cluster 5 and cluster 8 on the basis of their yield and yield related traits because they having the same phenotypic and genotypic characteristics.

The seed traits of the selected genotypes with bran and without bran were analyzed by the measurement of the different traits. The rice genotypes can be differentiated by the measurement of their size and shape. The ANOVA revealed that differences for seed length, seed width, seed thickness and seed length width ratio between the genotypes were significant ( $P < 0.01$  &  $0.05$ ) for all the components under study. Similar results were also reported by (Kasem *et al.*, 2009).

The eigen values of the first two principal components was very high both in the seed traits of the genotypes with bran and without bran and accounted for the variation more than 88% as shown in the Table VII. The comparison between the rice genotypes by their Eigen values and principal component number with bran and without bran were also shown in the Fig. 3 and 4. It is cleared that first two principal component showed more variability among the genotypes with respect to other principal component. In this study, first two principal components associated with length width ratio that determines the grain size and shape of the each genotype by the measurement of the traits under study. Rice genotypes variability on the basis of grain size and shape and other seed parameters have also been reported by other scientists (Bai *et al.*, 2010; Iwata *et al.*, 2010). On the other hand, genotypes were also classified in to different clusters based on their seed traits. Genotypes having the same seed traits were placed in the same cluster.

A good number of genotypes have been identified on the basis of plant and grain morphological traits. Finally, the genotypes with better yield potential (CB-17, CB-40, CB-42, Basmati-198, Super basmati & Basmati-385) would be used for the improvement and development of new rice varieties through breeding programs. These genotypes are diverse and would produce significant transgressive segregants. Seeds per panicle and seed weight per panicle could be used as indirect selection criteria for the identification of high yielding rice genotypes.

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