CHARACTERIZATION AND GENETIC DIVERSITY ANALYSIS OF STEM AMARANTH (*Amaranthus viridus* L.)

BY

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CERTIFICATE

This is to certify that thesis entitled, "**CHARACTERIZATION AND GENETIC DIVERSITY ANALYSIS OF STEM AMARANTH (*Amaranthus viridus L.*)**" submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE** in **GENETICS AND PLANT BREEDING**, embodies the result of a piece of bona fide research work carried out by, **SYEDA AMENA SULTANA** Registration No. **03-01181** under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

I further certify that such help or source of information, as has been availed of during the course of this investigation has duly been acknowledged.

Dated: December, 2008
Place: Dhaka, Bangladesh

(Dr. Md. Shahidur Rashid Bhuiyan)
Professor
Supervisor

Dedicated to
My
Beloved Parents

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Place: SAU, Dhaka.

SOME COMMONLY USED ABBREVIATIONS AND SYMBOLS

Abbreviations	Full word
%	Percent
^{0}C	Degree celsius
@	At the rate
σ^2_p	Phenotypic vriance
σ^2_e	Error variance
σ^2_g	Genotypic variance
h^2_b	Heritability in broad sense
AEZ	Agro –ecological Zone
Agric.	Agriculture
Agril.	Agricultural
Agron.	Agronomy
ANOVA	Analysis of variance
BARI	Bangladesh Agricultural Research Institue
BBS	Bangladesh Bureau of Satistics
Breed.	Breeding
BSMRAU	Bangabundhu Sheikh Mujibur Rahaman Agricultural University
cm	Centi –meter
CLV	Cluster Analysis
CV%	Percentage of Coefficient of Variation
CVA	Canonical Variate Analysis
D	Distance

SOME COMMONLY USED ABBREVIATIONS AND SYMBOLS (Cont'd)

Abbreviations	Full word
DF	Days to flowering
DG	Days to germination
DAS	Days After Sowing
Df	Degrees of Freedom
E	East
EMS	Error mean sum of square
et al.	And others
etc.	Etcetera
g	Gram (s)
G	Genotype
GA	Genetic advance
GCV	Genotypic coefficient of variation
Genet.	Genetics
GMS	Genotypic mean sum of square
GN.	Genotype Number
Hort.	Horticulture
j.	Journal
K	Setection intensity
Kg	Kilogram (s)
L	Liter
LL	Leaf length
LW	Leaf width

SOME COMMONLY USED ABBREVIATIONS AND SYMBOLS (Cont'd)

Abbreviations	Full word
ml	Milliter
MLBLB	Mean length of basal lateral branches
MLTLB	Mean length of top lateral branches
M P	Muriate of Potash
m^2	Squar meter
MSS	Mean sum of square
No.	Number
NBP	Number of branches per plant
NS	Not Significant
PCA	Principal Component Analysis
PCO	Principal Coordinate Analysis
PCV	Phenotypic coefficient of variation
RCBD	Randomized Complete Block Design
Res.	Research
SAU	Sher-e-Bangla Agricultural University
Sci.	Science
SD	Stem diameter
SWP	Seed weight per plant
T S P	Triple super Phosphate
t/ha	Tonnes per hectare
Univ.	University
Viz.	Namely

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CHARACTERIZATION AND GENETIC DIVERSITY ANALYSIS OF STEM AMARANTH (*Amaranthus viridus* L.)

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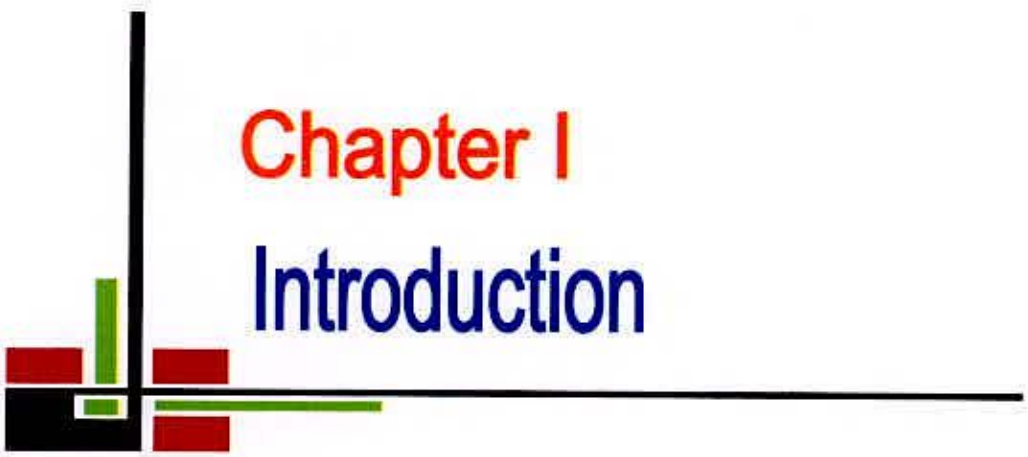
ABSTRACT

A field experiment was conducted with 40 stem amaranth genotypes at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka to study the characterization and genetic diversity analysis of stem amaranth (*Amaranthus viridus* L.) during April 2008 to June 2008. Significant variation was observed among all the genotypes for all the characters studied. Considering genetic parameters high genotypic coefficient of variation (GCV) was observed for seed weight per plant followed by mean length of basal lateral branches, mean length of top lateral branches, whereas leaf width showed low GCV. High heritability with low genetic advance in percent of mean was observed for days to flowering which indicated that non-additive gene effects were involved for the expression of this character and selection for such trait may not be rewarding. High heritability with moderate genetic advance in percent of mean was observed for days to germination indicated that this trait was under additive gene control and selection for genetic improvement for this trait would be effective. By using different multivariate techniques all the genotypes were grouped into five clusters. Principal Component Analysis, Principal Coordinate Analysis, Cluster Analysis, Canonical Variate Analysis gave similar results. Cluster IV had maximum (16) and cluster II had minimum (3) number of genotypes. The highest intra-cluster distance was found in cluster III and the lowest in cluster II among five clusters. The highest inter-cluster distance was observed between cluster II and III and the lowest between cluster I and II. The characters-days to germination, plant height, seed weight per plant and yield per plant contributed maximum towards divergence. Considering diversity pattern and other agronomic performances, the genotypes G9 and G25 from cluster I; G4, G22 and G37 from III; G10, G12, G16, G17 and G34 from IV and G24 and G30 from cluster V might be selected as suitable parents for future uses in hybridization program.



Chapter I

Introduction

CHAPTER I

INTRODUCTION

Stem Amaranth (*Amaranthus viridus* L.) belongs to the genus *Amaranthus* in the family Amaranthaceae. The family Amaranthaceae comprises 65 genera and 850 species. The genus *Amaranthus* includes 50 to 60 species, the leaves and stems of which are edible. This is the most important vegetables of the tropical countries of South Asia, South East Asia, East Africa, Central Africa, West Africa, Ethiopia, the Pacific and far East (Muthukrishnan and Irrulappan, 1986).

The stem amaranth is said to be the native of India (Nath, 1976). The centers of diversity for amaranths are central and South America, India, South East Asia and the secondary diversity is in West Africa and East Africa (Grubben, 1977). A wide variation is reported to exist within each species in growth habit, disease resistant, taste and quality thus offering considerable scope for future breeding programs.

In Bangladesh, during 2007 – 08 total vegetables production was about 81 lacs tons, of which 50 lacs tons was produced in rabi season and 30 lacs tons in kharif season (DAE, 2007 - 2008). So it is clear that the vegetables production in kharif season is very low. However, the maximum production of different vegetables are concentrated during the month of November to April. Thus there is a serious scarcity of vegetables during the month of May to September. As a result the price of vegetables remain high during this period.

The fresh tender leaves and stems of amaranth are delicious when cooked. The fibre of amaranth works against constipation. Its lysine content is nearly three times higher than corn and nearly twice than that of wheat (Muthkrishnan and Irulappan, 1986; Shanmugavelu, 1989). The leaves and tender stems of amaranth are rich in protein, fat, calcium, phosphorus, β-carotene, riboflavin, niacin, sodium, iron and ascorbic acid. Again it contains food energy of about 40 calorie per 100g edible portion, which is higher than common vegetables except potato and taro leaf (Chowdhury, 1967). Amaranth leaves are a good source of carotene, iron, calcium, vitamin C, folic acid and other micronutrients. Amaranth protein is a valuable contribution to the diet when protein intake is marginal (Shanmugavelu, 1989). The seed protein is rich in sulphur containing amino acid and lysine.

Stem amaranth is popular vegetables in Bangladesh for their quick growth and higher yield potential. It is cultivated in 5263 ha land with a production of 240 thousand tons in Bangladesh with average yield of 46.9 ton/ha (BBS, 2005). The low yield is mainly attributed due to the use of low yielding cultivars and lack of proper cultural practices (Hossain, 1996).

The development of high yielding lines with other desirable characters are badly needed to improve the yield status of this crop. The research work in this direction is very limited in Bangladesh. More work is needed for making a tangible improvement of this crop.

Yield is a complex characters associated with many component characters. It is the multiplicative and product of many factors, which jointly or singly influenced the yield. Hence, the primary requirement for

Hence, the primary requirement for a plant breeder is to have information on variability association of different characters and the direct and indirect effect of the yield contributing characters.

Traditional varieties, primitive cultivars and land races of stem amaranth are still used in cultivation in Bangladesh. The amaranth yield is very low. For this reason, superior parents with high breeding values are needed. Variability and genetic diversity are the fundamental law of plant breeding which is a major tool being used in parent selection for efficient hybridization program (Bhatt, 1973).

There are variations in different characters in the genotypes available in our country. Some of these variations can be exploited if they are well characterized. There are lots of variations which easily identified at the morphological level. Thus morphological characterization is key to identify the valuable genotypes which can be utilized in future breeding program.

Identification of yield contributing characters is necessary to establish a successful breeding program to develop high yielding varieties. Information of genetic variability is useful to formulate selection criteria for improvement of yield. The importance of genetic diversity in the improvement of a crop has been stressed in both self and cross pollinated crop (Griffing and Lindstrom, 1954). The quantification of genetic diversity through biometrical procedures such as Mahalanobis's D^2 statistics canonical variate Analysis (CVA) have made it possible to choose genetically diverse parents for a successful hybridization program.

In Bangladesh, information about the availability of genetic diversity in the amaranth germplasm is not enough. Thus the information that will be generated from this experiment might be useful for further improvement of amaranth genotypes. However, the objectives of the study were-

1. To characterize the genotypes on the basis of different morphological and yield contributing characters.
2. To study the genetic variability and genetic diversity for different quantitative characters involved among stem amaranth genotypes.
3. To select the genetically diverged parents to involve them in the future hybridization program.

Chapter II

Review of literature

CHAPTER II
REVIEW OF LITERATURE

Stem amaranth commonly used as leafy as well as stem vegetable in Bangladesh and in many other countries of the world. The crops have received much attention by a large number of researchers for its easy production and food value. Many studies on the variability, interrelationship, heritability and genetic advance have been carried out in many countries of the world. The review of the important research work relevant to the present study are stated below-

2.1 Characterization

Tyagi (2001) ovserved that plant height is an important character which is largely influenced by genotype, soil, water availability and temperature etc. Variation was highest for plant height of parents and their hybrids.

Singh *et al.* (1991) were evaluated increasing the number of branches is a mean of increasing yield, since the number of top and basal lateral branches have a significant positive correlation with yield .

Shukla *et al.* (2004) studied in 39 strains of vegetable amaranth (*A. tricolor*) to assess the genetic parameter for different quantitative and qualitative traits. Each strain was sown in a randomized block design in plot size of 1 m^2 with row-to-tow and plant-to-plant distance of 25 and 15 cm respectively. Data was recorded for 8 agronomic traits. Simultaneously another experiment was also conducted in RBD with three replications to record the total foliage yield and 7 quality traits. The

plot size was 2 m^2 for each strain with row-to-row distance 25 cm and plant-to-plant 15 cm. During crop season four foliage cuttings were performed and data on total foliage yield per plot (kg) was taken comprising all the cuttings. The strain AV-41 showed highest foliage yield (5.99 kg/plot), followed by AV-42, AV-30, AV-13 and AV-31. The heritability estimates were high for all the traits except branches/plant and moisture content. The genetic advance varied from 0.996% for moisture to 98.30% for seed yield. A breeding plant for the enhancement of foliage yield and the quality characters is discussed.

Hamid *et al.* (1989) reported that significant variation were present among 12 (Twelve) amaranth lines (4 exotic and 8 local) for plant height, number of leaves, stem diameter and yield. Height and stem diameter were positively correlated with yield.

Bhuiyan and Hoque (1983) studied the possibilities of growing some exotic varieties of grain amaranth during summer season in Bangladesh. The variety R-149 gave the highest yield of 20.60 kg/ha followed by R-104 with 14.90 kg/ha, which is extremely poor compared to the potential yield of 2-3 t/ha.

According to Prasad *et al.* (1980) correlation coefficient at phenotypic level showed that the yield has increased with an increase in leaf length and the leaf width. The leaf length has also increased with an increase in leaf width. But as the leaf number increases, the yield, leaf length and leaf width decreases. Thus it is interpreted that leaf size has a positive association with yield. Hence more emphasis should be given during selection to the size of leaf than to the number of leaves which is negatively correlated with yield.

Mohideen and Subramanian (1974) reported that the yield of green matter was significantly associated with different characters sush as weigth of plant, plant height, length of leaves, leaf width and stem diameter. It was further reported by them that the leaf width contributed substantially to leaf yield and suggested that leaf width plant height and stem diameter are reliable characters for exercising selection in amaranthus.

Vijayakumur (1980) found the plant height to have a positive and significant correlation with the green yield. According to him, leaf length/width ratio also showed a positive correlation with yield of greens on the 30 day of harvest.

2.2 Genetic Diversity

Das *et al.* (1991) informed on heritability and yield correlations which was derived from 8 characters in 35 genotypes collected at Lucknow, Uttar Pradesh, and grown during kharif under rainfed conditions at Nadia. Panicle weight, which had the highest estimates of heritability and genetic advance percentage and 100-grain weight contributed most to grain yield.

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Sudhir and Singh (2003) were assessed the genetic variability, heritability and genetic advance in 66 derivatives of *Amaranthus hypochondriacus* and *A. cruentus* in a field experiment of Lucknow, Uttar pradesh, India during 1977-97 . High phenotypic and genotypic coefficient of variation were observed for number of inflorescence per plant, leaf size, number of nodes per plant, number of spikelet per spike and grain yield. In general, the phenotypic coefficient of variation the characters examined. Heritability was high for all the characters examined. Genetic gain was

highest for the number of inflorescence per plant, number of nodes per plant, leaf size and number of primary branches per plant.

Sudhir and Singh (2000) worked on coefficient of variability and genetic advance (*Amaranthus*) at National Botanical Research Institute, Locknow, India. The foliage yield/plot was variable between 1.18-3.29 kg, with average yield of 2.25 ± 0.21 kg. The range and mean of individual cuttings for plant height, leaves/plant and foliage yield generally increased in ascending cutting and was maximum in fourth cutting, while range and mean were maximum in third cutting for size (38.07 ± 3.99) and branches/plant (11.90 ± 0.78). The heritability estimates in broad sense ranged from 33.24 to 75.00%. High heritability coupled with high genetic advance was noticed for foliage yield (75%), leaf size (74.98) and leaves/plant (73.73), indicating the preavalent role of additive gene effects.

Waghmode *et al.* (1993) were evaluated for 10 seed yield-related characters of 50 genotypes of *A. hypochondrious* at Rahuri. Cluster analysis revealed that genetic diversity was not correlated with geographic diversity. Of the 16 clusters, V and X had the highest average inter cluster distance (38.92), followed by clusters IX and X (37.27), III and X (34.59) and V and XI (30.52), suggesting that these groups of genotypes are highly divergent from each other.

Alba *et al.* (1997) experimented with twelve morphological, yield-related, quality and developmental traits to measure in 24 Amaranthus accessions, comprising 5 species, during 1991-95 in south Italy. Greatest variation was observed for biological yiedl, yield of terminal inflorescence, grain yield and height. Following principal component analysis, the first

component was associated with yield triats, qualitative traits such as oil and protein content characterized the second component, whilst the third component comprised traits directly connected with adaptability to agroclimatic conditions. Accessions were classified into 7 groups by hierarchical cluster analysis, irrespective of geographic origin or species tested.

Kamble *et al.* (2005) was studied genetic diversity among 50 genotypes of amaranthus grain collected from different geographic regions in India Considerable variation among genotypes for all ten metric characters was observed. Statistical analysis exhibited adequate genetic diversity among genotypes which were group into 11 clusters of which six were solitary and the remaining 5 clusters consisted of 2 to 20 genotypes. No parallelism was observed between geographic diversity and genetic diversity. Other traits such as height, length of inflorescence, number of spikelets and leaf area per plant appeared as the major sources of diversity. On the basis of genetic distance, cluster means and performance of a crossbreeding program involving diverse genotypes was suggested to obtain superior cultivars for yield improvement in grain amaranthus.

Erasmo *et al.* (2004) conducted the present work to evaluate of productive potential of grain amaranthus (*Amaranthus spp.*) in the State of Tocantins, Brazil, as alternative species in crop rotation on no tillage. Five cultivars (Oscar Blanco, AM 2264, AM 5189, PI 477913 and Japonica), were evaluated in an complete randomized block experiment with five repetitions, were the plots consisted of 20 m^2 (5×4 m), with rows equally spaced by 0.5 m and density of 25 plants/m. The experiment was conducted in the 1998-1999 crop season, under a Yellow Red Latossol (Ferralsol, FAO). All cultivars reached maturity 74 days after

the emergence. The largest values for plant height and residual biomass were verified in cultivars Japonica and AM 2264, corresponding, respectively to 1.79 and 1.56 m and 9.1 and 8.1 t/ha. The cultivars that were more productive O.Blanco and Japonica with 1.0 and 0.95 t/ha of grains, respectively. These results, although preliminary, indicate the potential for grain amaranth cultivation in the savannah of Tocantins, Brazil.

Rana *et al.* (2005) studied on a total of 100 accessions (50 from India and 50 from exotic sources) of grain amaranth (*Amaranthus hypochondriacus*) germplasm were grown in compete randomized block design. Data were recorded on protein content, oil content, plant height, inflorescence length, number of leaves, leaf length, leaf width and seed yield per plant. A wide range of means was observed for all the characters. All the genotypes, irrespective of their place of collection, were grouped into 10 different clusters. Clusters I, VII, VIII IX and X had high genetic distance with all other clusters. Inflorescence length and number of leaves and plant height significance for selecting better yielding genotypes.

Hazra *et al.* (2004) was determined the genetic divergence in 47 genotypes of amaranth (*Amaranthus spp.*) of Indian and exotic origin using the Mahalanobis D^2 statistic. The materials were grown during the kharif season of 2001-02 in West Bengal, India. The genotypes were grouped in to 22 clusters. Intracluster distance was highest for cluster VII followed by cluster II which included 13 genotypes from different states in India. The highest intercluster distance was recorded between cluster XII and XIII followed by cluster VI and XVII.

Pan *et al.* (1992) were studied on Forty-five indigenous and exotic genotypes of *Amaranthus tricolor* for genetic divergence based on 10 quantitative traits (days to first clipping, diameter of stem, length of internode, length of lamina, width of lamina, days to flowering, leaf-stem ratio, number of clippings, duration of harvest and total yield/0.45 m^2 plot). Analysis of variance revealed differences among the genotypes for all 10 characters. Using multivariate analysis, the genotypes were grouped into 10 clusters. The number of genotypes in clusters 1 to 10 were 7, 8, 5, 7, 4, 5, 3, 3, 2 and 1, respectively. The intracluster value was least in cluster 4 and highest in cluster 8. The intercluster value was maximum between cluster 1 and 3, suggesting that the genotypes in these clusters were highly divergent from each other. The genotypes in clusters 4 and 7 were the least divergent at the intercluster level. Clustering pattern was not associated with geographic distribution. Cluster 7 had low mean values for days to first clipping and leaf-stem ratio and high mean values for diameter of stem, length of lamina and internode, and total yield. Cluster 3 had the highest mean value for width of lamina and number of clippings. Cluster 6 had the highest mean values for days to flowering and duration of harvest. About 84% of the genetic diversity present in the 45 genotypes occurred in the first 2 canonical roots. Duration of harvest and total yield accounted for most of the variation present.

Devadas *et al.* (1992) were evaluated a total of 25 accessions of *Amaranthus tricolor*, *A dubius*, *A. spinosus* and A. vifidis for 13 biometric characters. The accessions were grouped into 7 clusters. The study of inter- and intra-cluster differences revealed that variability was greatest in varieties of *A. trioclor*.

Lohithaswa and Nagaraj (1996) were evaluated the genetic variability, heritability and genetic advance for 11 characters in 144 genotypes of grain amaranth (4 *Amaranthus spp.*) A considerable amount of phenotypic and genotypic variability was observed for plant FW, inflorescence FW, rachis/inflorescence, grain yield followed by stem DW, stem diameter at collar region and plant height. High heritability coupled with moderate genetic advance was observed for plant height and days to 50% flowering indicating that additive gene effects were operating for these characters and selection pressure could be applied on them for yield improvement. Moderate heritability with moderate genetic advance values were observed for both plant and inflorescence FW, rachis/inflorescence and stem diameter at collar region indicating the importance of both additive and non-additive gene actions for these characters.

Joshi and Rana (1995) conducted an experiment with a set of 20 genetically diverse genotypes of grain amaranth (*Amaranthus*) to analyse genetic variability at Shimla, Himachal Pradesh, in 1991-92. Phenotypic and genotypic variation coefficients, heritability and genetic advance were highest for inflorescence length, grain yield and spikelets per spike. Grain yield showed some significant positive correlation with plant height, leaf length and breadth, inflorescence length and spilelets/spike. Leaf length showed maximum direct effect on grain yield, followed by number of leaves, plant height and 1000 grain weight. On the basis of these results inflorescence length and spikelets/spike were the traits with the most potential for genetic improvement.

Joshi (1986) were observed wide variability for height, number of leaves per plant, leaf length and width, inflorescence length, number of spikelets

per plant, days to maturity, 1000-seed weight, seed popping size, seed protein content and seed yield per plant among 20 genotypes of *Amaranthus hybpchondricacus* grown from seed collected in Himachal Pradesh and Uttar Pradesh. Heritability estimates and expected genetic advance were high for 1000-seed weight, inflorescence length and height. High variability was also observed for inflorescence colour.

Revanappa and Madalageri (2004) were studied with forty Amaranthus genotypes which collected from Tamil nadu and Karanataka were evaluated at Bangalore. Phenotypic coefficients of variability (PCV) were higher than genotypic coefficients of variability (GCV) for all characters studied. Genotypes 84=2n and A104 had the best yield parameters. PCV and GCV were maximum for leaf stem ratio, number of leaves and fresh weight of leaves.

Ivara and Ayiecho (1991) conducted an experiment with two populations of *Amarnthus hypochondriacus* (Jumla and 1023), 2 of *A. cruentus* (1011 and 434) and 2 of *A. caudatus* (1113A and 982) were grown druing 1986 and 1987 and evaluated for 8 yield components. Analysis of variance revealed differences between the populations for all characters. Eight S1 families, derived from 8 selfed plants of each population grown in 1986, were evaluated for the same 8 characters during 1987. Analysis of variance revealed that within each population the level of heterogeneity varied for each character. Populations 1011 and Jumla were the most heterogeneous as they showed significant variation for 7 and 6 traits, respectively. Genetic variability within populations was confirmed by large values for genotypic variances and estimates of heritability for some characters.

Shukla *et al.* (2006) were grown twenty nine strains of vegetable amaranth (*Amaranthus triclor*) for two successive seasons to study different selection parameters for foliage yield and its nine contributing morphological and quality traits. The strains AV-38 (5.06 kg/plot) and AV-31 (5.04 kg/plot) recorded highest foliage yield, followed by AV-30 (4.78 kg/plot) and AV-23 (4.70 kg/plot). The protein and carotenoid content averaged 1.24 ± 0.03 mg/100 mg and 0.83 ± 0.02 mg/g respectively. The leaves of *A. tricolor* also have considerable quantities of ascorbic acid (112.33 ± 5.00 mg/100 g) and fibre (8.39 ± 0.10%). The mean of individual cuttings for plant height, leaf size, stem diameter, foliage yield, protein, ascorbic acid and fibre content increased with successive cuttings till third cutting and thereafter showed a decline. Genotypic coefficient of variation (GCV) values ranged from 6.80 to 28.25%. However, the fibre content, branches/plant, leaves/plant, plant height and stem diameter showed lowest values of GCV. The values of heritability estimates were high for all the traits in all the cuttings as well as on pooled basis and ranged from 0.89 for branches/plant to 0.98 for foliage yield. Highest expected genetic advance was noticed for ascorbic acid (57.48%), followed by foliage yield (48.30%) and leaf size (29.51%).

Singh *et al.* (2005) was carried out an investigation to study different selection parameters for foliage yield and its important yield contributing traits in 296 strains of vegetable amaranth (*A. tricolor*). The data were recorded for plant height (cm), stem diameter (cm), branches per plant, leaves per plant, leaf size (cm^2) and protein content (mg/100) of each cutting. Foliage yield (kg) was recorded on a per plot basis comprising 4 cuttings. The highest foliage yield per plot was recorded for strain AV-38, followed by AV-23 and AV-31. Generally, protein content was high

in the 2nd cutting in all strains. The heritability estimates were, in general, high for all the characters in all the cuttings and ranged from 74.87 to 93.33%. Genetic advance was maximum for foliage yield (42.50%), followed by leaf size (31.02%) and stem diameter (21.13%). It is concluded that foliage yield could be increased substantially in vegetable amaranth through indirect selection based on the characters leaf size and stem diameter.

Chapter III

Materials and Methods

CHAPTER III

MATERIALS AND METHODS

3.1 Experimental site

The investigation was carried out in the experimental farm of Sher-e-Bangla Agricultural University, Dhaka during April 2008 to June 2008. The location of the site was $23^0 74'$ N latitude and $90^0 35'$ E longitude with an elevation of 8.20 meter from sea level.

3.2 Climate and soil

The experimental site was situated in the subtropical zone. The soil of the experimental site lies in Agro-ecological regions of 'Madupur Tract' (AEZ No. 28). The soil is sandy loam in texture and olive gray with common fine to medium distinct dark yellowish brown mottles. The pH is 5.47 to 5.63 and organic carbon content is 0.82% (Appendix-I). The records of air temperature, humidity and rainfall during the period of experiment were noted from the Bangladesh Meteorological Department, Agargaon, Dhaka (Appendix II).

3.3 Genotypes

A total number of 40 (forty) stem amaranth genotypes were used in this experiment. The seeds of the thirty genotypes were collected from the Genetic Resources Centre of Bangladesh Agricultural Research Institute (BARI), two collected from the Horticulture division of BARI and rest of the eight genotypes were collected from the local market. The name of the genotypes is mentioned in Table 1.

Table 1. List of the 40 Stem amaranth genotypes used in the experiment

SL. No.	Code No.	Genotype	Source of Genotypes	SL. No.	Code No.	Genotype	Source of Genotypes
01	G1	BARIdata 1	BARI	21	G21	BD-2959	BARI
02	G2	BARIdata 2	BARI	22	G22	BD-2966	BARI
03	G3	Baromasi drutorj	Local market	23	G23	BD-8316	BARI
04	G4	Bashpata data	Local market	24	G24	BD-8317	BARI
05	G5	BD-2468	BARI	25	G25	BD-8319	BARI
06	G6	BD-2470	BARI	26	G26	BD-8320	BARI
07	G7	BD-2533	BARI	27	G27	BD8323	BARI
08	G8	BD-2632	BARI	28	G28	BD-8324	BARI
09	G9	BD-2922	BARI	29	G29	BD-8325	BARI
10	G10	BD-2930	BARI	30	G30	BD-8326	BARI
11	G11	BD-2932	BARI	31	G31	BD-8327	BARI
12	G12	BD-2933	BARI	32	G32	BD-8328	BARI
13	G13	BD-2935	BARI	33	G33	BD-8329	BARI
14	G14	BD-2937	BARI	34	G34	BD-9004	BARI
15	G15	BD-2939	BARI	35	G35	Bhuttan data	Local Market
16	G16	BD-2945	BARI	36	G36	Panna data	Local Market
17	G17	BD-2947	BARI	37	G37	Red queen data	Local Market
18	G18	BD-2953	BARI	38	G38	Red tower data	Local Market
19	G19	BD-2957	BARI	39	G39	Sada data	Local Market
20	G20	BD-2958	BARI	40	G40	Suressory data	Local Market

3.4 Land preparation

The experimental plot was prepared by several ploughing and cross ploughing followed by laddering and harrowing with power tiller and country plough to bring about good tilth. Weeds and other stubbles were removed carefully from the experimental plot and leveled properly.

3.5 Fertilizer application

Fertilizers such as urea, triple super phosphate (TSP), muriate of potash (MP) and manure like cowdung were applied at the rate of 200 kg, 100 kg, 200 kg and 20 ton per hectare respectively. The entire amounts of MP were applied during the final preparation of land. Urea was applied in three equal installments at 15, 30 and 45 days after seed sowing of stem amaranth. Well rotten cowdung also applied during final land preparation (Rashid, 1999).

3.6 Experimental design

Field lay out was done after final land preparation. The materials were laid out in Randomized Complete Block Design (RCBD) with three replications. The plot size was 15m × 13 m. Each block was 10 m long and 35 wide and 5 cm height from the ground level. A distance of 1.5 m from block to block, 30 cm from row to row and 20 cm from plant to plant was maintained. Photograph of field view are presented in Plate 1a and Plate 1.b.

3.7 Sowing of seeds and intercultural operation

The seeds of 40 stem amaranth genotypes were sown in lines in the experimental plot on 2 April, 2008. When the seedlings started to emerge the field was always kept under careful observation. After emergence of seedlings, various intercultural operations such as irrigation, drainage,

Plate 1.a . Field view of t the experimental site

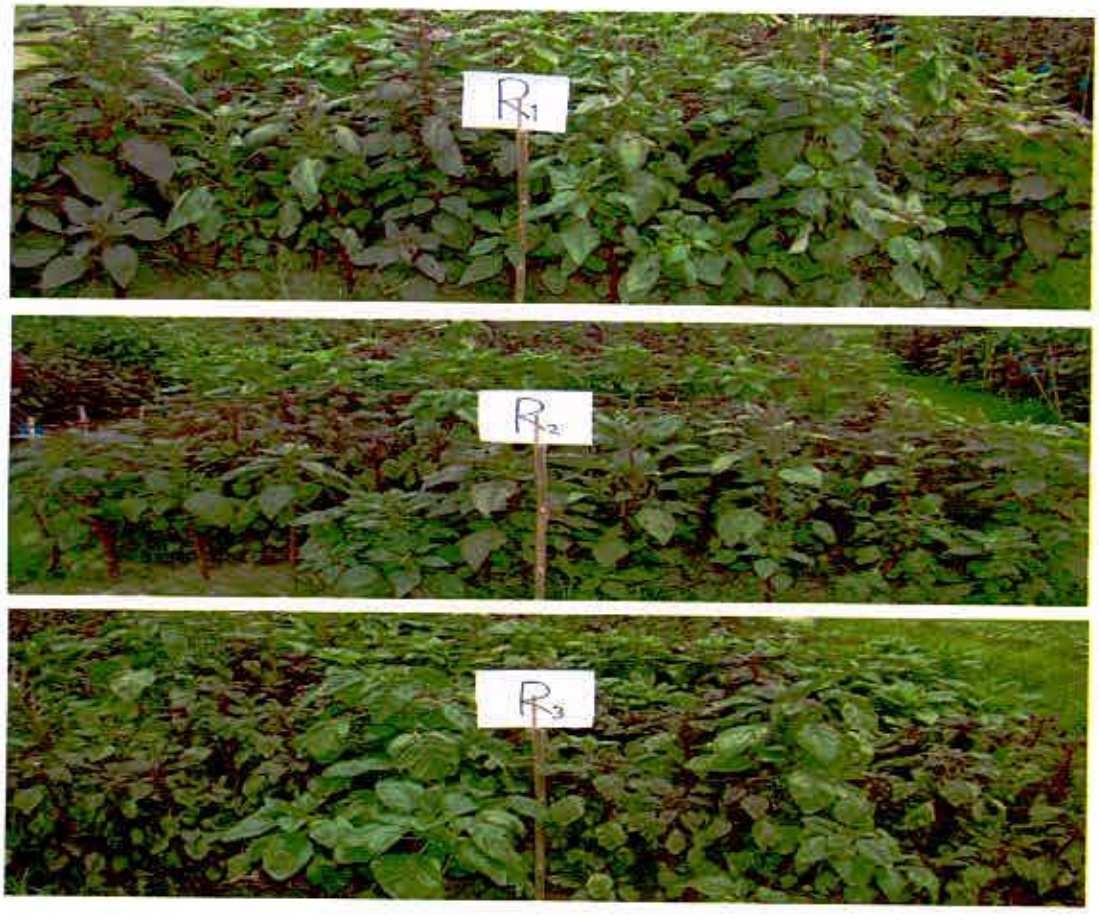


Plate 1.b. Field view of the experimental site (replication wise)

thinning, weeding and top dressing were accomplished for better growth and development of the stem amaranth seedlings.

3.7.1 Irrigation and drainage

Irrigation was provided with a watering came to the plots after germination in every alternate day in the evening upto 1st thinning. Further irrigation was provided when needed. Stagnant water was effectively drained out at the time of heavy rain.

3.7.2 Thinning

First thinning was done 15 days after sowing (DAS). 2nd thinning was done 15 days after the first and 3rd and 4th were done 15 days interval for proper growth and development of stem amaranth seedlings.

3.7.3 Weeding

Weeding was done to keep the plots free from weeds, easy aeration of soil, which ultimately ensured better growth and development. The newly emerged weeds were uprooted carefully whenever it is necessary. Breaking the crust of the soil was done when needed.

3.7.4 Top dressing

After basal dose, the remaining doses of urea were top dressed in 3 equal installments at 15 day after sowing (DAS), 30 DAS and 45 DAS. The fertilizers were applied on both sides of plants rows and mixed well with the soil.

3.7.5 Plant protection

For controlling leaf caterpillars Nogos @ 1ml/L water were applied 2 times at an interval of 10 days, starting soon after the appearance of infestation. There was no remarkable attack of diseases.

3.8 Harvesting

Different genotypes matured at different times. The harvesting was completed by 20 June, 2008. Ten plants from each block of each row were randomly selected to collect data and these were harvested by uprooting. Border plants were discarded to avoid border effect.

3.9 Recording of experimental data

Data on the following characters were recorded on individual plant basis from 10 randomly selected plants per genotypes in each replication. The observations for characterization and genetic diversity analysis were recorded under field condition and in the laboratory after harvest.

3.9. 1 Growth habit

Plant growth characters were recorded according to the performance of canopy and branches performance of canopy and branches were observed under the following habits:

- Erect
- Prostrate

3.9.2 Leaf shape

The leaf of different genotypes showed differences in their shape. The leaf of every genotype was recorded as per as the following shapes:

- Lanceolate
- Elliptical
- Ovatainate
- Rhombic

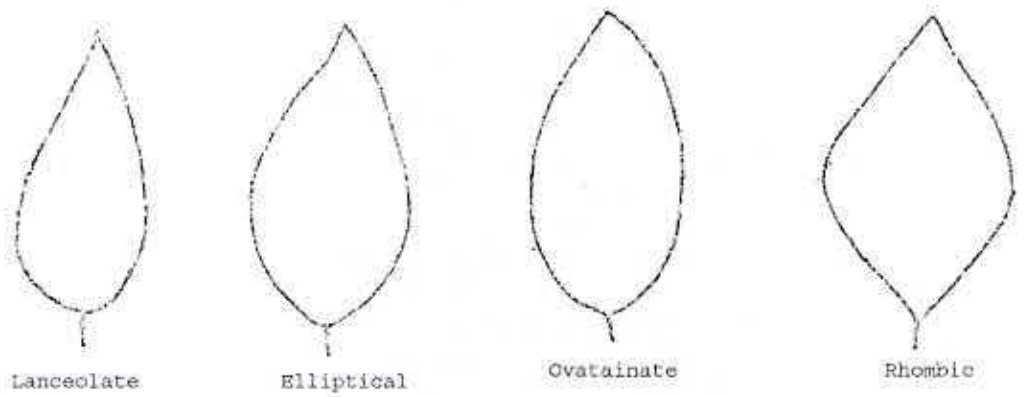


Figure. 1 Different shape of Leaf

3.9. 3 Leaf margin

The data were recorded by observing leaf structure phenotypic ally as per as the following marginal structure:

- Entire
- Crenate
- Undulate

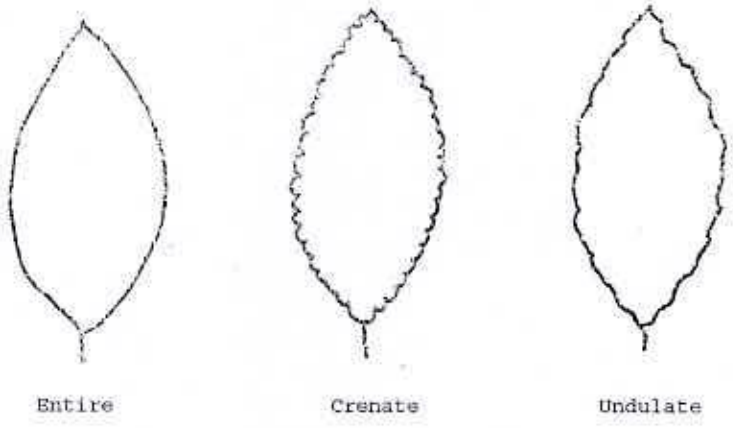


Figure. 2 Different types of leaf margin

3.9.4 Prominence of leaf veins

It was recorded by the following headings:

- Smooth
- Rugose (veins prominent)

3.9.5 Plant pubescence

The presence of pubescence of on leaf and stem was recorded during the mature stage of the plant by touching the leaf and stem of the plant.

3.9.6 Plant pigmentation

Leaf, stem and inflorescence colours were recorded by observing different stem amaranth genotypes phenotypically as per as the following colours:

- Purple/pink
- Green
- Dark green

3.9.7 Terminal inflorescence shape

The data were recorded by observing the following shape of the terminal inflorescences of different genotypes:

- Club-shaped at tips
- Panicle with short branches
- Spike (dense)
- None

3.9.8 Days to germination

Days to germination were recorded from seed sowing to the emergence of the seedling of every genotype.

3.9.9 Plant height

Length of main stem from ground level to the longest tip of the stem was measured at middle stage of harvesting period. The data were measured in centimeter (cm).

3.9.10 Number of branches per plant

The total number of branches of each plant present in each genotype were counted and recorded.

3.9.11 Mean length of basal lateral branches

The length of basal lateral branch of each plant was recorded and their average mean was calculated. The data were measured in centimeter.

3.9.12 Mean length of top lateral branches

The length of top lateral branch of each plant was recorded and their average mean was calculated. The data measured in centimeter.

3.9.13 Stem diameter

The stem diameter of every genotype measured along the middle part of the harvestable mature stem in centimeter (cm) and recorded.

3.9.14 Leaf length

Length from the tip to the basal end of 5 initially matured leaves per plant was measured in centimeter (cm) and recorded.

3.9.15 Leaf width

The width of 5 initially matured leaves per plant was measured by the middle part of each leaf. The data were measured in centimeter.

3.9.16 Days to flowering

Difference between the date of sowing to the date of flowering of an entry was counted as days to flowering.

3.9.17 Seed weight per plant

Weight of the total seeds from each of the sample plant was recorded in gram (g).

3.9.18 Yield per plant

Individual selected plant in each replication of each genotypes was weighed in kilogram (kg) and yield per plant was recorded.

3.10 Statistical Analysis

All the collected data of the study were used to statistical analysis for each character, analysis of variance (ANOVA), mean, range were calculated by using MSTATC software then analyzed for genotypic and phenotypic variance, genotypic and heritability, genetic advance and

genetic advance in % of mean. Mean data for each character were subjected to both univariate and multivariate analysis. For Univariate Analysis , analysis of variance was done individually by F-test (Panse and Shukatme, 1978). Multivariate analysis viz., Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CLU) and Canonical Vector Analysis (CVA) were done by using GENSTAT[5] software program (Copyright, 1987, Lawes Agricultural Trust, Rothamasted Experimental Station, UK).

3.10.1 Characterization of Stem Amaranth

3.10.1.1 Estimation Phenotypic and Genotypic Variance

Genotypic and phenotypic variances were estimated by Johnoson *et al.* (1955). Genotypic variance (σ^2_g) was obtained by subtracting error mean sum of square from the genotype mean sum of square and dividing by the number of replications as shown below:

$$\sigma^2_g = \frac{GMS - EMS}{r}$$

Where,

GMS = Genotypic mean sum of square

EMS = Error mean sum of square

r = Number of replication

The phenotypic variances (σ^2_p) were derived by adding genotypic variances (σ^2_g) with error variances (σ^2_e) as given by the following formula:

$$\sigma^2_p = \sigma^2_g + \sigma^2_e$$

3.10.1.2 Estimation genotypic and phenotypic Coefficient of variation

Genotypic and phenotypic coefficient of variations were estimated

according to the formula given by Johnson *et al.* (1955).

$$\text{Genotypic Coefficient of Variation (GCV)} = \frac{\sigma_g}{\overline{X}} \times 100$$

Where,

σ_g = Genotypic standard deviation

$\overline{X}$ = Grand mean

$$\text{Phenotypic Coefficient of Variation (PCV)} = \frac{\sigma_p}{\overline{X}} \times 100$$

Where,

σ_p = Phenotypic standard deviations

$\overline{X}$ = Grand mean

3.10.1.3 Estimation of Heritability

Broad sense heritability was estimated by the formula suggested by Johnson *et al.* (1995).

$$\% \, h^2_b = \frac{\sigma^2_b}{\sigma^2_p} \times 100$$

Where,

h^2_b = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

3.10.1.4 Estimation of Genetic Advance

The expected genetic advance for different characters under selection was estimated using the formula suggested by Johnoson *et al.* (1955).

$$\text{Genetic Advance (GA)} = h^2_b \, K. \, \sigma_p$$

Where,

h^2_b = Heritability in broad sense

K = Selection intensity, the value of which is 2.06 at 5% selection intensity

σ_p = Phenotypic standard deviation

3.10.1.5 Estimation of Genetic Advance in Percentage of Mean

Genetic advance in percentage of mean was calculated from the formula given by Comstock and Robinson (1952).

$$\text{Genetic in Percentage of Mean} = \frac{\text{Genetic advance}}{\text{Grand mean}} \times 100$$

3.10.2 Genetic Diversity Analysis

3.10.2.1 Principal Component Analysis (PCA)

Principal component analysis, one of the multivariate techniques, is used to examine the inter-relationship among several characters and can be done from the sum of squares and product matrix for the characters. Therefore, Principal components were computed from the correlation matrix and genotype scores obtained from the first components (which has the property of accounting for maximum variance) and succeeding components with latent roots greater than the unity (Jager *et al.*, 1983). Contribution of the different morphological characters towards divergence is discussed from the latent vectors of the first two principal components.

3.10.2.2 Principal Coordinate Analysis (PCO)

Principal coordinate analysis is equivalent to principal component analysis but it is used to calculate inter-unit distances. Through the use of all dimensions of P it gives the maximum distances between each pair of the n point using similarity matrix (Digby *et al.*, 1989).

3.10.2.3 Clustering

To divide the genotypes of the study into some number of mutually exclusive groups clustering was done using non-hierarchical classification. Starting from some initial classification of the genotypes into required groups, the algorithm repeatedly transfers genotypes from one group to another so long as such transfers improve the value of the criterion. When no further transfer can be found to improve the criterion, the algorithm switches to a second stage which examine the effect of swapping two genotypes of different classes and so on.

3.10.2.4 Canonical Variate Analysis (CVA)

Using canonical variate analysis a linear combination of original variabilities that maximize the ratio in between group to within group variation to be finding out and thereby giving functions of the original variabilities that can be used to discriminate between groups. Thus, in this analysis a series of orthogonal transformations sequentially maximizing the ratio of the among groups to the within group variations.

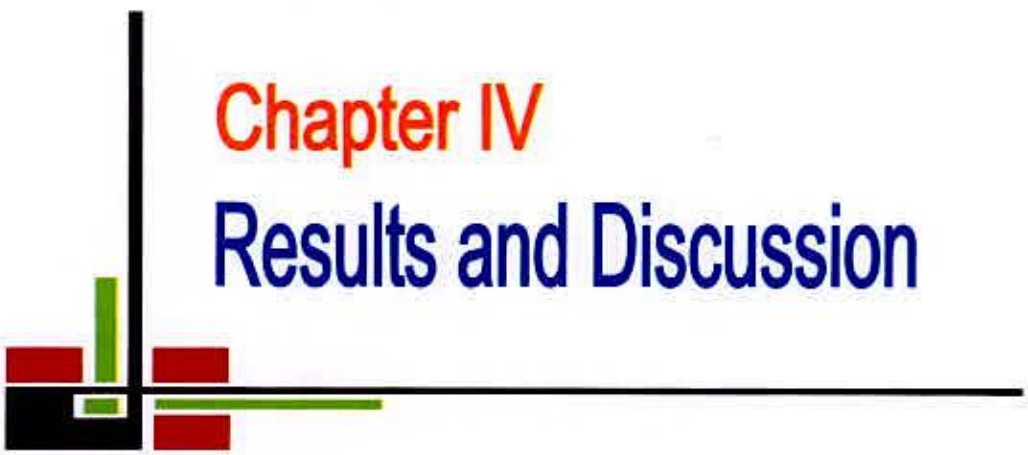
3.10.2.5 Computation of Average Intra-cluster Distances

When the clusters were formed, the average intra-cluster distances for each cluster was calculated by taking possible D^2 values within the member of a cluster obtained from the Principal Coordinate Analysis (PCO). The formula used was D^2/n, where D^2 is sum of distances

between all possible combinations (n) of the genotypes included in the cluster. The square root of the average D^2 values represents the distances (D) within cluster.

3.10.2.6 Cluster Diagram

Cluster diagram was drawn using the intra and inter cluster distance. If gives a brief idea of the pattern of diversity among the genotypes included in a cluster.



Chapter IV
Results and Discussion

CHAPTER IV

RESULTS AND DISCUSSION

The knowledge of genotypic variation within genotypes in relation to morphology, phenology and yield would help to screen better genotypes. Therefore, to generate information in the degree of diversity of forty (40) genotypes of stem amaranth were raised in the growing season of 2008 at the field of Sher-e-Bangla Agricultural University, Dhaka. This chapter comprises the presentation and discussion of the findings obtained from the study. The data pertaining to eleven characters were computed and statistically analyzed and the results obtained are described below:

4.1 Characterization of stem amaranth

4.1.1 Morphological character

4.1.1.1 Growth habit

Plant architecture is an important character to the breeders for improvement of plant ideotype under given environment. The lines studied have been grouped into two distinct characteristics viz. erect and prostrate. The genotypes G31, G9, G11, G1, G14, G13, G15, G32, G40, G2, G25 and G5 were prostrate in growth habit while the rest 28 genotypes were erect in growth habit (Table. 2).

4.1.1.2 Leaf shape

Various types of stem amaranth were found with different types of leaf shape. Among the forty genotypes, rhombic, lanceolate, ovatainate, elliptical shaped leaves were observed. The genotypes G31, G9, G6, G23, G16, G11, G14, G40, G29, G24, G7, G5, G39 and G27 produced rhombic leaves. Genotypes G21, G10, G13, G34, G34, G3, G19, G39 and

Table 2. Characterization of stem amaranth genotypes based on morphological traits

Gen. No.	Name of Genotypes	Growth habit	Leaf shape	Leaf margin	Prominence of leaf veins	Plant pubescence		Plant pigmentation			Terminal inflorescence shape
						Leaf	Stem	Leaf	Stem	Inflorescence	
1	BARI data 1	Prostrate	Lanceolate	Undulate	Rugose	Low	Conspicuous	Dark green	Purple	Green	Club shaped
2	BARI data 2	Prostrate	Lanceolate	Entire	Smooth	None	Conspicuous	Normal green	Green	Green	Club shaped
3	Baromasi drutoraj	Erect	Ovatainate	Undulate	Smooth	None	Low	Dark green	Purple	No	No
4	Bashpate data	Erect	Lanceolate	Entire	Rugose	Low	Low	Normal green	Green	No	No
5	BD-2468	Prostrate	Rhombic	Entire	Rugose	None	None	Entire lamina purple	Purple	Red	Spike (dense)
6	BD-2470	Erect	Rhombic	Entire	Rugose	None	Conspicuous	Entire lamina purple	Purple	Red	Spike (dense)
7	BD-2533	Erect	Rhombic	Entire	Rugose	None	None	Margin & vein pigmented	Purple	Red	Spike (dense)
8	BD-2632	Erect	Laneolate	Entire	Smooth	None	None	Entire laminar purple	Purple	Green	Club shaped
9	BD-2922	Prostrate	Rhombic	Entire	Rugose	None	Low	Entire lamina purple	Purple	Red	Spike (dense)
10	BD-2930	Erect	Ovatainate	Undulate	Smooth	None	None	Dark green	Purple	Green	Club shaped
11	BD-2932	Prostrate	Rhombic	Undulate	Rugose	None	None	Entire lamina purple	Purple	Pink	Panicle with short branch
12	BD-2933	Erect	Ovatainate	Undulate	Smooth	Low	Conspicuous	Dark green	Purple	Green	Club shaped
13	BD-2937	Prostrate	Ovatainate	Crenate	Rugose	None	None	Normal green	Purple	Green	Club shaped
14	BD-2937	Prostrate	Rhombic	Entire	Rugose	None	None	Normal green	Green	Green	Spike (dense)
15	BD-2939	Prostrate	Elliptical	Undulate	Rugose	None	None	Normal green	Purple	Pink	Spike (dense)
16	BD-2945	Erect	Rhombic	Undulate	Rugose	None	None	Normal green	Purple	Green	Club shaped
17	BD-2947	Erect	Lanceolate	Undulate	Rugose	None	None	Dark green	Purple	Green	Club shaped
18	BD-2953	Erect	Lanceolate	Undulate	Rugose	None	None	Entire lamina purple	Purple	Green	Club shaped
19	BD-2957	Erect	Ovatainate	Undulate	Smooth	None	Low	Dark green	Purple	Green	Club shaped
20	BD-2958	Erect	Lanceolate	Undulate	Rugose	None	None	Dark green	Purple	Green	Club shaped

Table 2 (cont'd).

Gen. No.	Name of Genotypes	Growth habit	Leaf shape	Leaf margin	Prominence of leaf veins	Plant pubescence		Plant pigmentation			Terminal inflorescence shape
						Leaf	Stem	Leaf	Stem	Inflorescence	
21	BD-2959	Erect	Ovatainate	Crenate	Rugose	None	Conspicuous	Dark green	Purple	Green	Panicle with short branch
22	BD-2966	Erect	Lanceolate	Entire	Rugose	None	None	Dark green	Purple	Green	Club shaped
23	BD-8316	Erect	Rhombic	Entire	Rugose	None	None	Normal green	Green	Green	Spike (dense)
24	BD-8317	Erect	Rhombic	Entire	Smooth	None	None	Normal green	Green	Green	Club shaped
25	BD-8319	Prostrate	Lanceolate	Entire	Rugose	None	None	Dark green	Purple	Red	Spike (dense)
26	BD-8320	Erect	Lanceolate	Entire	Rugose	None	None	Dark green	Purple	Pink	Spike (dense)
27	BD-8323	Erect	Rhombic	Entire	Smooth	None	Low	Dark green	Purple	Pink	Spike (dense)
28	BD-8324	Erect	Lanceolate	Entire	Smooth	None	Low	Dark green	Purple	Green	Spike (dense)
29	BD-8325	Erect	Rhombic	Entire	Smooth	None	None	Dark green	Purple	Pink	Spike (dense)
30	BD-8326	Erect	Lanceolate	Entire	Rugose	None	None	Dark green	Green	Green	Club shaped
31	BD-8327	Prostrate	Rhombic	Entire	Rugose	None	Low	Dark green	Purple	Pink	Spike (dense)
32	BD-8328	Prostrate	Lanceolate	Undulate	Smooth	Low	Conspicuous	Normal green	Purple	Pink	Spike (dense)
33	BD-8329	Erect	Elliptical	Undulate	Rugose	None	None	Dark green	Purple	Red	Spike (dense)
34	BD-9004	Erect	Ovatainate	Undulate	Rugose	None	Low	Dark green	Purple	Green	Club shaped
35	Bhuttan data	Erect	Lanceolate	Undulate	Rugose	Low	Low	Dark green	Purple	Pink	Spike (dense)
36	Panna data	Erect	Ovatainate	Undulate	Rugose	None	None	Dark green	Green	Pink	Club shaped
37	Red queen data	Erect	Lanceolate	Undulate	Rugose	None	None	Dark green	Purple	No	No
38	Red tower data	Erect	Lanceolate	Entire	Rugose	Low	Low	Normal green	Purple	No	No
39	Sada data	Erect	Rhombic	Entire	Smooth	None	None	Normal green	Green	Green	Spike (dense)
40	Suressory data	Prostrate	Rhombic	Undulate	Smooth	Low	Low	Normal green	Purple	Pink	Spike (dense)

G12 produced ovatainate leaves and genotypes G14 and G26 produced elliptical leaves (Plate 2). The rest of the genotypes produced lanceolate leaves (Table 2).

4.1.1.3 Leaf margin

Leaf margin can help to a breeder to know the information on photosynthesis rate. Leaf margin is recorded under the following categories: entire, crenate and undulate. The genotypes G31, G9, G6, G23, G8, G14, G4, G26, G28, G29, G24, G30, G38, G2, G25, G7, G5, G39, G22 and G27 had entire leaf margin, G21 and G13 showed crenate leaf margin and rest of the genotypes were of undulate type (Table 2).

4.1.1.4 Prominence of leaf veins

Prominence of leaf vein is a trait for consumer preference in stem amaranth. Genotypes G10, G8, G32, G28, G40, G29, G24, G2, G3, G19, G39, G12 and G27 had smooth leaf veins and rest of the genotypes had rugose leaf veins. (Table 2). A comparative leaf veins of amaranth is presented in Plate 3.

4.1.1.5 Plant pubescence

Plant pubescence is an important character of stem amaranth plant for consumer preference and marketing. This character is related to its resistance against pest. The more densely pubescence plant is more resistance against pest. Pubescence was observed by touching leaf and stem. Forty stem amaranth genotypes were grouped into none, low and conspicuous amount of pubescence. Among the 40 genotypes G31, G9, G4, G35, G28, G38, G34, G3, G19 and G27 had low pubescence; G21, G6, G1, G32, G2 and G12 had conspicuous pubescence on their stem. Rest of the genotypes had no pubescence on their stem. In case of leaf pubescence, genotypes G15, G4,

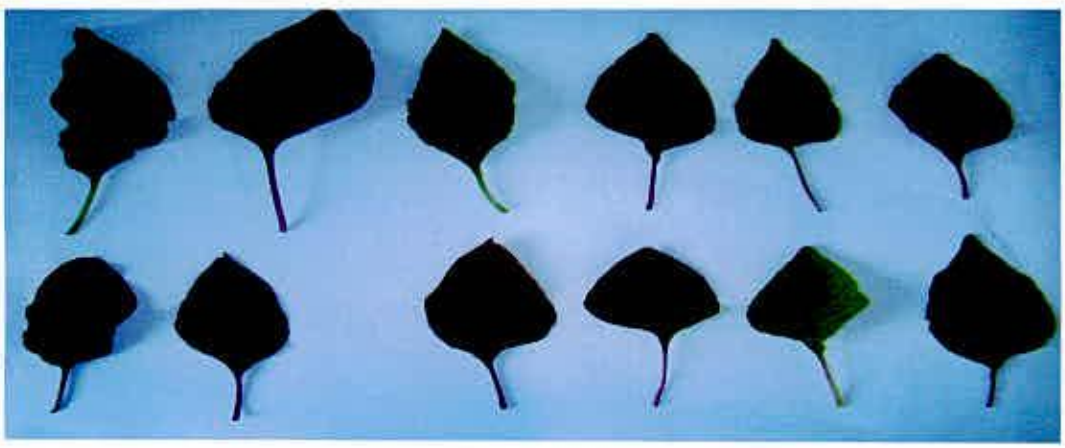


Plate 2. Photograph showing variation between different leaf shape

Plate 3. Photograph showing variation between different prominence of leaf veins

G35, G40, G38 and G12 had low pubescence and rest of the genotypes had no pubescence on their leaf.

4.1.1.6 Plant pigmentation

Plant pigmentation is one of the important morphological traits that has a direct effect on consumer preference and marketing value of stem amaranth. Plant pigmentation data were recorded by observing the pigment of leaves, stems and inflorescences of different stem amaranth genotypes. Among the 40 genotypes studied, leaf pigmentation of G23, G16, G14, G13, G15, G32, G4, G40, G24, G38, G2 and G39 were normal green, G99, G6, G8, G11, G18 and G5 were seen entire lamina purple, G7 was observed with margin and vein pigmented and rest of the genotypes had dark green pigmentation of their leaves. The genotypes G23, G14, G4, G24, G30, G2, G36 and G39 had green pigment on their stems and rest of the genotypes were seen purple pigment. In case of inflorescence pigmentation, the genotypes G31, G11, G15, G32, G35, G26, G40, G29, G36 and G27 were pink, G9, G6, G33, G25, G7 and G5 were red and rest of the genotypes were green (Table 2, Plate 4) but genotypes G4, G38, G3 and G37 were produced no inflorescence.

4.1.1.7 Terminal inflorescence shape

Various types of inflorescence were observed in the terminal portion of stem amaranth. Among the 40 genotypes G16, G20, G10, G8, G1, G13, G17, G24, G38, G2, G34, G19, G18, G36, G12, G22 were having club shape inflorescence at tip; G11 and G21 had panicle with short branches; genotypes G4, G3, G37, G38 produced no terminal inflorescence and rest of the genotypes were produced spike (dense) type of inflorescence (Table 2, Plate 5).

Plate 4. Photograph showing variation in plant pigmentation among different genotypes

Plate 5. Photograph showing different terminal inflorescenec shape

4.1.2 Characterization of stem amaranth genotypes on the basis of yield and yield contributing characters

4.1.2.1 Days to germination

A small variation was observed in respect of duration of germination among the genotypes. The genotype G2 took shortest time (1 day) for germination from the date of sowing, which was identical to G7, G12, G14 and G18 (Table 3). The G21 took the longest time (3.33 days) for germination.

4.1.2.2 Plant height

The plant height of different lines exhibited wide variation (Table 3). The plant height was maximum in genotype G4 (113.10 cm), which was more or less identical to G37 and G38. The genotypes G15 was the shortest plant (62.28 cm). The remaining genotypes were intermediate in this regard (Table 3). The genotype G4 produced the tallest plant than rest of the genotypes. Plant height is largely influenced by genotype which was observed by Tyagi (2001). Vijaykumar (1980) found that plant height had a positive correlation with the green yield. Alba *et al.* (1997) was observed greatest variation for plant height.

4.1.2.3 Number of branches (NB) per plant

Number of branches is an important morphological character which indicates the amount of yield per plant. It was observed that the maximum number of branches was produced by the genotype G19 (21.67) which was statistically superior to the rest of the genotypes. The genotypes G3, G4, G37 and G38 produced no branches. Singh *et al.* (1991) reported increasing the number of branches were a mean of increasing yield.

Plate 6. Photograph showing different number of branches

Table 3. Mean performances of eleven characters of forty stem amaranth genotypes

Genotype No.	DG	PH (cm)	NBP	MLBLB (cm)	MLTLB (cm)	SD (cm)	LL (cm)	LW (cm)	DF	SWP (gm)	YPP (gm)
1	2.00	86.91	8.00	9.80	4.96	7.33	13.34	7.87	40.00	2.68	263.27
2	1.00	98.61	10.67	9.56	7.27	6.33	15.87	9.63	40.00	5.34	252.53
3	2.00	95.75	0.00	0.00	0.00	7.91	13.53	9.26	42.00	4.78	306.67
4	3.00	113.10	0.00	0.00	0.00	8.39	16.85	8.59	47.00	3.21	350.00
5	2.00	66.17	9.00	16.82	8.72	3.75	14.04	8.93	31.00	7.62	122.40
6	2.00	65.58	9.67	17.58	9.69	3.29	13.52	8.14	32.00	8.00	100.50
7	1.00	100.77	15.67	14.89	10.09	7.14	14.77	10.05	32.00	5.42	307.37
8	2.00	86.60	12.00	22.35	12.50	6.30	13.67	8.63	36.00	0.72	253.67
9	2.00	72.06	7.00	9.70	11.42	4.32	14.40	9.22	31.00	10.46	130.37
10	2.00	87.17	16.67	21.85	5.87	7.34	13.09	7.06	44.00	5.36	265.40
11	2.00	84.07	11.00	16.01	9.64	5.99	12.43	7.95	40.00	4.68	175.17
12	1.00	98.37	10.67	22.60	7.95	6.85	11.90	6.89	45.00	3.62	269.67
13	2.00	86.01	10.00	17.29	4.93	6.56	11.80	7.91	44.00	0.26	239.47
14	1.00	65.74	11.00	14.71	4.90	4.51	12.82	7.88	31.00	6.40	121.83
15	2.33	62.28	9.00	14.35	6.59	4.05	15.02	8.36	33.00	4.78	94.00
16	3.00	85.71	14.33	17.97	6.45	7.27	10.50	6.81	40.00	4.18	254.67
17	2.00	94.13	13.00	26.07	8.17	7.33	10.59	6.93	40.00	0.04	280.67
18	1.00	89.82	16.67	22.11	14.53	7.28	11.57	7.92	36.00	0.05	253.30
19	2.00	81.19	21.67	13.17	5.77	5.87	11.52	7.91	40.00	0.28	190.30
20	3.00	97.50	13.33	18.59	6.29	7.31	11.80	7.87	44.00	0.16	283.13
21	3.33	93.40	11.00	18.03	9.05	6.74	12.16	7.42	48.00	7.50	338.80
22	2.33	103.00	9.00	20.23	10.87	8.53	10.79	7.16	32.00	2.35	342.50
23	2.00	82.83	9.67	22.74	21.43	6.07	14.85	8.57	32.00	4.90	225.67
24	3.00	92.98	20.00	17.34	6.85	5.66	16.05	9.28	33.00	2.12	215.93
25	2.00	75.53	8.00	3.81	4.99	4.97	14.51	8.70	40.00	10.06	134.83
26	3.00	84.23	9.00	6.68	11.45	4.38	13.87	8.41	33.00	4.08	171.00
27	2.00	91.27	12.33	9.61	10.94	6.49	17.54	10.34	36.00	7.20	232.33
28	2.00	79.10	9.67	8.72	14.70	6.77	14.17	8.95	41.00	7.30	236.50
29	3.00	73.76	11.00	12.52	8.93	4.32	14.28	9.65	36.00	2.98	118.33
30	2.00	95.82	15.67	8.84	4.20	5.27	15.68	8.84	33.00	1.38	209.17
31	2.00	79.53	10.33	8.03	7.01	5.14	13.30	8.27	36.00	2.18	177.03
32	2.67	84.32	11.33	7.38	13.45	6.40	18.23	9.68	36.00	7.42	168.03
33	2.00	96.60	10.67	20.15	9.78	6.61	14.98	9.17	43.00	2.50	285.87
34	3.00	85.53	11.67	17.14	7.53	7.27	11.53	7.17	40.00	4.10	275.73
35	2.00	95.63	10.00	6.47	11.27	7.27	16.55	9.27	44.00	2.96	297.33
36	3.00	81.40	12.33	4.67	9.92	7.14	13.99	9.52	36.00	7.46	236.93
37	3.00	111.13	0.00	0.00	0.00	7.93	14.43	9.11	48.00	4.29	351.33
38	2.33	109.00	0.00	0.00	0.00	7.53	15.75	8.91	32.00	3.67	325.00
39	2.00	64.49	9.67	4.33	9.52	4.80	15.29	8.89	32.00	9.50	88.80
40	3.00	85.12	12.67	8.76	6.22	5.48	13.75	8.00	37.00	5.50	191.50

DG = Days to germination, PH = Plant height (cm), NBP = Number of branches per plant, MLBLB = Mean length of basal lateral branches (cm), MLTLB = Mean length of top lateral branches (cm), SD = Stem diameter (cm), LL = Leaf length (cm), LW = Leaf width (cm), DF = Days to flowering, SWP = Seed weight per plant (gm), YPP = Yield per plant (gm).

4.1.2.4 Mean length of basal lateral branches

The length of basal lateral branch of each plant was recorded and their average mean was calculated. The genotype G17, produced the longest basal lateral branch which was 26.07 cm followed by G23 (22.74 cm). However, found that the genotype G25 produced shortest basal lateral branch (3.81cm).

4.1.2.5 Mean length of top lateral branches

The length of top lateral branch of each plant was recorded and their average mean was calculated. It was found that the genotype G23 produced the highest length of top lateral branch and the genotype G30 produced lowest (4.20cm) length of top lateral branch.

4.1.2.6 Stem diameter

The average diameter of stem showed marked difference among the genotypes. In respect of diameter, the experimental data showed that the genotype G2 was the widest (8.53 cm) followed by G4 (8.39 cm). The lowest diameter was observed in G6 (3.29 cm). Hamid *et al.* (1989) showed that height and stem diameter were positively correlated with yield.

4.1.2.7 Leaf length

The average marked difference among the genotypes was observed. The leaf of the genotype G32 (18.23 cm) were found to be the longest followed by the genotype G27 (17.54 cm) and G4 (16.85 cm). The genotype G16 produced the shortest leaf (10.50 cm). Prasad et al. (1980) showed that the yield had increased with an increase in leaf length. Leaf length showed maximum direct effect on grain yield, followed by number of leaves, plant height and seed weight were reported by Joshi *et al.* (1995).

4.1.2.8 Leaf width

The genotype G27 produced the widest leaf which was 10.34 cm followed by G7 (10.05 cm). It is also found that the genotype G16 produced least widest leaf (6.81 cm), which was identical to G12 (6.89 cm) and (6.93 cm). The differences in the average width of the leaf of different genotypes of stem amaranth were observed. The G27 produced the widest leaf while the narrow leaf was produced by the genotypes G16 (Table 3). Mohideen *et al.* (1974) reported that the leaf width contributed substantially to leaf yield.

4.1.2.9 Days to flowering

A small range of variability was observed in respect of flowering time among the genotypes. The genotypes G5 took the shortest time (31 days) for flowering from sowing which were similar to genotype G9 and G14. On the other hand, the genotype G21 took the longest time (48 days) to flower (Table 3). Sambandam (1960) studied the number of days required for flowering in different stem amaranth genotypes and concluded that the variation was due to the varietal characteristics. Sudhir *et al.* (2002) reported that a wide range of variation for days to flowering.

4.1.2.10 Seed weight per plant

The genotypes showed difference in producing seed weight per plant. The seed of harvestable stem amaranth genotype was collected and weighed in electrical balance. The genotype G17 produced the lowest amount of seed (0.04 gm) and the genotype G9 produced the highest (10.46 gm) amount of seed per plant.

4.1.2.11 Yield per plant

The genotypes showed a difference in producing yield per plant (Table 3). The data indicated that genotype G37 produced the highest yield of 351.33

gm followed by G4 (350.00 gm) and G22 (342.50 gm). Though the genotype G39 had the lowest yield per plant of 88.80 gm, which was more or lass identical with G15 (94.00 gm) and G6 (100.50 gm).

4.2 Variability of stem amaranth genotypes on the basis of yield and yield contributing characters

Range, mean and co-efficient of variation of eleven characters of stem amaranth namely days to germination, plant height, number of branches per plant, mean length of basal lateral branches, stem diameter, leaf length, leaf width, days to flowering, seed weight per plant and yield per plant have been presented in Table 4 . The mean values of above parameters were 2 days, 87.06 cm, 10.58, 12.77 cm, 8.096 cm, 6.25 cm, 13.87 cm, 8.48 cm, 38 days, 4.43 gm and 228.6 gm respectively and the co-efficient of variation of the above parameters were 9.11, 13.35, 13.29, 16.33, 16.57, 13.80, 13.63, 12.75, 4.35, 3.25 and 13.08% respectively which indicated considerable variation existing among the genotypes. Analysis of variance showed that the stem amaranth genotypes varied significantly with each other (Table 5). But replicatioon MSS for plant height, leaf length, leaf width,days to flowering, seed weight per plant were significant because of ununiform field where the study was conducted.

4.2.1 Genetic variability, heritability and genetic advance in stem amaranth genotypes

The genotypes varied significantly for all the characters (Table 5). The extent of variation among the genotypes in respect of 11 characters were studied for mean value, MSS, EMSS, genotypic variance (σ^2g), phenotypic variance (σ^2p), genotypic co-efficient of variation (GCV), phenotypic co-efficient of variation (PCV), heritability (h^2b), genetic advance (GA) and genetic advance in percent of mean have been presented in Table 6. The

Table 4. Grand mean, range and coefficient of variation

Characters	Minimum	Maximum	Grand mean	CV%
Days to germination	1.000	3.330	2.200	9.11
Plant height	62.28	113.10	87.06	13.35
Number of Branches	0.00	21.67	10.58	13.29
Mean length of basal lateral branches	0.00	26.07	12.77	16.33
Mean length of top lateral branches	0.00	21.43.	8.096	16.57
Stem diameter	3.29	8.53	6.247	13.80
Leaf length	10.50	18.23	13.87	13.63
Leaf width	6.81	10.34	8.478	12.75
Days to flowering	31.00	48.00	37.92	4.35
Seed wt./pl	0.04	10.46	4.437	3.25
Yield/plant	88.80	351.3	228.6	13.08

Table 5. Mean sum squares from the ANOVA of 40 stem amaranth genotypes in respect of 11 characters

Characters	d.f			Mean sum of square		
	Replication	Genotype	Error	Replication	Genotype	Error
Days to germination	2	39	78	0.100	1.227**	0.040
Plant height (cm)	2	39	78	1700.324**	482.053**	135.122
No. of branches per plant	2	39	78	0.148	31.726**	2.443
Mean length of basal lateral branches (cm)	2	39	78	1.279	112.601**	5.371
Mean length of top lateral branches (cm)	2	39	78	1.021	36.827**	2.222
Stem diameter (cm)	2	39	78	1.374	5.355**	0.743
Leaf length (cm)	2	39	78	33.629**	10.741**	3.571
Leaf width (cm)	2	39	78	6.184**	2.501**	1.169
Days to flowering	2	39	78	104.925**	81.752**	2.720
Seed weight per plant (gm)	2	39	78	1.959**	23.968**	0.021
Yield per plant (gm)	2	39	78	477.268	17206.481**	894.411

**** Significant at 1% level of probability**

Table 6. Variability, genetic parameter, heritability (h^2b),genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), genetic advance (GA), genetic advance in percent of mean for 11 yield and yield contributingcharacters of stem amaranth

Characters	GM	MSS	Error	σ^2g	σ^2p	GCV	PCV	h^2b	GA (%)	GA in % of mean (5%)
Days to germination	2.200	1.227**	0.040	0.40	0.44	28.59	30.00	90.82	1.23	56.13
Plant height (cm)	87.06	482.053**	135.122	115.64	250.77	12.35	18.19	46.12	15.04	17.28
No. of branches per plant	10.58	31.726**	2.443	9.76	12.20	26.57	29.71	79.98	5.76	48.95
Mean length of basal lateral branches (cm)	12.77	112.601**	5.371	35.74	41.11	42.13	45.19	86.94	11.48	80.93
Mean length of top lateral branches (cm)	8.096	36.827**	2.222	11.54	13.76	37.75	41.23	83.85	6.41	71.22
Stem diameter (cm)	6.247	5.355**	0.743	1.54	2.28	19.85	24.17	67.42	2.10	33.57
Leaf length (cm)	13.87	10.741**	3.571	2.39	5.96	11.15	17.61	40.09	2.02	14.54
Leaf width (cm)	8.478	2.501**	1.169	0.44	1.61	7.86	14.98	27.53	0.72	8.49
Days to flowering	37.92	81.752**	2.720	26.34	29.06	13.53	14.22	90.64	10.07	26.54
Seed weight per plant (gm)	4.437	23.968**	0.021	7.98	8.00	63.66	63.75	99.74	5.81	130.97
Yield per plant (gm)	228.6	17206.481**	894.411	5437.36	6331.77	32.25	34.80	85.87	140.76	61.56

mean value of all genotypes for each character is also given in Table 4. Performances of the genotypes are described below for each characters.

4.2.1.1 Days to germination

Analysis of variance for days to germination showed significant mean sum of square due to genotypic differences (Table 5). The mean value was ranged from 1.0 (G7) to 3.33 (G21). The phenotypic variance (0.44) was slightly higher than the genotypic variance (0.40). The difference present among the genotypic and phenotypic variances is indicating the effect of environment for the expression of the trait is low (Table 6). The phenotypic coefficient of variation was little higher than the genotypic coefficient of variation indicating that the apparent variation not only due to genotypes but also due to the influence of environment. A heritability estimate was also high (90.82%) with moderate genetic advance in percent of mean (Table 6).

4.2.1.2 Plant height (PH)

Significant mean sum of square for plant height indicated considerable differences among the genotypes studied (Table 5). The highest and lowest plant heights among the genotypes were 113.10 cm (G4) and 62.28 cm (G15) respectively with the mean value of 87.07 cm (Table 4). The phenotypic and genotypic variances for this trait were comparatively high (250.77 and 115.64). The phenotypic variance appeared more double with respect to than the genotypic variance suggesting considerable influence of environment on the expression of the genes controlling this trait. The phenotypic coefficient of variation (18.19) was higher than the genotypic coefficient of variation (12.35) (Table 6), which suggested that environment had a significant role on the expression of this trait. Heritability estimate was moderate (46.12%) with low genetic advance (15.04%) and genetic advance in percent of mean (17.28) was considerable for this trait indicating apparent variation was due to genotypes.

So, selection based on this trait would be effective. This result also has the agreement with the findings of Singh *et al.*, (2005).Joshi *et al.* (1986) reported that heritability estimates and expected genetic advance were high for plant height.

4.2.1.3 Number of branches per plant

Number of primary branches per plant was significant indicating considerable differences among the genotypes studied (Table 5). The maximum no. of branches and minimum no. of branches per plant among the genotypes were 0.00 (G3) and 21.67 (G19) respectively with the mean value of 10.58 (Table 5). The phenotypic variance (12.20) is higher than the genotypic variance (9.76) as presented in Table 6. This feature indicated higher influences of environment on the expression of the trait. This character showed moderate genotypic and phenotypic coefficient of variation (26.57 to 29.71) respectively. In this regard, the phenotypic coefficient of variation was higher than the genotypic coefficient of variation indicating the apparent variation not only due to genotypes but also due to the influence of environment. Estimated heritability of trait was high with moderate genetic advance in percent of mean (48.95) (Table 6). Lowest genotypic coefficient of variation for branches per plant was found by Shukla *et al.* (2006). Sudhir and Singh (2003) reported genetic advance was highest for number of branches per plant.

4.2.1.4 Mean length of basal lateral branches

Different types of genotypes showed differences in terms of length of basal lateral branches and their mean length was calculated. The range of mean length was from the highest 26.07 cm to lowest 0.00 cm (Table 4). The phenotypic variance (41.11) was higher than the genotypic variance (35.74). There was small difference between GCV and PCV. The estimated heritability was found

very high (86.94%). The genetic advance was low (11.48) with the high genetic advance in percent of mean (80.93) (Table 6).

4.2.1.5 Mean length of top lateral branches

Various types of genotypes exhibited differences in terms of length of top lateral branches and their mean length was calculated. The range of mean length was from the highest 21.43 cm to lowest 0.00 cm (Table 4). The phenotypic variance (13.76) was little higher than the genotypic variance (11.54). There was small difference between GCV and PCV (Table 6). The estimated heritability was found high (83.85%). The genetic advance was low (6.41) with the high genetic advance in percent of mean (71.22).

4.2.1.6 Stem diameter

Stem diameter of different plants were of different types (Table 3). The highest stem diameter was observed in G22 (8.53 cm) and the lowest stem diameter was G6 (3.29 cm) with the mean value of 6.25 (Table 4). The phenotypic variance (2.28) was slightly higher than the genotypic variance (1.54). There was small difference between GCV and PCV (Table 6). The estimated heritability was found high (67.42%). The genetic advance was low (2.10) with the moderate genetic advance in percent of mean (33.57) (Table 6). Singh *et al.* (2005) reported that genetic advance was moderate for stem diameter. Lohithaswa and Nagaraj (1996) were reported that moderate heritability with moderate genetic advance for stem diameter.

4.2.1.7 Leaf length

The highest leaf length was found in G32 (18.23) and lowest leaf length was found in G16 (10.50) with mean value of 13.87 (Table 4). The phenotypic variance (5.96) was much higher than genotypic variance (2.39). The phenotypic coefficient of variation (17.61) and genotypic coefficient of

variation (11.55) were low. Heritability estimates was moderate (40.09). The genetic advance was very low (2.02) with low genetic advance in percent of mean (14.54) (Table 6). Sudhir and Singh (2000) reported high heritability coupled with high genetic advance for leaf size.

4.2.1.8 Leaf width

A highly significant mean sum of square was found in Table 5, which indicated considerable differences among the genotypes studied. The maximum leaf width was found in G27 (10.34) and minimum leaf with was found in G16 (6.81) with mean value of 4.48 (Table 4). The phenotypic variance (1.61) was little higher than the genotypic variance (0.44). The phenotypic coefficient of variation (14.98) was comparatively higher than the genotypic coefficient of variation (7.86) which indicating the apparent variation not only due to genotypes but also due to the influence of environment. The estimated heritability was found low (27.53). The genetic advance was very low (0.72) with the low genetic advance in percent of mean (8.49) (Table 6). Sudhir *et al.* (2000) reported high heritability with high genetic advance.

4.2.1.9 Days to flowering

Analysis of variance for days to flowering showed highly significant mean sum of square due to genotypic differences (Table 5). The mean value with respect this trait ranged from 31.00 (G5) to 48.00 (G21). The phenotypic variance (29.06) was slightly higher than the genotypic variance (26.34). The difference present among the genotypic and phenotypic variances is indicating the effect of environment for the expression of the trait is low (Table 6). The phenotypic coefficient of variation was little higher than the genotypic coefficient of variation indicating the apparent variation not only due to genotypes but also due to the influence of environment. A heritability estimate was very high

(90.64) with moderate genetic advance in percent of mean (Table 6). This result also has the agreement with the findings of Lohithaswa and Nagaraj (1996).

4.2.1.10 Seed weight per plant

There were significant differences for seed weight among the every single plant of the different genotypes (Table 5). The highest seed weight was found in G9 (10.46 gm) and the lowest seed weight were found in genotype G17 (0.04 gm) with the mean value of 4.48. The phenotypic variance 8.00 was slightly higher than the genotypic variance 7.98. The PCV (63.75) was little higher than the GCV (63.66) indicating the apparent variation not only due to genotypes but also due to the influence of environment. A highest heritability among the eleven characters was estimated 99.74%, with very high genetic advance in percent of mean (130.97) (Table 6). This result also has the agreement with the findings of Joshi *et al.* (1986).

4.2.1.11 Yield per plant (YPP)

As there were variations in height and weight of the individual stem amaranth. Thus the yield of the different genotypes showed variations among the genotypes. The yield per plant was maximum in G37 (351.33 kg) and the minimum yield per plant was found in genotype G39 (88.80 kg) with the mean value of 228.6 kg (Table 4). The phenotypic variance (6331.77) was higher than the genotypic variance (5437.36). The genotypic coefficient of variation was (32.25) and the phenotypic coefficient of variation was (34.80), that means PCV was little higher than GCV. The estimated heritability was found high (85.87) with very high genetic advance (140.76) and moderate genetic advance in percent of mean (61.56) (Table 6). Singh *et al.* (2005) was carried out an investigation and observed that genetic advance was maximum for yield.

4.3 Diversity of the stem amaranth genotypes

Genetic diversity in stem amaranth was analyzed by using GENSTAT software program. Genetic diversity analysis involved several steps i.e., estimation of distance between the genotypes, clusters and analysis of inter-cluster distance. Therefore, more than one multivariate technique was required to represent the results more clearly and it was obvious from the results of many researchers (Bashar, 2002, Juned *et al.* 1988 and Ario, 1987). In the analysis of genetic diversity in stem amaranth multivariate techniques were used.

4.3.1 Construction of scatter diagram

Depending on the value of principal component scores 2 and 1 obtained from the principal component analysis, a two dimensional scatter diagram ($Z_1 - Z_2$) using component score 1 as X-axis and component score 2 as Y-axis was constructed, which has been presented in figure 3. The position of the genotypes in the scatter diagram was apparently distributed into five groups, which indicated that there existed considerable diversity among the genotypes.

4.3.2 Principal Component Analysis (PCA)

The principal component analysis produce Eigen values of principal component axes of coordination of genotypes with first axes totally accounted for the variation among the genotypes, whereas three of these Eigen values above unity accounted for 91.31% (Table 7). The first two principal axes accounted for 86.30 of the total variation among the 11 characters describing 40 stem amaranth genotypes. On the basis of principal axes I and II, a two dimentional chart ($Z_1 - Z_2$) of the genotypes are presented in Figure 3. The scatter diagram revealed that there were five apparent clusters. The genotypes were distantly located from each other (Figure 4).

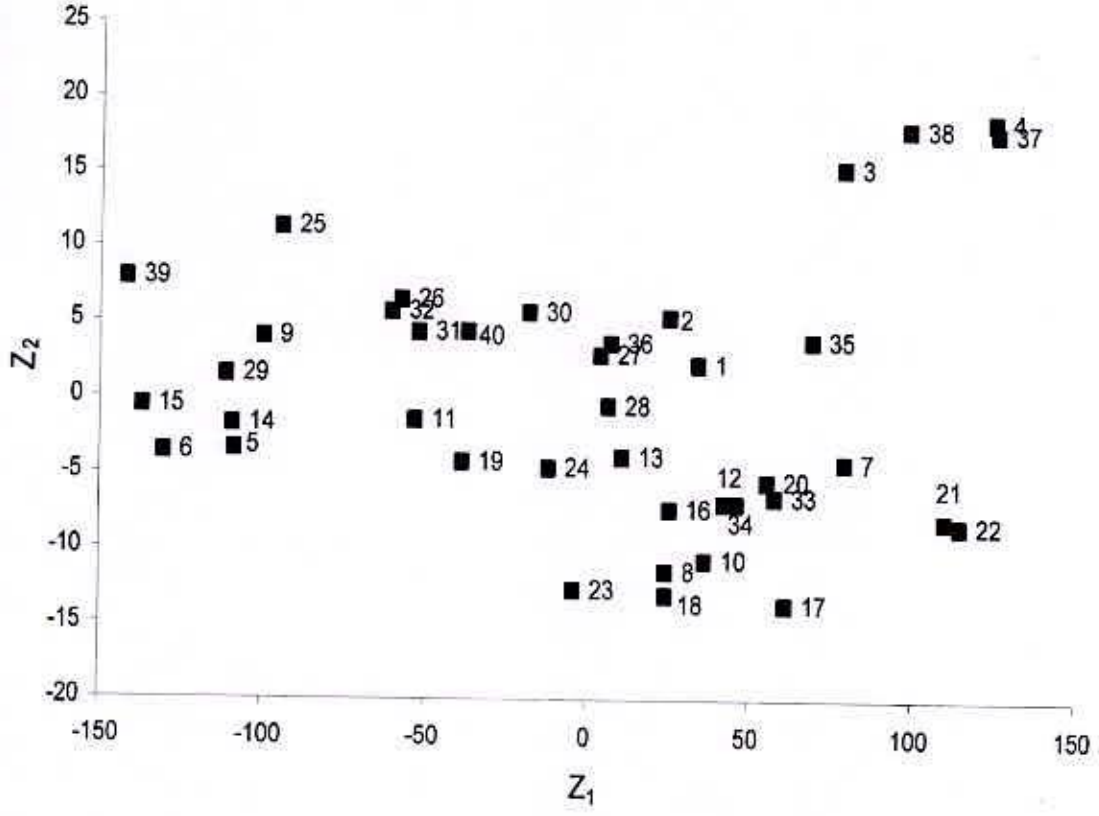


Figure 3. Scattered distribution of 40 stem amaranth genotypes based on the principal component scores

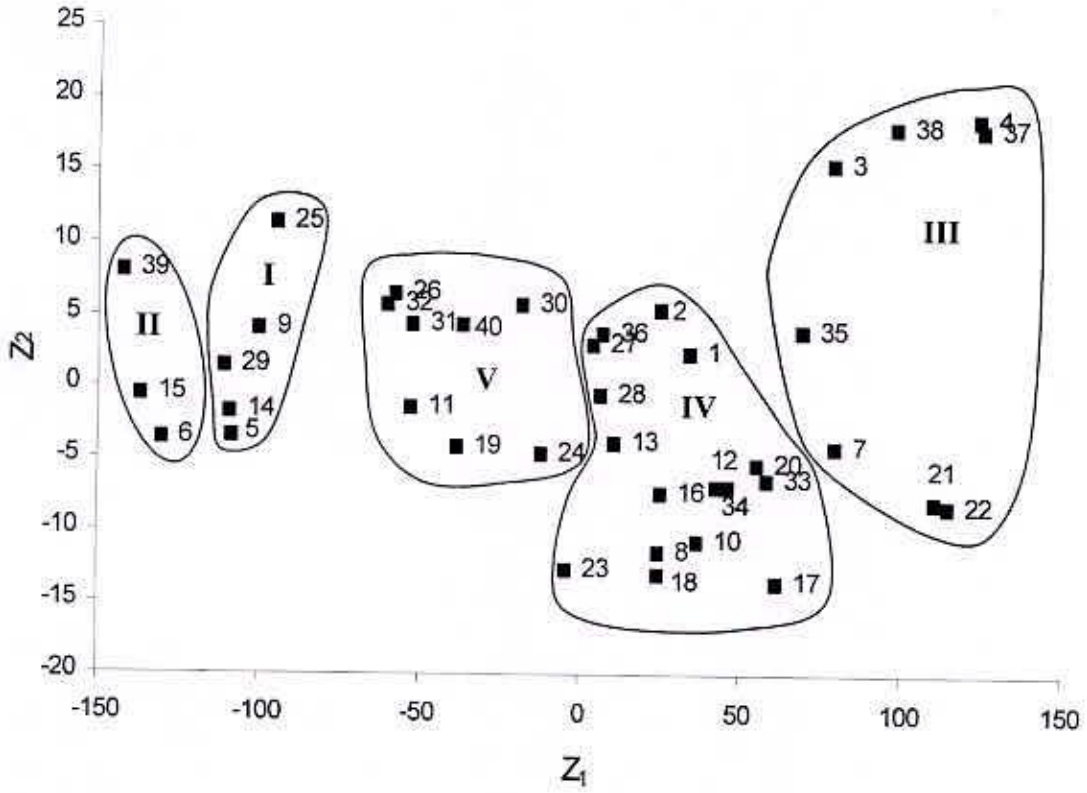


Figure 4. Scatter distribution of 40 stem amaranth genotypes based on their principal component scores superimposed with clustering

Table 7. Eigen values and percentage of variation in respect of 11 characters in 40 stem amaranth genotypes

Principal component axis	Eigen values	% of total variation accounted for	Cumulative percent
I	72.747	67.30	67.30
II	20.542	19.00	86.30
III	5.412	5.01	91.31
IV	3.780	3.50	94.81
V	2.703	2.50	97.31
VI	1.688	1.56	98.87
VII	0.561	0.52	99.39
VIII	0.364	0.34	99.73
IX	0.162	0.15	99.88
X	0.085	0.08	99.96
XI	0.051	0.04	100.00

4.3.3 Principal Coordinate Analysis (PCO)

Principal coordinate analysis was performed on auxiliary of principal component analysis. Inter genotypic distances obtained from principal coordinate analysis showed that the highest distance (5.387) was observed between the genotypes G37 and G18 followed by G18 and G3 (5.368), G18 and and G4 (5.102) and the lowest distance was observed between the genotypes G34 and G16 (0.269) followed by G6 and G5 (0.273), G37 and G4 (0.282), G37 and G3 (0.389) (Table 8). By using these distances from distance matrix intra-cluster distances were calculated (Table 9) as suggested by Singh and Chowdhury (1979). The highest intra-cluster distance was observed in cluster III (2.892), which is composed of 8 genotypes followed by cluster IV (1.367) with 16 genotypes. The cluster II showed the lowest intra-cluster distance (1.074) composed of only three genotypes (Table 10). These results revealed that the genotypes in cluster III were distantly related. On the other hand the genotypes in cluster II were closely related.

4.3.4 Non-Hierarchical Clustering

Using co-variance matrix with the application of non-hierarchical clustering, the 40 genotypes were grouped into five clusters. These results confirmed the clustering pattern of the genotypes obtained through principal component analysis. Khan (2006) reported five clustering, Islam (2005) reported four clusters and Kumar *et al.*, (1998) reported six distinct cluster in stem amaranth. Composition of different clusters with their corresponding genotypes in each cluster are presented in Table 10.

Cluster I constituted of five genotypes namely G5, G9, G14, G25 and G29. This group possessed genotypes with the highest cluster mean for leaf width (8.88) and seed weight per plant (7.50). The lowest mean found in days to germination (2.00) (Table 11).

Table 8. Ten of each higher and lower inter genotypic distance (D^2) between pains of stem amaranth genotypes

10 higher D2 values	Genotypes combination	10 lower D2 values	Genotypes combination
5.387	G37 & G18	0.269	G34 & G16
5.368	G18 & G3	0.273	G6 & G5
5.330	G18 & G4	0.282	G37 & G4
5.322	G38 & G18	0.389	G37 & G3
5.102	G23 & G4	0.412	G38 & G3
5.089	G37 & G23	0.454	G38 & G4
5.072	G37 & G17	0.470	G38 & G37
5.062	G38 & G23	0.477	G28 & G27
5.056	G23 & G3	0.489	G16 & G10
5.029	G38 & G17	0.505	G32 & G27

Table 9. Average inter cluster distance (D^2) and Intra cluster distance (bold) for 40 stem amaranth

Cluster	1	2	3	4	5
1	**1.139**				
2	2.757	**1.074**			
3	17.596	20.322	**2.892**		
4	11.607	14.313	6.037	**1.367**	
5	5.690	7.802	13.647	7.752	**1.173**

Table 10. Distribution of 40 genotypes of stem amaranth in five clusters

Cluster	Member of genotypes	Name of genotypes
1	5	BD-2468 (5), BD-2922 (9), BD-2937 (14) BD-8319 (25), BD-8325 (29)
2	3	BD-2470 (6), BD-2939 (15), Sada data (39)
3	8	Baromasi drutoraj (3), Bashpata data (4), BD-2533 (7), BD-2959 (21), BD-2966 (22), Bhuttan data (35), Red queen data (37), Red tower data (38)
4	16	BARI data (1), BARI data 2 (2), BD-2632 (8), BD-2930 (10), BD-2933 (12), BD-2935 (13), BD-2945 (16), BD-2947 (17), BD-2953 (18), BD-2958 (20), BD-8316 (23), BD-8323 (27), BD-8324 (28), BD-8329 (33), BD-9004 (34), Panna data (36)
5	8	BD-2932 (11), BD-2957 (19), BD- 8317 (24) BD-8320 (26), BD-8326 (30), BD-8327 (31) BD-8328 (32), Suressory data (40)

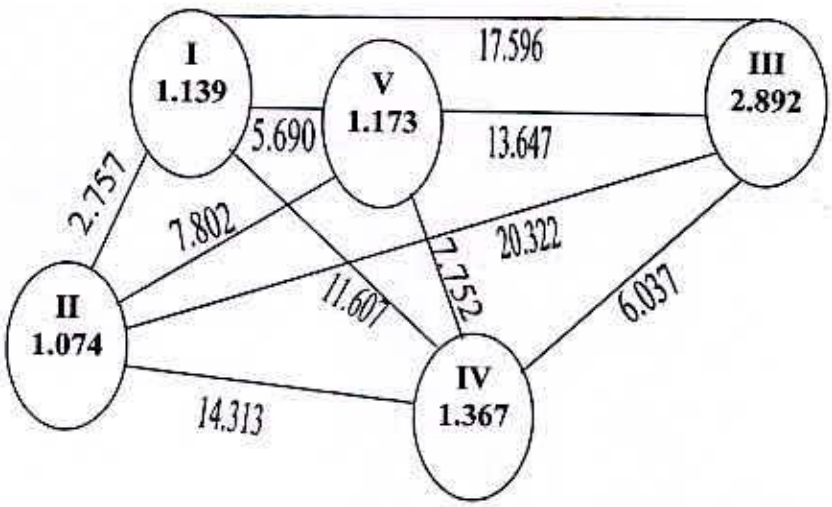


Figure 5. Diagram showing intra and inter cluster distances ($\sqrt{D^2}$) of 40 stem amaranth genotypes.

Table 11. Cluster mean for 11 characters of 40 stem amaranth genotypes

SL. No	Characters	Cluster				
		I	II	III	IV	V
1	Days to germination	2.00	2.11	2.37	2.06	2.46
2	Plant height	70.65	64.12	102.72	89.00	85.91
3	Number of Branches	9.20	9.45	5.71	11.98	13.96
4	Mean length of basal lateral branches	11.51	12.08	7.45	16.95	10.78
5	Mean length of top lateral branches	7.79	8.60	5.16	9.58	8.07
6	Stem diameter	4.37	4.05	7.68	6.89	5.52
7	Leaf length	14.01	14.61	14.35	13.20	14.35
8	Leaf width	8.88	8.46	8.72	8.20	8.54
9	Days to flowering	33.80	32.33	40.63	39.88	36.00
10	Seed wt./pl	7.50	7.43	4.27	3.49	3.46
11	Yield/plant	125.55	94.42	327.38	257.36	187.27

Cluster II had minimum number of (3) genotypes namely G6, G5 and G39. The cluster obtained first position in respect of cluster mean for leaf length (14.61) and the second in mean length of basal lateral branches (12.08) and seed weight per plant. It is lowest for plant height (64.12), stem diameter (4.05), days to flowering (7.43) and yield per plant (94.42). This cluster contains the shortest plant.

Cluster III was composed of 8 genotypes namely G3, G4, G7, G21, G22, G35, G37 and G38. Cluster III had the highest cluster mean for plant height (102.72), days to flowering (40.63) and yield per plant (327.38) and the lowest mean for number of branches per plant (5.71), mean length of basal lateral branches (7.45) and mean length of top lateral branches (5.16). This cluster contain tallest plant.

Cluster IV had the maximum number of (16) genotypes namely G1, G2, G10, G12, G13, G16, G17, G18, G20, G23, G27, G28, G33, G34 and G36. These genotypes produced the highest cluster mean for mean length of basal lateral branches (16.95) and mean length of top lateral branches (9.58), lowest for leaf length (13.20) and leaf width (8.20).

Eight genotypes formed cluster V. This cluster contained genotypes G11, G19, G24, G26, G30, G31, G32 and G40. This cluster obtained first position in respect of cluster mean for days to germination and number of branches per plant. On the other hand cluster mean for seed weight per plant was the lowest (3.46).

4.3.5 Canonical Variate Analysis (CVA)

To compute the inter-cluster Mahalanobis's D^2 values canonical variate analysis was used. The Table 9 indicates the intra and inter-cluster distance (D^2) values.

The inter-cluster distances were higher than the intra-cluster distances suggesting wider genetic diversity among the genotypes of different groups. Results indicating that the highest inter cluster distance was observed between II and cluster III (20.322) followed by between cluster I to cluster III (17.596), cluster V to cluster III (13.647). (Figure 4).

The lowest inter-cluster distance was observed between the cluster II and cluster I (2.757), followed by cluster I and cluster V (5.690), cluster IV to cluster III (6.037) and cluster II to cluster V (7.802) (Figure 4). The inter-cluster distances were larger than the intra cluster distances suggesting wider genetic diversity among the genotypes of different groups (Table 9).

Islam *et al.*, (1995) carried out on experiment on amaranth (*Amaranthus tricalor*) and obtained larger inter-cluster distances than the intra cluster distances in a multivariate analysis.

However the maximum inter cluster distance was observed between the cluster II and cluster III (20.322) maintaining more distances than other clusters and the lowest inter-cluster distance found between cluster II to cluster I (2.757), maintaining less distance than other cluster. Genotypes from the cluster II and cluster III (distances 20.322) if involved in hybridization might produce a wide spectrum of segregating populations, as genetic variation was very distinct among these groups. Similar reports were also made by Bansal *et al.*, (1999) and Singh *et al.*, (1996), Zhang *et al.*, (1987) reported that the greater genetic distances implying higher heterosis than those with similar genetic distances. The intra-cluster distance varied from 1.074 to 2.892, maximum for cluster III (2.892), which contained of 8 genotypes, while the minimum distance was found in cluster II (1.074) that comprises 3 genotypes.

Results of different multivariate analysis were superimposed in Figure from which it may be concluded from the above results that different multivariate techniques supplemented and confirmed one another. The clustering pattern of the lines revealed that varieties/lines originating from the some places did not form a single cluster because of direct selection pressure.

It has been observed that geographic diversity is not always related to genetic diversity and therefore, it is not adequate as an index of genetic diversity. Murty and Arunnachalam (1966) studied that genetic drift and selection in different environment could cause greater diversity them geographic distance.

Furthermore, there is a free exchange of seed material among different region as a consequence, the characters constellation that might be associated with particular region in nature loose their individuality under human interference and however, in some cases effect of geographic origin influenced clustering that is why geographic distribution was not the sole criterion of genetic diversity. The free cluster of the lines suggested dependence upon directional selection pressure applied for realizing maximum yield in different regions, that nicely evolved homeostatic devices would favour constancy of the associated characters. This would suggest that it was not necessary to choose diversity parents for diverse geographic regions for hybridization.

4.3.6 Contribution of characters towards Divergence of the Genotypes

Contribution of the characters towards divergence is presented in Table 12. The character contributing maximum to the divergence were given greater emphasis for deciding on the cluster for the purpose of further selection and choice of parents for hybridization (Jagadev *et al.*, 1991). The vector-1 (Z_1) obtained from PCA, the important characters responsible for genetic divergence in the major axis of differentiation were days to germination (0.7640), plant height (0.1349),

Table 12. Latent vectors for 11 characters of 4 stem amaranth genotypes

Parameters	Vectors I	Vectors II
Days to germination	0.7640	-0.4658
Plant height	0.1349	-0.1508
branches	0.0667	-0.2526
B.L.B length	0.0818	0.2083
T.L.B len	-0.1752	-0.1860
Stem dia	-0.4184	0.3185
Leaf length	0.0743	-0.0914
Leaf width	-0.6345	1.0698
Days to flower	-0.0058	-0.0012
Seed wt./pl	0.0570	0.2173
Weight/plant	-0.1020	0.0154

number of branches per plant (0.0667), mean length of basal lateral branches (0.0818), leaf length (0.0743) and seed weight per plant (0.0570). (Table 12). In vector II (Z_2) that was the second axis of differentiation of basal lateral branches (0.2083), stem diameter (0.3185), leaf width (1.0698), seed weight per plant (0.2173) and yield per plant (0.0154) (Table 12). The role of mean length of basal lateral branches and seed weight per plant for both the vectors was positive across two axis indicating the important components of genetic divergence in these materials.

4.3.7 Comparison of Different Multivariate Techniques

The cluster pattern of D^2 analysis through non-hierarchical clustering has taken care of simultaneous variation in all the characters under study. The distribution of genotypes in different clusters of the D^2 analysis has followed more or less similar trend of the Z_1 (Principal component score I) and Z_2 (Principal component score II) vectors of the principal component analysis. The D^2 and principal component analysis were found to be alternative methods in giving the information regarding the contribution of characters towards divergence in stem amaranth.

4.3.8 Selection of Genotypes for future Hybridization Programme

Selection of genetically divergent genotypes is an important step for hybridization programme. So, the genotypes were to be selected on the basis of specific objectives. A higher heterosis could be produced from the crosses between genetically distant parents (Falconer, 1960), Moll *et al.*, 1962, Ramanujam *et al.*, 1974, Main and Bhal, 1989).

Considering the magnitude of genetic distance and other agronomic performance, the genotypes G9 and G25 from cluster I, G4, G22 and G37 from III, G10, G12, G16, G17 and G34 from IV and G24 and G30 from V were

selected as promising germplasms for higher yield, number of seed per plant, days to germination and plant height. Therefore considering group distance, genetic distance and other agronomic performances, the inter-genotypic crosses between G37 and G18, G18 and G3, G18 and G4, G38 and G18, G23 and G4, G37 and G23, G37 and G17, might be suggested to use for future hybridization program.

Chapter V

Summary and Conclusion

CHAPTER V

SUMMARY AND CONCLUSION

In order to study the various characters and genetic diversity, an experiment was conducted with 40 stem amaranth genotypes at the experimental farm of Sher-e-Bangla Agricultural University during April, 2008 to June, 2008. Seeds were sown in the main field in a RCBD with three replications. Data on different morphological and yield contributing characters like growth habit, leaf shape, leaf margin, prominence of leaf veins, plant pubescence, plant pigmentation, terminal inflorescence shape, days to germination, plant height, number of branches per plant, mean length of basal lateral branches, mean length of top lateral branches, stem diameter, leaf length, leaf width, days to flowering, seed weight per plant and yield per plant were recorded. Analysis of variance revealed significant differences among all the genotypes for all the characters under study.

The phenotypic variance was higher than the corresponding genotypic variance for all the characters indicating greater influence of environment for the expression of these characters. The phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the characters. The maximum differences between phenotypic and genotypic coefficient of variation were 7.86 and 144.98 respectively which indicated that the leaf width was mostly depended on the environmental condition.

Amongst the characters the highest genotypic coefficient of variation was recorded for seed weight per plant (63.66) followed by mean length of basal lateral branches (42.13) and mean length of top lateral branches (37.75).

The highest estimated heritability amongst forth characters of stem amaranth was 99.74% for seed weight per plant and the lowest was 27.53% for leaf width. The highest GA amongst all the characters was found in yield per plant 140.76 gm and the lowest genetic advance was carried out in leaf width (0.72).

The maximum genetic advance in percent of mean was observed for seed weight per plant (130.97), followed by mean length of basal lateral branches (80.93) and mean length of top lateral branches (71.22), where as the lowest was for leaf width (8.49) and followed by leaf length (14.54) and plant height (17.28). The heritability (90.64%) with low genetic advance in percent of mean (26.54) indicated non-additive gene action for expression of the characters.

The significant variations among the genotypes for forth characters of stem amaranth were observed. Multivariate analysis was performed through principal component analysis, principal coordinate analysis, cluster analysis and canonical variate analysis using GEN STAT 513 software program. The first three principal component characters with eigen values were grater than unity contributed a total of 91.31% variation towards divergence. As per as principal component analysis (PCA), D^2 and cluster analysis, the genotypes were grouped into five different clusters. These clusters were found from a scatter diagram formed by Z_1 and Z_2 values obtained from PCA. Cluster I, II, III, IV and V composed of five, three, eight, sixteen and eight genotypes respectively. The highest inter-genotypic distance was found between genotypes G37 and G18 (Table 8) and the lowest distance between G34 and G16 (Table 8). The maximum inter-cluster distance was observed between the clusters II and III (20.322), followed by cluster I and cluster III (17.596). The lowest inter cluster distance was found between the cluster I and cluster II (2.757), followed by cluster I and cluster V (5.690).

The highest intra-cluster distance was identified in cluster III (2.892) and the lowest intra-cluster distance was found in cluster II (1.074). Genotypes included in cluster I were suitable for leaf width (8.88) and seed weight per plant (7.50), cluster III for having the highest plant height (102.72), stem diameter (7.68), days to flowering (40.63) and yield per plant (327.38), cluster IV for mean length of basal lateral branches (16.95) and mean length of top lateral branches (9.58) and cluster V for days to germination (2.46) and no-of branches per plant (13.96).

Findings of the present investigation indicated significant differences among the genotypes for all the characters studied. Generally, diversity was influenced by the morphological characters, but not by the distribution of genotypes, which indicated the importance of consumer preference and growers suitability. Considering diversity pattern and other agronomic performances, the genotypes G9 and G25 from cluster I; G4, G22 and G37 from III; G10, G12, G16, G17 and G34 from IV and genotypes G24 and G30 from cluster V could be considered as suitable parents for efficient hybridization in future breeding program. Inter-genotypic crosses between the diverse genotypes, viz. G37 and G18, G18 and G3, G18 and G4, G23 and G4, G37 and G23, might be able to produce desirable segregants.

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Appendices

Appendix I. Physical and chemical characteristics of initial soil (0-15 cm depth)

A. Physical composition of soil

Soil separates	%	Method employed
Sand	36.90	Hydrometer method (Day, 1915)
Silt	26.40	Do
Clay	36.66	Do
Texture class	Clay loam	Do

B. Chemical Composition of the soil

Sl. No.	Soil characteristics	Analytical data	Methods employed
1	Organic carbon (%)	0.82	Walkley and Black, 1947
2	Total N (kg/ha)	1790.00	Bremner and Mulvancy, 1965
3	Total S (ppm)	225.00	Bardsle and Lanester, 1965
4	Total P (ppm)	840.00	Olsen and Sommers, 1982
5	Available N (kg/ha)	54.00	Bremner, 1965
6	Available P (kg/ha)	69.00	Olsen and Dean, 1965
7	Exchangeable K (kg/ha)	89.00	Pratt, 1965
8	Available S (kg/ha)	16.00	Hunter, 1984
9	Ph (1:2.5 soil to water)	5.55	Jackson, 1958
10	CEC	11.23	Chapman, 1965

Source: Central library, Sher-e-Bangla Agricultural University, Dhaka.

Appendix II. Monthly average temperature, relative humidity, total rainfall and sunshine (hours/day) of the experimental site during the period from (April, 08 to June, 08)

Month	Average Temperature ^{0}C		RH%	Average Rainfall (mm)	Sunshine (hours/Month)
	Maximum	Minimum			
April	34.50	24.50	66	91	381.23
May	34.70	24.90	72	206	411.85
June	32.40	26.30	83	446	407.20

Source: Bangladesh Meterological Department Agargaon, Dhaka.