Heritability and Diversity Analysis of Quantitative Traits in Rice

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Summary

Genetic diversity is prerequisite for any crop improvement program as it helps breeders in the development of superior recombinants. This study was conducted with the aim of evaluating genetic parameters and phenotypic divergence in a germplasm consisted of twenty rice varieties. High estimates of heritability coupled with high genetic advance found for total grains per panicle, filled grains per panicle, tiller number and grain yield make these traits suitable for selection. Principle component analysis (PCA) showed that four components explained more than 90 percent of total variation. Cluster analysis of genotypes using Ward's minimum method and Euclidian distance criterion classified rice varieties in three different groups. Observed differences among the three groups in mean values of agronomic traits suggest the need for conducting crosses between genotypes of clusters II and III and subsequent selection for grains per panicle, filled grains per panicle and panicles per plant in segregating generations in order to develop new high yielding rice lines.

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Introduction

Rice is a staple food in Iran cultivated on 570,000 hectares of irrigated area with total production of 2.4 million tonnes of milled rice. Iran still largely depends on rice imports up to 0.8 million tonnes per year to meet the domestic consumer's demand (Nematzadeh et al., 2006). Local high quality rice varieties account for more than 70% of the total rice acreage in Iran, that are of the Basmati type with yield ranging from 2.5 to 4 t/ha (Nematzadeh & Khush, 1993). These varieties are tall, susceptible to lodging, have long grains, slender shape, intermediate amylose content and gelatinization temperature, soft gel consistency, good grain elongation and scent and are susceptible to blast and stem borer (Singh et al., 2000).

The rice breeding programs in Iran is based mainly on pedigree breeding method for cultivar development. Efforts are focused on development of varieties with high yield potential and acceptable cooking quality through hybridization of local aromatic, high yielding varieties. These high yielding improved varieties replaced the traditional varieties. However, improved varieties shared common ancestry, which could result in an erosion of genetic diversity. Diversity analysis can help in selection of genetically divergent parents, which can produce new recombinants with suitable traits when crossed to each other. 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; Kiani 2012). This study aimed to evaluate the extent of variability for yield attributing characters within local and improved varieties to provide basis for yield improvement through hybridization programmes in rice.

Materials and methods

Twenty varieties of rice (Table 1) were used in this study. The experiment was conducted in a randomized complete block design (RCBD) with three replications in Sari University of Agricultural Sciences and Natural Resources during 2011. 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).

Agronomic traits like plant height (cm), panicles per plant, panicle length (cm), total grains per panicle, filled grains per panicle, grain length (mm), grain width (mm), 1000 grains weight (g) and grain yield (t/ha) were recorded based on the standard evaluation system (SES) of rice (IRRI, 2002).

Statistical and genetic parameters like PCV (phenotypic coefficient of variation), GCV (genotypic coefficient of variation), H_{bs} (broad sense heritability) and GA (genetic advance) were calculated using formulas 1 to 4, respectively.

PCV= $(\sigma^2_p/X) \times 100$ (1)

GCV= $(\sigma^2_g/X) \times 100$ (2)

H_{bs}= $(\sigma^2_g/\sigma^2_p) \times 100$ (3)

GA= $i\, \sigma^2_p\, H_{bs}$ (4)

Where σ^2_p, σ^2_g and X are phenotypic variance, genotypic variance and the mean of a trait, respectively, whereas i is the selection intensity (i=2.06 when the proportion of selected parents is 5%).

Table 1. Rice varieties used in this study

Entry No.	Variety name	Type	Origin
1	Khazar	Improved	Iran
2	Tabesh	Local	Iran
3	Sang tarom	Local	Iran
4	Tarom mahalli	Local	Iran
5	Hashemi	Local	Iran
6	Astaneh	Local	Iran
7	Shastak	Local	Iran
8	Hassani	Local	Iran
9	Tarom deylamani	Local	Iran
10	Neda	Improved	Iran
11	Nemat	Improved	Iran
12	Dasht	Improved	Iran
13	Champa	Local	Iran
14	Amol-3	Improved	Iran
15	Sepidroud	Improved	Iran
16	Pajouhesh	Improved	Iran
17	Pouya	Improved	Iran
18	IR68061	Improved	Philippines
19	IR5931	Improved	Philippines
20	IR50	Improved	Philippines

Cluster analysis was performed using Ward's minimum method and Euclidian distance among varieties. All of statistical analyses, including analysis of variance, estimation of descriptive statistics, principal component analysis and cluster analysis, were performed using SPSS version 14 statistical package.

Results and discussion

The results of analysis of variance are presented in Table 2. High significant differences were observed among genotypes for all traits.

Estimation of statistical and genetic parameters is shown in Table 3. High phenotypic and genotypic variances were exhibited by total grains per panicle (6070.25 and 5951.98) followed by filled grains per panicle (2645.86 and 2553.61) and plant height (411.80 and 405.95). For all the traits phenotypic variance was higher than the genotypic variances indicating the influences of environmental factors on these traits (Devi et al., 2006). The PCV and GCV were the highest for total grains per panicle (40.20 and 39.81) followed by grain yield (39.91 and 31.48), panicles per plant (34.59 and 29.66) and filled grains per panicle (34.20 and 33.60). The lowest PCV and GCV were observed for grain length (8.17 and 7.97) and panicle length (9.03 and 7.35). High PCV and GCV for grain yield and number of spikelets per panicle and low PCV and GCV for panicle length was reported by Prajapati et al. (2011).

Heritability estimates ranged from 62.34% (grain yield) to 98.58% (plant height) (Table 3). Maximum and minimum genetic advance (as the percentage of mean) was observed for total grains per panicle (81.20%) and panicle length (12.34%), respectively. High estimates of heritability coupled with high genetic advance, expressed as the percentage of mean, was observed for total grains per panicle (98.05%, 81.20%) followed by filled grains per panicle (96.51%, 68.00%), panicles per plant (73.52%, 52.39%)

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Table 2. Analysis of variance for nine agronomic traits of twenty rice varieties

Sources of variation	Degrees of freedom	Mean squares								
		PH	PP	PL	TGN	FGP	GL	GW	TGW	GY
Genotype	19	1223.70**	65.88**	15.20**	17974.22**	7753.07**	2.06**	0.279**	46.47**	5.42**
Replicate	2	5.93 ns	14.87 ns	0.129 ns	181.55 ns	44.15 ns	0.016 ns	0.002 ns	3.43 ns	0.508 ns
Error	38	5.85	7.06	2.20	118.27	92.25	0.035	0.004	2.67	0.909

PH= Plant height, PP= Panicles per plant, PL= Panicle length, TGP= Total grains per panicle, FGP= Filled grains per panicle, GL= Grain length, GW= Grain width, TGW= 1000 grains weight, GY= Grain yield; ** = significant at P<0.01, ns = not significant

Table 3. Statistical and genetic parameters for nine agronomic traits in twenty rice varieties

Traits	Range	Mean	Standard deviation	σ^2_p	σ^2_g	PCV (%)	GCV (%)	H_{bs} (%)	GA (% of mean)
PH	167.67-99.83	123.62	20.20	411.80	405.95	16.41	16.30	98.58	41.21 (33.33)
PP	26.00-8.33	14.93	4.69	26.67	19.61	34.59	29.66	73.52	7.82 (52.39)
PL	32.67-24.33	28.29	2.25	6.53	4.33	9.03	7.35	66.34	3.49 (12.34)
TGP	347.33-73.00	193.80	77.40	6070.25	5951.98	40.20	39.81	98.05	157.37 (81.20)
FGP	273.00-68.00	150.40	50.84	2645.86	2553.61	34.20	33.60	96.51	102.27 (68.00)
GL	11.86-8.99	10.31	0.828	0.710	0.675	8.17	7.97	95.07	1.65 (16.01)
GW	3.27-1.90	2.35	0.305	0.096	0.092	13.18	12.91	95.82	0.612 (26.03)
TGW	34.13-18.96	27.24	3.94	17.27	14.60	15.26	14.03	84.54	7.24 (26.57)
GY	6.57-1.97	3.89	1.34	2.41	1.50	39.91	31.48	62.34	1.99 (51.17)

PH= Plant height, PP= Panicles per plant, PL= Panicle length, TGP= Total grains per panicle, FGP= filled grains per panicle, GL= grain length, GW= grain width, TGW= 1000 grains weight, GY= Grain yield

and grain yield (62.34%, 51.17%). Therefore, it is expected that selection will be successful in improving these traits. High estimates of heritability with moderate genetic advance were observed for plant height (98.58%, 33.33%), grain width (95.82%, 26.03%) and 1000 grains weight (84.54%, 26.57%). Characters including grain length (95.07%, 16.01%) and panicle length (66.34%, 12.34%) exhibited high heritability with low genetic advance. So, these traits could be improved by inter-mating of superior genotypes of segregation population developed through recombination breeding.

Principal component analysis (PCA) based on nine agronomic traits showed that four components accounted for 90.53% of total variation (Table 4). First component with variance of 40.43% from total variance related to negative association between panicles per plant with grain width and 1000 grains weight. Second component explained 22.84% of total variance showing importance and positive relationship between total grains per panicle and filled grains per panicle. This component may be named as 'grain filling' characteristics. Third component explained 15.82% of total variance showing importance of positive relationship between panicle length and grain length. Fourth component, with the variance of 11.44% showed competition between reproductive (plant height) and vegetative part (grain yield). Based on the results of PCA, a plant type for increasing grain yield should have high panicle length with higher filled seeds and moderate plant height and productive tillers.

Cluster analysis grouped 20 rice genotypes into three major clusters (Figure 1). Cluster I comprised seven local genotypes namely 'Tabesh', 'Sang Tarom', 'Tarom Mahalli', 'Astaneh', 'Shastak', 'Hassani' and 'Tarom Deylamani'. Cluster II as the largest cluster comprised nine genotypes 'Khazar', 'Hashemi',

'Neda', 'Nemat', 'Dasht', 'Champa', 'Amol-3', 'Pouya' and 'IR50'. However, two Philippine cultivars 'IR68061' and 'IR5931' along with two Iranian improved cultivars 'Sepidroud' and 'Pajouhesh' were grouped in cluster III. Cluster analysis separated local low yielding varieties from improved high-yielding varieties. Foreign varieties IR68061 and IR5931 (except IR50) along with two improved Iranian varieties 'Sepidroud' and 'Pajouhesh' formed a separate group. 'Sepidroud' originated from 'IR8/Domsiah' and 'Pajouhesh' was derived from the cross 'Sepidroud'/'Sang Jo'. So placement of these cultivars in the same cluster seems to be logical.

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

Trait	Principal Components			
	Comp 1	Comp 2	Comp 3	Comp 4
PH	0.038	-0.183	0.085	-0.913
PP	-0.595	-0.631	-0.258	0.352
PL	-0.300	0.136	0.859	-0.171
TGP	-0.268	0.887	0.054	0.286
FGP	-0.245	0.894	0.055	0.216
GL	0.240	0.013	0.918	0.123
GW	0.819	-0.253	-0.378	-0.184
TGW	0.902	-0.258	0.181	-0.120
GY	-0.486	0.203	0.131	0.743
Eigen value	3.639	2.055	1.424	1.029
Variance	40.43	22.84	15.82	11.44
Cumulative variance	40.43	63.27	79.09	90.53

PH= Plant height, PP= Panicles per plant, PL= Panicle length, TGP= Total grains per panicle, FGP= Filled grains per panicle, GL= Grain length, GW= Grain width, TGW= 1000 grains weight, GY= Grain yield

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Table 5. Mean and deviation (%) from total mean (in parenthesis) of three clusters of rice varieties for nine agronomic traits

Cluster	Varieties	PH	PP	PL	TGN	FGP	GL	GW	TGW	GY
I	2, 3, 4, 6, 7, 8, 9	141.90 (+14.79)	14.43 (-3.35)	26.81 (-5.23)	124.48 (-35.77)	107.14 (-28.76)	9.92 (-3.78)	2.62 (+11.49)	29.80 (+9.40)	2.66 (-31.62)
II	1, 5, 10, 11, 12, 13, 14, 17, 20	115.65 (-6.45)	11.93 (-20.09)	29.59 (+4.59)	244.70 (+1.88)	183.63 (+22.09)	10.78 (+4.56)	2.25 (-4.25)	27.47 (+0.84)	4.20 (+7.97)
III	18, 19, 15, 16	109.54 (-11.39)	22.58 (+51.24)	27.96 (-1.17)	200.58 (+26.26)	151.33 (+0.62)	9.94 (-3.59)	2.08 (-11.49)	22.24 (-18.35)	5.35 (+37.53)
	Total Mean	123.62	14.93	28.29	193.80	150.40	10.31	2.35	27.24	3.89

PH= Plant height, PP= Panicles per plant, PL= Panicle length, TGP= Total grains per panicle, FGP= Filled grains per panicle, GL= Grain length, GW= Grain width, TGW= 1000 grains weight, GY= Grain yield
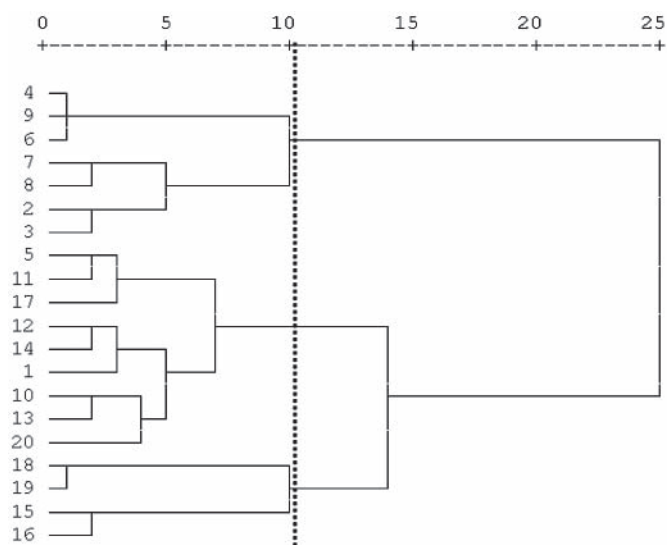

Figure 1. Clustering of twenty rice genotypes based on nine agronomic traits. For varieties names see Table 1.

The mean performance of three groups of rice varieties, revealed through cluster analysis, for nine agronomic traits is presented in Table 5. The highest grain yield (5.35 t/ha), panicles per plant (22.58), moderate total grains per panicle (200.58) and filled grains per panicle (151.33) were recorded for cluster III. Varieties from cluster II had the highest values for panicle length (29.59 cm), total grains per panicle (244.70), filled grains per panicle (183.63) and grain length (10.78), also they exhibited moderate plant height (115.65 cm), 1000 grains weight (27.47 g) and grain yield (4.20 t/ha). Cluster III showed the highest mean values for traits like plant height, grain width and 1000 grains weight.

Based on mean values of the three clusters, none of them 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 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; Kiani; 2012). Due to high values of cluster III for grain yield and panicles per plant and cluster II for most of yield contributing traits (total grains per panicle, filled grains per panicle, panicle length, grain length and 1000 grains weight) crossing varieties in cluster II with varieties in cluster III are expected to give promising and desirable recombinants in the segregating generations for most of traits.

Conclusion

In summary, the results of this study suggested crosses between genotypes of clusters II and III followed by selection based on total grains per panicle, filled grains per panicle and panicles per plant in segregating generations in order to develop new high yielding rice lines.

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