ORIGINAL ARTICLE

Cluster analysis of 24 Genotypes of Modified rice According to Qualitative and Quantitative traits

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ABSTRACT

Rice supplied main food of more than half of the worlds and a large part of Asia which supplied more than 80 % of the calories and 75 % of the consuming protein of the people. One of the methods to increased production was using Eugenic techniques and election is most important tool at Eugenic techniques. For this purpose, an experiment was done to evaluate the quantitative and qualitative characteristics of 24 different genotypes of modified native rice on 2011 at the Rasht Rice Research Institute. The experiment was done in a randomized complete block design with three replications during the 24 traits including yield and physiological characteristics and quality. A cluster analysis based on Ward's method showed that genotypes were tested in three main clusters; they were divided in three clusters. The most Available genotype in cluster A are Nemat genotypes, 203 and 416, Cluster II: Gharib and Khezr, Cluster III: Saleh, Sallari, Hasan Sarai, Binam and Hassani. Comparing clustering average based on Duncan test showed highest yield (6.25 tons per acre) of the cluster I. lowest yield were IIIb, II, IIIa and IIIc clusters with no significant differences.
Keywords: native and modified rice, qualitative and quantitative traits, cluster analysis

INTRODUCTION

Increasing world population and hunger which threat present and future human situation cannot be controlled except by increasing agricultural production .more than 50 percent of consuming foods are supplied by Cereals. Rice is most productive among them [1 and 2]. This plant is the main food of more than half of the world's [3]. Oryza has twenty species with 12 base chromosomes which O.Sativa is divided to three geographical races like Indica, Japonica and Javanica (Bulla) [4]. Also, in the twenty-first century cereal is still important and supplements resource of protein for human. Rice contains 8-9 % protein and most important food crop of more than a third of the world's population in the world. The area under rice cultivation is more than 150 million acre in the world. In order to supply food Resources of world population to provide food for a growing, rice production must double by 2025 [5]. According to General Agricultural Census in 2002, the area under rice cultivation was 465,453 acre and its production was 1,819,990 tons. Iran's average rice yield was about 4200 kg per acre and annual consumption of have been reported 32 kg [6]. In other hand, sufficient knowledge of genetic variation and classification of germ plasma is necessary to select appropriate parental for breeding purposes. Sarawgi and Rostogi [7] examined the genetic diversity in 132 genotypes of rice and placed cluster analysis in 10 different categories. Mutaka and Mehetre [8] used 25 genotypes to investigate the genetic diversity of rice and have been divided to 5 clusters according to yield performance. According to importance of issue, the purpose of this article is to study 24 genotypes of native and modified rice according to farming traits and cluster analysis according to qualitative and quantitative data.

MATERIAL AND METHODS

In this study was surveyed in rice Research Institute at Rasht in form of random block. Seeds of 24 genotypes of native and modified Rice were prepared in Rasht. Seedling was planting at main about 12 to 12 cm of density and 25 cm spacing. Planting Operation like preparing the main land, transplanting, irrigation, weeds and diseases and fertilizer were conducted in accordance with local custom. In this

study, Total tiller number, number of fertile tillers, days to 50% flowering, number of grains per cluster, number of fertile grains in clusters, number of empty grains in a cluster, plant height, 100 seed weight, plant weight, stem length, flag leaf length, flag leaf width, cluster outflow sheath, panicle length, raw grain length , raw grain width, grain shape, grain length cooked, grain elongated, amylose content, gelatinization temperature, the percentage of consistency and gels and yield were evaluated. 10 plants of each cultivar were selected randomly to evaluate traits. Then observations mean for each trait was used for statistical analysis. Statistical analysis and a cluster analysis using SPSS and a mean comparison using Duncan's multiple range tests were performed.

RESULTS AND DISCUSSION
Cluster analysis of 24 rice genotypes based on quantitative and qualitative traits and using ward of cutting the gap to 13 units methods (Fig. 1) showed that rice genotypes were grouped in three clusters. Third cluster with 14 genotypes is largest cluster and include of three groups IIIa with 7 genotypes, such as Salari and Hassan Sarai , Group IIb consisted of 4 genotypes include binam and hassani, group (IIIc) with 3 genotypes include mu10 line and Saleh. Second cluster with 7 genotypes such as Gharib and Khezr, in 416 and 203 were in first cluster with 3 genotypes. In This study 24 traits were examined in order to create clusters of mean comparing of all clusters (Table 1). Therefore, first cluster were higher than other in term of yield. Respectively third cluster (IIIb) and second cluster were ranked. Lowest yield belonged to third cluster (IIIa).

Sarawgi and Rostogi [7] examined the genetic diversity of 132 genotypes rice using cluster analysis and action figures in 10 different categories. Mokata and Mehetre [8] were used 25 genotypes to investigate the genetic diversity which were divided into five clusters according to yield components. Hanamaratti and Patile [9] have evaluated 50 genotypes rice under different growing conditions. Their research showed that, independent of the geographic origin, cultivars are grown on the highlands and regions and respectively, 17 and 18 clusters are generated. Liping and Jianfei [10] studied about 163 native species and 16 commercial Variety of japonica, as well as analysis cluster have been divided to 5 groups and 13 Brigades in order to evaluate Yield. Kandhola and Panwar [11] studied the genetic diversity among 52 genotypes rice and have divided them to 11 clusters according to 16 qualitative and morphological – farming traits.
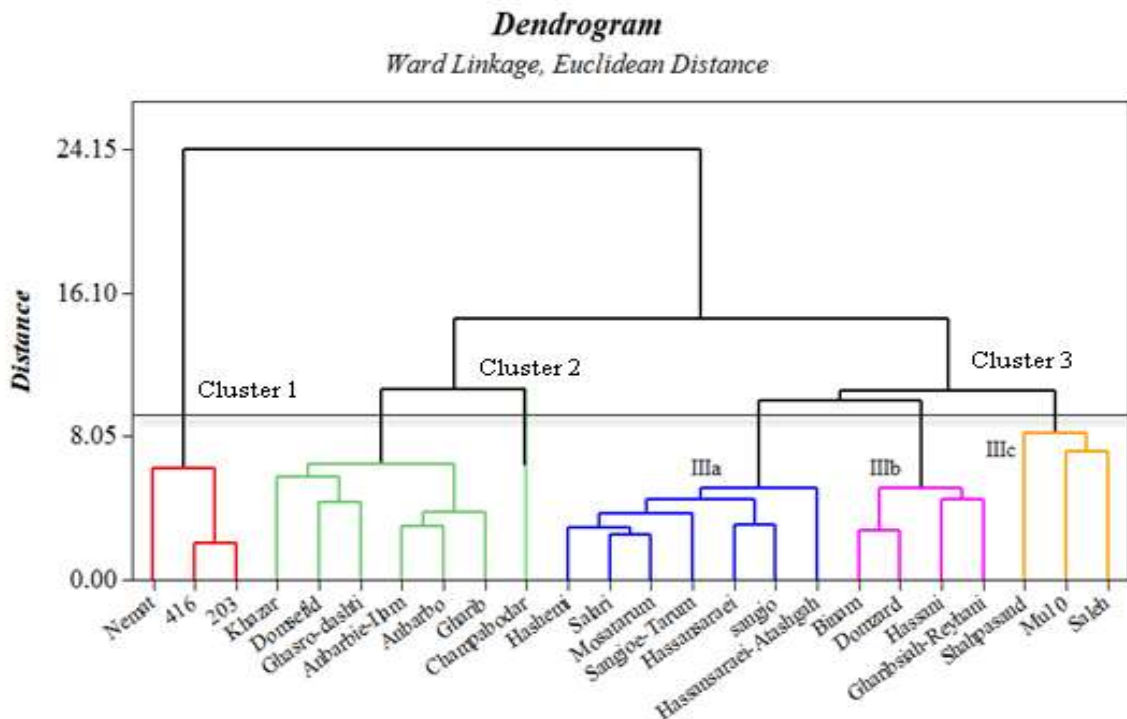

Figure 1. Dendrogram of Cluster Analysis through Variance Method (Ward) On the Basis 24 Genotypes of Native and Modified Rice

Table 1 – Comparing Average of Qualitative and Quantitative Traits According To Yield Cluster of Cluster Analysis

Traits	Cluster 1		Cluster 2		Cluster 3					
					I		II		III	
total tiller number	19.20	a	12.78	b	12.78	a	16.63	a	10.57	b
fertile tiller number	17.73	a	11.47	b	12.01	a	15.13	a	10.05	b
days to 50% flowering	113.83	a	108.64	a	98.50	b	97.66	b	95.25	b
grain number per ear	144.56	a	145.41	a	111.98	b	97.03	b	96.87	b
fertile grain number per ear	123.1	ab	129.73	a	103.48	bc	85.10	c	89.72	c
hollow grain number per ear	21.83	a	15.69	ab	8.57	bc	11.93	bc	7.22	c
plant height	111.8	c	151.46	a	140.93	ab	122.66	bc	127.27	bc
100 grain weight	2.77	ab	2.53	ab	2.43	b	2.69	ab	2.92	a
plant weight	37.3	a	37.3	b	22.67	b	29.67	b	23.95	b
Culm length	83.93	c	83.9*3	a	133.43	ab	96.33	bc	100.35	abc
length of flag leaf	37.93	a	37.93	a	32.68	ab	33.11	ab	29.12	b
width of flag leaf	1.3	ab	1.3	ab	1.08	b	1.4	a	1.07	b
length to width ratio of flag leaf	11.55	b	11.55	a	29.94	a	27.43	a	27.67	a
ear exposure rate from sheath	3.93	b	3.93	a	10.75	a	1.79	b	10.32	a
ear length	30.86	a	30.86	a	27.46	b	26.33	b	26.92	b
raw grain length	7.96	a	6.45	c	7.13	bc	7.24	b	6.4	c
raw grain width	1.86	c	2.25	ab	1.92	c	2.1	bc	2.43	a
grain shape	4.33	a	2.88	cd	3.63	b	3.41	bc	2.65	d
length of cooked grain	11.98	ab	11.31	b	12.76	a	12.1	ab	13.30	a
grain lengthening	1.48	c	1.77	bc	1.81	ab	1.88	ab	2.1	a
amylase rate	24.69	a	21.66	ab	20.63	b	24.37	a	19.75	b
gelatinization temperature	6.67	a	3.33	b	3.44	b	4.4	b	4.17	b
stability and consistency rate of gel	28.66	b	55.86	a	53.56	a	51.67	a	56.25	a
grain yield	6.29	a	4.10	b	3.48	b	4.5	b	3.57	b

Differences between averages of each column which have common characters are not significant at probability level of 5%.

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