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Study of the Genetic Diversity of Garlic

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Abstract

The experiment was carried out at the research field of Spices Research Centre, Shibganj, Bogra, Bangladesh to find out the Genetic di versity among 13 germplasms of Garlic (*Allium sativum* L) during Rabi 2013-14 using morphological traits. D^2 analysis of 13 garlic lines and analysis of variance were done. The lines were grouped into four clusters. The-inter cluster distance was larger than the intra-cluster distances. Maximum inter cluster distance was found between cluster I and II (11.433) followed by cluster III and IV (11.420) and I and IV (11.146). It may be concluded that the line in cluster II (5) and the line in cluster IV (4, 6 10, 11 and 12) grouped here is superior to all other clusters and could be used for future breeding work.

Keywords: *Allium sativum*, Genetic diversity, Garlic germplasms, D^2 analysis, Clustering

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1. INTRODUCTION

Garlic (*Allium sativum*) is one of the important spice crops grown in Bangladesh. It is widely cultivated during winter season. It is also being used as green stalks and young leaves are eaten fresh or cooked and furthermore, large quantities of garlic used for pharmaceutical purposes (7). Historical and cultural significance of Allium has been well documented in an ancient scripture in Garuda Purana, where it regarded as aphrodisiac food in India (1). Garlic is sensitive to growing temperature and photoperiod. Short days are favorable for the formation of bulbs of garlic (10). Low growing temperature in the early stage enhances plant growth and gave early initiation of bulbs in garlic (11). The average yield of garlic in our country is very low. However, clonal images species show a remarkably high degree of diversity in bulb size, color, growth habits and agronomic traits such as stress and drought tolerance (2). The characterization of garlic germplasm has been based mainly on phenotypic characteristics. The agricultural traits of garlic germplasms have normally shown wide variations in characteristics such as bulb weight, coat layer, leaf length, growth habit, and stress resistance (3,8,13). Assessment of germplasm resources is necessary for their effective use (6). Systematic study is therefore needed to evaluate the existing germplasm of garlic. Thinking the idea in mind 13 lines was evaluated to know their performances in Bangladesh.

The variability among different lines of a species is known as genetic diversity. Genetic diversity arises either due to geographical separation or due to genetic barriers to cross ability. D^2 statistic proposed by Mahalanobi's is one of the potent techniques for measuring the genetic divergence both in intra and inters cluster level. Genetic diversity plays an important role plant breeding to development of high yielding varieties. Such a study also permits to select the genetically divergent parents to obtain the desirable recombination of the segregating generations. The present study was undertaken in order to find out or selects suitable lines on the basis of genetic diversity.

2. MATERIALS AND METHODS

The study was conducted at Spices Research Centre, Bogra during rabi season 2013-2014 to select the promising garlic lines for releasing a variety. The experiment was laid out in RCB design with three replications. Twelve different garlic lines (GC001, GC005, GC0012, GC0013, GC0017, GC0027, GC0028, GC0029, GC0030, GC0031, GC0035 and GC0036) were collected and evaluated along with BARI Garlic -1 as a check. Planting was done on 15 November 2013, maintaining 10 cm x 10 cm. spacing. The unit plot size was 4.0 m x 1.2 m. In addition to 5 t/ha of cow dung, the crop was fertilized with N_{100} P_{54} K_{166} S_{20} kg/ha. The entire quantity of cow dung, P, K, S and ½ of N was applied during land preparation. The rest of N was applied in two equal splits at 25 and 50 DAP. To control tip, burn disease the crop was sprayed with Rovral 50WP@2g/l of water three times at 35, 45 and 55

DAP. Three irrigations were done at 10-20 days' interval during vegetative growth stage. Irrigation was stopped before 20 days of crop maturity. The crop was harvested on 18 March 2014.

The data were subjected to analysis of variance and Mahalanobis's (1936) generalized distance (D^2) extended by Rao (1952) MSTATC and Genstat programs of computer laboratory of SRC, BARI, Bogra. The genotypes were grouped into 4 (Four) different clusters following the method discussed by Tocher (12).

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance

The analysis of variance showed significant differences among the entries for all the characters studied. The range, mean, variance and standard deviation of eight characters have shown in Table 1. Among the 8 characters studied, the maximum variation was obtained in the character of yield (t/ha) followed by yield/plant (g) and bulb width (cm). Hence there is enough scope for selection of potential genotype/ lines for breeding program. Thirteen garlic lines were grouped in to four different clusters by using clustering techniques. The distribution of the genotypes in different clusters is presented in Table 2. The maximum number of genotypes (5) was grouped in clusters III and cluster IV.

Table 1. Variabilities of 8 characters of garlic lines

Characters	Range		Mean	Standard deviation	CV (%)
	Minimum	Maximum			
Plant height (cm)	62.8	83.70	74.87	3.82	5.10
No. of leaves/plant	6.20	8.90	7.54	0.62	8.25
Bulb length (cm)	2.96	3.99	3.39	0.23	6.81
Bulb width (cm)	2.50	4.38	3.18	0.30	9.56
Clove length (cm)	1.86	2.54	2.21	0.15	6.60
Clove width (cm)	0.60	0.82	0.73	0.05	7.55
Bulb yield/plant (g)	12.00	24.00	16.85	2.71	16.09
Bulb yield (t/ha)	4.00	12.17	7.79	2.17	27.86

Table 2. Distribution of different selected garlic lines in different clusters

Clusters	Line	Number of lines	Line with their accession number
I	1, 3	2	GC001, GC0012
II	5	1	GC0017
III	2,7,8,9,13	5	GC005, GC0028, GC0029, GC0030, BARI Garlic-1
IV	4,6,10,11,12	5	GC0013, GC0027, GC0031, GC0035, GC0036

The intra-and inter-cluster values within and among the clusters are presented in Table 3. Intra-group distance appeared much smaller than the inter-groups. It suggests wider genetic diversity of the lines among the clusters. The intra-cluster distances in all the clusters were found low indicating that genotypes within the clusters are closely related. Similar results were reported by (4).

Intra-cluster distances varied from 0.1513 to 0.096, comparatively higher intra-cluster distances were observed in cluster III and IV. Inter-cluster distances ranged from 7.952 to 11.433. The maximum inter-cluster distance was observed between cluster I and II (11.433). Medium or intermediate distances were observed between cluster III and IV (11.420) and I and IV (11.146). The lowest distance was shown between cluster II and IV (5.910). Clustering revealed instability due to low divergence and widely diverged clusters remains stable in different environment.

Table 3. Inter and intra-cluster (bold) distance (D^2) for 13 garlic lines obtained by canonical variate analysis

Clusters	I	II	III	IV
I	**0.096**			
II	11.433	**0.000**		
III	7.952	7.519	**0.1513**	
IV	11.146	5.910	11.420	**0.1166**

The genetic differences between clusters were reflected in their cluster means. Mean values for different clusters are presented in Table 4. The highest mean values for bulb yield (t/ha), yield/plant (cm), clove length (cm), clove width (cm), bulb width (cm), number of leaves/plant and plant height (cm) were observed in the same cluster II (Table 4). That means lines included in this group are better for those parameters. The highest bulb length was found in cluster III. Cluster I had the lowest value for plant height. The mean of yield/ plant (g) and yield (t/ha) was the lowest value in cluster I.

Contribution of the characters towards divergence is presented in Table 5. Results showed that, vector I obtained from PCA expressed that the important characters responsible for genetic divergence in the major axis of differentiation. Plant height, no. of leaves/plant, bulb length (cm), bulb width (cm), clove length (cm), clove width (cm), yield/plant (g) and yield (t/ha) showed negative value in respect to vector I. In vector II, which is the second axis of differentiation, the responsible characters were bulb

length (cm) and yield/plant (g) played their major role on genetic divergence. The other characters of both the axis played a minor role in the genetic divergence. This means that considerable emphasis should be given on those parameters responsible for genetic divergence. Maximum contribution of bulb length (cm) and yield/plant (g) towards diversity of garlic was also found.

Table 4. Cluster means for 8 different characters of 13 garlic lines

Characters	Clusters			
	I	II	III	IV
Plant height (cm)	70.98	78.47	73.95	76.63
No. of leaves/plant	6.93	8.40	7.37	7.77
Bulb length (cm)	3.23	3.36	3.38	3.43
Bulb width (cm)	3.04	3.44	3.08	3.28
Clove length (cm)	2.06	2.34	2.19	2.28
Clove width (cm)	0.67	0.77	0.71	0.76
Bulb yield/plant (g)	13.50	21.33	16.27	17.87
Bulb yield (t/ha)	5.17	11.30	6.54	9.37

Table 5. Contribution of different character towards divergence in garlic

Characters	Vector I	Vector II
Plant height (cm)	-0.3681	-0.0257
No. of leaves/plant	-0.3661	-0.0929
Bulb length (cm)	-0.2937	0.8999
Bulb width (cm)	-0.343	-0.095
Clove length (cm)	-0.360	-0.277
Clove width (cm)	-0.360	-0.250
Yield/plant (g)	-0.365	0.131
Yield (t/ha)	-0.367	-0.127

4. CONCLUSION

Considering pant architecture and other traits the different lines are clustered into 4 diverged groups. It is expected that genotypic lines belonging high to medium D^2 values tend to produce high yield potential. It may be concluded that the line in cluster II (5) and the line in cluster IV (4, 6 10, 11 and 12) grouped here is superior to all other clusters and could be used for future breeding work.

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