

Diversity assessment among some restorer lines using agronomic traits in rice (*Oryza sativa* L.)

Ghaffar KIANI

Department of Agronomy and Plant Breeding, Sari Agricultural Sciences and Natural Resources University,
P.O. Box: 578, Sari, Iran; E-mail: ghkiani@gmail.com

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Abstract. The aim of this study was to evaluate the phenotypic divergence in a germplasm consisted of thirty-seven restorer varieties. Coefficients of phenotypic variations were high for most of the traits revealing the existence of sufficient variation for the studied traits. The principle component analysis (PCA) showed that three components explained 68.22% of total variation. The first component was related to grain filling characteristics, while the second component showed importance and positive correlation of grain number with panicle length and the third component showed competition between reproductive and vegetative parts. The cluster analysis of genotypes using Ward's minimum method and Euclidian distance criteria classified the rice varieties in three different groups. The results of this study suggested crossing the Iranian cultivars with genotypes in cluster III for development of new desirable lines.

Keywords: rice, phenotypic variation, agronomic traits, cluster analysis, principle component analysis.

Introduction

Rice is staple food in Iran cultivated on 570,000 hectares of irrigated area and 2.4 million tonnes of milled rice is produced. Iran still largely depends on rice imports to the tune of 0.8 million tonnes each year to meet the domestic consumer's demand. Therefore, hybrid rice with 20-25% yield heterosis over conventional varieties happens to be a viable option to enhance the production and productivity levels, since the area under rice cultivation cannot be further increased due to water shortages (Nematzadeh et al. 2006). Exploitation of heterosis phenomenon through commercial F₁ hybrid seed plays a significant role in increasing the production and productivity of rice. Despite developing new CMS (Cytoplasmic Male Sterile) lines like Neda, Nemat, Dasht, Champa, Amol-3 in Iran, hybrid seed technology has not progressed due to the lack of suitable restore lines. However, a number of restorer lines were developed but, they are not applicable for hybrid seed production because of their unsuitable phenotypic properties for cross pollination with the aforesaid CMS lines. So, it is essential to bring these cultivars to R×R improvement program to develop suitable recombinant restore lines. In this way, diversity analysis permits to select the genetically diverged parents, which can produce new recombinants with suitable traits when crossed together. Several reports have emphasized the importance of genetic variation for selection of desirable parents (Sinha et al. 1991, Rahman et al. 1997, Bose & Pradhan 2005, Akter et al. 2009). This study aimed to evaluate the variation within a rice germplasm for selection of desirable parents for development of new restorer line through hybridization breeding programmes in Iran.

Materials and methods

Thirty-seven varieties (Table 1) were used in this study. Seeds were obtained from Rice Research Institute of Iran, Amol, Mazandaran province. The experiment was laid out in a randomized complete block design (RCBD) with three replications at Sari University of Agricultural Sciences and Natural Resources during 2010. Thirty-day-old seedlings were transplanted in six rows, each row having 30 plants with 25×25 cm planting pattern (a single plant per hill). NPK

fertilizers were applied at the rate of 200, 100 and 50 Kg/ha, respectively.

Agronomic traits like yield (t/ha), plant height (cm), tiller number, number of filled grains per panicle, number of non-filled grains per panicle, total grain number per panicle and panicle length (cm) were recorded based on the standard evaluation system (SES) of rice (IRRI, 2002).

All of the statistical analyses, including analysis of variance, estimation of descriptive statistics, principal component analysis and cluster analysis, were performed using SPSS (vers. 14).

Results

The results of the analysis of variance are presented in Table 2. Highly significant differences were observed between genotypes for all of the traits. Maximum standard deviation belonged to total grain number per panicle (3.80) followed by plant height (1.95) (Table 3). Agronomic traits, non-filled grains per panicle, yield, tiller number and total grain number per the panicle with the CVs of 45.59, 22.85, 22.80 and 22.55 percent had more phenotypic variations, respectively. While days to heading and panicle length had less variation.

The principal component analysis was based on eight agronomic features, which showed that three components accounted for 68.22% of total variation (Table 4). The first component with variance of 28.99% from total variance related to grain filling characteristics. In this component, days to heading and non-filled grains per panicle with positive coefficient and number of filled grains per panicle with negative coefficient related with each other conversely. The second component explained 21.29% of total variance showing importance and positive relationship between panicle length and total grain number per panicle. The third component with the variance of 17.94% showed competition between reproductive and vegetative parts (Table 4). In this component there are days to heading and grain yield with positive coefficients and plant height with negative coefficient indicating negative relationship between plant height with grain yield and days to heading.

Cluster analysis was applied in the distance criteria of 10 grouped genotypes into three clusters (Fig. 1). Cluster I comprised of 7 genotypes (19%) viz. 229, IR67924, IR65623,

Table 1. Rice varieties used in this study

Entry No.	Variety name	Origin	Entry No.	Variety name	Origin
1	Sepidrood	Iran	20	IR62037	IRRI
2	DN-33-18	Iran	21	SA1	IRRI
3	IR42686	IRRI	22	SA2	IRRI
4	IR60966	IRRI	23	SA11	IRRI
5	IR60819	IRRI	24	IR69714	IRRI
6	229	IRRI	25	IR7301395	IRRI
7	IR13155	IRRI	26	IR68448	IRRI
8	IR58082	IRRI	27	IR69707	IRRI
9	IR58110	IRRI	28	IR73885	IRRI
10	IR60819	IRRI	29	IR50360	IRRI
11	IR62161	IRRI	30	IR71604	IRRI
12	IR63879	IRRI	31	IR57298	IRRI
13	IR65623	IRRI	32	IR57301	IRRI
14	IR68926	IRRI	33	IR72102	IRRI
15	IR67924	IRRI	34	IR72102	IRRI
16	IR69726	IRRI	35	IR71604	IRRI
17	IR60819	IRRI	36	IR72102	IRRI
18	IR65383	IRRI	37	IR69723	IRRI
19	IR51078	IRRI			

Table 2. Analysis of variance in thirty-seven rice varieties for agronomic traits.

Sources of variation	Degree of freedom	Mean squares							
		Days to heading	Yield	Plant height	Tiller number	Filled grain per panicle	Un-filled grain per panicle	Total grain number	Panicle length
Treatment	36	36.98**	3.42**	349.18**	84.14**	8.76**	112.53**	99.71**	10.79**
Block	2	22.15**	0.04 ^{ns}	222.87**	19.47 ^{ns}	23.22**	71.78**	0.09 ^{ns}	12.26**
Error	72	3.66	0.88	25.70	14.02	2.75	4.10	4.94	2.21

** and ^{ns} are high-significant and non-significant at 1 percent statistical level, respectively.

Table 3. Descriptive statistics in thirty-seven rice varieties for agronomic traits.

Traits	Range	Mean	Standard deviation	Coefficient of variation (%)
DH	35-131	117.70	1.50	7.72
GY	2.49-7.42	5.13	0.19	22.85
PH	89-141	108.11	1.95	10.94
TN	9-26	14.92	0.56	22.80
FGP	35.28-91.89	76.70	1.75	13.85
NFG	8.11-64.72	23.30	1.75	45.59
TGN	62.20-168.80	106.08	3.80	22.55
PL	22.80-30.20	26.63	0.27	6.38

DH= Days to heading, GY= Grain yield, PH= Plant height, TN= Tiller number, FGP= Filled grains per panicle, NFG= Non-filled grains per panicle, TGN= Total grain number per panicle, PL= Panicle length

Table 4. Principal components with latent root values more than 1 in thirty-seven rice genotypes for agronomic traits.

Trait	Principal Components		
	Component 1	Component 2	Component 3
DH	0.51	0.11	0.57
GY	-0.28	-0.42	0.51
PH	0.04	0.12	-0.84
TN	0.06	0.48	0.47
FGP	-0.98	-0.01	0.03
NFG	0.98	0.01	-0.03
TGN	-0.10	0.86	0.03
PL	0.07	0.70	-0.16
Eigent value	2.32	1.70	1.44
Variance	28.99	21.29	17.94
Cumulative variance	28.99	50.28	68.22

DH= Days to heading, GY= Grain yield, PH= Plant height, TN= Tiller number, FGP= Filled grains per panicle, NFG= Non-filled grains per panicle, TGN= Total grain number per panicle, PL= Panicle length

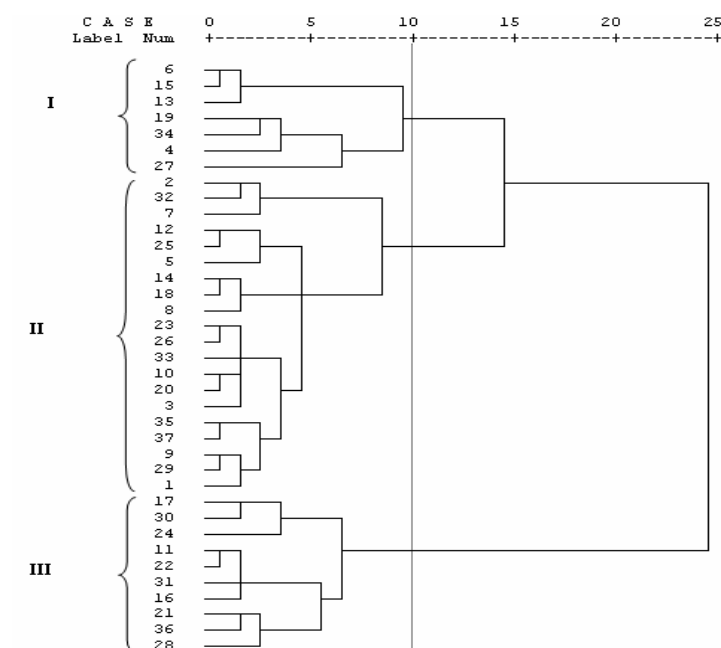


Figure 1. Clustering of thirty-seven rice genotypes based on eight agronomic traits. For the names of the varieties see Table 1.

Table 5. Mean and percentage of deviation from total mean (in parenthesis) in three clusters for different characters.

Cluster	Genotypes	DH	GY	PH	TN	FGP	NFG	TGN	PL
I	6, 15, 13, 19, 34, 4, 27	120	5.36	107.14	13	70.48	29.52	74.74	25.79
		(+1.95)	(+4.48)	(-0.89)	(-12.87)	(-8.11)	(+26.70)	(-29.54)	(-3.15)
II	2, 32, 7, 12, 25, 5, 14,	116.05	5.35	108.75	15.20	79.52	20.48	102.65	26.38
	18, 8, 23, 26, 33, 10, 20,	(-1.40)	(+4.29)	(+0.59)	(+1.88)	(+3.68)	(-12.10)	(-3.23)	(-0.94)
III	3, 35, 37, 9, 29, 1	119.40	4.53	107.50	15.70	75.43	24.57	134.86	27.73
	17, 30, 24, 11, 22, 31,	(+1.44)	(-11.70)	(-0.56)	(+5.23)	(-1.66)	(+5.45)	(+27.13)	(+4.13)
	16, 21, 36, 28								
	Total Mean	117.70	5.13	108.11	14.92	76.70	23.30	106.08	26.63

DH= Days to heading, GY= Grain yield, PH= Plant height, TN= Tiller number, FGP= Filled grains per panicle, NFG= Non-filled grains per panicle, TGN= Total grain number per panicle, PL= Panicle length

IR51078, IR72102, IR60966 and IR69707. Cluster II is the largest cluster comprising 20 genotypes (54%) and Iranian cultivars Sepidroud and DN-33-18 were placed in it. While there are 10 genotypes (27%) in cluster III.

The mean performance of eight characters in three clusters is presented in Table 5. In order to show the value of each cluster for agronomic traits, deviation of cluster mean from total mean was also estimated. High grain yield (5.36 t/ha) and days to heading (120) were recorded from cluster I but the other traits contained the lowest values. Genotypes of cluster II had better yield (5.35 t/ha), high plant height (108.75 cm), better tiller number (15.20) and high filled grains per panicle (79.52). While cluster III represented the highest mean values for three characters, like tiller number (15.70), total grain number per panicle (134.86) and panicle length (27.73 cm).

Discussion

Analysis of variance revealed the existence of considerable diversity for important yield relating traits among genotypes. More than 68 percent of the observed variations, explained by three independent components, indicated further

utilization of divergent varieties in future recombination-breeding programmers.

Cluster analysis suggested that none of the clusters contained genotypes with all the desirable characters, which could be directly selected and utilized. The hybridization between genotypes of different clusters is essential for the development of desirable genotypes. Recombination breeding between genotypes of different clusters has been suggested by Sinha et al. (1991) and Singh et al. (1996). Iftekharuddaula et al. (2002) reported that the crosses involving the parents belonging to distinct clusters would offer prime scope in the development of high yielding irrigated rice. There are several studies on rice diversity and clustering using agronomic traits (Sabesan et al. 2009, Lasalita-Zapico et al. 2010, Saravanan & Sabesan 2010).

Two Iranian varieties Sepidroud and DN-33-18 were placed in cluster II. DN-33-18 originated from Sepidroud/Sangejo, so placing these cultivars in the same cluster seems to be logical. The high values of cluster II for grain yield, tiller number and filled grain per panicle and cluster III for tiller number, total grain number per panicle and panicle length crossing Sepidroud and DN-33-18 (in cluster II) with varieties IR60819, IR71604, IR69714, IR62161, SA2, IR57298, IR69726, SA1, IR72102 and IR73885 (in cluster III)

are expected to give promising and desirable recombinants in the segregating generations for most of traits .

Conclusion

The results of this study suggested a crossing between Iranian cultivars (Sepidroud and DN-33-18) with genotypes in cluster III for developing new desirable lines.

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