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Short Research Article

Association, Principle Component and Genetic Divergnce Study in Recombinant Inbred Lines (RIL's) Population of Rice

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Abstract

Morphological characterization of seventy one rice breeding lines using 18 agronomic traits was performed. The aim of study was to determine the variability and extent of genetic diversity. Principal Component Analysis (PCA) was also performed to uncover similarities between variable and classify the genotypes. Only plant height exhibited high genetic advance and high heritability, whereas seedling height, biological yield and grain yield exhibited moderate heritability and high genetic advance. Character association of the yield attributing traits revealed significantly positive association of grain yield plant^{-1} with root pulling resistance, days to 50% flowering, tillers number, flag leaf width, second leaf width, spikelet fertility and biological yield. According to UPGMA cluster analysis all accessions were clustered into eleven groups. Cluster I was the biggest (including 29 lines) and cluster II, V, VIII and XI were the smallest (only one line) group. Under principal component analysis study, first six components contribute 77.54% of the variability. Component one had the contribution from the traits such as seedling height, shoot biomass, plant height, panicle length, flag leaf length, second leaf length and length of last inter-node which accounted 27.57% of the total variability. PC-2, PC-3, PC-4, PC-5 and PC-6 had 20.14%, 12.09%, 6.46%, 5.91% and 5.38% contribution to the total genotypic variability, respectively.

1. Introduction

Rice (*Oryza sativa* L.) is one of the pivotal staple cereal crops feeding more than half of the world population. In view of the growing population, the basic objective of the plant breeders would always be towards yield improvement in staple food crops. It has been estimated that the world will have to produce 60% more rice by 2030 than what it produced in 1995. Therefore, to increase production of rice plays a very important role in food security and poverty alleviation. Rice fulfills the nutritional requirements of half of the world's population. In India, rice is amajor food crop supplying 30% of the calorie requirement to the Indian population (Maclean, 2002). Keeping all these things in mind we have taken the recombinant inbred line (RIL) of rice, developed from a cross between a popular variety Swarna Sub-1 (susceptible to water stress) and an improved lines from IRRI, IR-86918-305-B (Water stress tolerant). Vaiation was present in recombinant inbred lines, hence, the present study was done to determine the extent of variability and to understand the magnitude of variability in the population which is fundamental for genetic improvement in all crop species. The estimation of character association could identify the relative importance of independent character (s). Genetic diversity is the basis of plant breeding, so understanding and assessing it is important for crop management, crop improvement by selection, use of crop germplasm, detection of genome structure, and transfer of desirable traits to other plants (Sasaki, 2005; McCouch et al., 1988). Multivariate statistical tools include Principal Component Analysis (PCA) and Cluster analysis. Principal Component Analysis (PCA) can be used to uncover similarities between variable and classify the cases (genotypes), while cluster analysis onthe other hand is concerned with classifying previously unclassified materials. This study was aimed to determine the level of morphological variation present in the population and to asses the genetic diversity.

2. Materials and Methods

The experiment was carried out under optimum irrigated condition in *kharif* 2015 in the research farm located at IGKV, Raipur, (21°16′ N and 81°36′ E at altitude of 289.6 meter above sea level) Chhattisgarh. The seventy one lines of the cross between Swarna Sub-1×IR 86918-B-305 were sown in Randomized Block Design (RBD) with two replications. Recommended packages of practices were followed during the crop growth period.

Observations were recorded for eighteen characters viz., seedling height (SH), root pulling resistance (RPR), shoot biomass (SBM), days to 50% flowering (DTF), tillers number (TLN), plant height in cm (PH), panicle length in cm (PL), flag leaf length in cm (FLL), flag leaf width in cm (FLW), 2nd leaf length in cm (SLL), 2nd leaf width in cm (SLW), length of last internode in cm (LLI), 100 seed weight (100SW), spikelet fertility (SPF), spikelet sterility (SPS), biological yield (BY) in g, harvest index (HI) in percent and grain yield in g (GY). The data after compilation for each character was subjected to standard method of analysis of variance following Panse and Sukhatme (1967), genotypic coefficient of variation (GCV) in percent and phenotypic coefficient of variation (PCV) in per cent, heritability in broad sense in per cent (h^2) and genetic advance as per cent of mean were estimated by the formula as suggested by Burton (1952); Johanson et al. (1955). Correlation coefficients were calculated as per Steel and Torrie (1997). Multivariate tool used for analyzing data was principal component analysis (PCA). The PCA was calculated by XLSTAT 2014.5.03. The PCA analysis reduces the dimensions of a multivariate data to a few principal axes, generates an Eigen vector for each axis and produces component scores for the characters Ariya et al. (1991); Sneath et al. (1973).

3. Results and Discussion

Eleven traits including seedling height, root puling resistance, shoot biomass, days to 50% flowering, plant height, flag leaf width, second leaf length, second leaf width, spikelet sterility, biological yield, harvest index and grain yield showed highly significant ($p \le 0.01$) variation and few panicle length and spikelet fertility were significant ($p \le 0.05$) among all the lines (Table 1).

The First order Statistical measures i.e. maximum, minimum, mean, phenotypic coefficient of Variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance, for the measured traits are presented in Table 2.

The magnitude of PCV (Table 3) was higher than the GCV. The PCV and GCV provide a measure to compare the variability present in the traits. Phenotypic coefficient of variation

Table 1: List of quantitative traits

Sl. No.		Traits	Sl. No.		Traits	Sl. No.		Traits
1.	SH	Seedling height	7.	PL	Panicle length	13.	100 SW	100 Seed weight
2.	RPR	Root pulling strength	8.	FLL	Flag leaf Length	14.	SPF	Spikelet fertility
3.	SBM	Shoot biomass	9.	FLW	Flag leaf width	15.	SPS	Spikelet sterility
4.	DTF	Days to 50% flowering	10.	SLL	Second leaf length	16.	BY	Biological yield
5.	TLN	Tillers number	11.	SLW	Second leaf width	17.	HI	Harvest index (%)
6.	PH	Plant height	12.	LLI	Length of last internode	18.	GY	Grain yield

Table 2: Mean squares of analysis of variance for 18 traits

Source of	df	Mean sum of square																	
		vari-ation	RPR	SBM	DTF	TLN	PH	PL	FLL	FLW	SLL	SLW	LLI	100 SW	SPF	SPS	BY	HI (%)	GY
Repli-cation	1	226.21**	57.68	287.81**	14.9	18.03	226.65*	3.53	39.09	0.38**	225.64*	0.00	26.94**	1.1**	82.31	82.32	243481.69	783.77**	365882.14**
Treat-ment	70	73.13**	28.79**	16.95**	172.43**	19.74	914.86**	3.79*	53.97	0.04**	115.68**	0.02**	14.77**	0.12	120.15*	120.15*	808500.88**	64.75**	81694.86**
Error	70	13.71	28.31	15.83	8.71	13.81	51.44	2.33	43.51	0.01	43.9	0.01	4.47	0.11	70.61	70.57	161104.72	23.49	26783.74

Table 3: Genetic variance of 18 morphological characteristics

Traits	Range		GM	PCV (%)	GCV (%)	h^2 (%)	GA as per cent of mean
	Min.	Max.					
SH	26.69	49.70	35.78	18.42	15.24	68.41	25.96
RPR	19.00	39.25	29.66	17.97	2.08	1.34	0.49
SBM	4.03	23.70	8.73	46.37	8.59	3.43	3.28
DTF	68.00	105.00	92.27	10.31	9.81	90.39	19.21
TLN	10.10	26.40	15.65	25.91	10.37	16.02	8.55
PH	74.40	164.80	105.27	20.88	19.74	89.35	38.43
PL	19.50	26.30	22.28	7.85	3.83	23.80	3.85
FLL	21.10	55.80	27.55	25.34	8.30	10.73	5.60
FLW	1.12	1.75	1.40	11.44	9.23	64.99	15.32
SLL	27.20	75.60	35.86	24.91	16.71	44.98	23.08
SLW	0.98	1.44	1.21	10.77	7.17	44.30	9.83
LLI	26.60	37.28	31.46	9.86	7.21	53.52	10.87
100SW	1.82	3.27	2.47	13.62	1.79	1.72	0.48
SPF	58.82	96.10	79.86	12.23	6.23	26.00	6.55
SPS	3.90	41.19	20.14	48.50	24.73	26.00	25.97
BY	1511.00	4405.50	2664.30	26.13	21.35	66.77	35.95
HI (%)	22.93	53.28	37.82	17.56	12.01	46.76	16.92
GY	602.00	1513.00	985.80	23.62	16.80	50.61	24.63

(PCV) were higher than those of genotypic coefficient of variation (GCV) for all the traits studied, indicating that they all interacted with the environment with the same degree. The GCV especially helps to compare the genetic variability in the traits. GCV and PCV were classified as suggested by Sivasubramanian and Madhavamenon (1973). Spikelet sterility exhibited maximum PCV followed by shoot biomass, while panicle length and length of last internode exhibited minimum PCV. Spikelet sterility shows maximum GCV followed by biological yield and plant height. Minimum GCV was recorded for 100 seed weight followed by root pulling resistance and panicle length. Board sense heritability ranged from 1.34 to 90.39%. The broad sense heritability can be used as a predictor in the selection procedure (Allard, 1960). The highest and the lowest amount of heritability was recorded at root pulling resistance and days to 50% flowering, respectively. The estimates of heritability were high for days to 50% flowering (90.39%) and plant height (89.35%). whereas other characters like SH (68.41%), FLW (64.99%), SLL (44.98%), SLW (44.30%), LLI (55.52%), BY (66.77%), HI (46.76%) and GY (50.61%) showed relatively moderate heritability. It revealed that character was governed by additive gene effects and low to moderate heritability was being exhibited due to high environmental effect and selection might be effective. GA as percent of mean ranged from 0.48% for 100 seed weight to 38.43% for plant height. Only plant height exhibited high GA and high heritability, whereas seedling height, biological yield and grain yield exhibited moderate heritability and high GA. These two parameters helpful for selection to improve grain yield in rice. This was in consonance with the findings of Chandra et al. (2009); Bekele et al. (2013) for plant height, Bekele et al. (2013) for biological yield plant^{-1}. The results got support from the Findings of Verma (2010) and Anandrao et al. (2011); Akhtar et al. (2011); Shrivastava et al. (2014).

3.1. *Association between traits*

Association between traits is so important because ithelps the breeder to select importantcharacters from the studied traits. Most of the traits such as yield and yield component traits are influenced by interaction of genotype and environment, and, therefore, selection based on correlation coefficient makes it easy for plant breeders (Ahmadikhah et al., 2008). Pearson's correlation coefficient was computed between 18 quantitative traits among 71 lines of rice (Table 4).

Phenotypic and genotypic correlations between yield and yield components were computed separately for rice genotypes. The results are presented in Table 4. The results revealed that the estimates of genotypic coefficients were higher than phenotypic correlation coefficients for most of the characters under study which indicated strong inherent

Table 4: Pearson's correlation coefficient among 12 quantitative traits

	SH	RPR	SBM	DTF	TLN	PH	PL	FLL	FLW	SLL	SLW	LLI
SH		-0.094	0.96**	-0.57**	-0.86**	0.82**	0.97**	0.56**	0.21*	0.91**	0.01	0.95**
RPR	0.13		0.59**	0.92**	0.93**	0.85**	-0.86**	-0.41**	4.26**	0.43**	4.39**	-0.94**
SBM	0.35**	0.12		-0.59**	-0.94**	0.97**	0.64**	0.95**	0.85**	0.97**	0.66**	0.92**
DTF	-0.48**	0.23*	-0.17		0.47**	-0.11	-0.54**	-0.30**	0.53**	-0.34**	0.38**	-0.61**
TLN	-0.31**	-0.001	-0.06	0.17		-0.84**	-0.71**	-0.3**	-0.16	-0.61**	-0.82**	-0.45**
PH	0.65**	0.13	0.24*	-0.10	-0.27**		0.88**	0.72**	0.13	0.80**	-0.05	0.86**
PL	0.52**	0.02	0.25*	-0.25*	-0.16	0.54**		0.99**	-0.04	0.82**	-0.07	-0.91**
FLL	0.25**	0.01	0.03	-0.09	-0.06	0.2*	0.18		0.23*	0.78**	-0.11	0.96**
FLW	0.08	0.33**	0.13	0.43**	-0.03	0.17	0.21*	0.04		0.45**	0.76**	-0.17
9	0.55**	0.2*	0.3**	-0.21*	-0.14	0.54**	0.36**	0.17	0.34**		0.41**	0.87**
SLW	-0.03	0.18*	0.02	0.23*	0.00	0.04	0.16	-0.03	0.66**	0.22*		-0.26**
LLI	0.66**	0.01	0.30**	-0.42**	-0.28**	0.68**	0.59**	0.23**	0.05	0.47**	-0.13	
100 SW	-0.01	-0.06	0.05	0.10	0.03	-0.04	-0.03	0.003	0.16	0.03	0.14	-0.12
SPF	0.04	0.04	0.05	0.08	-0.10	0.05	-0.04	-0.02	-0.02	0.02	-0.05	-0.03
SPS	-0.04	-0.04	-0.05	-0.08	0.10	-0.05	0.04	0.02	0.017	-0.023	0.05	0.026
BY	-0.28**	0.34**	-0.02	0.64**	0.21*	-0.16	-0.22*	-0.06	0.49**	-0.07	0.42**	-0.31**
HI	-0.09	-0.16	-0.04	-0.29**	0.02	-0.15	0.16	-0.05	-0.20*	-0.11	-0.25**	0.05
GY	-0.37**	0.22*	-0.04	0.48**	0.23**	-0.25*	-0.09	-0.09	0.39**	-0.14	0.26**	-0.27**

Table 4 continue..

	100 SW	SPF	SPS	BY	HI	GY
SH	-0.67**	0.14	-0.14	-0.51**	-0.06	-0.62**
RPR	0.96**	0.52**	-0.52**	0.98**	-0.73**	0.97**
SBM	0.93**	0.72**	-0.72**	-0.08	-0.96	-0.93
DTF	0.91**	0.18*	-0.18*	0.79**	-0.44**	0.68**
TLN	-0.98**	0.07	-0.07	0.47**	0.002	0.45**
PH	-0.51**	0.22*	-0.22*	-0.2*	-0.33**	-0.43**
PL	-0.95	0.39**	-0.39**	-0.62**	0.29**	-0.46**
FLL	-0.97**	-0.62**	0.62**	-0.42**	-0.33**	-0.67**
FLW	0.78**	0.39**	-0.39**	0.63**	-0.49**	0.41**
9	-0.24*	0.17	-0.17	-0.15	-0.50**	-0.53**
SLW	0.27**	0.13	-0.13	0.69**	-0.56**	0.41**
LLI	0.36**	0.24**	-0.24*	-0.56**	-0.01	-0.63**
100 SW		0.29**	-0.29**	0.76**	-0.79**	0.21*
SPF	0.06		-0.99	0.09	0.50**	0.57**
SPS	-0.05	-0.99**		-0.09	-0.49**	-0.56**
BY	0.22*	0.10	-0.10		-0.58**	0.81**
HI	-0.002	0.05	-0.04	-0.47**		0.02
GY	0.24*	0.14	-0.13	0.71**	0.28**	

association between the characters which might be due to masking or modifying effects of environment. At phenotypic level grain yield is positively and highly significantly correlated with days to 50% flowering, flag leaf width, second leaf width, biological yield at 1% probability level and also significant ($p \leq 0.05$) and positively correlated with root pulling resistance, tillers number and 100 seed weight.

Positive genotypic correlation was found between most of traits. Grain yield was highly significant ($p<0.01$) and positively correlated with most of traits such as root pulling resistance, days to 50% flowering, tillers number, flag leaf width, second leaf width, spikelet fertility and biological yield at 1% probability level and also significant ($p \leq 0.05$) and positively correlated with 100 seed weight (r=0.34). Veni et al. (2013); Babu et al. (2012); Augustina et al. (2013) also reported similar kind of result. Biological yield was highly significant and positively correlated with root pulling resistance, days to 50% flowering, tillers number, flag leaf width, second leaf width and 100 seed weight at 1% probability level. These results for number of filled grains panicle^{-1} were in accordance with Janardhanam et al. (2001); Kavitha and Reddi (2001); Yogameenakshi et al. (2004); Sharma and Sharma (2007); Babu et al. (2012). The results for the trait 1000 grain weight are in unison with Gopinath et al. (1984), Yogameenakshi et al. (2004); Augustina et al. (2013). The results for tillers numbers are in unison with Redy et al. (1997); Babu et al. (2012); Augustina et al. (2013).

3.2. Cluster analysis

Seventyone lines rice wereclustered into eleven groups by 18 quantitative traits. As evident from Figure 1 and Table 5 cluster I was the biggest (29 lines) and cluster II, V, VIII and XI were the smallest (only one member) group. Cluster III, IV, VI, VII, IX and X consisted of 12, 8, 3, 2, 6 and 7 members, respectively. The seventh group had the highest average in comparision with other groups considering six traits (Table 6) such as seedling height, shoot biomass, plant height, panicle lenth, length of last internode and spikelet fertility. Cluster VIII had the highest cluster mean for flag leaf width, second leaf width, 100 seed weight, biological yield and grain yield. Cluster II had highest average for root pulling resistance and harvest index, similarily cluster V had high average value for flag leaf length and second leaf length. Cluster IX, X and XI had highest average value for spikelet sterility, days to 50% flowering and tillers number, respectively. Spikelet sterility contributed maximum towards genetic divergence followed by shoot biomass and second leaf length. These characters were considered to be most important for the genetic diversity. Lowest contribution was made by panicle length followed by length of last internode and second leaf width.

The results clearly underlines that different clusters showed wide variation from one another in respect of cluster means. This indicated that genotypes having distinctly different mean performance for various characters were separated in to different clusters. Mean performance of different clusters revealed wide range of differences between clusters. Thus these genotypes hold great promise as parental stock to create genetic variability for selection as well as suitable donor for these characters in hybridization programme. Thus upon hybridization between these genotypes, we can create genetic variability for selection. The factors responsible for differentiation of intra- and inter-cluster levels were different in different environments as indicated by cluster means of various characters (Patil et al., 2003).

3.3. Principal component analysis (PCA)

Principal component analysis (PCA) was employed to reduce the complexity of the data set while retaining the variation within the data set as far as possible (Ringner, 2008). PCA measure the importance and contribution of each component to total variance and PCA can be used for measurement of independent impact of a particular character to the total variance whereas each coefficient of proper vectors indicates the degree of contribution of every original variable with which each principal component is associated. The PCA resulted in 18 independent principal components that had a cumulative explained variance of 100%. Following the Proportion of Variance Criterion (O'Rourke and Hatcher, 2013), six component in PCA analysis contribute 77.54% of

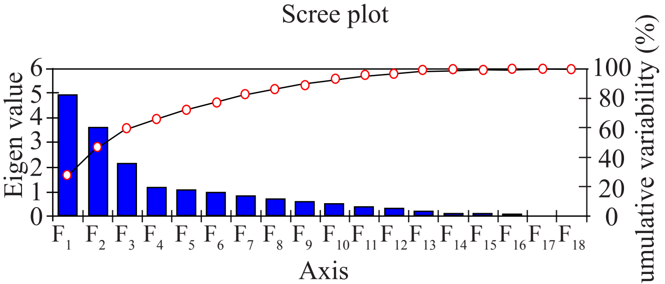

Figure 1: Scree plot showing Eigen value variation

Table 5: Clustering patterns of seventy one rice lines on the basis of diversity analysis

Sl. No.	Cluster	No. of lines	Lines
1.	I	29	G7 G8 G9 G10 G13 G14 G15 G16 G17 G18 G19 G20 G23 G32 G33 G34 G35 G39 G40 G41 G44 G45 G58 G59 G64 G65 G66
2.	II	1	G2
3.	III	12	G3 G4 G5 G11 G12 G22 G55 G57 G60 G61 G62 G63
4.	IV	8	G21 G25 G26 G27 G28 G29 G30 G42
5.	V	1	G24
6.	VI	3	G31 G37 G43
7.	VII	2	G36 G38
8.	VIII	1	G46
9.	IX	6	G47 G48 G50 G52 G53 G68
10.	X	7	G49 G51 G54 G56 G67 G69 G70
11.	XI	1	G71

Table 6: Cluster mean values for different characters

Cluster	SH	RPR	SBM	DTF	TLN	PH	PL	FLL	FLW	SLL	SLW	LLI	100 SW	SPF
I	38.72	28.25	7.69	86.50	11.80	112.00	21.70	33.20	1.46	40.80	1.16	35.00	1.89	79.44
II	38.98	34.50	6.49	88.50	13.30	111.20	23.10	22.80	1.31	37.00	1.19	33.40	2.53	88.76
III	32.85	29.50	7.11	96.00	14.10	93.90	21.30	28.80	1.53	29.70	1.30	30.20	2.68	81.89
IV	43.78	26.00	8.30	69.50	17.60	88.00	22.85	30.30	1.32	32.80	1.11	34.10	2.26	82.69
V	42.84	27.75	11.56	102.00	13.70	158.90	22.90	35.60	1.49	49.70	1.27	34.80	2.40	87.88
VI	39.77	24.00	7.20	91.00	11.80	116.00	23.70	25.10	1.39	36.40	1.27	32.50	2.45	83.22
VII	49.53	31.50	11.74	91.00	10.10	164.80	24.00	29.10	1.32	47.10	1.11	37.28	2.48	96.10
VIII	31.37	31.75	6.02	104.00	19.40	84.70	22.90	24.50	1.65	36.50	1.41	28.10	2.78	82.45
IX	30.11	28.00	9.32	104.50	15.40	86.60	22.00	26.20	1.54	32.70	1.34	30.90	2.56	62.85
X	29.94	33.00	6.28	105.00	12.50	89.70	21.50	28.60	1.51	30.50	1.33	28.50	2.38	80.76
XI	31.95	32.50	7.17	97.50	20.00	87.20	20.70	23.80	1.39	30.60	1.22	29.80	2.59	65.13

Table 6 continue..

Cluster	SPS	BY	HI	GY
I	20.57	2340.50	41.42	959.50
II	11.24	2314.00	53.28	1262.00
III	18.12	2847.50	39.07	1126.00
IV	17.31	1702.50	39.92	679.00
V	12.12	3151.50	22.93	730.00
VI	16.78	2056.00	38.07	770.00
VII	3.90	2691.50	25.42	694.50
VIII	17.56	4405.50	34.34	1513.00
IX	37.15	3795.00	33.07	1264.50
X	19.24	3357.50	36.28	1203.50
XI	34.87	3694.00	24.52	855.50

the variability with eigen values>1 among total genotypic variability for 18 quantitative characters of 71 lines are represented in Table 7. Principal component-7 (PC-7) to principal component-18 (PC-18) possesses eigen value <1. PC-1 with eigen value of 4.96 contribute 27.57% of the total variability, whereas PC-2, PC-3, PC-4, PC-5 and PC-6 had eigen value of 3.62, 2.18, 1.16, 1.06 and 0.99 possess 20.14, 12.09 6.46, 5.91 and 5.38% contribution to the total genotypic variability, respectively.

Analysis of the factor loadings of the characters in the retained PCs showed that phenotypic traits that contributed to yield showed high positive loadings in PC-1 (Table 8). These traits were seedling height, shoot biomass, plant height, panicle length, flag leaf length, second leaf length and length of last internode with factor loadings of 0.884, 0.433, 0.734, 0.707, 0.389, 0.649 and 0.878, respectively. These seven morphological characters could have contributed to the

Table 7: Computed eigenvalues of the different principal components of 18 agro-morphological characters of 71 line of RIL population of rice with corresponding proportion and cumulative explained variance

	PC-1	PC-2	PC-3	PC-4	PC-5	PC-6	PC-7	PC-8	PC-9	PC-10	PC-11	PC-12	PC-13	PC-14	PC-15	PC-16	PC-17	PC-18
Eigen value	4.96	3.62	2.18	1.16	1.06	0.99	0.88	0.73	0.61	0.56	0.40	0.33	0.23	0.12	0.12	0.07	0.01	0.00
Variability (%)	27.57	20.14	12.09	6.46	5.91	5.38	4.86	4.04	3.39	3.10	2.22	1.86	1.25	0.68	0.65	0.37	0.03	0.00
Cumulative %	27.57	47.71	59.79	66.25	72.17	77.54	82.41	86.44	89.83	92.94	95.15	97.01	98.27	98.95	99.60	99.97	100.00	100.00

maximum variability in PC-1 which explained 27.57% of the total variation in the data set. In second principal component, flag leaf width presented the highest factor loading of 0.852, followed by second leaf width (0.706), root pulling resistance (0.675), biological yield (0.650), days to 50% flowering (0.451) and spikelet fertility (0.256). In PC-3, only spikelet sterility (0.924) showed a high loading factor. PC-4 had high loading value for harvest index (0.621) and grain yield (0.419). PC-5 and PC-6 had high factor loading value for 100 seed weight (0.558) and tillers numbers (0.524), respectively.

Table 8: Factor loadings (Eigen vectors) for the different morphological characters for the principal components retained

	PC-1	PC-2	PC-3	PC-4	PC-5	PC-6
SH	0.884	0.283	-0.018	-0.028	0.058	0.048
RPR	-0.189	0.675	0.064	0.250	0.032	0.089
SBM	0.433	0.359	-0.025	-0.313	0.147	0.458
DTF	-0.664	0.451	0.032	-0.060	-0.266	-0.082
TLN	-0.462	-0.146	0.053	0.197	-0.438	0.524
PH	0.734	0.400	-0.008	-0.014	-0.230	-0.111
PL	0.707	0.225	-0.098	0.439	0.012	-0.030
FLL	0.389	0.115	0.202	0.205	-0.407	0.190
FLW	-0.131	0.852	0.105	0.160	0.079	-0.087
SLL	0.649	0.513	0.089	-0.023	-0.022	0.032
SLW	-0.179	0.706	0.215	0.080	0.279	-0.337
LLI	0.878	0.133	-0.063	0.119	-0.102	0.130
100 SW	-0.165	0.271	-0.062	-0.185	0.558	0.495
SPF	-0.011	0.256	-0.924	-0.197	-0.136	-0.060
SPS	0.011	-0.256	0.924	0.197	0.136	0.060
BY	-0.639	0.650	0.098	-0.056	-0.151	0.086
HI	0.050	-0.464	-0.495	0.621	0.299	0.055
GY	-0.659	0.404	-0.284	0.419	0.041	0.124

A scree plot (Figure 2) displays the eigen values associated with a component or factor in descending order versus the number of the component or factor. Researchers can use scree plots in principal components analysis and factor analysis to visually assess which components or factors explain most of the variability in the data. A factor analysis was conducted on 18 different agro-morphological characters. This scree plot shows that 6 of those factors explain most of the variability because the line starts to straighten after factor 6. The remaining factors explain a very small proportion of the variability and are likely unimportant.

The first component has phenological and yield related variables. Similar type of performance was obtained by Sanni (2012); Kayode (2008); Guei (2005) has obtained similar pattern for phonological variables in rice. Maji et al. (2012) reported that grain size that may be indicated by weight, volume, or length is one of the most important agronomic traits in rice. In current study also, grain yield along with harvest index had contributed 6.46% of total variability in component 4. Second component also include both phonological and yield related traits. Nachimuthu et al. (2014); Chakravorty et al. (2013) find similar kind of result. PC-4, PC-5 and PC-6

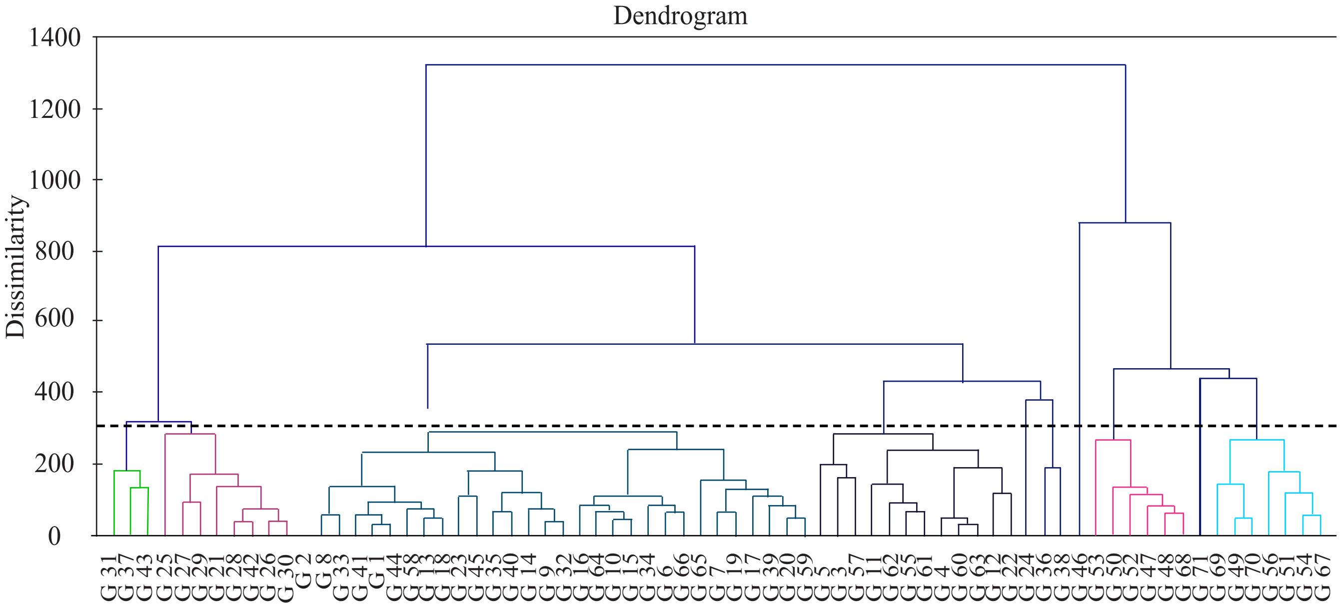

Figure 2: Dendrogram based on 18 morphological characters

included only yield related traits.

4. Conclusion

Seventy one lines of RIL's population of rice, were clustered into eleven main groups. Thus the genotypes from different groups can be used as parental stock. Principal component analysis indicated that first six components explain 77.54% of the total variation. Only plant height exhibited high heritability coupled with high genetic advance. Root pulling resistance, days to 50% flowering, tillers number, spikelet fertility and biological yield had positive correlations with grain yield, which is helpful for indirect selection for grain yield.

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