GENETIC DIVERSITY, CORRELATION AND PATH ANALYSIS IN STEM AMARANTH (*Amaranthus lividus* L.)

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BY

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CERTIFICATE

This is to certify that the thesis entitled, "**Genetic diversity, correlation and path analysis in stem amaranth (Amaranthus lividus 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 **Md. Abdulla Al Masum**, Registration number **13-05271** under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

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

Dated: June, 2020
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(Prof. Dr. Naheed Zeba)

Supervisor

Some commonly used abbreviations

Full word	Abbreviations	Full word	Abbreviations
Abstract	*Abstr*	Journal	*J.*
Advances/Advanced	*Adv.*	Limited	Ltd.
Agriculture	*Agric.*	Ministry	*Min.*
Agricultural	*Agril.*	Muriate of Potash	MP
Bangladesh Bureau of Statistics	BBS	Percentage	%
		Phenotypic Coefficient of Variation	PCV
Biology	*Biol.*		
Botany	*Bot.*	Physiology	*Physiol.*
Breeding	*Breed.*	Principle Component Analysis	PCA
Centimeter	cm		
Component variance	CV	Proceedings	*Proc.*
Cross between two dissimilar parents	X	Randomized Complete Block Design	RCBD
Degree Celsius	°C	Research	*Res.*
Division	*Div.*	Review	*Rev.*
Economic	*Econ.*	Science	*Sci.*
Environment	*Environ.*	Society	*Soc.*
Etcetera	etc.	Statistics	*Stat.*
Experimental	*Expt.*	That is	*i.e.*
Food and Agricultural Organization	FAO	The First Generation of a cross between two dissimilar parents	F_1
Gazette	*Gaz.*		
General	*Gen.*	Ton per Hectare	ton/h
Genetics	*Genet.*	Triple Super Phosphate	TSP
Gram	g	University	*Univ.*.
Horticulture/ Horticultural	*Hort.*	Variety	*Var*
		Vegetable	*Veg.*
Incorporated	Inc.	Videlicet (namely)	*viz.*
Information	*Inf.*	Weight	Wt.
International	*Intl.*	Yield Per Plant	YPP

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The Author

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GENETIC DIVERSITY, CORRELATION AND PATH ANALYSIS IN STEM AMARANTH (*Amaranthus lividus* L.)

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ABSTRACT

An experiment was conducted with the aim of assessments of genetic diversity, correlation and path analysis in stem amaranth (*Amaranthus lividus* L.).In this experiment thirty-seven stem amaranth genotypes were used as experimental materials. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. Variability, mean performance, correlation matrix, path analysis and genetic diversity analysis was performed. Analysis of variance revealed significant genotypic variation. Phenotypic co-efficient of variation (PCV) was higher than genotypic co-efficient of variation (GCV) for all the characters studied due to the influence of environment. High PCV and GCV was observed for plant gross weight, stem weight, ten leaf weight, plant height, stem height, stem diameter, number of branch per plant,number of leaves per branch, root shoot ratio, stem dry weight and plant weight without root indicating high variability among the genotypes and substantial scope of improvement in these traits in present material through selection. High heritability along with high genetic advance as percent of mean was observed for days to first flowering, days to 50% flowering, ten leaf weight, stem diameter, number of branch, number of leaves per branch, stem dry weight and plant weight without root. Hence, these characters need to be given more importance in selection as these are expected to be controlled by additive genes.Correlation revealed that plant weight without root had positive association with days to first flowering, days to fifty percent flowering, plant gross weight, stem weight, plant height, stem height, leaf length, leaf breath and stem diameter both at phenotypic and genotypic level. So, selection based on these traits would give better response for the improvement in yield in stem amaranth. Path analysis revealed that days to first flowering, plant gross weight, stem weight, ten leaf weight, plant height, stem height, leaf length, leaf breadth, stem diameter, number of branch, root shoot ratio, stem dry weight and thousand seed weight had positive direct effect on plant weight without root indicating these were the main contributors to yield per plant. Considering this diversity pattern, genetic status and other agronomic performances, G26, G25, G34, G36, G32 and G35 may perform better parents for efficient hybridization programme and the characters, days to first flowering, stem weight, stem height, stem breadth, number of branch, stem dry weight and thousand seed weight contributed maximum divergence among the stem amaranth genotypes.

CHAPTER I

INTRODUCTION

Stem amaranth (*Amaranthus lividus* L.) popularly known as danta, widely grown as vegetable crop. Stem amaranth is the herbaceous plant of the genus amaranthus, family Amaranthaceae.The amaranth native of India (Nath, 1976) and the centre of diversity for amaranths are Central and South America, India and South East Africa (Grubben, 1977). It is a very fast growing crop with and extremely high yield potential. The tender leaves and stems of stem amaranth are consumed as vegetable and it is rich in vitamin A and C, protein, fat, calcium, phosphorus, iron, riboflavin, niacin sodium, β-carotene and ascorbic acid than any other common vegetables (Ahammed *et al*., 2015).Two predominant types- leafy type and stem type are grown. The leafy type can be cultivated throughout the year but its production is high during winter season. The stem type is primarily a summer vegetable.

This vegetable crop grows well in the agro climatic condition of Bangladesh. The amaranth is a cross pollinated crop with chromosome number 2n=32 or 34 (Muthukrishnan *et al.,* 1989). *Amaranthus sp.* is erect, annual and up to 1.5 m tall with leaves shaped elliptical to lanceolate or brad ovate, dark green, light green or red. Fruit is dehiscent type, seeds are black, relatively large (Palada and Chang, 2008). The harvested amaranth is 50-80% edible (Oke, 1980). Amaranth leaves are rich and inexpensive source of dietary fibre, protein, vitamins and a wide range of minerals (Shukla *et al.,* 2006).The fresh tender leaves and stem of amaranth are delicious. It is cooked as vegetable soup by boiling and mixing with condiments. The seeds have various uses, as on ingredient in making sweet rolls, crepes, granola cereal, pancakes, cookies, crackers etc. Lysine content of stem amaranth is nearly three times higher than corn and twice than that of wheat (Muthukrishnan *et al.,* 1989).

Amaranth is mainly a summer and rainy vegetable in Bangladesh. The amaranth is an important and popular vegetable for its quick growing nature

and nutritional quality. The last documented area under this crop in Bangladesh is 26674 acres with production of 72277 tons (BBS, 2018), which is very low. It is because of the use of low yielding varieties and inefficient method of cultivation. To secure sustainable crop production there is no alternative of environmentally stable high yielding varieties. High yielding stable varieties will ensure more gross return to the farmers. Thus the farmers will be convinced to grow more and as a consequence the national economy will be strengthened. Though it is a very common crop in Bangladesh, very limited attempt had been taken for genetic improvement of this crop.

A better understanding of the nature and magnitude of variability among the genetic stocks should be the prime importance to the breeder. Genetic resources are vital not only to crop improvement program, but also for the very existence of the species in time and space (Swaminathan, 1983).Variability is essential for any plant breeding program. As per requirement of the farmers a new variety can be developed from a gathered diverse genetic stocks of a crop. So success of any breeding program largely depends on the genetic variability existing to the breeder and vigilant selection of parents. Genetic diversity is one of the important tools to measure genetic variability in crops (Ahammed *et al*., 2015; Gaur *et al*., 1978; Murty and Aurunachalam, 1966). The magnitude of genetic diversity through biometrical procedures has made it possible to choose genetically diverse parents for a successful hybridization program (Ahammed *et al*., 2013).Evaluation of genetic diversity is important to know the source of gene for a particular trait within the available germplasm (Tomaka, 1991). But studies pertaining to genetic diversity analysis of stem amaranth have barely been studied.

Genotypic and phenotypic coefficients of variation (GCV and PCV) are useful to detect the amount of variability present in the available genotypes. Heritability and genetic advance help in determining the influence of environment expression of the characters and the extent to which improvement is possible after selection. Crop improvement is related to the

genetic variability and it explains which the desirable characters are heritable. High heritability alone is not enough to make efficient selection in segregating generation, unless the information is accompanied for substantial amount of genetic advance (Johnson *et al.*, 1995). A breeder's first target is to increase yield, thus the knowledge of association between yield and its contributing traits is also important to know. According to Burton (1952), the extent of variability in a species is essential for improving any character in breeding. Therefore, it is important to know the genetic relationship between Amaranth species. As Amaranth is an environmental sensitive crop, stable genotypes are required to secure sustainable crop production.

It has been emphasized that the study of individual yield components can lead to simplification in genetic explanation of yield stability and hence, it is valuable to breeders in prediction and determination of environmental effects. It is important to identify the stable genotypes under different growing seasons which have great significance to the plant breeders for improvement of this crop. Bangladesh is very rich in amaranth germplasm but no systematic work has been undertaken to standardize the existing local germplasm and new varieties of stem amaranth. Hence, considering all spectrum of aforementioned requirement in stem amaranth, the present study was undertaken to find out and establish suitable selection criteria with the following objectives.

- To estimate genetic variation among the stem amaranth genotypes based on their yield and yield contributing traits.
- To know the nature of association of traits, their direct and indirect contribution to yield.
- To choose of genetically diverge parents to obtain desirable recombinant in segregating generations.

CHAPTER II

REVIEW OF LITERATURE

The review of literature includes reports of amaranth and other related crops studied by several investigators, which appears pertinent in understanding the problem and which may help in the explanation and interpretation of results of the present study. In this section, an attempt has been made to review the available information at home and abroad on genetic variability, co-relation and path co-efficient of different yield and yield contributing characters of different amaranth genotypes.

2.1 Genetic variability

It is well known fact that the genetic variability is the basic input for any plant breeding programme on which selection works are done to develop superior genotypes. Proper assessment of germplasm for various yield and yield attributing traits and reaction against major diseases is essential, as it provides potential genetic donors in crop breeding programme. Therefore, its proper understanding is very important for efficient utilization in crop improvement programme.

As early as 1883, Weisman described germplasm as “genetic material” which form the physical basis of inherited qualities and is transmitted from generation to generation by the cell. Later on, Vavilov (1926) realized the essential need for a broad genetic base of Germplasm for crop improvement. During 1951, he advocated genetic resource management and its enhancement through extensive explorations and systematic studies of the collection of landraces from various parts of the world. He suggested that the geographical centers of genetic diversity of cultivated species and their wild relatives should be exploited systematically.

Only a few systematic researches were found on stem amaranth which are presented here. Shukla *et al*. (2006) calculated populations in North India depend on a number of vegetable crops of which *Amaranthus spp.* is the most important since it is the only crop available in the hot summer months when no other foliage crop grows in the field. However, reports on mineral composition of leaves are rare with absolutely no information on the qualitative improvement of foliage yield with special reference to minerals. Studies on correlation among the minerals as well as with yield and leaf attributes are also lacking. Hence, they reported the proximate mineral composition in 30 strains of A. tricolor along with some suggestions for qualitative improvement of the foliage yield with reference to minerals. Their study showed that vegetable amaranth is a rich source of minerals like calcium, iron, and zinc. The heritability estimates were high for most of the traits, with potassium and calcium showing high values, while comparatively lower values were recorded for magnesium and nickel.

Anuja and Kader (2007) studied genetic variability and heritability involving 100 genotypes of Amaranthus germplasm in summer and monsoon seasons indicated that there were highly significant differences between the genotypes for green yield and thirteen other characters. Comparison of genotypic and phenotypic co-efficient variation for different traits indicated that the values of PCV were higher as compared to GCV due to the influence of environment. High genotypic co-efficient of variation was observed for number of leaves, yield of greens, root weight, leaf weight, stem weight and leaf area. Heritability estimates in general were high for most of the characters studied. High heritability coupled with high genetic advance (as per cent of mean) was observed for number of leaves, root length, root weight, leaf weight and stem

weight. Hence, these characters need to be given more importance in selection as these are expected to be controlled by additive genes. Similarly, in an experiment, Shukla *et al.* (2010) studied genetic diversity in a crop breeding programme helps in the identification of diverse parental combinations to create segregating progenies with maximum genetic variability and facilitates introgression of desirable genes from diverse germplasm into the available genetic base. In his study, 39 strains of vegetable amaranth (*Amaranthus tricolor*) were evaluated for eight morphological and seven quality traits for two test seasons to study the extent of genetic divergence among the strains. Multivariate analysis showed that the first four principal components contributed 67.55% of the variability. Cluster analysis grouped the strains into six clusters that displayed a wide range of diversity for most of the traits.

In an experiment of Ahammed *et al.* (2012), genetic variability and heritability analysis were done for yield and its component characters in twenty-two (22) diverse genotypes of stem amaranth. The highest PCV (87.85%) and GCV (81.67%) were observed for primary branches per plant while the lowest PCV (10.28%) was found in plant height and the lowest GCV (7.51%) was found in leaf width. Heritability estimates in broad sense were higher for leaf weight per plant (91.10%) followed by leaves per plant (86.83%), primary branches per plant (86.42%), stem weight per plant (82.56%) and yield per hectare (78.70%). Leaf weight per plant, stem weight per plant and yield per hectare exhibited high value of heritability (91.10%, 82.56% and 78.70%) along with high genetic advance (49.38%, 134.12% and 56.00%), respectively. In his another experiment in 2013, genetic divergence among 22 genotypes of stem amaranth was estimated using D^2 and Principal Component

Analysis. The genotypes were grouped into four clusters. Cluster I, II, III and IV composed of two, four, seven and nine genotypes in succession. No relationship was found between divergence and geographic distribution of the genotypes. Maximum inter cluster distance (12.326) was observed between cluster I and III and it was minimum (3.526) between cluster I and II. The crosses between the genotypes of cluster I with that of cluster III and cluster II with cluster III would exhibit high heterosis and also likely to produce new recombinants with desired characters in stem amaranth. The yield contributing characters were leaves per plant, petiole length, stem diameter, leaf weight per plant and stem weight per plant. Leaf width, petiole length and 1000 seed weight showed maximum contribution to the total divergence. The results obtained by D^2 analysis were confirmed by Principal Component Analysis (Ahammed *et al.*, 2013).

Akaneme and Ani (2013) reported in five amaranths accessions of the species obtained from National Centre for Genetic Resources and Biotechnology Ibadan, Nigeria, were evaluated in the field for variability in ten quantitative and nine qualitative traits in Completely Randomized Design with five replications per accession was employed. Analysis of variance revealed highly significant differences ($P<0.001$) for days to 50% flowering and 500 seed weight ($P<0.01$). The range, coefficient of variability, phenotypic and genotypic coefficients of variability also revealed high variability for each of the quantitative traits. The highest broad sense heritability (h^2bs), GCV, PCV and GA were obtained for days to 50% flowering. The dendrogram divided the accessions into cluster 1 comprising accessions 3 and 5 and cluster 2 comprising accessions 1, 2, 4. These variations provide ample opportunities for plant breeders to carry out selection while designing plant breeding

programmes for the improvement of the species. Again Ahammed *et al*. (2015) performed an experiment to evaluate of stem amaranth genotypes for growing in winter season in Bangladesh. Nineteen stem amaranth genotypes were used in this experiment to select suitable amaranth genotypes for winter season. The highest primary branch per plant was found in the genotype SA015 (6.83). The thickest stem diameter was observed in the genotype SA023 (22.05 mm) and the thinnest from SA015 (15.28 mm). The highest stem weight/plant was found in the genotype SA026 (205.32 g) and the lowest was in SA027 (79.12 g). The lowest leaf-stem ratio was found in the genotype SA005 (0.32). The genotype SA026 produced the highest stem yield (68.37t/ha) which was at par with SA023. The genotype SA015 was earlier (55.33 days) to flower and the genotype SA005 (104.00 days) was delayed in flowering. The highest edible portion (%) was observed in the genotype SA040 (71.20%) and the lowest was found in the genotype SA026 (51.76). The lowest fibre content (%) was found in the genotype SA040 (0.36%) at 70 days of sowing. The genotypes SA023, SA026, SA028 and SA040 were found promising in respect to amaranth stem production for winter season in Bangladesh (Ahammed *et al*., 2015).

Genetic variability, heritability and genetic advance (GA) for seven metrical traits in the cultivars of amaranth was studied by Parveen *et al.* (2013). The study indicated existence of considerable amount of genetic variability for all the characters studied except rachis per inflorescence. High estimate of heritability were also observed in the characters of seed yield per plant, length of inflorescence. The maximum values of PCV, GCV, heritability and GA was found for the characters *viz*., seed weight of 1000 seeds and seed yield per plant. Hence, these traits can be effectively improved through selection. Similarly, hundred germplasm of

amaranth during *Kharif*-2011 were evaluated by Venkatesh *et al.* (2014) for assessing the genetic variability for grain yield and yield related traits. Analysis of variance revealed significant differences among the genotypes for all the characters studied. High PCV and GCV were observed for stem girth, plant height, panicle length and grain yield per plant. On the other hand, low PCV and GCV were observed for days to maturity and grain protein content. All the studied traits exhibited high heritability. High genetic advance as per cent of mean was observed for days to 50 per cent flowering, plant height, panicle length and grain yield per plant indicating scope for improvement of the traits of interest through hybridization and selections.

Sarker *et al.* (2014) evaluated genotypic variability in 30 vegetable amaranth genotypes for nutrient composition, antioxidant content, and 12 yield contributing traits. High mean value, high range of variability and high genotypic variance were observed for all the traits except content of Ca, protein and beta-carotenoid. Close differences between genotypic and phenotypic variances and genotypic and phenotypic coefficient of variations were observed for all the traits. Considering all genetic parameters, selection based on contents of potassium, manganese, and ascorbic acid, plant height, leaves per plant, diameter of stem base, fiber content, leaf area and foliage yield per plot seemed to be effective for the improvement of vegetable amaranth. Again, Diwan *et al.*(2017) studied ten germplasm of amaranthus during the period from October, 2014 to February, 2015. The data were analyzed to work out the variability, correlation coefficient and path analysis for character viz., number of leaves per plant, leaf length (cm), leaf width (cm), plant height (cm), stem girth (cm), stem weight (g), leaf weight (g), stem weight (g), petiole length (cm), panicle length (cm), plant weight (g),

number of cutting, leaf yield (kg/plot), seed yield (g/plant), 1000 seed weight (g) and crop duration (sowing to last harvest). The analysis of variance indicated that the mean sum of square due to genotypes were highly significant for all the sixteen characters. Significant mean sum of squares due to leaf yield and attributing characters revealed existence of considerable variability in material studied for improvement of various traits. The highest leaf yield kg per plot was recorded in genotype 2012/AMVAR- 4 followed by 2012/AMVAR-7 (17.41 kg/plot), CG Amaranthus-1 (17.36 kg/plot). Moderate estimates of phenotypic and genotypic coefficient of variation for almost all traits except leaf weight show the high genotypic and phenotypic variation indicated that there was high variability offering ample scope for selection of desired variability. Heritability along with genetic advance as percent of mean for all the tested characters indicated that these characters were under additive gene action and there were excellent chances of effective selection for improvement of these traits.

Morphological characterization of plant genetic resources was studied by Gerrano *et al.* (2017) which generated important information for plant breeders useful for pre-breeding and breeding programmes of crops. A number of Amaranths species have been collected from different regions in the world and conserved in the gene bank of the Agricultural Research Council, Pretoria, South Africa. The objective of the study was to assess the genetic diversity of these conserved Amaranthus species using qualitative morphological characters. Thirty-two species of Amaranthus were evaluated for 16 qualitative morphological characters in the field using a randomized complete block design with three replications. The frequencies for each qualitative character were tabulated. The Shannon Weaver diversity index (HI) was calculated and the result revealed a low

to high diversity among the collection regions for the traits. The result of the study showed that the HI for all the species varied from 0.28 to 0.70, indicating the existence of a wide genetic diversity among species evaluated. The information obtained in this study could be used for the genetic improvement of Amaranthus species in South Africa for the development of cultivars.

Khezerlu and Tajbakhsh (2017) studied the seed organic pretreatment for morphological characteristics and quality according to forage desirable quality of amaranthus, as new plant in Iran, production deficit and forage qualitative reducing in this country on recent years, can be positive step to introduce this plant as forage security source. To study the means of morphological characteristics and forage quality of amaranthus under seed pretreatment, a trial was arranged as randomized completely block design with six treatments and three replications in research field of agricultural college of Uremia university. Treatments were including seed priming of pigeon manure (10%), concentrated vaniaze (68.39%) (Three in thousands) super macro plus nano chelate fertilizer (three in thousand), magnet water, Homeopathy 12x and control. The seeds were soaked in the listed treatments for 8 hours; therefore, those were brought to the initial moisture content for 24 hours at 25°C and transferred to field for planting. Ground preparation was concluded in the beginning of June as furrow-ridge. Seed were placed in 1-2 cm soil depth. Evaluated traits in current study were including plant height, secondary bough number, stem diagonal and forage quality. Harvest was at flowering stage in one square meter of each experimental unit. Samples were dried and milled. Therefore, near-infrared spectroscopy (NIR) technology was used for forage quality measurement. Results of analysis variance indicated that treatment effects on plant height and diagonal stem were

not significant, but was significant for leaf number and secondary bough number. Using priming led to plant height and stem diagonal increasing, but was statistically not significant. The highest leaf number was related to magnetic water pretreatment (395 leaves in square meter), then pigeon manure (362.3 leaves in square meter). The highest secondary bough was related to magnet water pretreatment. After primed seed establishment in soil, the seeds were germinated more monotonous, faster and better than no- treatment. Actually, plants derived from primed seeds were developed root systems on the shortest time as compared with seeds without pretreatment because of desirable suction of nutrition material and water, and ecological and biological sections production. Treatment effect was significant for all traits except to ash percent. The most crud protein percent and soluble carbohydrate and digestibility dry matter was related to pretreatment of pigeon manure respectively 25.4%, 11.8% and 51.5%. The highest percentage of soluble fiber on neutral detergents and soluble fiber on acidic detergent, and crude fiber were obtained for control respectively by 59.7%, 43/03% and 26/6%. Crude protein value of forage was significantly related to digestibility percent that is one of the most important factors determining forage quality. Increasing crude fiber will result in reduction of protein and nutrition value of crops. Amaranthus was placed on desirable qualitative degree for crude protein percentage and digestibility according to grass species categories for indicators values of forage quality. According to obtained results in current study, using organic seed pretreatment led to qualitative and quantitative enhancement of Amaranthus forage. Therefore, seeds treatment before planting using organic fertilizers produced in the field will lead to fertilizer preparation related the cost saving, and income value will be economically more

than the cost and cost-effective for farmers.

Shrivastav *et al.* (2017) reported grain yield is a complex quantitative trait, considerably affected by environment; therefore, selection of genotypes based on yield is not effective. Higher yield can be achieved by improving its component traits. Correlation studies alone are not indicative of inter relationships among heritable traits, this lead to negative results (Bhat,1973).The present study was undertaken on twenty-three diverse genotypes of Amaranthus (*Amaranthus paniculatus* L.) including three checks (GA 2, BGA 2 and RMA 7) in Randomized Block Design with three replications during Rabi 2014-15 at Students Instructional Farm, Kumarganj, Faizabad. The analysis of variance revealed that mean squares due to treatments were highly significant for all characters except seed volume weight (g/10ml). The magnitude of phenotypic coefficient of variation was higher than corresponding genotypic coefficient of variation for all the characters. The high estimates of genetic advance in per cent of mean (>20%) were recorded for harvest index (%) (54.15%), biological yield per plant (51.79%), plant height (35.23%), number of branches per plant (34.33%)and inflorescence length (30.86). All the genotypes were grouped into five different non overlapping clusters. Tiwari (2018) studied Twenty- seven genotypes of grain amaranth were used to study nature and genetic parameters with an aim to select superior genotypes. Phenotypic variance was higher than the genotypic variance for all the traits. The heritability estimates for all the characters were high and none of the characters showed moderate or low estimates. For the cluster analysis, 27 genotypes were grouped into four clusters in which third cluster was higher than other in terms of cluster mean. Lower cluster mean belonged to fourth cluster

2.2 Correlation coefficient

As yield is the resultant of combined effect of several component characters and environment, understanding the interaction of characters among themselves and with environment has been of great use in the plant breeding. Shukla *et al*. (2006) study showed that vegetable amaranth is a rich source of minerals like calcium, iron, and zinc. Nickel was the only mineral that showed positive correlation with all the minerals, as well as with leaf size and foliage yield. Zinc showed strong positive relationship with iron (0.66**) and manganese (0.74**), and was the only mineral exhibiting significant positive association with foliage yield. This study would be of use in enhancement of selected minerals in different regions according to local preferences and nutrient deficiency prevalent among the populations. Similarly, Pandey and Singh (2010) evaluated twenty-six accessions of grain amaranth (*Amaranthus hypochondriacus* L.) for salient biochemical and quantitative traits particularly reference to chlorophyll a and b, total chlorophyll, phenol content, leaf moisture, leaf protein content, test weight and yield per plant. Genetic divergence and association among these traits were analyzed. Leaf protein content revealed exceptional attributes for ameliorating protein deficiency strictly in the diet of vegetarian people. Leaf protein content was noted significant in four accessions, namely AG- 67/1(3.152mgg-1),AG-21(2.452mgg-1),AG-306(2.101mgg-1)and AG-1175 (2.101 mg g-1).1000 seed weight was found positive correlated with seed yield per plant and it is also highly direct effect to the seed yield using Euclidean cluster analysis 26 accessions were distributed in 3 clusters (at 9.0 Euclidean distance) of which cluster I contained maximum (13) accessions, cluster II (10) and cluster III (3) accessions. Cluster I and III were found more diverse than

others and therefore can be used for developing recombinants. Biochemical characters had no significant genetic association with grain yield per plant which revealed that biochemical traits can be improved without altering grain yield. Cluster I and III were found more diverse than others and therefore can be used for developing recombinants.

Ahammed *et al*. (2012) performed an experiment based on correlation analysis and he found that, leaves per plant, stem diameter, stem weight per plant, leaf weight per plant and plant height exhibited highly significant positive correlation with yield per hectare both at genotypic and phenotypic level. According to his experiment, selection based on these traits would give better response for the improvement in marketable yield in stem amaranth. On the other hand, Kumar *et al*. (2014) studied the correlation coefficient analysis showed that most of the traits were positively and significantly correlated at both the phenotypic and genotypic levels. In case of grain yield/plant, it was highly significant and positively associated with number of grains/plant and harvest index at both the levels. However, number of tillers/plant, weight/ear and number of grains/spike were positively correlated with harvest index at genotypic level.

Sarker *et al.* (2014) found in amaranth experiment that foliage yield had significant *positive* correlation with plant height, leaves per plant, diameter of stem base, fiber content and leaf area. Nutrient content and antioxidant traits exhibited interesting results, i.e., had insignificant genotypic correlations with foliage yield and most of the studied traits indicating that selection with these traits might be possible without compromising any yield loss. Therefore, concomitant selection for high nutrient, antioxidant and high foliage yield would be effective for

improvement of the vegetable amaranth. Based on mean, range, genetic parameters, correlation coefficient and path coefficient values, direct selection through three traits, i.e., fiber content, leaf area and diameter of stem base would significantly improve the foliage yield of vegetable amaranth. On the other hand, concomitant selection based on high nutrient and antioxidant content and high foliage yield would be effective selection method for improvement of vegetable amaranth with leaf area, shoot weight, shoot per root weight and stem base diameter. Insignificant genotypic correlation was observed among mineral, quality and agronomic traits, except K vs. Mg, protein vs. dietary fiber and stem base diameter vs. Ca. Some of these genotypes can be used for improvement of vegetable amaranth regarding mineral, protein and dietary fiber content without compromising yield loss. In the same year in 2014, Venkatesh *et al*. (2014) reported that one hundred genotypes of grain amaranth were used to estimate correlation co-efficient among 10 quantitative traits including grain yield in grain amaranth. At the phenotypic level, stem girth, number of leaves per plant, plant height, panicle length and seed weight exhibited significant positive correlation with grain yield, while its association with panicle width was negative and significant. Again, Ayehu *et al*. (2015) evaluated those 36 accessions of *Amaranthus spp*. in 6x6 simple lattices design at Tepi and Mizan experimental sites. The overall objective was to estimate the extent of genetic association among yield and yield related traits. Variances component method was used to estimate, genetic relationship among traits was also estimated by using standard method. Analysis of variance revealed that there was a significant difference ($p< 0.01$) among thirty-six germplasm accessions for all the characters studied except for thousand seed weight which was non-significant ($p>0.05$). Less value of

phenotypic correlation coefficient than the genotypic correlation coefficient were found in most of the characters.

In an experiment, Diwan *et al*. (2017) found highly significant and positive correlation with leaf yield with plant height, plant weight, stem girth and seed yield, whereas leaf length and petiole length showed negative association with green yield. In a similar experiment of Shrivastav *et al.* (2017), the seed yield per plant was found highly and positively associated with inflorescence length, plant height and biological yield per plant. Seed yield per plant showed negative correlation with days to 50% flowering and protein content; and non significant correlation with maturity. The characters showing significant positive correlation among yield and yield contributing characters would be highly effective and efficient in improving respective traits. Again, Tiwari (2018) observed that, Days to maturity got significant positive correlation with seed yield, plant height, length of inflorescence and 1000 seed weight (g). Plant height was also found to have significant positive correlation with seed yield and 1000 seed weight. Length of inflorescence and 1000 seed weight had significant and positive correlation with yield.

2.3 Path coefficient

A polygenic trait like seed yield is influenced by its various components directly as well as indirectly via other traits, which create a complex situation before a breeder for making selection. Therefore, path coefficient analysis could provide a more realistic picture of the interrelationship by partitioning it into direct and indirect effects of the variables. A few researches on Path coefficient analysis are revealed here. Haghighi *et al.* (2012) studied that direct and indirect

effect of each yield component on the final yield, by the means of path analysis is highly important. The result of principle component analysis indicated that in the first prim, traits such as plant height, stem yield, leaf yield, flower and biomass yield contributed to about 80% of variations. The result of stepwise analysis of the traits that affect the dependent variable (biomass yield) indicated that four traits including flower yield, stem yield, leaf yield and petiole yield entered to the model respectively. The result of path analysis showed that stem yield had the highest positive direct effect on biomass yield and had determination of 0.482 of the total variations. Flower yield which was the first trait entering the model, was the second most effective trait on biomass yield with determination of 0.294. Therefore, it can be concluded that stem yield had the highest effect on biomass yield and after that, flower yield; leaf yield and petiole yield were the most effective traits on biomass yield, respectively. Keshav *et al*. (2013) reported that inter relationship among direct and indirect influence of component characters of yield is important in detecting the correlated response to directional selection, and in the detection of traits as useful markers.

In a study of Venkatesh *et al*. (2014), he reported that one hundred genotypes of grain amaranth were used to estimate correlation and path co-efficient among 10 quantitative traits including grain yield in grain amaranth. Path co-efficient analysis revealed maximum positive direct effect of number of leaves per plant (0.575) on grain yield followed by seed weight (0.234), panicle length (0.221) and plant height (0.124). The study suggests that selection of varieties with higher number of leaves per plant, seed weight, panicle length and plant height will help the breeder to select the genotypes which can give better grain yield. Kumar *et al*. (2014) reported that path coefficient analysis was used to

determine the direct and indirect effects of different characters on grain yield. Path analysis revealed that the direct effects of number of grains per spike, biological yield per plant and harvest index on grain yield. These characters' merit special attention in formulating selection strategy in wheat for developing high yielding varieties.

Maximum positive direct effect was recorded by Ayehu *et al*. (2015) in biomass per plant, average branch length, leaf area, days to flowering, leaf width and plant height on the other hand, length of medium branch `exerted the highest negative direct effect on yield. Among others biomass per plant will be useful traits for indirect selection to increases green leaf yield. Similarly, Shrivastav *et al.* (2017) reported that path analysis revealed biological yield per plant and harvest index as important components having high order of direct effect and biological yield per plant via days to maturity followed by harvest index via protein content, inflorescence length via plant height. The characters identified above as important direct and indirect yield components would be helpful in formulating strategy for selecting high yielding varieties of Amaranthus. Again, Jangde *et al.* (2017) reported that path coefficient analysis revealed that fresh stem weight (1.100) and number of leaves per plant (0.014) showed the highest positive direct effect on leaf yield, whereas direct negative effect on leaf yield *viz*. Plant height (-0.071) for quantitative characters. In an experiment of Diwan *et al*. (2017), Path coefficient analysis revealed that stem weight, 1000 seed weight, number of leaves, intermodal length and panicle length were the most important yield components. Selection programme based on these characters is suggested for further improvement. Tiwari (2018) observed that in case of path analysis, days to maturity had direct effects on grain yield then 1000 seed weight, length of inflorescence and plant height.

CHAPTER III

MATERIALS AND METHODS

This chapter encompasses information regarding methodology used in execution of the experiment. It covers a brief description of locations of experimental site, planting materials, climate and soil, layout and design of the experiment, plot preparation, fertilizing, intercultural operations, harvesting, data recording procedure, statistical analysis etc. which are presented as follows:

3.1. Experimental site

The research was carried out in the research farm of Sher-e-Bangla Agricultural University, Sher-e-Bangla nagar, Dhaka during the Robi season of 2019-2020.The location of the site is 23°74' N latitude and 90°35' E longitudes at an elevation of 8.2 meters from sea level (Appendix I).

3.2 Soil

The soil belongs to "The Modhupur Tract", AEZ-28 that comprises of silty clay in texture at the top, olive-gray with common line to medium distinct dark yellowish brown mottles, soil pH ranged from 6.0-6.6 and organic carbon 0.45%. The experimental spot was flat, medium high land with available irrigation and drainage system and above sea level. The details are presented in Appendix II.

3.3 Climate

The experimental site is located under the sub-tropical climatic zone. It is characterized by three seasons- winter season from November to February and the pre-monsoon period or hot season from March to April and monsoon period from May to October. The cropping season of this experiment was the Robi season from mid-November to mid-March.The monthly average minimum and maximum temperature during the crop period was 12.00°C and 26.00°C and minimum and maximum relative humidity was 57% and 79%, respectively. The monthly average rainfall during the crop period was 17.59

mm. Details of the metrological data of air temperature, relative humidity, rainfall and sunshine hour during the period of the experiment was collected from the Weather Station of Bangladesh, Sher-e- Bangla Nagar, Dhaka-1207 and presented in Appendix III.

3.4 Planting materials

A total number of thirty-seven genotypes of stem amaranth were used in the study as parents (Table 1). The seeds were collected from the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Sher-e-Bangla Nagar, Dhaka and Bangladesh Agricultural Research Institute (BARI).

3.5 Design and layout of the experiment

The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. The field size was 20 m×20 m. Line to line distance was 20 cm. The whole field was divided into three-unit plot. The unit plot size was 20 m X 5 m accommodating thirty-seven lines in each plot. In each plot 37 genotypes were planted in three replications.

3.6 Land preparation

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

3.7 Seed sowing

Seeds of the thirty-seven genotypes were sown directly in line on 1st December, 2019.

3.8 Manure and fertilizers application

The entire quantity of cow dung and TSP were applied during the final land preparation a week before seed sowing. Urea & Murate of Potash (MP) were top dressed in three equal splits. The first, second and third top dressing were done at 15 days, 21 days and 28 days after sowings respectively.

Table 1. Name and source of stem amaranth genotypes used in the present study

Sl. No.	Genotypes No.	Name/Acc No.	Source
1	G1	BD-11527	BARI, Gazipur
2	G2	BD-11528	
3	G3	BD-11529	
4	G4	BD-11530	
5	G5	BD-11531	
6	G6	BD-11532	
7	G7	BD-11533	
8	G8	BD-11534	
9	G9	BD-11535	
10	G10	BD-11537	
11	G11	BD-11538	
12	G12	BD-11540	
13	G13	BD-11542	
14	G14	BD-11544	
15	G15	BD-11548	
16	G16	BD-11549	
17	G17	BD-11550	
18	G18	BD-11556	
19	G19	BD-11559	
20	G20	BD-11560	
21	G21	BD-11561	
22	G22	BD-11562	
23	G23	BD-11563	
24	G24	BD-11564	
25	G25	BD-11565	
26	G26	BD-11566	
27	G27	BD-10680	
28	G28	BD-10681	
29	G29	BD-10682	
30	G30	BD-10851	
31	G31	Aman danta	GEPB SAU
32	G32	Ghee Kanchan	
33	G33	Sharupa	
34	G34	Green tower	
35	G35	Red tower	
36	G36	Panna	
37	G37	Bhutan	

GEPB=Department of Genetics and Plant Breeding, SAU = Sher-e-Bangla Agricultural University, BARI= Bangladesh Agricultural Research Institute

3.9 Intercultural operations

Weeding and mulching of the plot was done as and when required. Then top dressing and irrigation were applied at 15 days' interval. The insecticide Diazinon was sprayed to prevent the damage of the plants by the fruit borer and white fly, the vector of TYLCV. Some pictorial view of intercultural operation is illustrated in (Plate 1)

3.9.1 Thinning

First thinning was done 25 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.

3.10 Harvesting

Different genotypes matured at different times. The final harvesting was done by 20 March, 2020. Ten plants from each replication were randomly selected to collect data and harvested by uprooting. Border plants were discarded to avoid border effect. Some pictorial views of the field are presented in Appendix IV.

3.11 Observation and collection of 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 co-rrelation, path co-efficient and genetic diversity analysis were recorded under field condition and in the laboratory after harvest.

3.11.1 Days to first flowering

Number of days for first flowering was counted from seed sowing date to first flowering.

3.11.2 Days to 50 % flowering

The number of days was required from the date of sowing to the date of 50% flowering of the plants of each replication.

3.11.3 Plant Gross weight (g)

The average weight of the whole plant from the root to the tip was measured.

Plate 1. Intercultural operation and data collection. A. Thinning, B. Weeding,and C. Measuring of stem height

3.11.4 Stem weight (g)

The average weight of the stem from the ground level to the tip was measured.

3.11.5 Ten Leaf weight (g)

Weight of ten leaves was measured from randomly selected plants.

3.11.6 Plant height (cm)

The average height of the whole plant from the root to the tip was measured.

3.11.7 Stem height (cm)

The average height of the stem from the ground level to the tip was measured.

3.11.8 Leaf length (cm)

Average length of leaf was measured including petiole.

3.11.9 Leaf breadth (cm)

Average breath of leaf was measured.

3.11.10 Stem perimeter (cm)

The average perimeter of the stem was measured.

3.11.11 Number of branch per plant

Number of branch of the each plant was counted.

3.11.12 Number of leaves per branch

Number of leaves in each branch from each plant was counted.

3.11.13 Root length (cm)

Average length of the root was measured.

3.11.14 Root shoot ratio

Ratio of shoot and root length was measured.

3.11.15 Stem dry weight (g)

Stem was oven dried at 60^{O} C temperature for five days and then the weight was recorded.

3.11.16 Thousand seed weight (g)

Weight of thousand seeds from each of the genotype which are randomly was recorded and expressed in grams.

3.11.17 Plant weight without root (g)

The average height of the whole plant without the root length was measured.

3.12 Statistical analysis

For each character the data were recorded and averaged to obtain mean data. Mean data of characters were subjected to multivariate analysis. Univariate analysis of the individual character was done for all characters under study using mean values (Singh and Chaudhary, 1985) and was estimated using MSTAT-C computer program. Duncan's Multiple Range Test (DMRT) was performed for all the characters to test the differences between the means of the genotypes. Mean, range, and co-efficient of variation (CV%) were also estimated using MSTAT-C, Multivariate analysis was done by computer using the GENESTAT and Microsoft Excel 2016 software through four techniques viz., Principal Component Analysis(PCA), Principle Co-ordinate Analysis (PCO), Cluster Analysis and Canonical Vector Analysis (CVA).

3.12.1 Estimation of genotypic and phenotypic variances

Genotypic and phenotypic variances were calculated by the following formulae given by Johnson *et al*. (1995).

a. Genotypic variance, $\delta^2 g = \frac{MSG - MSE}{r}$

Where, MSG=Mean sum of square for genotype

MSE=Mean sum of square for error, and

r = Number of replication

b. Phenotypic variance, $\delta^2 p = \delta^2 g + \delta^2 e$

Where, $\delta^2 g =$ Genotypic variance,

$\delta^2 e$ = Environmental variance=Mean square of error

3.12.2 Estimation of genotypic and phenotypic co-efficient of variation

The genotypic and phenotypic co-efficient of variation in percent were computed by the following formula (Burton, 1952).

Genotypic co-efficient of variation (GCV %) = $\frac{\delta_g \times 100}{\bar{X}}$

Phenotypic co-efficient of variation (PCV %) = $\frac{\delta_p \times 100}{\bar{X}}$

Where, δ_g = Genotypic standard deviation

δ_p = Phenotypic standard deviation

$\bar{X}$ = Population mean.

The PCV and GCV values are ranked as low, medium and high (Shivasubramanian and Menon, 1973) and are mentioned below:

0-10% - Low

10-20% - Moderate

>20% - High

3.12.3 Estimation of heritability

Broad sense heritability was estimated by the following formula, suggested by Johnson *et al*. (1955)

h^2_b (%) = $\frac{\delta^2 g}{\delta^2 p} \times 100$

Where,

h^2_b= Heritability in broad sense

$\delta^2 g$ = Genotypic variance

$\delta^2 p$ =Phenotypic variance

3.9.4 Estimation of genetic advance

Genetic advance was estimated for different characters under selection by using the formula suggested by Johnson *et al.* (1995)

$$GA = \frac{\delta^2 g}{\delta^2 p} K.\ \delta_p$$

Where, GA= Genetic advance

$\delta\ ^2_g$ = Genotypic variance

$\delta\ ^2_p$ = Phenotypic variance

δ_p = Phenotypic standard deviation

K = Selection differential which is equal to 2.06 at 5% selection intensity

3.12.5 Estimation of genetic advance in percentage of mean

Genetic advance in percentage of mean was calculated by the following formula given by Johnson *et al*. (1995).

Genetic Advance in percentage of mean = $\frac{Genetic\ \ Advance}{Grand\ \ mean} \times 100$

Genetic advance in percent of mean was classified as low, moderate and high (Johnson *et al*., 1955) and values are given below:

0-10% - Low

10-20% - Moderate

20% and above - High

3.12.6 Estimation of simple correlation co-efficient

Simple correlation co-efficient was estimated by the following formula (Clarke, 1980; Singh and Chaudhary, 1985).

$$r = \frac{\sum xy - \frac{\sum x . \sum y}{N}}{\sqrt{[\{\sum x2 - \frac{(\sum x)2}{N}\}\{\sum y2 - \frac{(\sum y)2}{N}\}]}}$$

Where,

$\sum$ = Summation

x and y are two variable correlated

N = Number of observations

3.12.7 Estimation of genotypic and phenotypic correlation co-efficient

The genotypic and phenotypic correlation co-efficient was estimated by the formula (Johnson *et al.*1995; Hanson *et al.* 1956).

Genotypic correlation $(r_{gxy}) = \frac{GCOVxy}{\sqrt{GVx.GVy}} = \frac{\sigma_{gxy}}{\sqrt{(\sigma^2_{gx} . \sigma^2_{gy})}}$

Where, σ_{gxy} = Genotypic co-variance between the traits x and y

σ^2_{gx} = Genotypic variance of the trait x

σ^2_{gy} = Genotypic variance of the trait y

Phenotypic correlation $(r_{xy}) = \frac{PCOVxy}{\sqrt{PVx.PVy}} = \frac{\sigma_{pxy}}{\sqrt{(\sigma^2_{px} . \sigma^2_{py})}}$

Where, σ_{pxy} = Phenotypic co-variance between the traits x and y

σ^2_{px} = Phenotypic variance of the trait x

σ^2_{py} = Phenotypic variance of the trait y

3.12.8 Estimation of path co-efficient analysis

Path co-efficient analysis was carried out according to the procedure employed by Dewey and Lu (1959) also quoted in Singh and Chaudhary (1985), using simple correlation values. In path analysis, correlation co-efficient is partitioned into direct and indirect independent variables on the dependent variable.

In order to estimate direct and indirect effect of the correlated characters, say, xl, x2 and x3 yield y, a set of simultaneous equations (three equations in this example) is required to be formulated as shown below:

$r_{yx1} = P_{yxl} + P_{yx2} r_{xlx2} + P_{yx3} r_{x1x3}$

$r_{yx2} = P_{yxl} r_{x1x2} + P_{yx2} + P_{YX3} r_{x2x3}$

$r_{yx3} = P_{yxl} r_{x1x3} + P_{yx2} r_{x2x3} + P_{yx3}$

Where, r´s denotes simple correlation co-efficient and P´s denote path co-efficient (Unknown). P´s in the above equation may be conveniently solved by arranging them in matrix from.

Total correlation, say between x_1 and y is thus partitioned follows:

Pyx1= the direct effect of x1 via x_2 on y.

$P_{yx2} r_{x1x2}$= the indirect effect of x1 via x_2 on y.

$P_{yx3} r_{x1x3}$= the indirect effect of x1 via x_3 on y.

3.13 Multivariate analysis

Genetic diversity was estimated following Mahalanobis's (1936) generalized distance (D^2). Selection of parents in hybridization programme based on Mahalanobis's D^2 statistic is more reliable as requisite knowledge of parents in respect of a mass of characteristics is available prior to crossing. Rao (1952) reported that the quantification of genetic diversity through biometrical procedures had made it possible to choose genetically diverse parents for a

successful hybridization program. Statistical analysis such as Mahalanobis D^2 and Canonical Variate Analysis (CVA), which quantify the differences among several quantitative traits are efficient method of evaluating genetic diversity. Mean data of each quantitative character were subjected to both univariate and multivariate analysis. Mean, range, co-efficient of variation (CV) and correlation was estimated using MSTAT computer program. Multivariate analysis *viz.*, Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CLU) and Canonical Variate Analysis (CVA) were done by using GENSTAT program.

3.13.1 Principle component analysis

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

3.13.2 Principle Co-ordinate analysis

Principal coordinate analysis is equivalent to PCA but it is used to calculate inter unit distances. Through the use of all dimensions of P it gives the minimum distance between each pair of the N points using similarity matrix (Digby *et al*., 1989).

3.13.3 Cluster analysis (CA)

To divide the genotypes of a data set into some number of mutually exclusive groups clustering was done using non-hierarchical classification. In GENSTAT, algorithm was used to search for optimal values of chosen criteria. Starting from some initial classification of the genotypes into required number

of groups, the algorithm repeatedly transferred genotypes from one group to another so long as such transfer improved the value of the criterion. When no further transfer can be found to improve the criterion, the algorithm switches to a second stage which examines the effect of swooping two genotypes of different classes and so on.

3.13.4 Canonical variate analysis (CVA)

Canonical Variate Analysis, complementary to D2 statistic, is a sort of multivariate analysis where canonical vectors and roots representing different axes of differentiation and the amount of variation accounted for by each of such axes respectively and derived. Canonical Variate Analysis computed linear combination of original variability that maximized the ratio between ground and within group variations, thereby giving functions of the original variables that could be used to discriminate between the groups. Thus in this analysis, a series of orthogonal transformation was done sequentially for maximizing the ratio of the groups to within group variations.

3.13.5 Calculation of D^2 values

The Mahalanobis's distance (D^2) values are calculated from transformed uncorrelated means of characters according to Rao (1952) and Singh and Chaudhury (1985). The D^2 values were estimated for all possible combinations between genotypes. In simpler form D^2 statastic is defined by the formula

$$D^2 = \sum_i^x d_i^2 = \sum_i^x \left(Y_i^j - Y_j^k\right) \qquad \textbf{(j≠k)}$$

Where,

Y= Uncorrelated variable (character) which varies from i=1 to x

X= Number of characters

Superscript j and k to Y = A pair of any two genotypes.

3.13.6 Computation of average intra-cluster distances

Average intra-cluster distances were calculated by the following formula as suggested by Singh and Chaudhury (1985)

Average intra-cluster distance = $\frac{\sum D_i^2}{n}$

Where,

D_i^2 = the sum of distances between all possible combinations (n) genotypes included in a cluster.

n= number of all possible combinations between the populations in cluster.

3.13.7 Computation of average inter-cluster distances

Average inter-cluster distances were calculated by the following formula as suggested by Singh and Chaudhury (1985)

Average inter-cluster distance = $\frac{\sum D_{ij}^2}{n_i \times n_j}$

$\sum \boldsymbol{D_{ij}^2}$ = The sum of distances between all possible combinations of the populations in clusters i and j.

n_i = Number of populations in cluster i.

n_j = Number of populations in cluster j.

3.13.8 Cluster diagram

Using the values of intra and inter cluster distances (D=$\sqrt{D^2}$), a cluster diagram, was drawn as suggested by Singh and Chaudhury (1985). It gives a brief idea of the pattern of diversity among the genotypes included in a cluster.

CHAPTER IV

RESULTS AND DISCUSSION

The experiment was conducted to identify the breeding values in respect of genotypic effects and comparative performances of different stem amaranth genotypes. The study was carried out to find out the phenotypic and genotypic variability, co-efficient of variation, heritability, genetic advance, genetic advance as percent of mean, correlation, path analysis and genetic diversity among different genotypes to estimate the direct and indirect effect of yield contributing traits on yield. Seventeen characters such as days to first flowering, days to 50% flowering, plant gross weight (g), stem weight (g), 10 leaf weight (g), plant height (cm), stem height (cm), leaf length (cm), leaf breadth (cm), stem breadth (cm), number of branch, number of leaf per branch, root length (cm), root shoot ratio, stem dry weight, thousand seed weight (g) and plant weight without root (g)were studied in respect of thirty-seven genotypes. This chapter comprises the presentation and discussion of the findings obtained from the study. Pictorial differences of the leaf and stem of the genotypes are presented in Plate (2-4). Data pertaining to seventeen yield and its contributing characters were computed and statistically analyzed and the results of the present investigation are presented in this chapter.

4.1 Genetic variability, heritability and genetic advance

The analysis of variance for seventeen different characters of stem amaranth is presented in Table 2. The mean values for each character of all the genotypes are shown in Table 3. Performance of the genotypes is described below for each character. The extent of variation among the genotypes in respect of seventeen characters was studied and mean sum of square, phenotypic variance (σ^2p), genotypic variance (σ^2g), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2b), genetic advance (GA), genetic advance in percent of mean and coefficient of variation (CV) presented in (Table 4). The extent of variability as measured by GCV and PCV

Plate 2. Front side of leaves of thirty-seven genotypes of stem amaranth

Plate 3. Back side of leaves of thirty-seven genotypes of stem amaranth

Plate 4. Stem of thirty-seven genotypes of stem amaranth

Table 2. Analysis of variance (MS Value) for seventeen different characters of stem amaranth

Characters	Mean sum of square		
	Replication (r-1) = 2	Genotype (g-1) = 36	Error (r-1)(g-1) = 72
DFF	0.55	96.91**	9.47
DFPF	12.06	121.32**	5.24
PGW(g)	7787.80	27232.90**	4145.00
SW(g)	147.04	8510.67**	1388.56
10LW(g)	51.14	203.03**	16.23
PH(cm)	1661.84	970.78**	110.75
SH(cm)	1684.22	884.40**	107.72
LL(cm)	52.18	27.44**	7.83
LB(cm)	4.08	8.44**	2.47
SD(cm)	4.09	9.15**	0.70
NBr	1.25	22.23**	0.87
NLBr	37.90	155.48**	14.17
RL(cm)	27.01	26.84**	10.06
RLSH	0.03	0.02**	0.003
SDW(g)	29.82	85.75**	1.41
TSW(g)	0.01	0.02**	0.004
PWWR(g)	1780.20	23405.40**	3111.50

DFF-Days to 1st flowering, DFPF-Days to 50% flowering, PGW(g)- Plant gross weight, SW- Stem weight, 10LW- Ten leaf weight, PH (g)- Plant height, SH- Stem height, LL- Leaf length, LB- Leaf breath, SD- Stem diameter, NBr- Number of branch per plant, NLBr- Number of leaf per branch, RL(cm)- Root length, RLSH- Shoot:Root, SDW(g)- Shoot dry weight, TSW (g)- Thousand seed weight, PWWR (g)- Plant weight without root

* Significant at 5% level of probability

** Significant at 1% level of probability

Table 3. Mean performance of various growth parameter and yield components of seventeen characters of thirty-seven genotypes of stem amaranth

Geno-type	DFF	DFPF	PGW (g)	SW (g)	10 LW (g)	PH (cm)	SH (cm)	LL (cm)	LB (cm)	SD (cm)	NBr	NLBr	RL (cm)	RLSH	SDW (g)	TSW (g)	PWWR (g)
G1	51.00	62.00	303.67	204.33	38.00	74.00	61.00	21.67	6.83	7.17	3.33	19.00	23.47	0.47	12.03	0.64	276.67
G2	35.67	45.33	180.33	116.33	12.33	60.00	45.67	22.33	8.50	6.73	4.00	18.33	19.17	0.42	21.12	0.80	157.67
G3	47.33	57.00	273.67	137.67	26.67	54.33	43.00	15.50	4.67	14.00	9.67	60.00	18.67	0.44	14.66	0.68	185.33
G4	35.00	46.67	352.33	225.33	32.00	71.67	53.00	22.33	8.17	6.40	7.00	23.00	21.07	0.40	21.76	0.77	288.00
G5	43.33	54.67	308.00	155.00	31.00	71.00	54.33	20.67	8.17	6.00	7.33	20.67	19.73	0.36	5.78	0.51	251.33
G6	50.00	62.33	212.33	142.00	21.33	78.33	62.00	24.67	6.57	6.33	2.33	19.00	17.33	0.28	15.49	0.71	173.00
G7	36.00	46.00	356.00	182.00	35.67	80.33	63.00	22.50	7.50	5.67	8.00	17.00	21.00	0.34	7.79	0.77	277.67
G8	45.00	55.67	271.33	140.00	26.00	83.33	64.67	21.00	7.17	5.50	7.33	16.67	18.50	0.29	10.37	0.79	226.33
G9	36.33	46.00	288.00	159.33	29.33	83.00	62.00	25.33	8.33	7.17	1.33	19.67	18.83	0.35	11.22	0.78	262.00
G10	43.33	50.00	273.67	171.00	29.00	84.33	63.33	25.33	8.50	7.90	2.00	18.67	17.00	0.30	17.44	0.73	262.67
G11	52.67	63.33	424.33	261.00	39.00	107.33	93.00	23.67	8.33	8.00	2.33	23.67	20.23	0.22	5.44	0.91	359.67
G12	48.00	67.00	382.67	232.00	41.33	100.00	84.67	25.67	10.67	8.67	5.00	18.33	21.13	0.26	5.72	0.82	338.33
G13	54.00	59.67	338.33	186.00	31.67	98.00	79.67	25.67	7.67	6.50	1.67	22.67	16.00	0.21	5.33	0.79	283.33
G14	48.00	63.33	590.33	261.33	34.00	92.00	67.33	27.00	7.00	7.10	8.33	20.67	18.83	0.31	9.34	0.70	372.33
G15	40.33	60.33	206.67	128.33	18.67	53.67	47.67	19.00	5.67	3.83	8.00	20.00	15.67	0.41	7.92	0.73	174.00
G16	56.00	55.33	378.33	156.33	32.33	86.00	67.00	24.67	12.33	5.73	7.00	17.67	20.33	0.34	8.42	0.80	317.00
G17	48.33	51.67	326.00	172.67	21.33	81.00	69.33	20.33	7.17	6.00	7.67	20.67	15.83	0.23	11.23	0.90	383.00
G18	46.33	46.00	265.67	117.00	19.00	70.00	51.33	22.67	7.00	5.33	7.00	20.67	16.00	0.31	8.26	0.83	220.00

Table 3. (Cont'd)

Geno -type	DFF	DFPF	PGW (g)	SW (g)	10 LW (g)	PH (cm)	SH (cm)	LL (cm)	LB (cm)	SD (cm)	NBr	NLBr	RL (cm)	RLSH	SDW (g)	TSW (g)	PWWR (g)
G19	43.33	56.67	377.00	195.00	39.33	80.00	61.00	27.33	10.67	7.57	3.00	20.00	16.17	0.26	9.46	0.85	348.67
G20	44.33	46.00	329.33	155.00	37.33	79.67	65.00	20.33	7.00	5.67	1.67	21.67	18.67	0.29	12.83	0.67	239.00
G21	54.33	62.00	340.67	156.00	32.67	73.67	55.67	25.00	9.00	6.33	1.67	23.00	14.87	0.28	12.70	0.83	287.33
G22	53.00	50.67	350.33	165.33	38.00	68.67	50.33	22.00	7.33	5.63	5.00	20.33	16.33	0.33	20.26	0.72	281.00
G23	45.33	61.00	397.00	200.00	38.33	81.00	67.33	19.33	7.60	6.83	2.33	22.00	21.33	0.33	12.06	0.88	333.67
G24	37.33	50.33	393.33	200.33	47.33	77.00	62.00	21.33	7.33	6.83	2.67	20.00	20.33	0.33	15.09	0.84	307.33
G25	48.33	54.33	415.67	213.67	41.67	80.67	65.00	23.00	8.33	6.67	2.00	19.67	17.17	0.26	23.19	0.84	329.67
G26	51.67	57.33	234.00	118.00	15.67	40.67	25.67	16.00	5.17	2.83	8.00	17.67	9.67	0.38	4.82	0.84	210.67
G27	53.00	55.67	473.33	221.00	21.67	90.00	75.00	24.67	7.50	6.83	5.00	23.67	16.17	0.22	6.23	0.94	311.00
G28	43.33	64.00	290.00	148.33	32.33	78.33	61.67	25.33	7.67	5.73	2.33	18.00	14.83	0.24	8.80	0.80	199.67
G29	42.00	50.00	251.67	149.00	42.00	91.00	68.33	28.67	10.67	7.67	3.00	17.67	17.00	0.30	13.45	0.72	180.33
G30	42.67	54.00	378.33	234.67	29.67	117.33	104.33	25.67	9.00	6.73	7.67	18.67	17.17	0.16	6.07	0.76	391.00
G31	51.33	56.67	362.67	282.33	29.00	103.33	87.33	26.00	10.00	6.83	9.00	21.67	14.83	0.17	14.67	0.66	362.67
G32	46.00	60.33	554.33	250.33	18.00	131.33	111.67	24.67	9.00	10.00	7.67	27.33	17.00	0.15	15.44	0.71	572.00
G33	43.33	61.33	220.67	109.33	27.00	82.33	63.67	22.67	8.67	5.33	6.33	13.33	12.17	0.24	7.13	0.69	187.33
G34	49.00	59.67	372.67	255.67	34.33	111.00	89.67	28.67	11.00	7.33	7.33	17.67	22.33	0.26	17.78	0.77	359.00
G35	52.67	57.33	555.67	303.00	25.00	108.33	92.67	24.33	8.00	7.50	7.33	29.67	23.00	0.26	5.40	0.78	483.33
G36	42.00	64.00	431.00	295.67	36.00	89.33	74.33	24.33	11.00	6.33	2.00	17.00	20.50	0.30	21.87	0.79	361.33
G37	46.67	45.67	339.00	168.00	29.67	79.00	63.33	25.00	9.67	6.17	9.00	20.00	21.83	0.29	9.59	0.64	310.67
Min	35.00	45.33	180.33	109.33	12.33	40.67	25.67	15.50	4.67	2.83	1.33	13.33	9.67	0.15	4.82	0.51	157.67
Max	56.00	67.00	590.33	303.00	47.33	131.33	111.67	28.67	12.33	14.00	9.67	60.00	23.47	0.47	23.19	0.94	572.00
Mean	46.12	55.66	345.90	188.33	30.64	83.54	66.92	23.36	8.24	6.73	5.20	21.23	18.11	0.30	11.79	0.77	293.62

DFF-Days to 1st flowering, DFPF-Days to 50% flowering, PGW(g)- Plant gross weight, SW- Stem weight, 10LW- Ten leaf weight, PH (g)- Plant height, SH- Stem height, LL- Leaf length, LB- Leaf breath, SD- Stem diameter, NBr- Number of branch per plant, NLBr- Number of leaf per branch, RL (CM)- Root length, RLSH- Shoot:Root, SDW(g)- Shoot dry weight, TSW (g)- Thousand seed weight, PWWR (g)- Plant weight without root

Table 4. Estimation of genetic parameters in seventeen characters of ten genotypes in stem Amaranth

Parameters	Mean	σ^2p	σ^2g	σ^2e	PCV	GCV	ECV	Heri-tability	Genetic Advance (5%)	Genetic Advance (% of mean)	CV (%)
Days to First Flowering	46.12	38.61	29.15	9.47	13.47	11.71	1.77	75.49	9.66	20.95	6.67
Days to 50% Flowering	55.66	43.93	38.70	5.24	11.91	11.18	0.73	88.08	12.03	21.61	4.11
Plant Gross Weight (g)	345.90	11840.97	7695.97	4145.00	31.46	25.36	6.10	64.99	145.69	42.12	18.61
Stem Weight (g)	188.33	3762.60	2374.04	1388.56	32.57	25.87	6.70	63.10	79.73	42.33	19.79
10 Leaf Weight (g)	30.64	78.49	62.27	16.23	28.92	25.75	3.16	79.33	14.48	47.25	13.15
Plant Height (cm)	83.54	397.43	286.68	110.75	23.86	20.27	3.60	72.13	29.62	35.46	12.6
Stem Height (cm)	66.92	366.61	258.89	107.72	28.61	24.04	4.57	70.62	27.85	41.62	15.51
Leaf Length (cm)	23.36	14.36	6.54	7.83	16.22	10.95	5.28	45.51	3.55	15.21	11.98
Leaf Breadth (cm)	8.24	4.46	1.99	2.47	25.63	17.13	8.50	44.66	1.94	23.58	19.06
Stem diameter (cm)	6.73	3.52	2.82	0.70	27.88	24.96	2.92	80.15	3.10	46.03	12.42
Number of Branch per plant	5.20	7.99	7.12	0.87	54.38	51.33	3.05	89.08	5.19	99.80	17.97
Number of Leaf per Branch	21.23	61.27	47.10	14.17	36.88	32.34	4.54	76.88	12.40	58.40	17.73
Root Length (cm)	18.11	15.66	5.59	10.06	21.84	13.05	8.79	35.71	2.91	16.07	17.52
Root shoot ratio	0.30	0.01	0.00	0.00	30.06	22.72	7.34	57.14	0.11	35.38	19.69
Stem Dry Weight (g)	11.79	29.52	28.11	1.41	46.09	44.98	1.11	95.23	10.66	90.42	10.07
Thousand Seed Weight (g)	0.77	0.01	0.01	0.00	13.25	10.15	3.10	58.66	0.12	16.01	8.51
Plant weight without root (g)	293.62	9876.13	6764.63	3111.50	33.85	28.01	5.83	68.49	140.22	47.76	19

σ^2p: Phenotypic variance PCV: Phenotypic coefficient of variation GA (5%): Genetic advance

σ^2g: Genotypic variance GCV: Genotypic co-efficient of variation GAM: Genetic advance (% of mean)

σ^2e: Environmental variance ECV: Environmental co-efficient of variation CV (%) = coefficient of variation

provides information regarding the relative amount of variation in different characters. Selection of traits based on heritability and genetic advance as percent of mean is of great importance to the breeder for making criteria for improvement in a complex character (Tusharkumar *et al*., 2019). The data were analyzed and possible interpretations are given here based on established scales. According to Deshmukh *et al.* (1986) PCV and GCV can be categorized as low (<10%), moderate (10-20%) and high (>20%). Wide difference between PCV and GCV for the traits implies their susceptibility to environmental fluctuation, whereas narrow difference suggested their relative resistance to environmental variation. Heritability is the percentage of phenotypic variance that is attributed to genetic variance. Heritability of a trait is considered as vary high or high at values 80% or more and moderate when it ranged from 40-80% and when it is less than 40%, it is low (Singh, 2009). The estimates of heritability alone fail to indicate the response to selection (Johnson *et al*., 1955). Therefore, the heritability estimates appear to be more meaningful when accompanied by estimates of genetic advance and the genetic advance at percentage of mean. Deshmukh *et al.* (1986) classified genetic advance as percentage of mean as low (<10%), moderate (10-20%) and high (>20%).

4.1.1 Days to first flowering

Highly significant variation was observed among all the genotypes (96.91) studied for this character (Table 2). The mean value of days to first flowering was observed significantly the lowest in G4 (35.00 days) (Table 3) indicating first flower emerges earlier than other genotypes after sowing. The highest days took to first flowering was found in G16 (56.00 days). Genotypic and phenotypic variance of days to first flowering was observed 29.15 and 38.61, respectively with high differences between them indicating that they were more responsive to environmental factor for their phenotypic expression and estimates of genotypic co-efficient of variation and phenotypic co-efficient of variation were moderate(11.71% and 13.47% respectively) (Table 4)indicated that there was moderate variability and offering scope for selection of desired variability.Days to first flowering showed relatively high heritability (75.49%)

with high genetic advance as percentage of mean (20.95%) indicated that this character was under additive gene action and there were excellent chances of effective selection for improvement of these traits.

4.1.2 Days to 50% flowering

Highly significant variation was observed among all the genotypes (121.32) studied for this character (Table 2). The mean value of Days to 50% flowering was observed significantly the lowest in G2 (45.33 days) (Table 3). The highest days took to 50% flowering was found in G12 (67.00 days). Genotypic and phenotypic variance of days to 50% flowering was observed 43.93 and 38.70, respectively with moderate differences between them indicating that they were moderately responsive to environmental factor for their phenotypic expression. The GCV (11.18 %) and PCV (11.91 %) were moderate indicating moderate variability among the genotypes (Table 4). Akaneme and Ani (2013) reported slightly different result where they found high GCV and PCV. However, in both cases moderate or high, there are scope of selection for this character. Narrow difference between GCV and PCV suggested their relative resistance to environmental variation. Days to 50% flowering showed high heritability (88.08%) with high genetic advance as percentage of mean (21.61%) indicating the presence of additive gene action and scope for improvement of the trait through hybridization and selections. The results regarding high heritability along with high genetic advance are in accordance with that of Venkatesh *et al*. (2014) and Akaneme and Ani (2013) for days to 50% flowering. GCV and PCV that were sharing value equally and well supported by high heritability value will greatly important for plant development program (Anas *et al*., 2013).

4.1.3 Plant gross weight (g)

Highly significant variation was observed among all the genotypes (27232.90) studied for this character (Table 2). The mean value of plant gross weight was observed significantly the lowest in G2 (180.33 g) (Table 3). The highest plant gross weight was found in G14 (590.33 g). Genotypic and phenotypic variance of plant gross weight was observed 11840.97and 7695.97, respectively with

high differences between them indicating that they were more responsive to environmental factor for their phenotypic expression and values of genotypic co-efficient of variation and phenotypic co-efficient of variation were high (25.36% and 31.46% respectively) which indicated high variability among the genotypes (Table 4). Plant gross weight showed moderately high heritability (64.99%) with high genetic advance (145.69) and genetic advance in percentage of mean (42.12%) indicating additive gene effect is present and selection could be effective for this trait.

4.1.4 Stem weight (g)

Highly significant variation was observed among all the genotypes (8510.67) studied for this character (Table 2). The mean value of stem weight was observed significantly the lowest in G33 (109.33g) (Table 3). The highest weight of stem weight was found in G35 (303.00 g). Genotypic and phenotypic variance of stem weight was observed 2374.04 and 3762.60 respectively (Table 4), with high differences between them indicating that they were more responsive to environmental factor for their phenotypic expression. High genotypic and phenotypic coefficient variation (25.87% and 32.57% respectively) indicated that there was high variability offering ample scope for selection of desired variability. Genotypic co-efficient of variation and phenotypic co-efficient of variation were indicated wide differences between them and implies their susceptibility to environmental fluctuation. stem weight showed high heritability (63.10%) with high genetic advance (79.73) and genetic advance in percentage of mean (42.33%) indicating additive gene effect is present and selection can be effective for the trait. Anuja and Kader (2007) also found higher PCV than GCV as well as high heritability along with high genetic advance as percent of mean for stem weight. Ahammed *et al.* (2012) also found high heritability along with high genetic advance for stem weight. So this character in amaranth is important in selection as it is expected to be controlled by additive genes.

4.1.5 Leaf weight (g)

Highly significant variation was observed among all the genotypes (203.03) studied for this character (Table 2). The mean value of Ten Leaf Weight was observed significantly the lowest in G2 (12.33 g) (Table 3). The highest weight of Ten Leaf Weight was found in G24 (47.33 g). Genotypic and phenotypic variance of ten leaf weight were observed 62.27 and 78.49, respectively with high differences between them indicating that they were more responsive to environmental factor for their phenotypic expression. The estimates of genotypic co-efficient of variation and phenotypic co-efficient of variation were high(25.75% and 28.92% respectively) indicating high variability among the genotypes offering ample scope for selection of desired variability. Diwan *et al.* (2017) and Anuja and Kader (2007) also reported high GCV and PCV for this character. Wide differences between GCV and PCV in the present study indicated high environmental influence on the genes controlling this trait. Ten leaf weight showed high heritability (79.33%) with high genetic advance in percentage of mean (47.25%) indicated that these characters were under additive gene action and there were excellent chances of effective selection for improvement of these traits. Ahammed *et al*. (2012) andAnuja and Kader (2007) also reported high heritability along with high genetic advance in percent of mean for leaf weight.

4.1.6 Plant height (cm)

Highly significant variation was observed among all the genotypes (970.78) studied for this character (Table 2). The mean value of plant height was observed significantly the lowest in G16 (40.67 cm) (Table 3). The highest value of plant height was found in G32 (131.33 cm). Genotypic and phenotypic variance of plant height was observed 286.68 and 397.43, respectively (Table 4). Phenotypic variance is higher (23.86%) than the genotypic variation (20.27%) indicating the environmental influence on the genes controlling this trait. The result of high GCV and PCV (>20 %) for this trait in amaranth agreed with the result of Shrivastav *et al.* (2017). High GCV and PCV indicated considerable amount of variability among the genotypes and this trait needs to

be given importance for selection. Venkatesh *et al.* (2014)also reported the similar result of high GCV and PCV. Wide gap of genotypic co-efficient of variation and phenotypic co-efficient of variation implies their susceptibility to environmental fluctuation. Plant height showed relatively high heritability (72.13%) with high genetic advance (29.62) and genetic advance in percentage of mean (35.46%). Hence, this character need to be given more importance in selection as this is expected to be controlled by additive genes. Tiwari *et al.* (2018), Shrivastav *et al.* (2017) and Venkatesh *et al.* (2014) reported the similar result of high heritability along with high genetic advance as percent of mean for this trait in amaranth.

4.1.7 Stem height (cm)

Highly significant variation was observed among all the genotypes (884.40) studied for this character (Table 2). The mean value of Stem height was observed significantly the lowest in G26 (25.67 cm) (Table 3). The highest stem height was found in G32 (111.67 cm). Genotypic and phenotypic variance of stem height was observed 258.89 and 366.61, respectively with high differences between them indicating that they were more responsive to environmental factor for their phenotypic expression. Phenotypic coefficient of variation was greater (28.61%) than the genotypic coefficient of variation (24.04%) for this trait (Table 4) suggesting the environment influences on the expression of this trait. Since PCV estimates the effects of genotypes and environment, higher PCV versus GCV indicates a significant contribution of environment and genotypes by environment interaction in the expression of this trait. Stem height showed high heritability (70.62%) with high genetic advance (27.85) and genetic advance in percentage of mean (41.62%) indicating additive gene effect is present and selection can be effective for the trait.

4.1.8 Leaf length (cm)

Highly significant variation was observed among all the genotypes (27.44) studied for this character (Table 2). The mean value of leaf length was observed significantly the lowest in G3 (15.50 cm) (Table 3). The highest value

of Leaf length was found in both of G29 and G32 (28.67 cm). Genotypic and phenotypic variance of Leaf length were observed 6.54 and 14.36, respectively with high differences between them indicating that they were more responsive to environmental factor for their phenotypic expression and wide gap of genotypic co-efficient of variation and phenotypic co-efficient of variation (10.95% and 16.22% respectively) indicated the influence of environment on the expression of the genes controlling this trait (Table 4). Leaf length showed moderate heritability (45.51%) with low genetic advance (3.55) and genetic advance in percentage of mean (15.21%) indicating presence of non-additive gene action and selection would not be effective for the character.

4.1.9 Leaf breadth (cm)

Highly significant variation was observed among all the genotypes (8.44) studied for this character (Table 2). The mean value of leaf breadth was observed significantly the lowest in G3 (4.67 cm) (Table 3). The highest value of Leaf breadth was found in G16 (12.33 cm). The genotypic and phenotypic variance was observed 1.99 and 4.46, respectively for leaf breadth with high environmental influence. The phenotypic co-efficient of variation (25.63) was higher than the genotypic co-efficient of variation (17.13), indicated environmental influence on the expression of genes controlling this trait(Table 4). Leaf breadth showed moderate heritability (44.66%) with low genetic advance (1.94) and genetic advance in percentage of mean (23.58%) indicating presence of non-additive gene action and selection may be ineffective for the character.

4.1.10 Stem diameter (cm)

Highly significant variation was observed among all the genotypes (9.15) studied for this character (Table 2). The mean value of stem breadth was observed significantly the lowest in G26 in (2.83cm) (Table 3). The highest value of stem diameter was found in G3 (14.00cm). Genotypic and phenotypic variance of stem diameter was observed 2.82 and 3.52, respectively suggested no influence of environment on the expression of the genes controlling this

trait. The estimates of high genotypic co-efficient of variation and phenotypic co-efficient of variation (24.96% and 27.88% respectively) indicated high variability among the genotypes (Table 4). The result of high GCV and PCV were in accordance with that of Venkatesh *et al.* (2014) for stem diameter. Stem diameter showed high heritability (80.15%) along with high genetic advance in percentage of mean (46.03%) indicating the presence of additive gene action and improvement through selection would be effective for the trait.

4.1.11 Number of branches per plant

Highly significant variation was observed among all the genotypes (22.23) studied for this character (Table 2). The mean value of number of branch was observed significantly the lowest in G9 (1.33) (Table 3). The highest value of number of branch was found in G9 (9.67). Genotypic and phenotypic variance of no of branch were observed 7.12 and 7.99, respectively with low differences between them indicating that they were less responsive to environmental factor for their phenotypic expression. High GCV (51.33 %) and PCV (54.38 %) indicated the high variability among the genotypes offering ample scope for selection of desired variability(Table 4). The results are in accordance with that of Shrivastav *et al.* (2017) and Ahammed *et al.* (2012) for high GCV and PCV for this character. Narrow gap between genotypic co-efficient of variation and phenotypic co-efficient of variation indicated the minimal influence of environment on the genes controlling this trait. Number of branch showed high heritability (89.08%) with high genetic advance in percentage of mean (99.80%) indicating the presence of additive gene action and improvement through selection could be effective for the trait. Similar results were reported by Shrivastav *et al.*(2017) for high heritability along with high genetic advance for this trait.

4.1.12 Number of leaves per branch

Highly significant variation was observed among all the genotypes (155.48) studied for this character (Table 2).The mean value of number of leaf per branch was observed significantly the lowest in G33 (13.33) (Table 3). The

highest value of number of Leaf per branch was found in G3 (60.00). Genotypic and phenotypic variance of number of leaf per branch was observed 47.10 and 61.27, respectively with high differences between them indicating that they were more responsive to environmental factor for their phenotypic expression. The phenotypic co-efficient of variation (36.88) was higher than the genotypic co-efficient of variation (32.34),indicates that the apparent variation is not only due to genotypes but also due to influence of the environment (Table 4).Both GCV and PCV were high (>20%) indicating high variability among the genotypes. The results of Anuja and Kader (2007)in amaranth agreed with the result of the present study for high GCV in amaranth. In his experiment they also found higher PCV than GCV due to the environmental influence. Number of leaf per branch showed high heritability (76.88%) along with high genetic advance in percentage of mean (58.40%) indicated that this trait was controlled by additive gene and selection for this character would be effective. Anuja and Kader (2007) observed similar result of high heritability and high genetic advance as percent of mean in their experiment.

4.1.13 Root length (cm)

Highly significant variation was observed among all the genotypes (26.84) studied for this character (Table 2). The mean value of root length was observed significantly the lowest in G26 (9.67 cm) (Table 3). The highest value of root length was found in G1 (23.47 cm). Genotypic and phenotypic variance of root length were observed 5.59 and 15.66, respectively with high differences between them indicating that they were more responsive to environmental factor for their phenotypic expression. Phenotypic coefficient of variation was higher (21.84 %) than the corresponding genotypic coefficients of variation (13.05 %) for root length indicating considerable influence of environment on the expression of genes controlling this trait(Table 4). The results are in accordance with that of Anuja and Kader (2007). Root length showed low heritability (35.71%) with low genetic advance (2.91) and genetic advance in percentage of mean (16.07%) indicating presence of non-additive gene action

and improvement through selection can't be effective. The results of Anuja and Kader (2007) contradict with that of present study. They found high heritability with high genetic advance as percent of mean in their experiment.

4.1.14 Root shoot ratio

Highly significant variation was observed among all the genotypes (0.02) studied for this character (Table 2). The mean value of root shoot ratio was observed significantly the lowest in G32 (0.15) (Table 3). The highest value of root shoot ratio mature was found in G1 (0.47). Genotypic and phenotypic variance of root shoot ratio were observed 0.00 and 0.01, respectively with negligible difference between them indicating that they were not responsive to environmental factor for their phenotypic expression. High genotypic co-efficient of variation and phenotypic co-efficient of variation (22.72% and 30.06% respectively) indicated that the variability is high among the genotypes and adequate scope is present for selection (Table 4). Root shoot ratio showed moderate heritability (57.14%) with low genetic advance (0.11) and genetic advance in percentage of mean (35.38%) indicating presence of non-additive gene action and improvement through selection can't be effective.

4.1.15 Stem dry weight (g)

Highly significant variation was observed among all the genotypes (85.75) studied for this character (Table 2). The mean value of stem dry weight was observed significantly the lowest in G26 (4.82g) (Table 2). The highest value of stem dry weight was found in G25 (23.19 g). Genotypic and phenotypic variance of stem dry weight were observed 28.11 and 29.52, respectively with low differences between them indicating that they were less responsive to environmental factor for their phenotypic expression and values of genotypic co-efficient of variation and phenotypic co-efficient of variation were 44.98% and 46.09% respectively (Table 4). This character exhibited high estimates of phenotypic as well as genotypic coefficient of variation indicating high variability among the genotypes and substantial scope of improvement in this trait in present material through selection. Stem dry weight showed high

heritability (95.23%) with genetic advance in percentage of mean (90.42%) indicating the presence of additive gene action and selection could be effective for the improvement of this character.

4.1.16 Thousand seed weight (g)

Highly significant variation was observed among all the genotypes (0.02) studied for this character (Table 2). The mean value of thousand seed weight was observed significantly the lowest in G5 (0.51 g) in (Table 2). The highest value of thousand seed weight was found in G27 (0.94 g). Genotypic and phenotypic variance of thousand seed weight were observed 0.01 and 0.01, respectively without any differences between them indicating that there is no environmental influence on the expression of genes controlling this trait. The estimates of phenotypic co-efficient of variation was higher than genotypic co-efficient of variation and were 13.25% and 10.15% respectively which indicated that the apparent variation is not only due to the genotypes but also due to the influence of environment (Table 4). Parveen *et al*. (2013) found high GCV and PCV (>20 %) for this character. Thousand seed weight showed moderate heritability (58.66%) with low genetic advance (0.12) and genetic advance in percentage of mean (16.01%) indicating presence of non-additive gene action and improvement through selection can't be effective. This result contradicts with the result of Parveen *et al.* (2013) where they found maximum values of PCV, GCV, heritability and GA for the character of thousand seed weight.

4.1.17 Plant weight without root (g)

Highly significant variation was observed among all the genotypes (23405.40) studied for this character (Table 2). The mean value of plant weight without root (g) was observed significantly the lowest in G2 (157.67 g) in (Table 2). The highest value of plant weight without root (g) was found in G32 (572.00 g). Genotypic and phenotypic variance of plant weight without root (g) were observed 6764.63 and 9876.13, respectively. The phenotypic variance is higher than the genotypic variance indicating considerable amount of environmental

influence on the expression of the genes controlling this trait. The estimates of genotypic co-efficient of variation and phenotypic co-efficient of variation were high (28.01% and 33.85% respectively)indicating that there was high variability among the genotypes offering enough scope for selection of desired variability (Table 4). Similar high GCV and PCV was found in the result of Anuja and Kader (2007). Selection of traits based on heritability and genetic advance as percent of mean is of great importance to the breeder for making criteria for improvement in a complex character. Plant weight without root (g) showed moderately high heritability (68.49%) with high genetic advance (140.22) and genetic advance in percentage of mean (47.76%) suggesting additive gene effect is present and selection could be effective for the trait. Similar results of high heritability along with high genetic advance (>20%) was reported by Shrivastav *et al.* (2017), Ahammed *et al*. (2012) and Anuja and Kader (2007) for yield per plant.

4.2 CORRELATION ANALYSIS

Improvement of a particular character in all the breeding programs can be achieved by indirect selection via different characters. This wants a good understanding of the association of various characters with the target character and among the different characters themselves. It is necessary to have the estimates of correlation of yield with different characters that the genotype might be assessed visually. The makeup and constitution correlation reveals the extent of association between completely different characters, thus, it helps to base choice procedure to a needed balance, once two opposite fascinating characters moving the principal characters are being selected.

Simple correlation was partitioned into phenotypic (that can be directly observed), genotypic (inherent association between characters) components as suggested by (Singh and Chaudhary, 1985). As we know yield is a complex product being influence by several inter dependable quantitative characters. So selection may not be effective unless the other contributing components influence the yield directly or indirectly. When selection pressure is applied for

improvement of any character highly associated with yield, it simultaneously affects a number of other correlated characters. Hence knowledge regarding association of character with yield and among themselves provides guideline to the plant breeders for making improvement through selection with a clear understanding about the contribution in respect of establishing the association by genetic and non-genetic factors (Dewey and Lu, 1959).

A positive correlation happens because of coupling section of linkage and correlation arises because of repulsion section of linkage of genes dominant completely different traits. No correlation indicates that genes involved are situated so much apart on identical chromosome or they're situated on completely different bodies. Yield being a fancy character is governed by an outsized range of genes. The influence of every character on yield might be well-known through correlation studies with a view to see the extent and nature of relationships prevailing among yield and yield attributing characters. So, the constitution and phenotypic correlation co-efficient values for seventeen characters in stem amaranth genotypes studied are given in (Table 5).

4.2.1 Days to first flowering

Days to First Flowering showed highly significant and positive correlation with DFPF (G=0.516, P=0.396), plant gross weight (G=0.343, P=0.206), stem weight (G=0.222), Plant Height (G=0.216), stem height (G=0.226) and plant weight without root (G=0.304, P=0.211). It also observed that highly significant but negative correlation with root length (G=-0.228), root shoot ratio (G=-0.385, P=-0.220) and stem dry weight (G=-0.281, P=-0.242). Non-significant and positive correlation with stem weight (P=0.148), plant height (P=0.171), stem height (P=0.178), leaf length (G=0.156), leaf breadth (G=0.056, P=0.019), stem breadth (G=0.045,P=0.025), no of branch (G=0.054,P=0.044), no of leaf per branch (G=0.174,P=0.135) and thousand seed weight (G=0.139, P=0.104) and non-significant but negative correlation ten leaf weight (G=-0.032, P=-0.014), Leaf length (P=-0.001) and root length (P=-0.066).

Table 5. Genotypic and phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype stem Amaranth

character		DFF	DFPF	PGW (g)	SW (g)	10LW (g)	PH(cm)	SH(cm)	LL(cm)	LB(cm)	SD(cm)	NBr	NLBr	RL(cm)	RLSH	SDW (g)	TSW(g)
DFPF	G	0.516**															
	P	0.396**															
PGW (g)	G	0.343**	0.304**														
	P	0.206*	0.207*														
SW (g)	G	0.222*	0.379**	0.850**													
	P	0.148^{NS}	0.273**	0.788**													
10LW (g)	G	-0.032^{NS}	0.107^{NS}	0.276**	0.323**												
	P	-0.014^{NS}	0.104^{NS}	0.311**	0.347**												
PH(cm)	G	0.216*	0.269**	0.751**	0.831**	0.231*											
	P	0.171^{NS}	0.260**	0.500**	0.558**	0.167NS											
SH(cm)	G	0.226*	0.308**	0.738**	0.866**	0.204*	0.987**										
	P	0.178^{NS}	0.290**	0.482**	0.550**	0.127NS	0.974**										
LL(cm)	G	0.157^{NS}	0.129^{NS}	0.426**	0.553**	0.311**	0.776**	0.672**									
	P	-0.001^{NS}	0.107^{NS}	0.243**	0.301**	0.258**	0.560**	0.474**									
LB(cm)	G	0.056^{NS}	0.072^{NS}	0.324**	0.509**	0.400**	0.674**	0.627**	0.818**								
	P	0.019^{NS}	0.056^{NS}	0.172^{NS}	0.242**	0.314**	0.399**	0.330**	0.646**								
SD(cm)	G	0.045^{NS}	0.160^{NS}	0.309**	0.325**	0.155NS	0.345**	0.352**	0.034^{NS}	0.039^{NS}							
	P	0.025^{NS}	0.115^{NS}	0.263**	0.266**	0.169NS	0.291**	0.291**	0.168^{NS}	0.106^{NS}							
NBr	G	0.054^{NS}	-0.098^{NS}	0.099^{NS}	0.049^{NS}	-0.453**	-0.009^{NS}	0.013^{NS}	-0.283**	-0.157^{NS}	0.024^{NS}						
	P	0.044^{NS}	-0.095^{NS}	0.093^{NS}	0.027^{NS}	-0.399**	-0.005^{NS}	0.020^{NS}	-0.179^{NS}	-0.094^{NS}	0.042^{NS}						
NLBr	G	0.174^{NS}	0.044^{NS}	0.155^{NS}	0.070^{NS}	-0.144^{NS}	-0.168^{NS}	-0.113^{NS}	-0.541**	-0.481**	0.790**	0.267**					
	P	0.135^{NS}	0.047^{NS}	0.101^{NS}	0.023^{NS}	-0.094^{NS}	-0.009^{NS}	0.031^{NS}	-0.211*	-0.274**	0.713**	0.253**					
RL(cm)	G	-0.228*	-0.092^{NS}	0.355**	0.532**	0.476**	0.394**	0.419**	0.194*	0.353**	0.402**	-0.039^{NS}	0.114^{NS}				
	P	-0.066^{NS}	-0.068^{NS}	0.360**	0.379**	0.339**	0.157^{NS}	0.163^{NS}	0.096^{NS}	0.176^{NS}	0.277**	0.009^{NS}	0.105^{NS}				
RLSH	G	-0.385**	-0.270**	-0.574**	-0.585**	-0.068^{NS}	-0.824**	-0.804**	-0.677**	-0.509**	-0.064^{NS}	0.035^{NS}	0.246**	0.150^{NS}			
	P	-0.220*	-0.238*	-0.280**	-0.265**	-0.014^{NS}	-0.727**	-0.739**	-0.414**	-0.259**	-0.031^{NS}	0.053^{NS}	0.108^{NS}	0.351**			
SDW (g)	G	-0.281**	-0.242**	-0.057^{NS}	0.123^{NS}	0.143^{NS}	-0.098^{NS}	-0.128^{NS}	0.040^{NS}	0.155^{NS}	0.215*	-0.244**	0.062^{NS}	0.201*	0.234*		
	P	-0.242**	-0.216*	-0.042^{NS}	0.091^{NS}	0.125^{NS}	-0.095^{NS}	-0.122^{NS}	0.024^{NS}	0.113^{NS}	0.167^{NS}	-0.246**	0.031^{NS}	0.127^{NS}	0.176^{NS}		
TSW (g)	G	0.139^{NS}	0.107^{NS}	0.166^{NS}	0.096^{NS}	0.018^{NS}	0.091^{NS}	0.111^{NS}	0.111^{NS}	0.119^{NS}	-0.090^{NS}	-0.341**	-0.102^{NS}	-0.168^{NS}	-0.290**	-0.079^{NS}	
	P	0.104^{NS}	0.061^{NS}	0.220*	0.154^{NS}	0.008^{NS}	0.026^{NS}	0.054^{NS}	-0.046^{NS}	-0.033^{NS}	-0.118^{NS}	-0.240*	-0.118^{NS}	-0.092^{NS}	-0.172^{NS}	-0.070^{NS}	
PWWR (g)	G	0.304**	0.248**	0.891**	0.835**	0.123^{NS}	0.845**	0.865**	0.412**	0.486**	0.300**	0.180^{NS}	0.060^{NS}	0.317**	-0.679**	-0.018^{NS}	0.164^{NS}
	P	0.211*	0.176^{NS}	0.841**	0.788**	0.175^{NS}	0.630**	0.630**	0.260**	0.248**	0.249**	0.148^{NS}	0.057^{NS}	0.294**	-0.412**	-0.022^{NS}	0.191*

DFF-Days to 1st flowering, DFPF-Days to 50% flowering, PGW(g)- Plant gross weight, SW- Stem weight, 10LW- Ten leaf weight, PH (cm)- Plant height, SH- Stem height, LL- Leaf length, LB- Leaf breath, SD- Stem Diameter, NBr- Number of branch per plant, NLBr- Number of leaves per branch, RL (cm)- Root length, RLSH- Shoot:Root, SDW(g)- Shoot dry weight, TSW (g)- Thousand seed weight, PWWR (g)- Plant weight without root * Significant at 5% level of probability ** Significant at 1% level of probability

4.2.2 Days to 50% flowering

Days to fifty percent flowering showed highly significant and positive correlation with plant gross weight (G=0.304, P=0.207), stem weight (G=0.379, P=0.273), stem weight (G=0.269), plant height (G=0.260), stem height (G=0.308, P=0.290) and plant weight without root (G=0.248). It also observed that highly significant but negative correlation with root shoot ratio (G=-0.270, P=-0.238) and stem dry weight (G=-0.242, P=-0.216). Non-significant and positive correlation with ten leaf weight (G=0.107, P=0.104), leaf length (G=0.129, P=0.107), leaf breadth (G=0.072, P=0.056), stem breadth (G=0.160, P=0.115), no of leaves per branch (G=0.044, P=0.047), thousand seed weight (G=0.107, P=0.061) and plant weight without root (P=0.176) and non-significant but negative correlation no of branch per plant (G=-0.098, P=-0.095) and root length (G=-0.092, P=-0.068).

4.2.3 Plant gross weight (g)

Plant gross weight showed highly significant and positive correlation with stem weight (G=0.850, P=0.788), Ten leaves weight (G=0.076, P=0.311), plant height (G=0.751, P=0.500), stem height (G=0.738, P=0.482), leaf length (G=0.426, P=0.243), leaf breadth (G=0.324, P=0.309), stem breadth (G=0.309, P=0.263), root length (G=0.355, P=0.360), thousand seed weight (P=0.220) and plant weight without root (G=0.891, P=0.841). It also observed that highly significant but negative correlation with root shoot ratio (G=-0.574, P=-0.280). Non-significant and positive correlation with leaf breadth (P=0.172), no of branch per plant (G=0.099, P=093), no of leaves per branch (G=0.155, P=0.101) and thousand seed weight (G=0.166) and non-significant but negative correlation stem dry weight (G=-0.057, P=-0.042). As mentioned above, plant gross weight showed highly significant positive correlation with plant weight without root indicated that yield could be improved in stem amaranth if selection is based on plant gross weight. Diwan *et al*. (2017) found similar highly significant and positive correlation between plant weight and yield.

4.2.4 Stem weight (g)

Stem weight showed highly significant and positive correlation with ten leaf weight (G=0.323, P=0.347), plant height (G=0.831, P=0.558), stem height (G=0.866, P=0.550), leaf length (G=0.553, P=0.301), leaf breadth (G=0.509, P=0.242), stem breadth (G=0.325, P=0.266), root length (G=0.532, P=0.379) and plant weight without root (G=0.835, P=0.788). It also observed that highly significant but negative correlation with root shoot ratio (G=-0.588, P=-0.265). Non-significant and positive correlation with no of branch (G=0.049, P=0.027), no of leaf per branch (G=0.070, P=0.023), thousand seed weight (G=0.096, P=0.176) and stem dry weight (G=0.123, P=0.091).A significant and positive correlation was also reported by Ahammed *et al*. (2012) between stem weight and yield in amaranth both at genotypic and phenotypic level. Hence, selection based on stem weight trait would give better response for the improvement in marketable yield in stem amaranth.

4.2.5 Leaf weight (g)

Ten leaf weight showed highly significant and positive correlation with plant height (G=0.231), stem height (G=0.204), leaf length (G=0.311, P=0.258), leaf breadth (G=0.400, P=0.314) and root length (G=0.476, P=0.339). It also observed that highly significant but negative correlation with no of branch (G=-0.453, P=-0.399). Non-significant and positive correlation with plant height (P=0.167), stem height (P=0.127), stem breadth (G=0.155, P=0.169), stem dry weight (G=0.143, P=0.125), thousand seed weight (G=0.018, P=0.008) and plant weight without root (G=0.123P=0.175) and non-significant but negative correlation no of leaf per branch (G=-0.144, P=-0.094) and root shoot ratio (G=-0.068, P=-0.014).

4.2.6 Plant height (cm)

Plant height showed highly significant and positive correlation with stem height (G=0.987, P=0.974), leaf length (G=0.776, P=0.560), leaf breadth (G=0.674, P=0.399), stem breadth (G=0.345, P=0.291), plant weight without root (G=0.845, P=0.630) and root length (G=0.394). It also observed that

highly significant but negative correlation with root shoot ratio (G=-0.824, P=-0.727). Non-significant and positive correlation with root length (P=0.157) and thousand seed weight (G=0.091, P=0.026) and non-significant but negative correlation no of branch (G=-0.009, P=-0.005), no of leaf per branch (G=-0.168, P=-0.009) and stem dry weight (G=-0.098, P=-0.095).A highly significant and positive correlation with plant weight without root suggested that selection based on this trait would give better response for the improvement in yield in stem amaranth. Diwan *et al*. (2017), Sarker *et al*. (2014), Venkatesh *et al*. (2014) and Ahammed *et al.* (2012) reported a similar highly significant positive correlation of plant height with yield.

4.2.7 Stem height (cm)

Stem height showed highly significant and positive correlation with leaf length (G=0.672, P=0.474), leaf breadth (G=0.627, P=0.330), stem breadth (G=0.352, P=0.291), root length (G=0.419) and plant weight without root (G=0.865, P=0.630). It was observed that highly significant but negative correlation with root shoot ratio (G=-0.804, P=-0.739). Non-significant and positive correlation with number of branch (G=0.013, P=0.020), no of leaf per branch (G=0.013, P=0.020) and thousand seed weight (G=0.111, P=0.054) and non-significant but negative correlation no of leaf per branch (G=-0.113) and stem dry weight (G=-0.739, P=-0.122).

4.2.8 Leaf length (cm)

Leaf length showed highly significant and positive correlation with leaf breadth (G=0.818, P=0.646), root length (G=0.194) and plant weight without root (G=0.412, P=0.260). It also observed that highly significant but negative correlation with number of branch (G=-0.283), no of leaf per branch (G=-0.541, P=-0.211) and root shoot ratio (G=-0.677, P=-0.414). Non-significant and positive correlation with stem breadth (G=0.034, P=0.168), root length (P=0.096), stem dry weight (G=0.040, P=0.024) and thousand seed weight (P=0.111) and non-significant but negative correlation no of branch (P=-0.0179) and thousand seed weight (P=-0.046).

4.2.9 Leaf breadth (cm)

Leaf breadth showed highly significant and positive correlation with root length (G=0.353) and plant weight without root (G=0.486, P=0.248). It was observed that highly significant but negative correlation with no of leaf per branch (G=-0.481, P=-0.274) and root shoot ratio (G=-0.509, P=-0.259). Non-significant and positive correlation with stem breadth (G=0.039, P=0.106), root length (P=0.176), stem dry weight (G=0.155, P=0.113) and thousand seed weight (G=0.119) and non-significant but negative correlation no of branch (G=-0.157,P=-0.094) and thousand seed weight (P=-0.033).

4.2.10 Stem diameter (cm)

Stem diameter showed highly significant and positive correlation with no of leaf per branch (G=0.790, P=0.713), root length (G=0.402, P=0.277), stem dry weight (G=0.215) and plant weight without root (G=0.300, P=0.249). Non-significant and positive correlation with no of branch (G=0.024, P=0.042) and SDR (P=0.167) and non-significant but negative correlation root shoot ratio (G=-0.064, P=-0.031) and thousand seed weight (G=-0.090, P=-0.118).Significant and positive correlation with plant weight without root indicated yield could be improved in stem amaranth if selection is based on stem weight trait. Diwan *et al*. (2017), Sarker *et al*. (2014), Venkatesh *et al.* (2014) and Ahammed *et al*. (2012) exhibited a similar highly significant and positive correlation between stem diameter and yield.

4.2.11 Number of branches per plant

No of branch showed highly significant and positive correlation with no of leaf per branch (G=0.267, P=0.253). It also observed that highly significant but negative correlation with stem dry weight (G=-0.244, P=-0.246) and thousand seed weight (G=-0.341,P=-0.240). Non-significant and positive correlation with root length (P=0.009), root shoot ratio (G=0.035, P=0.053) and plant weight without root (G=0.180, P=0.148) and non-significant but negative correlation root length (G=-0.148).

4.2.12 Number of leaves per branch

No of leaf per branch showed highly significant and positive correlation with RLSH (G=0.246). Non-significant and positive correlation with Root Length (G=0.114, P=0.105), root shoot ratio (P=0.108), stem dry weight (G=0.062, P=0.031) and plant weight without root (G=0.168, P=0.057). Non-significant but negative correlation thousand seed weight (G=-0.168, P=-0.118). Number of leaves per branch showed here highly significant and positive correlation with plant weight without root indicating yield could be improved in stem amaranth if selection is based on number of leaf per branch. Venkatesh *et al*. (2014) reported a similar result where number of leaves and yield were highly significant and positively correlated.

4.2.13 Root length (cm)

Root length per branch showed highly significant and positive correlation with root shoot ratio(P=0.351), stem dry weight (G=0.201), plant weight without root (G=0.317, P=0.294). Non-significant and positive correlation with root shoot ratio (G=0.150) and stem dry weight (P=0.127). Non-significant but negative correlation thousand seed weight (G=-0.168,P=-0.092).

4.2.14 Root shoot ratio

Root shoot ratio showed highly significant and positive correlation with stem dry weight (G=0.234). It also observed that highly significant but negative correlation with thousand seed weight (G=-0.290) and plant weight without root (G=-0.679, P=-0.412). Non-significant and positive correlation with stem dry weight (P=0.176) and non-significant but negative correlation no of leaf per branch (P=-0.172).

4.2.15 Stem dry weight

Stem dry weight showed non-significant negative correlation 1000 seed weight (G=-0.079, P=-0.070) and plant weight without root (G=-0.018, P=-0.022).

4.2.16 Thousand seed weight (g)

Thousand seed weight showed highly significant and positive correlation with plant weight without root (P=0.191). It also observed that highly significant but negative correlation with plant weight without root (G=-0.164).

4.3 Path Co-efficient analysis

Correlation analysis indicates the association pattern of component traits with yield. They merely represent the influence of a selected attribute on yield instead of providing cause and impact relationship. The path coefficient analysis technique was developed by Wright (1921) and demonstrated by Deway and Lu (1959) facilitates the partitioning of correlation coefficients into direct and indirect contribution of various characters on yield. It's standardized partial parametric statistical analysis. As such, it measures the direct influence of one variable upon other. Such data would be of good value in enabling the breeder to specifically determine the necessary component traits of yield and utilize the genetic stock for improvement in a planned way. The direct and indirect effects of yield conductive characters on yield were found out by using path analysis. Here plant weight without root was considered as effect (dependent variable) and days to first flowering, days to fifty percent flowering, plant gross weight (g), stem weight (g), ten leaf weight (g), plant height (cm), stem height (cm), leaf length (cm), leaf breadth (cm), stem diameter (cm), number of branch, number of leaf per branch, root length (cm), root shoot ratio, stem dry weight and thousand seed weight were treated as independent variables. Path coefficient analysis was showed direct and indirect effects of different characters on yield of stem amaranth in (Table 6).

4.3.1 Days to first flowering

Path co-efficient analysis revealed that, days to first flowering had positive direct effect (0.265) on plant weight without root. Days to first flowering had positive indirect effect on days to plant gross weight (0.269), stem height (0.743), leaf breadth (0.008), stem diameter (0.014), number of branch (0.007),

Table 6. Path coefficient analysis showing direct (bold) and indirect effects of different characters on yield of Stem Amaranth

Direct Effects	DFF	DFPF	PGW (g)	SW (g)	10LW (g)	PH (cm)	SH (cm)	LL(cm)	LB (cm)	SB (cm)	NBr	NLBr	RL (cm)	RLSH	SDW (g)	TSW (g)	Genotypic correlation with PWWR (g)
DFF	**0.265**	-0.227	0.289	-0.046	-0.007	-0.257	0.743	-0.046	0.008	0.014	0.007	-0.087	0.269	-0.588	-0.047	0.013	0.304**
DFPF	0.137	**-0.439**	0.256	-0.079	0.025	-0.320	1.014	-0.038	0.011	0.051	-0.013	-0.022	0.108	-0.413	-0.040	0.010	0.248**
PGW (g)	0.091	-0.133	**0.841**	-0.177	0.064	-0.893	2.430	-0.124	0.048	0.099	0.013	-0.077	-0.419	-0.878	-0.009	0.015	0.891**
SW (g)	0.059	-0.166	0.715	**-0.208**	0.074	-0.989	2.852	-0.162	0.076	0.104	0.007	-0.035	-0.628	-0.894	0.020	0.009	0.835**
10LW (g)	-0.009	-0.047	0.232	-0.067	**0.230**	-0.275	0.670	-0.091	0.060	0.050	-0.062	0.071	-0.562	-0.103	0.024	0.002	0.123^{NS}
PH (cm)	0.057	-0.118	0.632	-0.173	0.053	**-1.190**	3.250	-0.227	0.101	0.111	-0.001	0.084	-0.465	-1.260	-0.016	0.008	0.845**
SH (cm)	0.060	-0.135	0.621	-0.180	0.047	-1.174	**3.294**	-0.196	0.094	0.113	0.002	0.056	-0.494	-1.230	-0.021	0.010	0.865**
LL (cm)	0.042	-0.057	0.358	-0.115	0.071	-0.923	2.212	**-0.292**	0.122	0.011	-0.039	0.269	-0.229	-1.036	0.007	0.010	0.412**
LB (cm)	0.015	-0.032	0.273	-0.106	0.092	-0.802	2.065	-0.239	**0.150**	0.012	-0.021	0.239	-0.417	-0.779	0.026	0.011	0.486**
SD (cm)	0.012	-0.070	0.260	-0.068	0.036	-0.411	1.158	-0.010	0.006	**0.321**	0.003	-0.392	-0.474	-0.099	0.036	-0.008	0.300**
NBr	0.014	0.043	0.083	-0.010	-0.104	0.010	0.044	0.083	-0.023	0.008	**0.137**	-0.133	0.046	0.054	-0.041	-0.031	0.180^{NS}
NLBr	0.046	-0.019	0.130	-0.015	-0.033	0.200	-0.373	0.158	-0.072	0.254	0.037	**-0.497**	-0.134	0.376	0.010	-0.009	0.060NS
RL(cm)	-0.061	0.040	0.298	-0.111	0.109	-0.469	1.379	-0.057	0.053	0.129	-0.005	-0.056	**-1.181**	0.229	0.034	-0.015	0.317**
RLSH	-0.102	0.119	-0.483	0.122	-0.016	0.980	-2.648	0.198	-0.076	-0.021	0.005	-0.122	-0.177	**1.530**	0.039	-0.026	-0.679**
SDW (g)	-0.075	0.106	-0.048	-0.026	0.033	0.117	-0.423	-0.012	0.023	0.069	-0.033	-0.031	-0.237	0.358	**0.167**	-0.007	-0.018^{NS}
TSW (g)	0.037	-0.047	0.140	-0.020	0.004	-0.108	0.366	-0.032	0.018	-0.029	-0.047	0.050	0.198	-0.443	-0.013	**0.090**	0.164^{NS}

DFF-Days to 1st flowering, DFPF-Days to 50% flowering, PGW(g)- Plant gross weight, SW- Stem weight, 10LW- Ten leaf weight, PH (cm)- Plant height, SH- Stem height, LL- Leaf length, LB- Leaf breath, SP- Stem perimeter, NBr- Number of branch per plant, NLBr- Number of leaf per branch, RL (cm)- Root length, RLSH- Shoot: Root, SDW(g)- Shoot dry weight, TSW (g)- Thousand seed weight, PWWR (g)- Plant weight without root

* Significant at 5% level of probability ** Significant at 1% level of probability

root length (0.269) and thousand seed weight (0.013) while negative indirect effect on days to fifty percent flowering (-0.227), stem weight (-0.046), ten leaf weight (-0.007), plant height (-0.257), leaf length (-0.046), number of leaf per branch (-0.087), stem dry weight(-0.047) and root shoot ratio (-0.588). Correlation was positive highly significant (0.304). It showed highly significant positive genotypic correlation (0.304) with plant weight without root.The study suggests that selection of genotypes with lowest days to first flowering will help to select the genotypes which can give better plant weight without root (yield/plant). Maximum positive direct effect of days to flowering on yield per plant was also recorded by Ayehu *et al*. (2015).

4.3.2 Days to 50% flowering

Path co-efficient analysis revealed that days to fifty percent flowering had negative direct effect (-0.439) on plant weight without root. Days to fifty percent flowering had positive indirect effect on days to days to first flowering (0.137), plant gross weight (0.289) , stem height (0.014), leaf breadth (0.014) , stem diameter (0.051), root length (0.108), thousand seed weight (0.010) and ten leaf weight (0.025).while negative indirect effect on stem weight (-0.079), plant height (-0.320), leaf length (-0.038), number of branch (-0.013), number of leaf per branch (-0.022), root shoot ratio (-0.413) and stem dry weight (-0.040). Correlation was positive highly significant (0.248). It showed highly significant positive genotypic correlation (0.248) with plant weight without root.

4.3.3 Plant gross weight (g)

Path co-efficient analysis revealed that plant gross weight had positive direct effect (0.841) on plant weight without root. Plant gross weight had positive indirect effect on days to days to first flowering (0.091), ten leaf weight (0.064) , stem height (2.430), leaf breadth (0.048) , stem diameter (0.099), number of branch (0.013) and thousand seed weight (0.015).while negative indirect effect on days to fifty percent flowering (-0.133), stem weight (-0.177), plant height (-0.893), leaf length (-0.124), number of leaf per

branch (-0.077), root length (-0.419), root shoot ratio (-0.878) and stem dry weight (-0.009). Correlation was positive highly significant (0.891). It showed highly significant positive genotypic correlation (0.891) with plant weight without root.

4.3.4 Stem weight (g)

Path co-efficient analysis revealed that stem weight had positive direct effect (0.265) on plant weight without root. Hence, stem weight would be helpful in formulating strategy for selecting high yielding varieties of Amaranthus. Jangde *et al.* (2017) and Diwan *et al*. (2017) recorded similar highest positive direct effect on yield.Stem weight had positive indirect effect on days to days to first flowering (0.059), plant gross weight (0.715) , ten leaf weight (0.074), stem height (2.252) , leaf breadth (0.076), stem diameter (0.104), number of branch (0.007), stem dry weight (0.020) and thousand seed weight (0.009)while negative indirect effect on days to fifty percent flowering (-0.166), plant height (-0.989), leaf length (-0.162), root length (-0.628), root shoot ratio (-0.894) and number of leaf per branch (-0.035). Correlation was positive highly significant (0.835). It showed highly significant positive genotypic correlation (0.835) with plant weight without root.

4.3.5 Ten leaf weight (g)

Path co-efficient analysis revealed that ten leaf weight had positive direct effect (0.230) on plant weight without root. Ten leaf weight had positive indirect effect on days to plant gross weight (0.232), stem height (0.670) , leaf breadth (0.068), stem diameter (0.050) , number of leaf per branch (0.071), stem dry weight (0.024) and thousand seed weight (0.002)while negative indirect effect on days to first flowering (-0.009), days to fifty percent flowering (-0.047), stem weight (-0.067), plant height (-0.275), leaf length (-0.091), number of branch (-0.062), root length (-0.562) and root shoot ratio (-0.103). Correlation was positive non-significant (0.123). It showed non-significant positive genotypic correlation (0.123) with plant weight without root.

4.3.6 Plant height (cm)

Path co-efficient analysis revealed that plant height had negative direct effect (-1.190) on plant weight without root indicated that plant height would be helpful in formulating strategy for selecting high yielding varieties of Amaranthus Jangde *et al.* (2017) reported similar direct negative effect on yield. The result of Tiwari *et al*. (2018) and Ayehu *et al*. (2015) oppose with the result of present study. They found Maximum positive direct effect of plant height on yield. Plant height had positive indirect effect on days to days to first flowering (0.057), plant gross weight (0.632) , ten leaf weight (0.053), stem height (3.250) , leaf breadth (0.101), stem diameter (0.111), number of leaf per branch (0.084) and thousand seed weight (0.008)while negative indirect effect on days to fifty percent flowering (-0.118), stem weight (-0.173), leaf length (-0.227), number of branch (-0.001), root length (-0.465), root shoot ratio (-1.260) and stem dry weight (-0.016). Correlation was positive highly significant (0.845). It showed highly significant positive genotypic correlation (0.845) with plant weight without root.

4.3.7 Stem height (cm)

Path co-efficient analysis revealed that stem height had positive direct effect (3.294) on plant weight without root. Stem height had positive indirect effect on days to days to first flowering (0.060), plant gross weight (0.321), ten leaf weight (0.047), leaf breadth (0.094), stem diameter (0.113), number of branch (0.002), number of leaf per branch (0.056) and stem dry weight (0.010). While negative indirect effect on days to fifty percent flowering (-0.135), stem weight (-0.180), plant height (-1.174), leaf length (-0.494), stem dry weight (-0.021), root length (-0.494) and root shoot ratio (-1.230). Correlation was positive non-significant (0.865). It showed non-significant positive genotypic correlation (0.865) with plant weight without root.

4.3.8 Leaf length (cm)

Path co-efficient analysis revealed that leaf length had negative direct effect (-0.292) on plant weight without root. Leaf length had positive indirect effect on

days to days to first flowering (0.042), plant gross weight (0.358) , ten leaf weight (0.071), stem height (2.212) , leaf breadth (0.122), stem diameter (0.111), number of leaf per branch (0.269), stem dry weight (0.007) and thousand seed weight (0.010) while negative indirect effect on days to fifty percent flowering (-0.057), stem weight (-0.115), plant height (-0.923), number of branch (-0.039), root length (-0.229) and root shoot ratio (-1.036). Correlation was positive highly significant (0.412). It showed highly significant positive genotypic correlation (0.412) with plant weight without root.

4.3.9 Leaf breadth (cm)

Path co-efficient analysis revealed that leaf breadth had positive direct effect (0.150) on plant weight without root indicated that selection of varieties with higher leaf breadth will help the breeder to select the genotypes which can give better grainyield. Ayehu *et al*. (2015) recorded similar maximum positive direct effect of leaf breadth on yield. Leaf breadth had positive indirect effect on days to days to first flowering (0.015), plant gross weight (0.273), ten leaf weight (0.092), stem height (0.065), stem diameter (0.012), number of leaf per branch (0.239) stem dry weight (0.026) and thousand seed weight (0.011) while negative indirect effect on days to fifty percent flowering (-0.032), plant height (-0.802), root length (-0.417), root length (-0.494), stem weight (-0.106) and root shoot ratio (-0.106). Correlation was positive non-significant (0.486). It showed non-significant positive genotypic correlation (0.486) with plant weight without root.

4.3.10 Stem diameter (cm)

Path co-efficient analysis revealed that stem diameter had positive direct effect (0.321) on plant weight without root. Stem diameter had positive indirect effect on days to days to first flowering (0.012), plant gross weight (0.260), ten leaf weight (0.036), stem height (1.158), leaf breadth (0.006), number of branch(0.003) and stem dry weight (0.007). While negative indirect effect on days to fifty percent flowering (-0.012), stem weight (-0.068), plant height (-

0.411), leaf length (-0.010) number of leaf per branch (-0.392), root length (-0.474), root shoot ratio (-0.099), and thousand seed weight (-0.008). Correlation was positive non-significant (0.300). It showed non-significant positive genotypic correlation (0.300) with plant weight without root.

4.3.11 Number of branches per plant

Path co-efficient analysis revealed that number of branch had positive direct effect (0.137) on plant weight without root. Number of branch had positive indirect effect on days to days to first flowering (0.014), days to fifty percent flowering (0.043), plant gross weight (0.083), plant height (0.010), stem height (0.044), leaf length (0.083), stem diameter (0.008), root length (0.046) and root shoot ratio (0.0.054), while negative indirect effect on stem weight (-0.010), ten leaf weight (-0.104), leaf breadth (-0.023), number of leaf per branch (-0.133), stem dry weight (-0.041) and thousand seed weight (-0.031). Correlation was positive non-significant (0.180). It showed non-significant positive genotypic correlation (0.180) with plant weight without root.

4.3.12 Number of leaves per branch

Path co-efficient analysis revealed that number of leaf per branch had negative direct effect (-0.497) on plant weight without root. Jangde *et al.* (2017) and Diwan *et al*. (2017) contradict with the result of the present study. They found that number of leaf per branch had positive direct effect on yield in amaranth. Number of leaf per branch had positive indirect effect on days to days to first flowering (0.046), plant gross weight (0.130), plant height (0.200), leaf length (0.0158), stem diameter (0.254), number of branch (0.037), root shoot ratio (0.054) and stem dry weight (0.010). While negative indirect effect on days to fifty percent flowering (-0.019), stem weight (-0.015), ten leaf weight (-0.033), stem height (-0.373), leaf breadth (-0.072), root length (-0.134) and thousand seed weight (-0.009). Correlation was positive non-significant (0.060). It showed non-significant positive genotypic correlation (0.060) with plant weight without root.

4.3.13 Root length (cm)

Path co-efficient analysis revealed that root length had negative direct effect (-1.181) on plant weight without root. Root length had positive indirect effect on days to days to fifty percent flowering (0.040), plant gross weight (0.298), ten leaf weight (0.109), stem height (1.379), leaf breadth (0.053), stem diameter (0.129), root shoot ratio (0.229) and stem dry weight (0.034). While negative indirect effect on days to first flowering (-0.040), stem weight (-0.111), plant height (-0.469), leaf length (-0.057), number of branch (-0.005), number of leaf per branch (-0.056) and thousand seed weight (-1.026). Correlation was positive highly significant (0.317). It showed highly significant positive genotypic correlation (0.317) with plant weight without root.

4.3.14 Root shoot ratio

Path co-efficient analysis revealed that root shoot ratio had positive direct effect (1.530) on plant weight without root. Root shoot ratio had positive indirect effect on days to days to fifty percent flowering (0.119), stem weight (0.122), plant height (0.980), leaf length (0.198), number of branch (0.005), and stem dry weight (0.039). While negative indirect effect on days to first flowering (-0.102), plant gross weight (-0.483), ten leaf weight (-0.016), stem height (-2.648), leaf breadth (-0.076), number of leaf per branch (-0.122), stem diameter (-0.021), root length (-0.177) and thousand seed weight (-0.026). Correlation was negative highly significant (-0.679). It showed highly significant negative genotypic correlation (-0.679) with plant weight without root.

4.3.15 Stem dry weight

Path co-efficient analysis revealed that stem dry weight had positive direct effect (0.167) on plant weight without root. Stem dry weight had positive indirect effect on days to days to fifty percent flowering (0.106), ten leaf weight (0.033), plant height (0.117), leaf breadth (0.023), stem diameter (0.096), and root shoot ratio (0.358). While negative indirect effect on days to first flowering (-0.075), plant gross weight (-0.048), stem weight (-0.026), stem height (-0.423), leaf length (-0.012), number of branch (-0.033), number of leaf

per branch (-0.031), root length (-0.237) and thousand seed weight (-0.007). Correlation was negative non-significant (-0.018). It showed non-significant negative genotypic correlation (-0.018) with plant weight without root.

4.3.16 Thousand seed weight

Path co-efficient analysis revealed that thousand seed weight had positive direct effect (0.090) on plant weight without root. Selection programme based on this character is suggested for further improvement. Tiwari *et al*. (2018) and Diwan *et al.* (2017) recorded similar positive direct effect of thousand seed weight on yield. Thousand seed weight had positive indirect effect on days to days to first flowering (0.037), plant gross weight (0.140), ten leaf weight (0.004), stem height (0.366), leaf breadth (0.018), number of leaf per branch (0.050), and root length (0.198). While negative indirect effect on days to fifty percent flowering (-0.047), stem weight (-0.020), plant height (-0.108), leaf length (-0.032), stem diameter (-0.029), root shoot ratio (-0.443), number of branch (-0.047) and stem dry weight (-0.013). Correlation WAS positive non-significant (0.164). It showed non-significant positive genotypic correlation (0.164) with plant weight without root.

4.4 Residual effects

The residual effect (R) of path co-efficient analysis was 0.06which reported that the traits under study contributed 94% of the plant weight without root. It is said that there were some other factors those contributed 6% to the plant weight without root that are not included in the present study could have significant effect on plant weight without root.

4.5 Multivariate analysis

Multivariate analysis techniques *viz*. Cluster Analysis (CA) and Principal Component Analysis (PCA) were used to study the genetic divergence pattern. One of the potent techniques of assessing genetic divergence is D^2 statistic proposed by Mahalanobis in 1936. This technique measures the forces of differentiation at two levels *viz.*, intra cluster and inter cluster that helps selection of genetically divergent parents for exploitation in hybridization

programmes. While selecting parents on the basis of D^2 statistic, three important points should be considered *viz*., i) the relative contribution of each character to the total genetic divergence, ii) the choice of clusters with the maximum statistical distance and iii) the selection of one or a few genotypes from such clusters. The success of the hybridization followed by selection depends largely on the selection of parents showing high genetic diversity for traits of interest (Murthy and Arunachalam, 1966). A large amount of genetic diversity has been reported in mung bean (Sinha *et al.* 1996; Francisco and Maeda, 1989) which indicates potential for genetic improvement of the crop. The genetic variability present among the different genotypes of a species may arise either due to geographical separation or due to genetic barriers to cross ability.

4.5.1 Cluster analysis

The experiment was conducted to investigate the genetic diversity of thirty-seven genotypes of stem amaranth. The genotypes were divided into five clusters according to D^2 analysis (Table 7). The cluster IV had (G4, G7, G13, G16, G17, G19, G21, G22, G23, G24 and G37) maximum number of genotypes (11) followed by cluster I and cluster II which had 8 genotypes. Cluster III and V had 3 and 7 genotypes respectively. Remarkably cluster I had (G2, G3, G6, G15, G18, G26, G29 and G33) whereas cluster II had (G11, G12, G25, G27, G30, G31, G34 and G36). Furthermore, cluster III had (G14, G32 and G35), cluster V showed seven genotypes (G1, G5, G8, G9, G10, G20 and G28). Clustering was done at random that indicate a broad genetic base of the genotypes. Mean of the cluster are shown in Table 8.

4.5.2 Principal component analysis (PCA)

Genetic divergence analysis quantifies the genetic distance among the selected genotypes and reflects the relative contribution of specific traits towards the total divergence and is an important tool for breeding program. The diversity analysis is useful to determine the magnitude of divergence among population. The Principal component analysis was studied with thirty-seven genotypes of stem amaranth. Eigen values and latent vectors of corresponding 17 principal

Table 7.Distribution of thirty-seven genotypes in different clusters

Cluster no.	Genotypes	No. of genotypes
I	G2, G3, G6, G15, G18, G26, G29, G33	8
II	G11, G12, G25, G27, G30, G31, G34, G36	8
III	G14, G32, G35	3
IV	G4, G7, G13, G16, G17, G19, G21,G22, G23, G24, G37	11
V	G1, G5, G8, G9, G10, G20, G28	7
	Total	**37**

Table 8. Cluster mean for seventeen yield and yield related characters in thirty-seven genotypes of Stem Amaranth

Characters	I	II	III	IV	V
Days to First Flowering	44.58	48.38	48.89	46.3	43.81
Days to 50% Flowering	54.96	59.33	60.33	53.24	54.05
Plant Gross Weight (g)	230.63	405.08	566.78	358.94	294.86
Stem Weight (g)	127.21	249.5	271.55	182.45	161.86
Ten Leaf Weight (g)	22.83	34.08	25.67	34.39	31.86
Plant Height (cm)	66.29	99.87	110.55	79.67	79.09
Stem Height (cm)	50.92	84.17	90.56	62.88	61.71
Leaf Length (cm)	21.44	25.21	25.33	23.23	22.81
Leaf Breadth (cm)	7.12	9.48	8	8.59	7.67
Stem Breadth (cm)	6.51	7.17	8.2	6.33	6.45
Number of Branch	6.04	5.04	7.78	5	3.62
Number of Leaf per Branch	23.33	20.04	25.89	20.58	19.19
Root Length (cm)	15.71	18.69	19.61	18.64	18.72
Root shoot ratio	0.35	0.23	0.24	0.3	0.33
Stem Dry Weight (g)	11.61	12.62	10.06	12.15	11.21
Thousand Seed Weight (g)	0.75	0.81	0.73	0.8	0.7
Plant weight without root (g)	186.04	351.58	475.89	310.7	245.38

component axes and % of total variation accounting for them obtained from the principal component analysis (Table 9). It represents that the cumulative Eigen values of first five principal components accounted for 74.14% of the total variation; the first principle component accounted for 33.93% of the total variation; the second, third, fourth and fifth components accounted for 13.78%, 12.67%, 8.37% and 6.39% of the total variation, respectively. The rest of the components accounted for only 24.85% of the total variation.

4.5.3 Construction of scatter diagram

According to the values of principal component scores 2 and 1 obtained from the principal component analysis, a two dimensional (Z1-Z2) scatter diagram was constructed, using component score 1 as X-axis and component score 2 as Y-axis which has been presented in figure 1. The positions of the genotypes in the scatter diagram were apparently distributed, which indicated the considerable diversity among the genotypes. The distribution of Thirty-Seven Stem Amaranth genotypes based on their principle component score with clusters indicated that the genotypes were apparently distributed into five groups (Figure 1). The scattered diagram for the stem amaranth genotypes of five cluster expressed that the genotypes G2, G3, G14, G17, G24, G35, G32, G36, G25 and G26 were distantly located which suggesting more diverged from rest of the genotypes.

4.5.4 Principal coordinate analysis

Principal coordinate analysis (PCO) was estimated on auxiliary principal component analysis. This analysis helps in estimating distances. Principal coordination analysis (PCO) indicated that the highest inter genotypes distance (2.969) was observed between the Stem Amaranth genotypes G26 and G32 followed by the genotypes G26 and G36. The tenth highest pair distance was (2.478) observed between G26 and G31. The lowest distance (0.451) was observed between the genotypes G23 and G24 followed by the genotypes G16 and G37. The tenth lowest distance (0.593) was observed between the genotypes G8 and G18. The difference between the highest and the lowest

Table 9. Eigen values and yield percent contribution of 17 characters of thirty-seven genotypes of Stem Amaranth

Principal component axes	Eigen values	Percent variation	Cumulative % of variation
I	5.769	33.93	33.93
II	2.343	13.78	47.71
III	2.155	12.67	60.38
IV	1.424	8.37	68.75
V	1.087	6.39	75.14
VI	1.063	6.25	81.39
VII	0.747	4.4	85.79
VIII	0.611	3.59	89.38
IX	0.541	3.18	92.56
X	0.433	2.55	95.11
XI	0.306	1.8	96.91
XII	0.214	1.26	98.17
XIII	0.129	0.76	98.93
XIV	0.083	0.49	99.42
XV	0.052	0.31	99.73
XVI	0.038	0.22	99.95
XVII	0.006	0.04	100

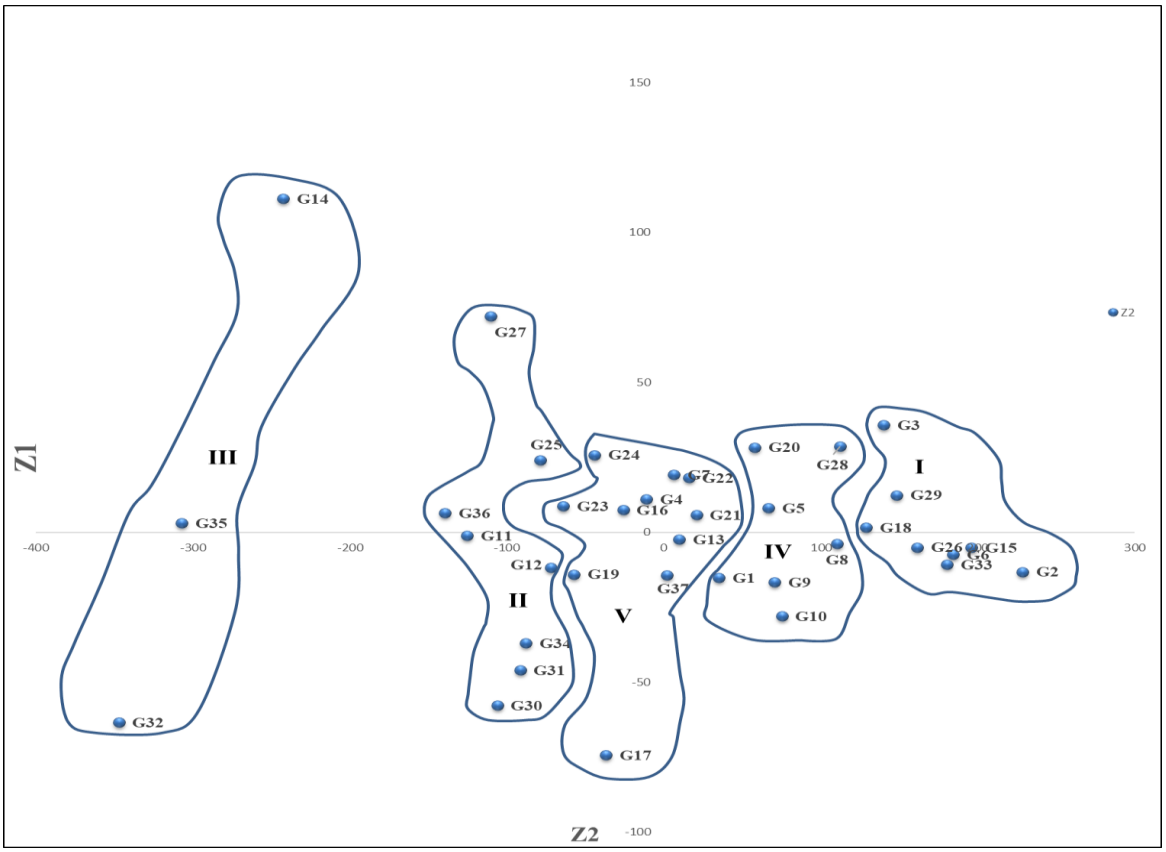


Figure 1. Cluster diagram showing genotypes grouping in different clusters of thirty-seven genotypes of stem amaranth.

inter-genotypes distance indicated the prevalence of variability among the 37 genotypes of stem amaranth (Table 10). According to Rahim *et al*. (2010) the hybrids of genotypes with maximum distance resulted in high yield, the cross between these genotypes can be used in breeding programs to achieve maximum heterosis. The maximum intra-cluster distance was presented in cluster I 1.514) which had eight genotypes (G2, G3, G6, G15, G18, G26, G29 and G33). The minimum intra-cluster distance was recorded in cluster V which containing seven genotypes (G1, G5, G8, G9, G10, G20 and G28).

4.6 Non-hierarchical clustering

Thirty-seven stem amaranth genotypes were grouped into five different clusters non-hierarchical clustering (Table 7). These results confirmed the clustering pattern of the genotypes obtained through PCA. Cluster means were computed for all the 17 characters studied and presented in (Table 8). However, if we consider the characters of the experiment then the following scenario would capture our attention.

4.6.1 Days to first flowering

It was observed that minimum days required in the cluster V (43.81 days). It revealed that most of the early flowering materials are laying in this group. On the other hand, late flowering materials were present in the cluster group III (48.89 9days).

4.6.2 Days to 50% flowering

The lowest days to fifty percent flowering materials were present in the cluster IV (53.24 days) and the highest days to fifty percent flowering materials were presented in the cluster group III (60.33 days).

4.6.3 Plant gross weight (g)

The highest weight of whole plant (g) was observed in the cluster III (566.78) and the lowest weight of whole plant (g) was observed in cluster I (230.63).

Table 10. Ten highest and ten lowest inter genotypic distance

Highest Distance			Lowest Distance		
Genotypes		Distance	Genotypes		Distance
G26	G32	2.969	G23	G24	0.451
G26	G36	2.908	G16	G37	0.498
G26	G34	2.736	G7	G37	0.513
G25	G26	2.711	G9	G20	0.53
G11	G26	2.672	G1	G23	0.535
G2	G32	2.637	G9	G10	0.547
G26	G35	2.623	G5	G7	0.569
G3	G36	2.528	G25	G36	0.572
G12	G26	2.48	G31	G34	0.576
G26	G31	2.478	G8	G18	0.593

Table 11. Intra (Bold) and inter cluster distances (D^2)

	I	II	III	IV	V
I	**1.514**				
II	12.367	**1.21**			
III	21.146	11.138	**1.069**		
IV	7.403	5.422	13.965	**1.048**	
V	3.622	9.723	17.627	4.348	**0.973**

4.6.4 Stem weight (g)

It was observed that the highest weight of stem weight (g) in the cluster III (271.55) and the lowest stem weight (g) was observed in cluster I (127.21).

4.6.5 Ten leaf weight (g)

The highest ten leaf weight (g)was observed in the cluster IV (34.39) and the lowest ten leaf weight (g)was observed in cluster I (22.83).

4.6.6 Plant height (cm)

In the experiment the highest plant height (cm) was observed in the cluster III (110.55) and the lowest plant height (cm) was observed in cluster I (66.29).

4.6.7 Stem height (cm)

It was observed that the highest stem height (cm) in the cluster III (90.56) and the lowest stem height (cm)is observed in cluster I (50.92).

4.6.8 Leaf length (cm)

The highest leaf length (cm) was observed in the cluster III (25.33) and the lowest leaf length (cm)was observed in cluster I (21.44).

4.6.9 Leaf breadth (cm)

In the experiment the highest leaf breadth (cm)was observed in the cluster II (9.48) and the lowest leaf breadth (cm) was observed in cluster I (7.12).

4.6.10 Stem diameter (cm)

The highest stem diameter (cm)was observed in the cluster III (8.2) and the lowest stem diameter (cm)was observed in cluster IV (6.33).

4.6.11 Number of branches per plant

The highest number of branch was observed in the cluster III (7.78) and the lowest number of branch was observed in cluster V (3.62).

4.6.12 Number of leaf per branch

It was observed that highest number of leaf per branch in the cluster III (25.89) and the lowest number of leaf per branch was observed in cluster V (19.19).

4.6.13 Root length (cm)

The highest root length (cm)was observed in the cluster III (19.61) and the lowest root length (cm) was observed in cluster I (15.71).

4.6.14 Root shoot ratio

In the experiment the highest root shoot ratio was observed in the cluster I (0.35) and the lowest root shoot ratio was observed in cluster II (0.23).

4.6.15 Stem dry weight (g)

The highest stem dry weight (g)was observed in the cluster II (12.62) and the lowest stem dry weight (g) was observed in cluster III (10.06).

4.6.16 Thousand Seed weight (g)

It was observed that the highest thousand seed weight (g)in the cluster II (0.81) and the lowest Thousand Seed Weight (g)was observed in cluster I (0.7).

4.6.17 Plant weight without root (g)

The highest plant weight without root was observed in the cluster III (475.89) and the lowest plant weight without root was observed in cluster I (186.04).

4.7 Canonical Variate Analysis

Canonical variate analysis (CVA) was done to identify the inter-cluster distance. (Table 11, Figure 2) were presented intra and inter-cluster distance (D^2) values. In this experiment the inter-cluster distances were higher from intra-cluster distances. It showed that the wide range of genetic variability among genotypes of stem amaranth. Based on the result it indicated that the highest inter cluster distance was observed between I and III (21.146), followed by III and V (17.627), III and IV (13.965), I and II (12.367) and II and III (11.138) (Table 11). The lowest inter-cluster distance was observed between I and V (3.622) followed by IV and V (4.348) and II and IV (5.422), whereas there is no any similar type of distance was found. With the help of D^2 values within and between clusters, an arbitrary cluster diagram was constructed, which showed the relationship between different genotypes. Diagram also showed the intra and inters cluster distance of thirty-seven genotype of Stem Amaranth.

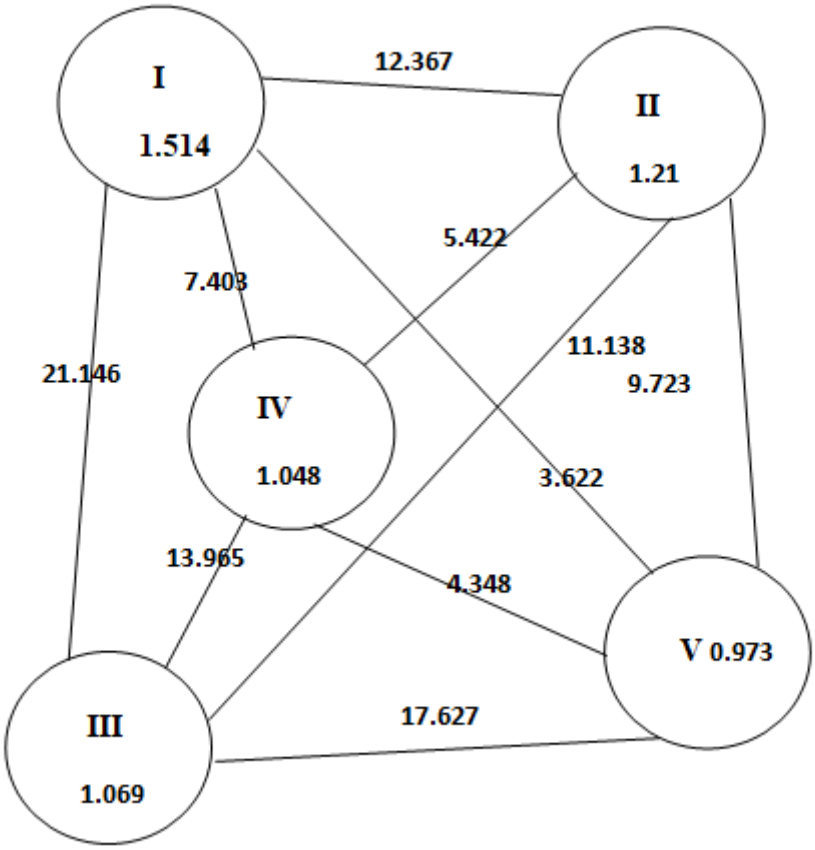


Figure2. Intra and inter cluster distances (D2) of thirty-seven genotypes of stem amaranth

However, the maximum inter-cluster distance was recorded between clusters I and III followed by between III and V. Genotypes from these clusters can be used in hybridization programme. The intra-cluster divergence varied from 0.973 to 1.514, maximum for cluster I, which was comprised of eight genotypes of diverse origin, while the minimum distance was observed in cluster V that comprised seven genotypes. Results obtained from different multivariate techniques were superimposed in Figure 2 from which it may be concluded that all the techniques gave more or less similar results and one technique supplemented and confirmed the results of another one.

4.8 Contribution of characters towards divergence of the cultivars

For deciding on the cluster for the purpose of further selection and choice of parents for hybridization the character contributing maximum to the divergence were given greater emphasis (Jagadev *et al.* 1991). The PCA revealed that in vector I (Z1) the important characters responsible for genetic divergence in the major axis of differentiation were days to first flowering, days to fifty percent flowering, plant gross weight (g), stem weight (g), stem height (cm), leaf length (cm), stem diameter (cm), number of branch, root length (cm), stem dry weight, thousand seed weight, plant weight without root (Table 12). In vector II (Z2) that was the second axis of differentiation days to first flowering, stem weight (g), ten leaf weight (g), stem height (cm), leaf breadth (cm), stem diameter (cm), number of branch, stem dry weight (g), thousand seed weight (g) were important. The role of days to first flowering, stem weight (g), stem height (cm), stem diameter (cm) stem dry weight (g), thousand seed weight (g) in both the vectors were positive across two axes indicating the important components of genetic divergence in those materials.

4.9 Selection of genotypes as parent for hybridization programme

Genetically dissimilar parent selection is the fundamental works for hybridization programme. So the genotypes were chosen according to specific Trait, maximum heterosis could be shown in offspring from the crosses between genetically diverse parents. Based on cluster mean and agronomic

Table 12. Relative contributions of the 17 agromorphogenic characters of 37 varieties to the total divergence

Characters	Vector 1	Vector 2
Days to First Flowering	0.0141	0.1177
Days to 50% Flowering	0.0511	-0.0822
Plant Gross Weight (g)	0.0407	-0.0053
Stem Weight (g)	0.0141	0.0381
10 Leaf Weight (g)	-0.0335	0.0736
Plant Height (cm)	-0.0771	-0.3139
Stem Height (cm)	0.0796	0.3067
Leaf Length (cm)	0.2815	-0.1621
Leaf Breadth (cm)	-0.2305	0.6138
Stem Breadth (cm)	0.0206	0.5508
Number of Branch	0.2559	0.2926
Number of Leaf per Branch	-0.0603	-0.1345
Root Length (cm)	0.0421	-0.1406
Root shoot ratio	-4.6125	-10.7687
Stem Dry Weight (g)	0.0951	0.0612
Thousand Seed Weight (g)	0.7212	10.8551
Plant weight without root (g)	0.0117	-0.0253

performance, the genotype G32 for maximum plant weight without root (g), plant height (cm), stem height (cm), G16 for leaf breadth (cm) and G34 for leaf length (cm) and G3 for Stem diameter (cm), number of branch, number of leaf per branch found promising. Therefore, considering group distance and other agronomic performance the inter genotypic crosses between G25, G26, G32, G34 and G36 and other improved variety and might be suggested for future hybridization program.

CHAPTER V

SUMMARY AND CONCLUSION

The experiment was conducted at the research field of the Sher-e-Bangla Agricultural University, Dhaka-1207 during the period from November to March in Robi season for genetic diversity, co-relation and path coefficient analysis in stem amaranth. In this experiment thirty-seven stem amaranth genotypes were used as experimental materials. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. Variability, mean performance, correlation matrix, path analysis and genetic diversity analysis on different yield and yield contributing character of stem amaranth genotypes was estimated and significant variation was observed for different stem amaranth genotypes.

Analysis of variance for seventeen different characters of stem amaranth revealed that there is significant variation among all the genotypes under study. The mean performance illustrated that the highest days to first flowering was found in G16 (56.00 days) and the lowest days to first flowering was found in G4 (35.00 days). The highest days to 50% flowering was found in G12 (67.00 days) and the lowest days to 50% flowering was found in G2 (45.33 days). The highest plant gross weight (g) was found in G114 (590.33g) and the lowest plant gross weight was found in G2 (180.33 g). The highest stem weight (g) was found in G35 (303.00g) and the lowest stem weight (g)was found in G33 (109.33 g). The highest ten leaf weight (g) was found in G24 (47.33 g) and the lowest ten leaf weight (g) was found in G2 (12.33 g). The highest plant height (cm) was found in G24 (47.33 g) and the lowest plant height (cm) was found in G2 (12.33 g). The highest stem height (cm) was found in G32 (111.67 cm) and the lowest stem height (cm) was found in G26 (25.67 cm). The highest leaf length (cm) was found in G29 & G32 (28.67 cm) and the lowest leaf length (cm) was found in G3 (15.50 cm). The highest leaf breadth (cm) was found in G16 (12.33 cm) and the lowest leaf breadth (cm) was found in G3 (4.67 cm). The highest stem breadth (cm) was found in G3 (14.00cm) and the lowest stem

breadth (cm) was found in G26 (2.83 cm). The highest number of branch was found in G9 (9.67) and the lowest number of branch was found in G9 (1.33). The highest number of leaf per branch was found in G3 (60.00) and the lowest number of leaf per branch was found in G33 (13.33). The highest root length (cm) was found in G1 (23.47 cm) and the lowest root length (cm) was found in G26 (9.67 cm). The highest root shoot ratio was found in G1 (0.47) and the lowest root shoot ratio was found in G32 (0.15). The highest stem dry weight (g) was found in G25 (23.19 g) and the lowest stem dry weight (gm) was found in G26 (4.82 g).

The phenotypic variance for all the character under study was considerably higher than the genotypic variance. Genotypic co-efficient of variation was lower than phenotypic co-efficient of variation for all the characters. Days to first flowering, days to 50% flowering, plant gross weight, stem weight, 10 leaf weight, plant height (cm), stem height (cm), stem diameter (cm), number of branch, number of leaves per branch, stem dry weight (g) and plant weight without root (g) showed high heritability along with high genetic advance in percentage of mean revealed the possibility of predominance of additive gene action in the inheritance of this character therefore, the characters could be improved through selection process.

Correlation revealed that plant weight without root had positive association with days to first flowering, days to fifty percent flowering, plant gross weight (g), stem weight (g), leaf weight (g), plant height (cm), stem height (cm), leaf length (cm), leaf breadth (cm), stem diameter (cm), number of branches per plant, number of leaf per branch, root length (cm), root shoot ratio and plant weight without root (g) both phenotypic and genotypic.

Path analysis revealed that days to first flowering, plant gross weight (g), ten leaf weight (g), stem height (cm), leaf breadth (cm), stem breadth (cm), number of branch, root shoot ratio, stem dry weight (g) and thousand seed weight (g) had positive direct effect on grain yield on plant indicating these were the main contributors to yield per plant.

Multivariate analysis, cluster analysis and canonical variate analysis revealed significant difference among the cluster. Genetic diversity among the genotypes was performed through Principal Component Analysis (PCA), cluster analysis, Canonical Variate Analysis (CVA) using GENSTAT According to PCA, PCO and Cluster analysis, the genotypes were grouped into five different clusters. The highest inter-cluster distance was observed between I and III and the lowest inter-cluster distance was observed between I and V. The highest and lowest intra-cluster distances were observed in cluster I and V respectively. Considering diversity pattern, genetic status and other agronomic performances, G26 from cluster I; G25, G34 and G36 from cluster II; G32 and G35 from cluster III might be considered better parents for efficient hybridization programme. Diverse genotypes in crossing programme may produce desirable segregants. So, divergent genotypes are recommended to use as parent in hybridization programme. The present study revealed the result that the characters days to first flowering, stem weight (g), stem height (cm), stem breadth (cm), number of branch, stem dry weight (g) and thousand seed weight (g) contributed maximum divergence among the red amaranth genotypes.

On the basis of present study, it can be concluded that days to first flowering, days to 50% flowering, plant gross weight, stem weight, leaf weight, plant height (cm), stem height (cm), stem diameter (cm), number of branches per plant, number of leaves per branch, stem dry weight (g) and plant weight without root (g) could be improved through selection process as these are expected to be controlled by additive genes. Days to first flowering, days to 50% flowering, Plant gross weight, stem weight, plant height, stem height, leaf length, leaf breadth and stem diameter showed significant and positive correlation with plant weight without root. So, selection based on these traits would give better response for the improvement in marketable yield in stem amaranth. All the characters except days to 50 % flowering, number of leaves per branch and root length had positive direct effect on plant weight without root. The study suggests that selection of varieties with the characters which

had positive direct effect will help the breeder to select the genotypes which can give better yield in stem amaranth.G26 from cluster I; G25, G34 and G36 from cluster II; G32 and G35 from cluster III might be considered better parents for efficient hybridization programme.

REFERENCE

Ahammed, A.U., Rahman, M.M. and Hossain, M.M. (2015). Evaluation of stem amaranth genotypes for growing in winter season in Bangladesh. *Anuals Bangladesh Agric*. **19**(2): 1-9.

Ahammed, A.U., Rahman, M.M. and Mian, M.A.K. (2013). Multivariate analysis in stem amaranth (*Amaranthus tricolor*). *Bangladesh J. Plant Breed. Genet.* 26(1): 11-17.

Ahammed, A.U, Rahman, M.M. and. Mian, M.A.K. (2012). Genetic variability, heritability and correlation in stem amaranth (*Amaranthus tricolor*). *Bangladesh J. Plant Breed. Genet.* **25**(2): 25-32.

Akaneme, F.I. and Ani, G.O. (2013).Morphological assessment of genetic variability among accessions Amaranthus hybrids. *World Applied Sci. J.***28**(4):568-577.

Anas, Meddy Rachmadi, Mansyur. (2013). Phenotypic and genotypic variance and heritability of stay green character among 22 elite sorghum (*Sorghum bicolor* (L.) moench) genotypes. International Conference on Biological Sciences (ICBS-2013). pp. 318-325.

Anuja, S. and Kader, M. (2007).Variability, heritability and genetic advance studies in amaranthus (*Amaranthus spp.). The Asian J. Hortic.* **2**(1):63-66.

Ayehu, F.H., Lal, S. and Sinatayehu, A. (2015). Estimation of Association Characters in Amaranths Germplasm Accessions (*Amaranthus* Spp.) under Mizan and Tepi Condtions. *South West Ethiopia.* **2**(1):2348-6848.

BBS. (2018). Yearbook of Agricultural Statistics-2017. pp. 274.

Bhatt, G.M. (1973). Significance of path co-efficient analysis in determining nature of character association. *Euphytica.* **22**: 338-343.

Burton, G.W. (1952). Quantitative interaction in grasses. **In**: Proc. *6th Intl.Grassland Congr*. **1**: 277-283.

Clarke, G.M. (1980). Statistics and experimental design. 2nd Edition. Edward Arnold. London. pp 196.

Deway, D.R. and Lu, K.N. (1959). A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agron. J.***51**: 515-518.

Deshmukh, S.N., Basu, M.S. and Reddy, P.S. (1986). Genetic variability, character association and path co-efficient of quantitative traits in Virginia bunch varieties of groundnut. *Indian J. Agric. Sci.***56**: 816-821.

Digby, P.N., Gaiway and Lane, P. (1989). Genstat 5, A second course. Oxford Science Publication, Oxford. pp: 103-108.

Diwan, I. S., Shukla, N. and Kurrey, V. (2017).Genetic studies in Amaranthus germplasm.*Intl.J. Curr Microbiol. Applied Sci.***6**(8): 2459-2470.

Francisco, P.B. Jr. and Maeda, K. (1989). Agro-physiological studies on the yield performance of mung bean. Cultivar differences in earliness in flowering and their relationships with growth and seed yield. *Japan J. Crop Sci*. **58**: 704-711.

Gaur, P.C., Gupta, P.K. and Kishore, H. (1978). Studies on genetic divergence in potato. *Euphytica*. **27**: 361-368.

Gerrano, S.A., Jansen W.S., Rensburg, V. Mavengahama, S., Bairu, M., Venter, S. and Adebola, P.O. (2017).Qualitative morphological diversity of *Amaranthus species*. *J. Tropical Agric*.**55**(1):12-20.

Grubben, G.J. (1997). Tropical vegetables and their genetic resources, Ed. H. pp. 123-124.

Haghighi, M.L., Abbaszadeh, B., Lebaschi M. H. and Shahrebabaki, M.A.V. (2012).Evaluating effective traits on yield of two medicinal amaranths (*Amaranthus hypochondriacus* L. var. Cim and var. Kharkofski) in Karaj, *Iran. Annals Biol. Res.* **3**(2):1014-1019.

Hanson, C.H., Robinson, H.F. and Comstock, R.E. (1956). Biometric studies of yield segregating population in Korean lespedeza. *Agron. J.***48**: 268-272.

Jagadev, P.N., Samal, K.M. and Lenka, L. (1991). Genetic divergence in rape mustard. *Indian J. Genet. Plant Breed.* **51**: 465-466.

Jangde, B., Asati, B.S., Sahu, P. and Tripathy, B. (2017**).** Correlation and Path coefficient analysis in vegetable Amaranthus (*Amaranthus tricolor* L.). *Intl. J. Chemical Studies.***6**(1): 1426-1431.

Johnson, H.W., Robinson, H.F. and R.E. Comstock. (1955). Estimates of genetic and environmental variability in soybean. *Agron. J.***47**: 314-318.

Johnson, H.W., Robinson, H.F. and Comstock, R.E., (1995) Estimation of genetic and environmental variability in soybean. *Agron. J.* **47**: 477-483.

Keshav, K.U. and Maurya, K. (2013). Genetic association between foliage yield and its biochemical parameters in vegetable Amaranthus (*Amaranthus tricolor*). *Intl. J. Advanced Res. Technol.* **1:** 56-74.

Khezerlu, S.M. and Tajbakhsh, M. (2017). Studied seed organic pretreatment for morphological characteristics and quality according to forage desirable quality of amaranthus (*Amaranthus hypochondriacus* L.) as new plant in Iran. *Iranian J. Field Crops Res.* **15**(1):103-112.

Kumar, R. and Mohammed, Y.G. (2014). Genotypic variability in grain amaranthus (*Amaranthus hypochondriacus* L.) under varied plant densities. *J. App. Hortic.***16**(2): 161164.

Mahalanobis, P.C. (1936). On the generalized distance in statistics. *Natl. Inst. Sci. India.* **12**: 49-55.

Murty, B.R. and Arunachalam, V. (1966). The nature of genetic divergence in relation to breeding system in crop plants. *Indian J. Genet*. **26**(A): 188-198.

Muthukrishnan, C.R., Bose, T.K., Som, M.G. and Irulappan, I. (1989). *Amranthus*: Vegetable Crops in India. Naya Prakash, Calcutta-six. India. pp. 670-679.

Nath, P. (1976). Vegetables for the tropical region, ICAR, New Delhi. **In**: Amaranthus. C.R. Muthukrishnan and I. Irulappan.Naya Prokash, Calcutta six. p. 670.

Oke, O.L. (1980). Amaranth in Nigeria. Proc. 2nd Amaranth Conf. Rodale Press Emmaus. PA. p. 22.

Palada, M.C. and Chang, L.C. (2008). AVDRC International Cooperators. *Agron. J.***100**: 344-351.

Pandey, R.M. and Singh, R. (2010). Genetic studies for biochemical and quantitative characters in grain amaranth (*Amaranthus hypochondriacus* L.). *Plant Omics J.* **3**(4):129-134.

Parveen, M., Chattopadhyay, N.C. and Tah, J. (2013). Biometric evaluation of genotypic variability and genetic advance inamaranth cultivars. *J. Sci. technol.* **2**(2):26-30.

Rahim, M.A., Mia, A.A., Mahmud, F., Zeba, N. and Afrin. K. (2010) Genetic variability, character association and genetic divergence in Mungbean (*Vigna radiata* L. Wilczek). *Plant Omic*. **3**: 1-6.

Rao, C.R. (1952). Advanced statistical methods in biometrical research. John Willy and sons. New York. p. 390.

Sarker, U., Islam, T.M., Rabbani, G.M. and Oba, S. (2014).Genotypic variability for nutrient, antioxidant, yield and yield contributing traits in vegetable amaranth. *J. Food Agric. Environ.***12**(34): 168-174.

Shivasubramanian, S. and Menon, M. (1973). Heterosis and inbreeding depression in rice. *Madras Agril. J.* **60**: 1139.

Shrivastav, S.P., Yadav, C.B., Lal, K. and Singh,V. (2017). Studied genetic variability, divergence, correlation and path coefficient analysis for contributing traits in Amaranthus (*Amaranthus paniculatus* L.). *Trends in Biosci.***10**(18): 3257-3264.

Singh, B.D. (2009). Plant breeding principles and methods. Kalyani Publisher, New Delhi, India.

Shukla, S., Bhargava, A., Chatterjee, A., Pandey, C.A. and Mishra, B.K. (2010). Studied diversity in phenotypic and nutritional traits in vegetable Amaranth (*Amaranthus tricolor*), a nutritionally underutilised crop. *J. Sci. Food and Agric.* **90**(1): 139-144.

Singh, R.K. and Chaudhary, B.D. (1985). Biometrical methods in quantitative genetic analysis. Kalayani Publisher, New Delhi, India.

Shukla, S., Bhargava, A., Chatterjee, A., Srivastava, J., Singh, N. and Singh, S.P. (2006). Mineral Profile and Variability in vegetable Amaranth *Amaranthus tricolor*). *Plant Foods Human Nutrition*. **61**(1): 21-26.

Shukla, S., Bhargava, A., Chatterjee, A., Srivastava, J. and Singh, S.P. (2006). Genotypic variability in vegetable amaranth (*Amaranthus tricolor* L.) for foliage yield and its contributing traits over successive cuttings and years. *Euphytica*. **151**(1):103-110.

Sinha R.P, Sinha S.P. and Kumar S. (1996). Genetic variation in mung bean (*V. radiata* L. Wilczek). *J Appl Biol*. **6**: 33-35.

Swaminathan, M.S. (1983). Genetic conservation: microb to man presidential Address. *Intl. Congr. Genetics.* New Delhi. p. 31.

Singh, R.K. and Chaudhury, B.D. (1985). Biometrical methods of quantitative genetic analysis. *Haryana J. Hort. Sci.* **12**(2): 151-156.

Tiwari, J.K. (2018). Studied variability and genetic parameters for different yield contributing traits in grain Amaranth, *J. Res. ANGRAU.* **46**(4): 11-16.

Tomoka, N. (1991). Genetic diversity and land race differentiation of mungbean (*Vigna radiate* (L.) wilczek) and evaluation of its wild relatives (The sub-genus cerato tropics) as breeding materials. Tech. Bull. Trop. Res. Centre, Japan, No. 28. Ministry of Agric. Forestry and Fisheries, Japan. p. 1.

Tusharkumar, A. Patel, B.N., Rumit Patel, Patil, G.B. and Chirag Solanki. (2019). Genetic variability, correlation and path coefficient analysis of yield and yield contributing characters in mung bean [*Vigna radiata* (L.) Wilczek]. *Intl. J. Chemical Studies*. **7**(4): 383-387.

Vavilov, N.I. (1926). Studied on the origins of cultivated plants. *Bull. Appl. Plant Breed.* **16**: 1-245.

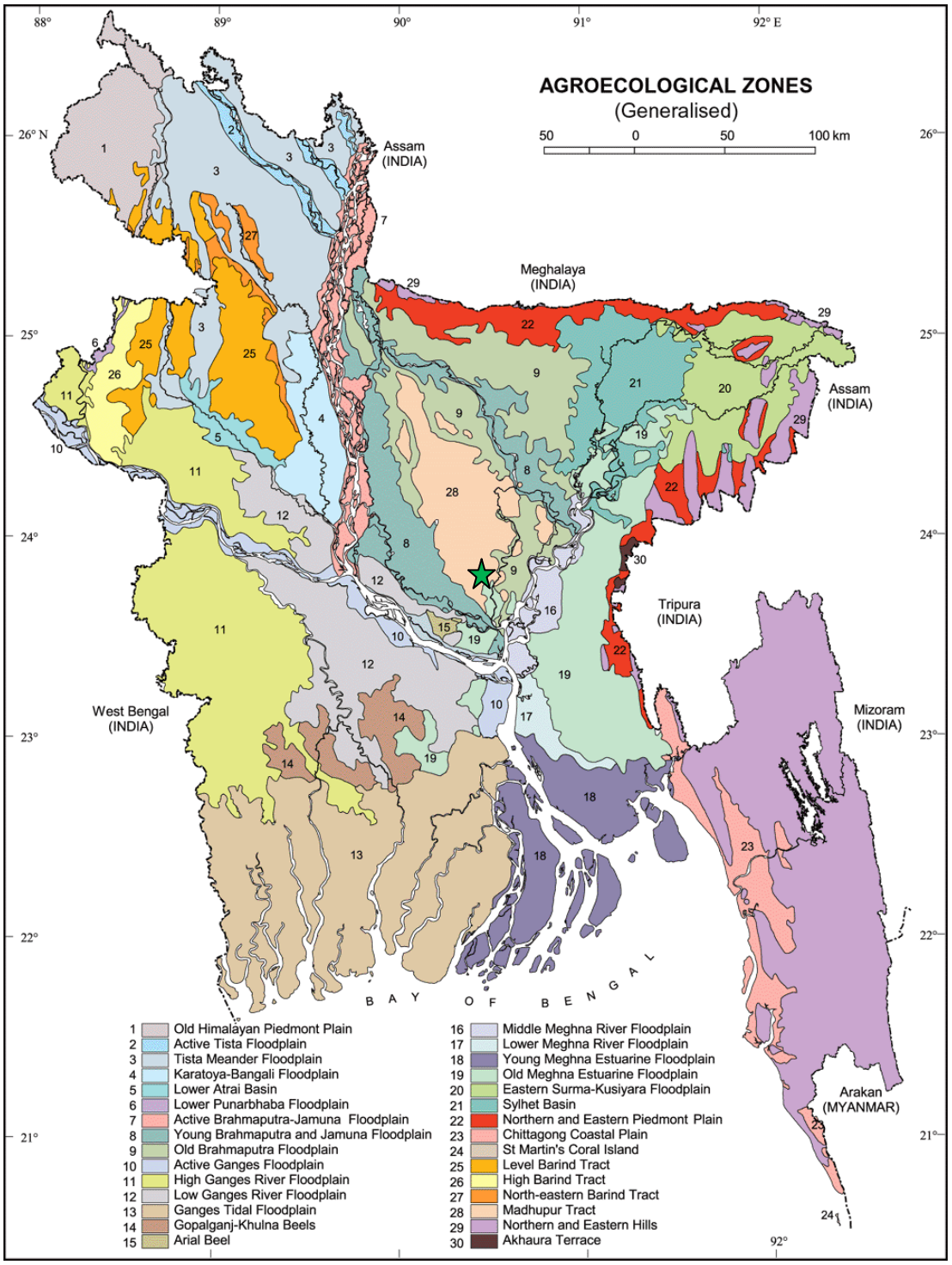
Venkatesh, L., Murthy, N., Nehru, S.D. and Manjappa (2014). Studied genetic variability, heritability and genetic advance in grain amaranth (*Amaranthus* spp.). *Asian J. Bio. Sci.* **9**(1): 67-70.

Weisman, A. (1883). Die Kontinuital des Keimplasmasals Crundlage siner, Theric der vererbung. **In**: Aufsatze Vber Vererbung and Kervantte Biologische Fragen. *Fisher. Jena.* 182-191.

Wright, S. (1921). Correlation and causation. *J. Agric. Res*. **20**: 557-558.

APPENDICES

Appendix I. Map showing the experimental site under the study



The experimental site under the study

★ The experimental site under the study

Appendix II. Morphological, physical and chemical characteristics of initial soil (0-15 cm depth) of the experimental site

A. Morphological characteristics of the experimental field

Morphological features	Characteristics
Location	Sher-e-Bangla Agricultural University Research Farm, Dhaka
AEZ	AEZ-28, Modhupur Tract
General Soil Type	Deep Red Brown Terrace Soil
Land type	High land
Soil series	Tejgaon
Topography	Fairly leveled

B. Physical composition of the soil

Soil separates	%	Methods employed
Sand	26	Hydrometer method (Day, 1915)
Silt	45	Do
Clay	29	Do
Texture class	Silty loam	Do

C. Chemical composition of the soil

Sl. No.	Soil characteristics	Analytical data	Methods employed
1	Organic carbon (%)	0.45	Walkley and Black, 1947
2	Total N (%)	0.03	Bremner and Mulvaney, 1965
3	Total S (ppm)	225.00	Bardsley 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 (ppm)	20.54	Olsen and Dean, 1965
7	Exchangeable K (me/100 g soil)	0.10	Pratt, 1965
8	Available S (ppm)	16.00	Hunter, 1984
9	pH (1:2.5 soil to water)	5.6	Jackson, 1958
10	CEC	11.23	Chapman, 1965

Source: Soil Resource and Development Institute (SRDI), Farmgate, Dhaka

Appendix III. Monthly average temperature, average relative humidity and total rainfall and average sunshine of the experimental site during the period from November, 2019 to March, 2020.

Month	Average temperature (°c)		Average RH (%)	Rainfall (mm) (total)	Average sunshine (hr)
	Minimum	**Maximum**			
Novenber, 2019	21	30	65	35	**8**
December, 2020	15	29	74	15	**9**
January, 2020	13	24	68	7	**9**
February, 2020	18	30	57	25	**8**
March, 2020	**20**	**33**	**57**	**65**	**7**

Source: Bangladesh Meteorological Department (Climate & Weather Division), Agargoan, Dhaka – 1212

Appendix IV. Some pictorial views of the experimental field.

Visit of research supervisor in the field