

Original Research Article

Genetic Diversity for Bulb Yield and Its Component Traits in Garlic (*Allium sativum* L.)

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ABSTRACT

The aim of this study was to estimate the genetic diversity among the collected genotypes within country and it's further in crop improvement. An experiment was laid out in a randomized block design with 25 garlic genotypes replicated three times separately at HRC, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut during *rabi* 2014-15. The observations were recorded on various growth and yield attributing parameters from the five randomly selected competitive plants of each plot for all replications. Mahalanobis D² analysis showed 25 genotypes grouped into six clusters. This makes the genotypes to become moderately divergent. The maximum inter cluster D² value (1142.147) was recorded between cluster V and III and the minimum average inter cluster D² value (87.991) was recorded between cluster VI and IV of the total variation. Over all the study confirmed the presence of sufficient genetic diversity in Indian genotypes and this could be exploited in the genetic improvement of the garlic crop through hybridization and simple selection.

Keywords

Genetic diversity,
Intra cluster,
Pseudostem, Bulb
yield, Garlic

Introduction

Garlic (*Allium sativum* L.) is one of the most important edible bulbous crop of the world. It is a monocot plant and belongs to the family Alliaceae. It is highly placed for its flavor enhancing capacity and high medicinal properties like antimicrobial, antidiabetic, anticarcinogenic action and also used in treatment of cardiovascular disease. Garlic has higher nutritional values than other bulbous vegetable crops as it bulb (100 g) contain moisture- 62.8%, protein-

6.3%, fat- 0.1%, fiber- 0.8%, carbohydrates- 29%, energy-145 calories and is good source of selenium, phosphorous, manganese, copper, iron, zinc, calcium, thiamine, riboflavin (Sodh *et al.*, 2016). 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 uses (Kik *et al.*, 2001). Garlic displays considerable diversity with respect to morphological features, yield,

quality features as well as resistance to important insect pests and diseases (Kumar *et al.*, 2015).

Garlic has been clonally propagated from a longer period, which may be speculated to result in a bottleneck for genetic variation in garlic. 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 (Bradley *et al.*, 1996). China is the leading garlic producer, which contributes over 85-90 per cent of the world's garlic production. India is the second largest producing country in world and contributes 21.19% of the total spices production of India. In past 20 years, production of garlic in India has increased more than two times. In 2015-16, garlic crop occupied 2.81 lakh ha with the production of 16.17 lakh tones. Madhya Pradesh, Gujarat, Uttar Pradesh, Rajasthan, Assam, Punjab, Maharashtra, West Bengal, Haryana and Odisha are the major onion producing states. Among these states Madhya Pradesh is the leading garlic producing state followed by Gujarat and Rajasthan during 2016 (Anonymous, 2016).

To achieve the national and international requirement, export demands, selection of suitable varieties with desired characters is always needful for improvement of garlic germplasm materials (Sharma *et al.*, 2016). Characterization of germplasm materials helps to ensure an efficient and effective use of genotypes for further crop improvement. Mahalanobis D^2 analysis helps in assessing the diversity among the genotypes and to select the divergent parents for future breeding programmes (Mahalanobis, 1936). Recently, such assessment is mainly based on a small number of phenotypic traits. However, environmental conditions may also affect the expression of various quantitative traits. Study of genetic diversity

is an essential requirement for any crop improvement programme because genetically diverse parents are commonly used to explore heterosis and to obtain superior recombinants.

Keeping in view importance of garlic an experiment was conducted to study the genetic diversity in garlic germplasm through morphological parameters and to exploit this diversity for further breeding programme.

Materials and Methods

A total of 25 accessions of garlic varieties (Table 1) were used in the present study collected from different reputed institutions of India raised during rabi season of 2014-2015 at Horticultural Research Centre (HRC) of SVPUA&T in Randomized Block Design (RBD) with three replications. The observations were recorded from five randomly selected competitive plants of each plot for all replications. Observations were taken for various growth and yield attributing parameters like plant height, length of longest leaf, width of longest leaf, number of green and dry leaves per plant, diameter and height of pseudo stem, bulb diameter, bulb length, weight of bulb, cloves per bulb, weight of single clove, days to maturity and bulb yield in q/ha. The recorded observations were subjected to biometrical and statistical analysis. The genetic diversity among twenty five garlic accessions was assessed by using D^2 Mahalanobis statistics. The grouping of accessions was done using Tocher's method, as described by Rao, (1952).

Results and Discussion

The D^2 analysis revealed the 25 diverse genotypes grouped in to six clusters by Mahalanobis Euclidean Distance method,

out of the six clusters (Table 2). Cluster VI and I contained maximum number of genotypes (7) comprising G-282, P G-9, Cheenia, Indian Garlic, F-1, Hari Rani, F-2 and Kadari-4, G-323, A V T G-1, PG-17, C F G-6, C F G-5, C F C-7 respectively. While, cluster IV comprising (6) genotypes namely C F G-1, P G-24, C F C-1, F-6, U.P Chatta and G-50, cluster II and V both containing (2) genotypes *viz.*, Sakha-44, G G-2 and Jawa, Rohni-2, respectively. Cluster III contained single genotypes namely F-3. All the clusters observed to be heterogeneous which included genotypes from different geographical regions. The clustering pattern obtained in the present experiment suggested that genetic diversity is not necessarily parallel to the geographical diversity. These results are similar to those reported earlier by several researchers in garlic regarding the geographical diversity (Singh *et al.*, 2012; Sandhu *et al.*, 2014; Singh and Dubey, 2011).

The average intra and inter cluster D^2 values are presented in Table 3. Maximum inter cluster D^2 value (1142.14) was recorded between cluster V and III and the minimum average inter cluster D^2 value (87.99) was recorded between cluster VI and IV. The intra cluster distance were found 33.46 for cluster VI, 42.54 for cluster III, 46.32 for cluster II, 61.43 for cluster IV, 75.48 for cluster I, 113.87 for cluster V. The maximum inter cluster D^2 value indicated that genotypes of cluster V and III are not so closely related whereas the genotypes of cluster VI and IV are closely related. It is apparent therefore, the genotypes of various clusters do not differ so significantly with regards to their relative genetic distance as indicated from the low variation of D^2 values. Therefore, it is suggested that selection of genotypes based upon large cluster distance from all the clusters may

lead to favorable broad spectrum genetic variability for bulb yield improvement. Similar findings were also reported by Singh *et al.*, (2013) and Sandhu *et al.*, (2014).

The grouping pattern of the genotypes suggested no parallelisms between genetic divergence and geographical distribution of genotypes. Crossing of genotypes belonging to the same cluster would not be expected to desirable segregants, as these are less divergent for enhancing bulb yield. Therefore, hybridization programme involving genetically diverse parents belonging to different distant cluster would provide an opportunity for bringing together gene constellations of diverse nature. Singh and Dubey, (2011) and Mohanty, (2000) also reported that genotype diversity was independent of geographical region. Arunachalam, (1981) also stated that genotypes belonging to the cluster with maximum inter cluster distance are genetically more divergent.

The cluster means for different traits are measures of inter cluster divergence and degree of homogeneity. Hence, cluster means were worked out which indicated that different clusters were superior with respect to various traits. The cluster mean calculated for fifteen economically important characters under study have been presented in Table 4. Plant height showed highest mean for cluster number VI (69.70) and lowest mean for cluster number III (65.00), length of longest leaf revealed highest mean for cluster number III (46.46) and lowest mean for cluster number II (45.06), width of longest leaf exhibited highest mean for cluster number VI (1.86) and lowest mean for cluster number III (1.57), number of green leaves per plant had highest mean for cluster number V (9.83) and lowest mean for cluster number II (5.63), number of dried leaves per plant revealed highest mean for

cluster number IV (3.00) and lowest mean for cluster III (1.00), pseudostem diameter exhibited highest mean for cluster number IV (1.21) and lowest mean for cluster number III (1.11), pseudostem height showed highest mean for cluster number VI (24.59) and lowest mean for cluster number IV (20.56), diameter of bulb exhibited highest mean for cluster number IV (4.25) and lowest mean for cluster number III (3.63), length of bulb had highest mean for cluster number V (4.42) and lowest mean for cluster number III (3.79), weight of bulb showed highest mean for cluster number IV (24.45) and lowest mean for cluster number II (20.33), number of cloves per bulb exhibited highest mean for cluster number I (26.38) and lowest mean for cluster number V (21.36), weight of clove showed highest mean for cluster number IV (1.96) and lowest mean for cluster number III (1.33), length of clove exhibited highest mean for cluster number V (3.87) and lowest mean for cluster number V (3.00), days of maturity showed highest mean for cluster number III (158.66) and lowest mean for cluster number V (133.33), bulb yield exhibited highest mean for cluster number I (165.67) and lowest mean for cluster number II (135.43).

The present study revealed considerable genetic diversity between the clusters on the basis of comparison cluster means for fifteen traits. Cluster IV showed highest mean values for number of dry leaves per plant, pseudostem diameter, bulb diameter, bulb weight, weight of cloves and length of longest clove whereas, cluster VI showed the highest mean values for plant height, width of longest leaf and pseudostem height. Hence on the basis high cluster mean for almost all important component traits, cluster IV and VI has been isolated as the most divergent cluster containing genotypes like CFG-1, PG-24, CFC-1, F-6, UP Chatta,

G-50, G-282, PG-9, Cheenia, Indian Garlic, F-1, Hari Rani and F-2. Thus, crosses involving the parents from these two clusters may exhibit high heterosis as well as bulb yield. Therefore, hybridization involving above mentioned genotypes is suggested in further breeding programme in order to achieve high heterotic combinations and thus produce large genetic variability and better recombinants in the segregating generations for high yield. Similar results were also reported by Sandhu *et al.*, (2014) and Singh *et al.*, (2013) in their study in garlic crop.

The individual characters contributing maximum to the D^2 values have greater emphasis for deciding the cluster for the purpose of further selection. The percentage contributions of different characters towards genetic divergence are presented in Table 5. Ranking character wise D^2 values and adding the ranks for each character for all the entries identified the variables, which contributed towards the divergence.

Bulb yield contributed maximum (45.05%) towards total divergence and this was followed number of dried leaves per plant (38.33%), number of green leaves per plant (14.33%), days of maturity (11.00%), weight of bulb (7.33%), weight of single clove (6.67%), number of cloves per bulb (6.00%), length of longest clove (2.00%), pseudostem height (1.67%), plant height (1.00%), pseudostem diameter (0.86%), bulb diameter (0.68), length of longest leaf (0.67), bulb length (0.33) and width of longest leaf (0.28%).

Thus, it is suggested that those traits which are highly contributing towards the genetic diversity will help while selecting elite genotypes for further improvement in garlic. Similar findings were also reported by Singh *et al.*, (2012) in garlic.

Table.1 List of garlic genotypes and their source of collection under experiment

S. No.	Genotypes	Source of collection
1.	KADARI-4	Locally collected from area Bareilly, Uttar Pradesh
2.	CFG-6	Locally collected from area Bareilly, Uttar Pradesh
3.	CFG-5	Locally collected from area Bareilly, Uttar Pradesh
4.	CFC-7	Locally collected from area Bareilly, Uttar Pradesh
5.	CFG-1	Locally collected from area Bareilly, Uttar Pradesh
6.	F-6	Punjab Agriculture University (PAU) Ludhiana, Punjab
7.	AVTG-1	Punjab Agriculture University (PAU) Ludhiana, Punjab
8.	G-282	National Horticulture Research and Development Foundation (NHRDF) Nasik
9.	PG-17	Punjab Agriculture University (PAU) Ludhiana, Punjab
10.	G-50	Directorate of Onion and Garlic Research,(Pune) Maharashtra
11.	UP CHATTA	Locally collected from area Bareilly, Uttar Pradesh
12.	PG-24	Punjab Agriculture University (PAU) Ludhiana, Punjab
13.	CFC-1	Locally collected from area Bareilly, Uttar Pradesh
14.	PG-9	Punjab Agriculture University (PAU) Ludhiana, Punjab
15.	JAWA	Locally collected from area Bareilly, Uttar Pradesh
16.	ROHNI	Locally collected from area Bareilly, Uttar Pradesh
17.	CHEENIA	Locally collected from area Bareilly, Uttar Pradesh
18.	HARI RANI	Locally collected from area Bareilly, Uttar Pradesh
19.	INDIAN GARLIC	Locally collected from area Bareilly, Uttar Pradesh
20.	G-323	National Horticulture Research and Development Foundation (NHRDF) Nasik
21.	F-2	Punjab Agriculture University (PAU) Ludhiana, Punjab
22.	F-1	Punjab Agriculture University (PAU) Ludhiana, Punjab
23.	SAKHA-44	Locally collected from area Bareilly, Uttar Pradesh
24.	F-3	Punjab Agriculture University (PAU) Ludhiana, Punjab
25.	GG-2	Directorate of Onion and Garlic Research, (Pune) Maharashtra

Table.2 Clustering pattern of 25 genotypes of Garlic on the basis of genetic divergence

Cluster numbers	No. of genotypes	Genotypes
I	7	Kadari-4, G-323, A V T G-1, PG-17, C F G-6, C F G-5, C F C-7
II	2	Sakha-44, G G-2
III	1	F-3
IV	6	C F G-1, P G-24, C F C-1, F-6, U.P Chatta, G-50
V	2	Jawa, Rohni-2
VI	7	G-282, P G-9, Cheenia, Indian Garlic, F-1, Hari Rani, F-2

Table.3 Average of intra and inter cluster distance

Cluster	I	II	III	IV	V	VI
I	75.44	132.56	338.74	305.51	375.40	318.51
II		46.32	276.86	397.28	424.69	318.18
III			42.54	1072.07	1142.14	1007.37
IV				61.43	141.57	87.99
V					113.87	198.41
VI						33.46

Values in parenthesis are square root of D² value

Table.4 Cluster wise mean values of 15 characters in garlic

Characters Clusters	PH	LL	WL	NGL	NDL	PsD	PsH	BD	BL	BW	NCB	CW	CL	DM	BY
I	67.09	45.14	1.69	8.17	2.06	1.15	24.01	4.20	4.39	24.41	26.38	1.92	3.73	157.38	165.67
II	68.06	45.06	1.64	5.63	2.00	1.11	22.70	3.76	4.06	20.33	22.42	1.54	3.63	146.33	135.43
III	65.00	46.46	1.57	5.66	1.00	1.11	20.93	3.63	3.79	23.38	23.73	1.33	3.00	158.66	155.75
IV	65.19	45.10	1.80	8.83	3.00	1.21	20.56	4.25	4.37	24.45	26.15	1.96	3.82	154.72	162.88
V	66.35	44.50	1.78	9.83	3.00	1.13	21.93	4.23	4.42	24.08	21.36	1.84	3.87	133.33	160.40
VI	69.70	45.69	1.86	6.52	3.00	1.17	24.59	4.13	4.16	22.59	23.71	1.78	3.68	157.14	151.04

Bold values are highest values for that character

On the basis of present study we can conclude that the Cluster IV and VI are more suitable for the further breeding programme as they contain most promising genotypes which are more diverse and may be utilized for future research to achieve high heterotic combinations in garlic.

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