# GENETIC DIVERSITY ANALYSIS OF RED AMARANTH

**(*Amaranthus cruentus* L.)**

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## (*Amaranthus cruentus* L.)

**BY**

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# CERTIFICATE

This is to certify that thesis entitled, **"GENETIC DIVERSITY ANALYSIS OF RED AMARANTH (*Amaranthus cruentus* L.)"** was 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 (MS)** in **GENETICS AND PLANT BREEDING,** embodies the result of a piece of bona fide research work carried out by **MD. SHAFIQUL ISLAM**, Registration No: **11-04498** under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

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

*Dated : June, 2021*
*Place: Dhaka, Bangladesh*

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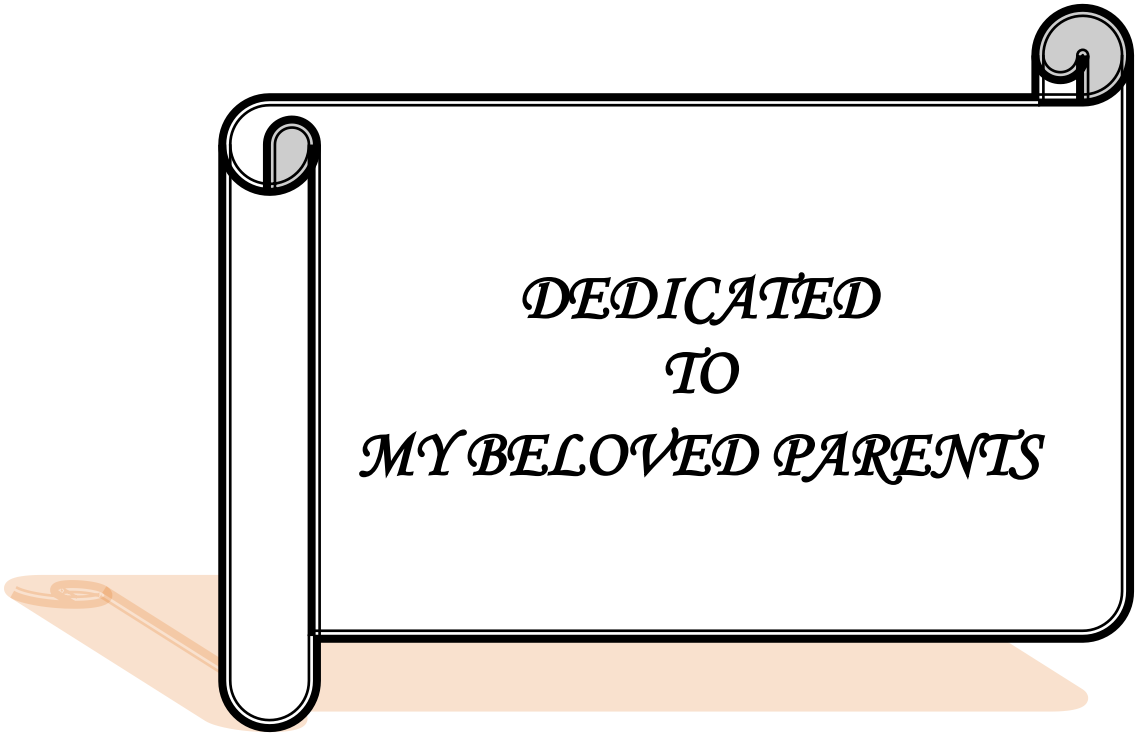
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TO
MY BELOVED PARENTS

## COMMONLY USED ABBREVIATIONS

| Full word | Abbreviation |
|---|---|
| At the rate | @ |
| Agro Ecological Zone | AEZ |
| Analysis of variance | ANOVA |
| And others | *et al.* |
| Bangladesh Agricultural Research Institute | BARI |
| Bangladesh Bureau of Statistics | BBS |
| Bangladesh | BD |
| By way of | Via |
| Cultivars | cv. |
| Centimeter | Cm |
| Canonical Variate Analysis | CVA |
| Cluster Analysis | CA |
| Degrees of Freedom | df |
| Duncan`s Multiple Range Test | DMRT |
| Etcetera | etc. |
| Environmental variance | $\sigma^2e$ |
| Food and Agricultural Organization | FAO |
| Genotypic variance | $\sigma^2g$ |
| Gram | g |
| Genotype | G |
| Genetic Advance | GA |
| Genotypic coefficient of variation | GCV |
| Genetic Advance | GA |
| Heritability in a broad sense | $h^2b$ |
| International Center for Agricultural Research in Dry Area | ICARDA |
| Indian Agricultural Research Institut | IARI |
| Journal | J. |
| Kilogram | Kg |
| Meter | M |
| Mean sum of square | MS |
| Murate of Potash | MP |
| Ministry of Agriculture | MOA |
| Number | No. |
| Namely | *Viz.* |

**COMMONLY USED SOME ABREVIATIONS (Cont'd)**

| Full word | Abbreviation |
|---|---|
| Principal Component Analysis | PCA |
| Principal Coordinate Analysis | PCO |
| Phenotypic coefficient of variation | PCV |
| Percent | % |
| Phenotypic variance | $\sigma^2p$ |
| Percentage of Co-efficient of Variation | CV% |
| Plant height | PH |
| Residual Effect | R |
| Randomized Complete Block Design | RCBD |
| Science | Sci. |
| Standard Error | SE |
| Square meter | $m^2$ |
| Sher-e-Bangla Agricultural University | SAU |
| Triple Super Phosphate | TSP |
| Thousand seed weight | TSW |
| University | Uni. |
| Variety | var. |

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**The Author**

# LIST OF CONTENTS

# LIST OF CONTENTS (Cont'd)

# LIST OF CONTENTS (Cont'd)

# LIST OF TABLES

# LIST OF FIGURES

# LIST OF PLATES

# LIST OF APPENDICES

# GENETIC DIVERSITY ANALYSIS OF RED AMARANTH (*Amaranthus cruentus* L.)

**BY**

**MD. SHAFIQUL ISLAM**

## ABSTRACT

A field experiment was conducted with 20 genotypes of red amaranth (*Amaranthus cruentus* L.) at the experimental field of Sher-e-Bangla Agricultural University, Dhaka to study the Genetic Diversity Analysis of Red Amaranth from November to December 2020. The genotypes were found significantly different for all the characters studied. Comparatively phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the traits. Experiment showed significant differences among the genotypes. Phenotypic variance was higher than that of genotypic variance for all the characters. High genotypic co-efficient of variation (GCV) was found for plant height and average leaf area plant$^{-1}$. High heritability with high genetic advance in percent of mean was observed in plant height, average stem diameter plant$^{-1}$ and yield plant$^{-1}$ (fresh weight) which indicated that these traits would be effective for genetic improvement. Correlation studies showed that positive and significant correlation of yield plant$^{-1}$ (fresh weight) with number of leaves plant$^{-1}$, average leaf length plant$^{-1}$, average leaf area plant$^{-1}$ and average stem diameter plant$^{-1}$. Path co-efficient analysis revealed that number of leaves plant$^{-1}$, average leaf area plant$^{-1}$ and average stem diameter plant$^{-1}$ had the positive direct effect on yield plant$^{-1}$ (fresh weight) whereas, plant height and average leaf length plant$^{-1}$ had the negative direct effect on yield plant$^{-1}$ (fresh weight). Diversity was estimated by cluster distance and the genotypes were grouped into five clusters. The highest inter-cluster distance was observed between clusters II and IV and the maximum intra-cluster distance was found in cluster II and the lowest inter-cluster distance was observed between clusters I and II and the minimum intra-cluster distance was found in cluster IV. Considering group distance and other agronomic performance, genotypes BD-7406 and BD-2964 in cluster IV and genotypes BD-2946 and BD-2934 in cluster III could be considered as suitable genotypes for efficient hybridization in future.

# CHAPTER I

# INTRODUCTION

The word "Amaranth" in Greek means "everlasting". National Academy of Sciences of the U.S in 1975 elected amaranths as the world's most promising crop with promising economic value. Amaranth is a herbaceous annual plant in the family Amaranthaceae. Plants in the genus *Amaranthus* have green or red leaves and branched flower stalks (heads). Mature plants bear small seeds, variable in colour from cream to gold to pink to shiny black. The genus *Amaranthus* consists of up to 70 species (in the form of cosmopolitan weed or cultivated plant) and is widely spread in all tropical and subtropical regions of the world (Espitia, 1994). Vegetable amaranthus is an herbaceous annual with upright growth habit, cultivated for both leaves and grain purpose (Panda *et al.*, 2017). Among the common species include *Amaranthus hybridus*, *A. cruentus*, *A. dubius*, *A. spinosus*, *A. blitum*, *A. caudatus*, *A. graecizans*, *A. lividus*, *A. tricolor* and *A. viridis* (Wambugu and Muthamia, 2009).

It is grown throughout the year since it has very quick growth and is suited for crop rotation. Most of the cultivated species are monoecious and wind pollinated (Khoshoo and Pal, 1970). The vegetable amaranth species (2n = 34) include *A. tricolor, A. dubius, A. lividus, A. blitum, A. tristis,* and *A. viridis,* while grain types (2n = 32) includes *A. cruentus A. caudatus* and *A. spinosus.* The diversity of amaranth are Central and South America, India and South East Asia with secondary centres of diversity in West and East Africa. Vegetable type of leaf red amaranth is *Amaranthus cruentus,* originated in south East Asia, particularly in India (Rai and Yadav, 2005). It is an important vegetable cultivated in Bangladesh for tender vegetable. The total area and production of red amaranth in Bangladesh is about 28436 acres and 53749 tonnes respectively (BBS, 2017).

Red amaranth (*Amaranthus cruentus*) is recognized as an easy-to-grow and extremely productive and nutritious vegetable. The vegetable amaranth is one of the popular leafy vegetables in the South-East Asia and is becoming increasingly popular everywhere due to its attractive leaf colour, taste and nutritional value.

Amaranth plant belongs to C4 plant group, it has a high rate of photosynthesis and excellent water use efficiency at high temperature and high radiation intensity (Panda *et al.*, 2017). The nutritional endowments of amaranths provide evidence that the plants deserve some scientific attention . Lysine and Sulphur containing amino acids have been found in their leaves (Dodok *et al*., 1997). Many vegetables and cereal grains lack these amino acids. Additionally the leaves are high in carbohydrates, several vitamins including beta- carotene, vitamin C and minerals such as iron, calcium, manganese and zinc (Gamel *et al*., 2016 and Das, 2016). It also contains high amount of protein, dietary fiber and has been rated equal or superior in taste to spinach and is considerably higher in protein (14-30% on dry weight basis) (Das, 2016). It fits well in multiple and mixed cropping system because of its short duration with high yield potential of edible matter per unit area (Panda *et al.*, 2017).

Considering the potentiality of this crop, there is need to develop varieties suitable for cultivation under specific agro-ecological conditions. The knowledge regarding the amount of genetic variability existing for various characters is essential for initiating the crop improvement program. With limited variability, much improvement cannot be achieved, hence, the breeders will have to enrich the germplasm or can be restored to create greater variability through hybridization, mutation and polyploidy breeding (Panda, 2015).

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

genotypes. Such studies are also useful in selection of parents for hybridization to recover superior transgressive segregates. Hence, the present investigation entitled “characterization and genetic diversity analysis of red amaranth” has been designed with the following objectives.

i. To assess the extent of genetic variability for yield and its component traits in red amaranthus genotypes

ii. To study the character association (correlation) and path analysis among yield and its contributing characters

# CHAPTER II

# REVIEW OF LITERATURE

Vegetable breeder is primarily concerned with the improvement of both quantitative and qualitative plant characters. Hence, adequate knowledge on genetics of various traits is very essential in vegetable breeding program for obtaining desired results in succeeding generations. However, the success of vegetable breeding depends on the extent and the magnitude of variability existing in the germplasm. At the same time, improvement is possible on the basis of heritable variation.

*Amaranthus* is a short duration, nutritious leafy vegetable. In India lot of variation has been observed in this crop leading to development of several new promising varieties/ lines. As there is every possibility, that the established varieties may lose their importance in course of time, hence to search for new cultivars is a continuous process. Further for crop improvement programs like selection and hybridization, a sound knowledge of nature of character association and genetic divergence in any crop is highly essential. In the present investigation, an attempt has been made to study the genetic variability, divergence, heritability, character association and path co-efficient analysis in amaranthus. Therefore, reviews relevant to amaranthus on these aspects have been presented below for interpretation of results under the following headings.

2.1 Genetic variability for yield and its component traits in amaranthus genotypes

2.2 Character association (correlation) and path analysis among yield and its contributing characters

2.3 Genetic diversity among the genotypes for yield and its component traits

## 2.1 Genetic variability for yield and its component traits in amaranthus genotypes

Selection of superior genotypes at one stage or the other is most important aspect in any plant improvement program and the effectiveness of selection is based on the existence of genetic variability within or among the population subjected to selection (Dixit *et al.*, 1971; Swamy, 1972; Tikka *et al.*, 1974). Therefore, a quantitative measure of genetic variability would be extremely important in breeding for improvement of quantitative traits.

Yogendra *et al.* (2018) studied the genetic variability available in amaranthus under Chhattisgarh plain condition for twenty-five genotypes. High magnitude of GCV and PCV were observed for seed yield per plot, followed by test weight, petiole length, number of leaves plant, stem girth, leaf breadth, leaf length, number of branches plant and leaf yield. The heritability estimates recorded to be high for the characters *viz.* dry matter per cent, fiber content, seed yield plot, stem girth, test weight, leaf yield per plot, petiole length, leaf breadth and root length, leaf length, number of branches plant, plant height. Highest estimates of genetic advance as percentage of mean was obtained for characters namely seed yield per plot and test weight, petiole length, number of leaves per plant, stem girth and leaf breadth.

Tiwari (2018) studied on genetic variability and genetic divergence for seed yield and its component characters in grain amaranth *(Amaranthus hypochondriacus* L.) germplasms. The maximum plant height (148.00 cm) was noticed in IC-95339. The genotype IC-82625 recorded highest seed yield per plant (46.69 g).

Malagan *et al.* (2018) conducted an experiment on genetic variability, heritability and genetic advance in grain amaranth (*Amaranthus* spp.) among forty-four genotypes and analysis of variance revealed significant differences among the genotypes for all the characters studied. High PCV and GCV was observed for number branches per plant, number of panicles per inflorescence,

number of inflorescence per plant, panicle length (cm), panicle breadth (cm), thousand seed weight (mg), seed yield per plant (g), inflorescence length (cm), plant height at 90 das (cm) and stem diameter (cm). On the other hand, low PCV and GCV were observed for days to seed maturity. All the traits studied exhibited high heritability. High genetic advance as per cent of mean was observed for number of branches per plant, number of inflorescence per plant, number of panicles per inflorescence, panicle length (cm), panicle breadth (cm), thousand seed weight (mg) and seed yield (g) indicating predominance of additive genetic component in expression of these traits. Thus, there is scope for improvement of seed yield by adopting selection.

Tejaswini *et al.* (2017) evaluated twenty-seven genotypes along with two checks (Arka Suguna and Arka Arunima) of vegetable amaranth *(Amaranthus tricolor* L.). for genetic variability, heritability and genetic advance for yield and yield attributing traits and found that the estimates of PCV and GCV were high for plant height, stem diameter, number of branches per plant, leaf area index, number of leaves per plant, leaf weight per plant, leaf stem ratio at 30, 60 and 90 DAS, leaf length at 30 and 90 DAS, stem weight per plant at 30 and 60 DAS, total foliage yield, total chlorophyll content, carotenoids, protein content, ascorbic acid and oxalate content indicating the existence of wider genetic variability for these traits in the germplasm. High heritability coupled with high genetic advance expressed in percentage of mean was observed for plant height, stem diameter, stem weight per plant, number of branches per plant, leaf length, leaf width, leaf area index, number of leaves per plant, leaf weight per plant, leaf/stem ratio at 30, 60 and 90 DAS, foliage yield per plant, total chlorophyll content, carotenoids, protein content, ascorbic acid, oxalate content, iron content, folic acid indicating that these traits were mainly governed by additive gene action and response for further improvement of these traits.

Panda *et al.* (2017) conducted an experiment to study genetic variability and varietal performance in vegetable amaranthus *(Amaranthus spp.)* among 12

genotypes. Expression of high to moderate PCV and GCV for characters like number of inflorescence per plant, leaf: stem ratio, stem weight, yield per plant, leaf weight and plant height indicated the presence of good amount of variability among the genotypes indicating selection for such characters would be effective in amaranthus.

Lokeshkumar and Murthy (2017) studied genetic variability and divergence for yield component traits in grain amaranth *(Amaranthus spp.)* and found high phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) was observed for all the traits except for chlorophyll content (SPAD chlorophyll meter reading), panicle width and 1000 seed weight.

Sarker *et al.* (2015) evaluated forty three vegetable amaranth *(Amaranthus tricolor* L.) genotypes selected from different eco-geographic regions of Bangladesh for genetic variability, heritability and genetic association among mineral elements and quality and agronomic traits and the analysis showed that vegetable amaranth is a rich source of K, Ca, Mg, proteins and dietary fiber with average values among the 43 genotypes showed a biological yield >2000 $g/m^2$ and high mineral, protein, and dietary fiber contents. Eleven genotypes had high amount of minerals, protein, and dietary fiber with above-average biological yield; nine genotypes had below average biological yield but were rich in minerals, protein, and dietary fiber.

Dhangrah *et al.* (2015) conducted an experiment on heritable variation and predicted selection response of green yield and its component traits in vegetable amaranth among twenty-two genotypes. The results revealed that high to moderate estimates of coefficients of variation (GCV and PCV), high heritability.

Yadav *et al.* (2014) conducted an experiment on analysis of variability parameters for morphological and agronomic traits in grain amaranth genotypes. Genotypic co-efficient of variation for different characters ranged from 11.60 to 42.73 per cent. The highest GCV was recorded with grain yield

per plant (42.73 %). High heritability exhibited for all the characters which ranged from 97.81 to 99.98 percent.

Venkatesh *et al.* (2014) studied genetic variability, heritability and genetic advance in grain amaranth *(Amaranthus* spp.) among 100 germplasm accessions evaluated, all the traits exhibited high heritability. High genetic advance as per cent mean was observed for days to 50 per cent flowering, stem girth, number of leaves per plant , plant height, panicle length, panicle width and grain yield per plant indicating scope for improvement of these traits of interest through hybridization and selection.

Sarker *et al.* (2014) studied genotypic variability for nutrient, anti oxidant, yield and yield contributing traits in vegetable amaranth and found 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 insignificant genotypic correlations with foliage yield, indicating selection with these traits might be possible without compromising any yield loss. On the other hand, concomitant selection based on high nutrient, antioxidant content and high foliage yield would be effective selection method for improvement of vegetable amaranth.

Mobina *et al.* (2014) studied the vegetative yield attributes for eight genotypes of amaranth cultivars, results indicated the existence of considerable amount of genetic variation for all the traits except leaf length in 60 days. GCV was highest for the leaf number and lowest in the leaf length. The heritability ranged between 0.265 (leaf length) to 0.913 (leaf per plant), the value genetic advance in the ranged from 2.3 (Leaf width) to 123.44 (leaf per plant).

Ramesh *et al.* (2013) studied genetic parameters in grain amaranthus *(A. hypochondriacus*) as influenced by plant densities. Among ten genotypes and reported high PCV and GCV for leaf area at 50 per cent flowering, length of inflorescence, grain yield, carbohydrates and protein. Medium PCV and GCV observed were for plant height, days to 50 per cent flowering and diameter of

the inflorescence whereas high heritability and GAM was observed for all the traits.

Hasan *et al*. (2013) studied genetic variability, correlation and path analysis, among seventeen genotypes of stem amaranth *(Amaranthus tricolor* L.) to determine the genetic variability, degree of association between yield and its component characters. High heritability with high genetic advance as per cent of mean was registered for number of leaf, leaf weight and marketable yield.

Chattopadhyay *et al.* (2013) estimated genetic parameters among 11 genotypes. High to moderate GCV and PCV values for shoot weight per plant, green yield per plant, shoot-leaf ratio, leaf weight, number of leaves per plant and plant height.

Akaneme and Ani (2013) conducted an experiment on morphological assessment of genetic variability among accessions of *Amaranthus hybridus.* Analysis of variance revealed highly significant differences ($P<0.001$) for leaf width, hypocotyls length, days to 50 per cent flowering, 500 seed weight ($P<0.01$) and leaf length ($P<0.05$). The range, co-efficient of variability, phenotypic and genotypic coefficient of variability also revealed high variability for each of the quantitative traits. The highest broad sense heritability ($h^2b$), GCV, PCV and GA were obtained for days to 50 percent flowering which was also positively correlated with leaf length and stem diameter.

Sravanthi *et al.* (2012) evaluated genetic parameters for grain yield and its associated traits by evaluating 40 germplasm lines along with 3 checks of *Amaranthus spp.* Analysis of variance revealed highly significant differences for genotypes, indicating magnificent variation among the genotypes for all the nineteen characters *viz.,* plant height, stem girth, stem weight, number of branches per plant, leaf area, leaf length, leaf width, petiole length, total leaf weight, number of leaves per plant, days to 50 per cent flowering, inflorescence length, lateral spikelet length, days to 80 per cent maturity of

seed, leaf: stem ratio, 1000 seed weight, protein content, dry matter content, seed yield per plant. High estimates of phenotypic and genotypic co-efficient of variation for almost all traits except protein content indicated that there was high variability offering ample scope for selection of desired variability. High estimates of heritability along with genetic advance as per cent of mean for all the characters indicated that these characters were under additive gene action and there were excellent chances of effective selection for improvement of these traits.

Sravanthi *et al.* (2012) observed high estimates (>60%) of heritability for plant height (83.59%), stem girth (87.65%), stem weight (98.90%), number of branches/plant (82.43%), petiole length (92.85%), leaf length (90.02%), leaf width (81.97%), leaf area (98.76%), total leaf weight (99.05%), number of leaves/plant (92.07%), days to 50% flowering (97.68%), inflorescence length (97.09%), lateral spikelet length (97.74%), days to 80% maturity of seed (88.67%),1000 seed weight (95.01%), protein content (96.41%), dry matter content (98.36%), leaf: stem ratio (96.17%) and seed yield (87.29%) in grain amaranth.

Pan *et al.* (2008) studied genetic variation and character association in vegetable amaranth *(Amaranthus tricolor* L.) and observed maximum extent of genetic variability for leaf: stem ratio followed by greens/plot, girth of stem and length of leaf.

Kusuma *et al.* (2007) evaluated grain amaranthus collections for productivity and quality traits and found that high GCV and PCV for panicle length, dry weight of panicle, dry weight of stem, harvest index and seed yield in grain amaranth. Low PCV and GCV were reported for 50 per cent flowering and days to maturity whereas moderate PCV and GCV for plant height and girth. High heritability and GAM recorded for panicle length, dry weight of panicle, dry weight of stem and moderate heritability and GAM for 50 per cent

flowering, maturity and stem girth. However, high heritability and moderate GAM were reported for plant height, harvest index and yield.

Anuja and Mohideen (2007) conducted an experiment on genetic variability and heritability in amarathus *(Amaranthus spp.),* High GCV was observed for number of leaf 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.

Vujacic (2005) conducted an experiment on variability and factor analysis of morphological and productive characteristics of species of the genus *amaranthus.* Among ten genotypes, variability within a specific trait was significant. In case of the plant height, it ranged between 93.18 cm and 160.78 (A. *mantegazzianus);* foliage per plant raged between 12.89 *(A. cruentus)* and 23.46 *(A. mantegazzianus);* average foliage length varied from 14.77 *(A. cruentus)* to 26.72 cm *(A. mantegazzianus);* average foliage width ranged between 6.30 *(A. cruentus)* and 14.46 cm *(A. mantegazzianus);* foliage mass per plant ranged between 94.05 *(A. molleros)* and 246.81 g *(A. mantegazzianus).* Seed mass per plant varied from 45.56 *(A. molleros)* to 67.55 g *(A. mantegazzianus).*

Hiremath (2005) studied the variability in grain amaranthus and found that high PCV, GCV, heritability and GAM for plant height, length of inflorescence and grain yield. Whereas low PCV, GCV, high heritability and moderate GAM for maturity and protein content. Days to 50 per cent flowering exhibited moderate PCV, low GCV, high heritability and moderate GAM.

## 2.2 Character association and path analysis among yield and its contributing characters

The most important economic character in crop plant is yield, which is complex one and is dependent on a number of directly or indirectly associated traits. Therefore, knowledge on the nature of association of different attributes with yield is essential. The nature of association between two components may be positive or negative. When any two attributes are positively associated then selection for one will indirectly result in selection of other. When any two attributes are negatively correlated, selection of one will have adverse effect for the selection of the other character.

Tiwari (2018) conducted an experiment to know variability and genetic parameters for different yield contributing traits in twenty- seven genotypes of grain amaranth and found that days to maturity got significant positive correlation with seed yield, plant height, length of inflorescence and seed weight (g). Plant height was also found to have significant positive correlation with seed yield and seed weight. Length of inflorescence and seed weight had significant and positive correlation with yield. In case of path analysis, days to maturity had direct effects on grain yield than seed weight, length of inflorescence and plant height.

Jangde *et al.* (2017) studied correlation and path co-efficient analysis in vegetable amaranthus *(Amaranthus tricolor* L.) among 25 genotypes and reported that leaf yield (kg) per plot showed positive and significant correlation with number of leaves per plant and fresh stem weight for quantitative characters. Chlorophyll-a showed a significant positive correlation with total chlorophyll at both phenotypic and genotypic level only. Chlorophyll-b showed significant positive correlation with total chlorophyll at both phenotypic and genotypic levels. Path co-efficient 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 plant height (0.071) exhibited direct negative effect on yield.

Dhangrah *et al.* (2015) conducted an experiment on heritable variation and predicted selection response of green yield and its component traits in vegetable amaranth among twenty-two genotypes. The correlations between green yield and its components such as leaf number, leaf length: width ratio, plant weight, stem fresh weight and leaf fresh weight were significant and positive indicating the possibility of indirect selection and realizing a correlated response. However, the leaf: stem ratio (fresh) showed negative correlation with green yield and positive correlation with marketable maturity which suggested selection of lower leaf : stem ratio (fresh) for obtaining high green yield with early maturity.

Hailu *et al.* (2015) reported lower value for phenotypic correlation co-efficient than the genotypic correlation co-efficient in most of the characters. The green leaf yield per plant showed a positive and significant relationship with the majority of the traits except lateral inflorescence which had negative significant association with green leaf yield in amaranthus.

Sarker *et al.* (2015) studied the variability, heritability and genetic association in vegetable amaranth *(Amaranthus tricolor* L.) and results indicated that biological yield exhibited a strong positive correlation with leaf area, shoot weight, shoot/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.

Yadav *et al.* (2014) studied the variability parameters for morphological and agronomic traits in grain amaranth *(Amaranthus spp.)* genotypes. At genotypic level, seed yield per plant showed highly significant positive correlation with days to 80 percent maturity and plant height and significant positive correlation

with days to 50 percent flowering. Inflorescence length had significant positive correlation with lateral spikelet length.

Patial *et al.* (2014) conducted an experiment on character association and path co-efficient analysis in grain amaranth *(Amaranthus spp.).* Twenty-two genotypes of amaranth were evaluated for 12 quantitative traits for two years and results indicated that all traits except days to seed fill possessed positive association with grain yield. Harvest index was positively correlated with days to maturity. Harvest index, aerial biomass per plant and days to maturity also had high phenotypic and genotypic direct effects on seed yield per plant, revealing that indirect selection for these traits would be effective in improving seed yield.

Chattopadhyay *et al.* (2013) studied genetic parameters, inter-relationships and genetic divergence of vegetable amaranthuhs. Among 11 genotypes. From the correlation and path analysis, they concluded that emphasis should be given to shoot weight per plant, stem diameter and leaf-shoot ratio for selecting high yielding genotypes.

Hasan *et al.* (2013) evaluated seventeen genotypes of stem amaranth (*Amaranthus tricolor* L.) to determine the genetic variability, degree of association between yield and its component characters. The correlation studies revealed strong positive association of yield with leaf weight, stem weight, stem diameter, dry weight with rind, and dry weight without rind. The result of path analysis indicated that stem weight had maximum direct effect on marketable yield followed by leaf weight, leaf number and dry weight without rind.

Kendre *et al.* (2013) studied correlation and path analysis in leafy *Amaranthus tricolor* L. and it revealed that, plant height and petiole length exhibited positive and significant association with the yield in amaranth and also indicated their relative importance in leaf yield. Path analysis revealed that, the character *viz.* stem diameter exerted highest direct effect over yield followed

by petiole length, leaf area and number of leaves. While plant height exhibited the negative direct effect on yield, however it exhibited significant correlation co-efficient value.

Khurana *et al.* (2013) studied correlation of quantitative characters and concluded that plant height was positively correlated with number of branches per plant, leaf length, leaf width, number of leaves per plant, leaf area index, total green yield, while number of leaves per plant was positively correlated with leaf area index, total green yield. Leaf area index was positively correlated with total green yield. The genotypic coefficient of correlation, in general, was high in magnitude than the corresponding phenotypic coefficient of correlation indicating that there is an inherent association among the various characters studied. Total green yield exhibited highly significant and positive correlation with plant height, number of branches per plant, leaf length, leaf width, number of leaves and leaf area index both at genotypic and phenotypic levels.

Ahammed *et al.* (2012) studied the correlation in amaranthus and 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.

Shankar *et al.* (2012) conducted an experiment on genetic variability, correlation and path analysis in grain amaranth and found that yield per plot had a significant positive correlation with leaf length, leaf width, stem weight, leaf weight, number of leaves per plant and shoot weight.

## 2.3 Genetic diversity among the genotypes for yield and its component traits

Clustering based on mean values of the traits of experimental material enables to distinguish genetically close and divergent types which is prerequisite for

both theoretical as well as practical plant breeding. Eco-geographical diversity has been regarded as an index of genetic diversity (Vavilov, 1926).

The technique of Mahalanobis $D^2$ statistic has been employed widely to resolve genetic divergence at inter-varietal, subspecies and species levels in several crops. A brief review of work carried out in this aspect in vegetable amaranth is presented below.

Tiwari (2018) studied on genetic variability and genetic divergence for seed yield and its component characters in grain amaranth *(Amaranthusm hypochondriacus* L.) germplasms. Fifty-four genotypes were grouped into eight different non-overlapping clusters. The highest inter cluster distance was observed between cluster III and cluster VIII (67.39) followed by cluster IV and cluster VII (64.30) suggesting wide diversity among these groups. Considering cluster mean and genetic distance, crossing between genotypes of cluster IV (IC-82625 and IC-95247) with cluster VIII (Durga) were likely to recombine the genes for high seed yield under temperate conditions of mid hills in Uttarakhand.

Lokeshkumar and Murthy (2017) investigated on genetic variability and divergence studies for yield component traits in grain amaranth *(Amaranthus spp.).* The divergence studies using K-means clusters analysis approach has grouped the test materials into seven clusters. Cluster V was the largest comprising of 25 genotypes while cluster VII was solitary with only one genotype. Inter-cluster distance was maximum between clusters II and cluster VII. The genotypes IC095204, SKGPA-70 and IC095244 superior over the standard check for grain yield.

Ogbangwor (2014) studied the extent of genetic divergence among 30 genotypes of vegetable amaranth, using 12 morphological and three qualitative characters. The statistical analysis revealed significant differences among the amaranth genotypes for stem diameter, petiole length, leaf length, fresh weight of leaf, stem, root and whole plant, leaf-stem ratio and leaf dry matter yield.

The result of cluster analysis using FASTCLUS grouped the genotypes into seven clusters. It displayed a wide range of diversity for most of the traits.

Akther *et al*. (2013) conducted an experiment on genetic divergence in stem amaranth (*Amaranthus tricolor* L.) genotypes for yield and its component characters and results indicated that the highest inter cluster distance was observed between IV and I, followed by the distance between cluster II and I showing wide diversity among the groups. The highest intra-cluster distance was observed for the cluster IV and the lowest for the cluster I. The genotypes of stem amaranth from cluster I and cluster IV may be selected as parents in future hybridization program.

Akaneme and Ani (2013) studied the morphological assessment of genetic variability among accessions of *Amaranthus hybridus.* Dendrogram divided the accessions into cluster I comprising accessions 3 and 5 and cluster II comprising accessions 1, 2 and 4. The qualitative traits differed among the accessions with the exception of growth habit, branching index and leaf shape. These variations provide ample opportunities for plant breeders to carry out selection while designing plant breeding program for the improvement of the species.

Chattopadhyay *et al.* (2013) studied genetic divergence of vegetable amaranthus. Among 11 genotypes, based on degree of divergence the genotypes were grouped into two clusters. The top two characters which contributed most towards genetic divergence were shoot weight per plant and leaf weight per plant, genotypes belonging to cluster I could be regarded as useful sources of gene for improving green yield of vegetable amaranthus.

Shankar *et al.* (2012), studied 28 accessions of amaranthus, comprising *A. tricolor*, *A. cruentus*, *A. hybridus* and *A. dubius* classified them into 12 cluster groups at 0.78 Euclidean distances: clusters I, II, III and V were major clusters having 14, 2, 2 and 2 accessions, respectively.

Pandey and Singh (2011) studied genetic divergence in grain amaranth (*Amaranthus hypochondriacus* L.). The 98 genotypes were grouped into 18 clusters in which cluster I contained maximum number of genotypes (42), Cluster II (11), Cluster III (7), Cluster IV and V (5 in each case) and Cluster VI has 4 genotypes. Cluster VII, VIII, IX, X have (3 in each), cluster XI, XII, XIII, XIV (2 in each) and clusters XV, XVI, XVII and XVIII (1in each case).

Pandey (2009) conducted an experiment on genetic divergence of parents and $F_2$ segregates in grain amaranthus, among twenty-six accessions including both indigenous and exotic introductions, based on $D^2$ analysis, the accessions were grouped into eleven clusters. The accession in cluster V had the greatest divergence, closely followed by those of clusters IV and I. The maximum and minimum divergences were revealed between clusters VIII and XI and between II and VII respectively. The parents involved in these eight potential crosses showed moderate genetic divergence.

Yashwant (2009) conducted an experiment on genetic diversity among the hundred genotypes of grain amaranth in summer and *kharif* seasons. Using estimated $D^2$ values, 100 genotypes were grouped into 12 and 14 clusters in the experiment done in summer and *kharif* season respectively. Clustering pattern in the summer experiment revealed that the cluster X to be the larger of all, consisting of 22 genotypes whereas 14 clusters were formed in *kharif* season and cluster I being largest of all with 23 genotypes. In this study, the intra-cluster $D^2$ value ranged from 24.4 to 62558.8 and 12.0 to 167150.0 in summer and *kharif* seasons respectively. The average intra-cluster distance was maximum for cluster XII followed by cluster II, X and I, while minimum was found in cluster III whereas, in *kharif* it was the cluster III which had maximum average intra-cluster distance and minimum intra-cluster distance was observed in cluster II. The inter-cluster $D^2$ values exhibited a wide range of cluster distance from 17.43 to 341.08 and 15.9 to 213.5 in summer and *kharif respectively*. Maximum and minimum inter-cluster distances were found

between cluster VIII and V and III and IX, respectively in summer and between VIII and IX and IX and IV in *kharif.*

Kusuma *et al*. (2007) studied genetic divergence among 64 grain amaranth genotypes using Mahalanobis $D^2$ statistic. The genotypes were grouped into 11 clusters, which revealed maximum inter cluster distance between III and cluster XI, followed by cluster VII and XI, cluster II and III. The trait Panicle fresh weight contributed maximum towards genetic divergence.

Hiremath (2005) studied the genetic diversity among 144 genotypes of grain amaranth *(Amaranthus spp.).* The genotypes were grouped into five clusters based on the $D^2$ values. Cluster V was the largest with 127 genotypes while cluster IV was a smallest cluster with two genotypes. The inter-cluster $D^2$ values ranged widely from 314.955 between cluster I and II and 155.637 between cluster IV and V indicating presence of genetic variability for physiological parameters in grain amaranth *(Amaranthus spp.* L.). The percent contribution of character indicated that grain protein content was the major contributor towards divergence followed by fresh weight and length of inflorescence.

# CHAPTER III

# MATERIALS AND METHODS

To carry out the experiment 20 selected genotypes of red amaranth *(Amaranthus cruentus* L.) were used as lines and these were done in Rabi season 2020. In Rabi season, the lines of red amaranth were grown in the experimental field.

## 3.1 Experimental site

The experiment was carried out at the experimental field of Sher-e-Bangla Agricultural University, Dhaka – 1207 during November to December 20. The location of the experimental site was situated at 23°74′N latitude and 90°35′E longitudes with an elevation of 8.6 meter from the sea level. Photograph showing experimental site (Appendix I).

## 3.2 Soil and Climate

The soil of the experimental site was in the subtropical zone which belongs to Agro ecological region of "Madhupur Tract" (AEZ No. 28). The soil was clay loam in texture and olive gray with common fine to medium distinct dark yellowish brown mottles. The pH was 5.47 to 5.63 and organic carbon content was 0.82% (Appendix II). The records of air temperature, humidity and rainfall during the period of experiment were noted from the Bangladesh Meteorological Department, Agargaon, Dhaka (Appendix III).

## 3.3 Experimental materials

The healthy seeds of 20 genotypes of red amaranth *(Amaranthus cruentus* L.) collected from the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, which were used as experimental materials. The materials used in that experiment is shown in Table 1.

**Table 1. Materials used for the experiment**

| Genotypic symbols | Genotypes | Source |
|---|---|---|
| $G_1$ | BD-2925 | PGRC, BARI |
| $G_2$ | BD-2928 | PGRC, BARI |
| $G_3$ | BD-2930 | PGRC, BARI |
| $G_4$ | BD-2934 | PGRC, BARI |
| $G_5$ | BD-2941 | PGRC, BARI |
| $G_6$ | BD-2942 | PGRC, BARI |
| $G_7$ | BD-2946 | PGRC, BARI |
| $G_8$ | BD-2947 | PGRC, BARI |
| $G_9$ | BD-2956 | PGRC, BARI |
| $G_{10}$ | BD-2957 | PGRC, BARI |
| $G_{11}$ | BD-2958 | PGRC, BARI |
| $G_{12}$ | BD-2961 | PGRC, BARI |
| $G_{13}$ | BD-2964 | PGRC, BARI |
| $G_{14}$ | BD-7400 | PGRC, BARI |
| $G_{15}$ | BD-7406 | PGRC, BARI |
| $G_{16}$ | BD-9004 | PGRC, BARI |
| $G_{17}$ | BD-9790 | PGRC, BARI |
| $G_{18}$ | BD-9795 | PGRC, BARI |
| $G_{19}$ | BD-9806 | PGRC, BARI |
| $G_{20}$ | BD-9815 | PGRC, BARI |

### 3.4 Land preparation

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

### 3.5 Application of manure and fertilizer

The crop was fertilized at the rate of 10 tons of Cow dung, 250 kg Urea, 150 kg Triple Super Phosphate (TSP), 200 kg Muriate of Potash (MP), 250. The half amount of urea, total amount of Cow-dung, TSP, MP were applied during final land preparation. The rest amount of urea was applied as top dressing after 15 days of sowing.

### 3.6 Experimental design and layout

Field layout was done after final land preparation. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. The total area of the experiment was 56 m × 14 m = 784 $m^2$. Each replication size was 1 m × 1 m, and the distance between replication to replication was 0.5 m.

### 3.7 Sowing of seeds

Seeds of red amaranth *(Amaranthus cruentus* L.) were sown in lines in the experimental plots on 20 November, 2020. The seeds were placed at about 1 cm depth in the soil. After sowing the seeds were covered with soil carefully so that no clods were on the seeds. Seeds were grown in separate line in the experimental field on 23 November, 2020. The row spacing was 30 cm having plant spacing 10 cm within the row. The seedlings emerged within three days.

### 3.8 Irrigation and drainage

The irrigation was given by sprinkler after sowing of seeds to bring proper moisture condition of the soil to ensure uniform germination of the seeds. A

good drainage system was maintained for the immediate release of rainwater from the experimental plot during the growing period.

### 3.9 Intercultural operation

Necessary intercultural operations were done during the crop period to ensure the normal growth and development of the plants. Thinning and 1st weeding was done after 10 days of sowing. Top-dressing was done after 15 days of sowing. For controlling leaf caterpillars, Nogos @ 1 mi/L water were applied 2 times at an interval of 7 days, starting soon after the appearance of infestation. There was no remarkable attack of diseases.

### 3.10 Harvesting of sample plants

The plants were harvested to obtain vegetative yield. The harvesting was completed by 15 December 2020. At the time of harvest, 10 plants were selected at random from the middle row of each plot. The sample plants were tagged properly and then harvested by uprooting. Data were recorded from these 10 plants. A pictorial view of all harvested plants (genotypes) at the vegetative stage is presented on plates 1 to 5.

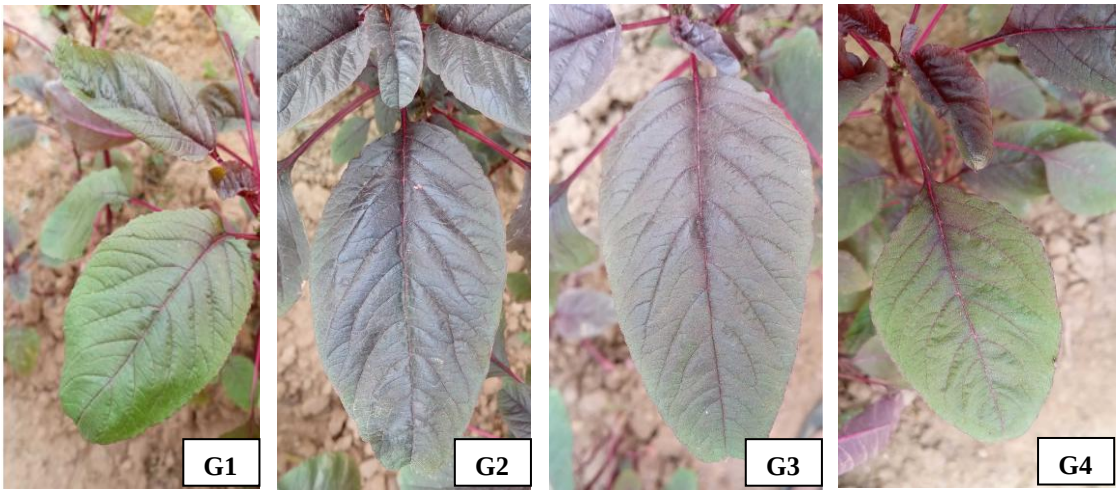


Plate 1. Pictorial view of harvested genotypes of G1–G4.

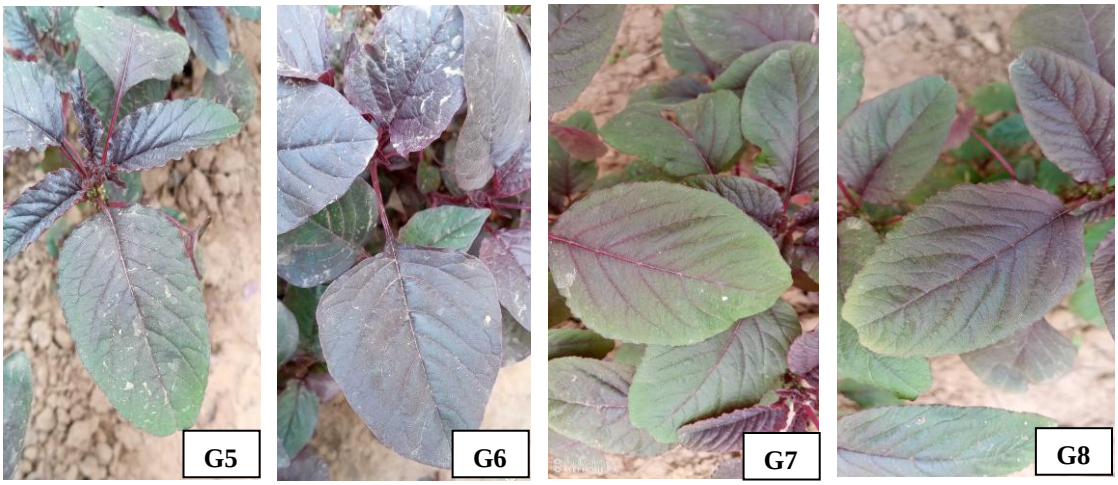


Plate 2. Pictorial view of harvested genotypes of G5–G8.

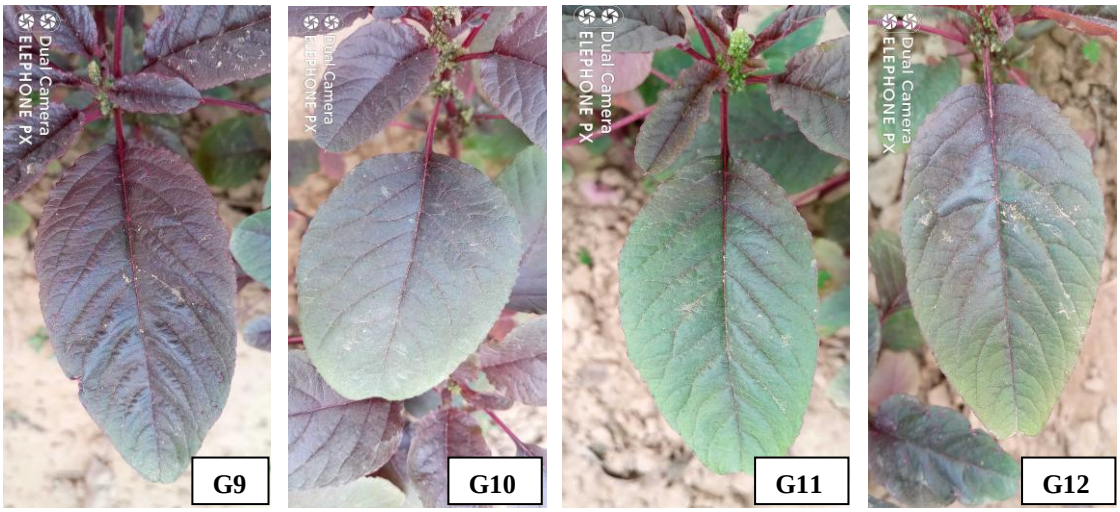


Plate 3. Pictorial view of harvested genotypes of G9–G12.

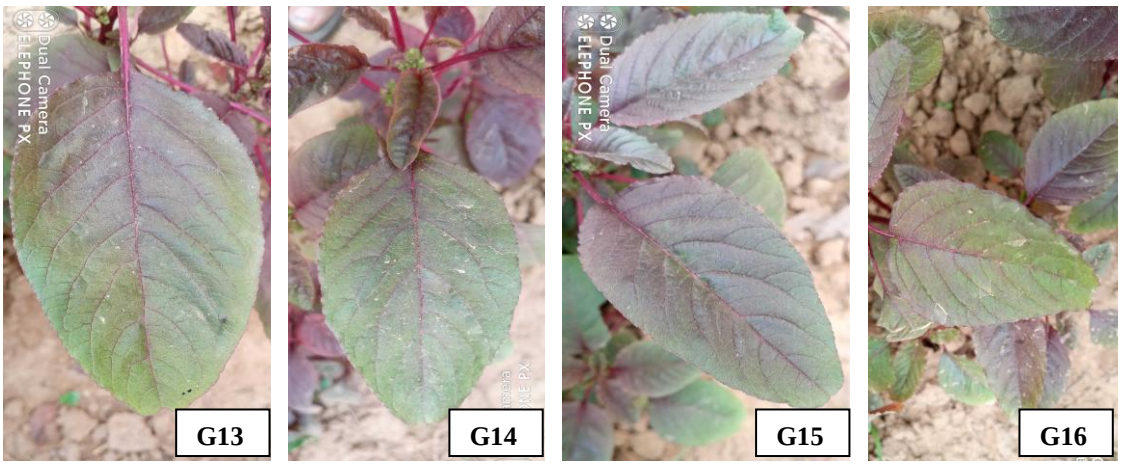


Plate 4. Pictorial view of harvested genotypes of G13–G16.

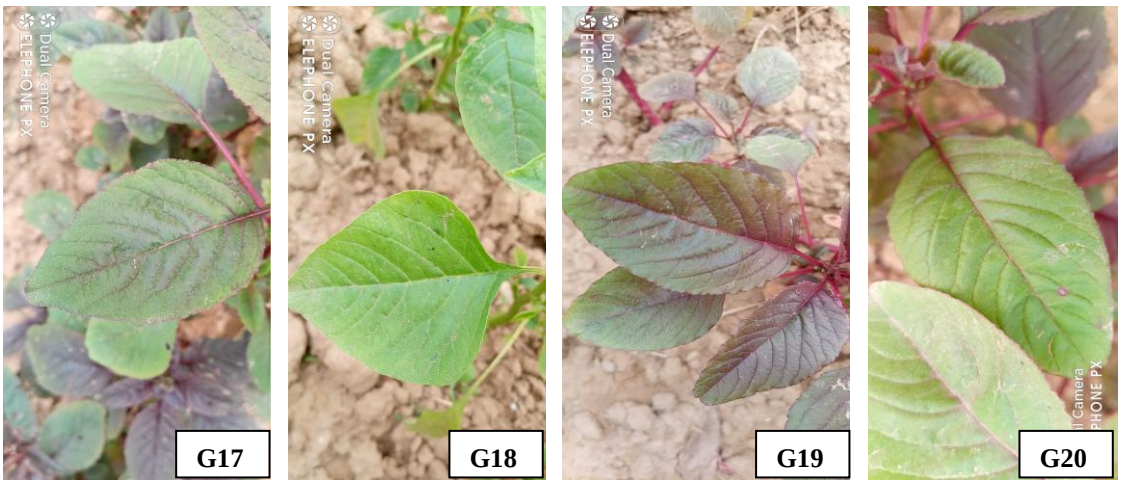


Plate 5. Pictorial view of harvested genotypes of G17–G20.

### 3.11 Data collection

For studying different genetic parameters and inter-relationships, six characters were taken into consideration. A pictorial view of observation and data collection is presented in Plate 6. The data were recorded on ten selected plants for each genotype (parent) on the following characters:

1) **Plant height (cm):** It was measured in centimeters (cm) from the base of the plant to the tip of the top leaf. Data were taken after harvesting.
2) **Number of leaves plant$^{-1}$:** The total number of leaves that appeared in the plant was counted from the sample of 10 plants and the mean value was recorded.
3) **Average leaf length plant$^{-1}$ (cm):** The leaves were selected randomly from a different position and their lengths were measured by recording the length starting from the tip of the leaves to the base of the petiole and expressed in centimeter (cm).
4) **Average leaf area plant$^{-1}$ (cm$^2$):** Leaf area was measured from 10 selected plants using a leaf area meter instrument expressed in cm$^2$.
5) **Average stem diameter plant$^{-1}$ (mm):** Stem diameter was measured at five cm above the ground level with the help of slide calipers and expressed in millimeters.
6) **Yield plant$^{-1}$ (fresh weight) (g):** Fresh weight of randomly selected 10 plants from each replication was recorded and the mean value was taken as fresh weight plant$^{-1}$ and was expressed in grams.

Plate 6. Experimental field showing data collection.

### 3.12 Statistical analysis

#### 3.12.1 Estimation of genetic parameters

Estimation of phenotypic ($\sigma^2p$), genotypic **(**$\sigma^2g$), and environmental ($\sigma^2e$) variance were calculated by the following formula (Johnson *et al.*, 1955).

$$\text{Genotypic variance } (\delta^2g) = \frac{MSG - MSE}{r}$$

Where,

*MSG* = Mean Square due to Genotypes.

*MSE* = Mean Square Error

*r* = Number of replication

Phenotypic variance ($\sigma^2p$) = $\sigma^2g + \sigma^2e$

Where,

$\sigma^2g$ = Genotypic variance

$\sigma^2e$ = Environmental variance = MSE

#### 3.12.2 Estimation of genotypic coefficient of variation and phenotypic coefficient of variation

Genotypic and phenotypic coefficients of variation were estimated according to the formula given by Burton (1952) and Singh and Chudhary (1985).

$$\text{Genotypic Co-efficient of Variation (GCV \%)} = \frac{\sqrt{\sigma^2g}}{\overline{X}} \times 100$$

Where,

$\sigma^2g$ = Genotypic variance

$\overline{X}$ = Population mean

$$\text{Phenotypic Co-efficient of Variation (PCV \%)} = \frac{\sqrt{\sigma^2p}}{\overline{X}} \times 100$$

Where,

$\sigma^2p$ = Phenotypic variance

$\overline{x}$ = Population mean

### 3.12.3 Estimation of heritability

Heritability in a broad sense was estimated using the given formula suggested by Johnson *et al*. (1955).

$$\text{Heritability, } h^2b = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$= Phenotypic variance

### 3.12.4 Estimation of genetic advance

Expected genetic advance under selection was estimated using the formula suggested by Johnson *et al*., 1955.

$$\text{Genetic advanced (GA)} = \frac{\sigma^2 g}{\sigma^2 p} \times K \times \sigma p$$

Where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$= Phenotypic variance

$\sigma p$ = Phenotypic standard deviation

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

### 3.12.5 Estimation of genetic advance in percent of mean GA(%)

The estimate by the following formula suggested by Comstock and Robinson (1952).

$$\text{Genetic advance in percent of mean GA(\%)} = \frac{\text{GA}}{\overline{\text{X}}} \times 100$$

Where,

GA = Expected Genetic Advance

$\overline{\text{X}}$ = Population mean

### 3.12.6 Estimation of correlation

The genotypic and phenotypic correlation is estimated by the formula suggested by Miller *et al.* (1958).

$$\text{Genotypic correlation } r_{gxy} = \frac{Cov_{gxy}}{\sqrt{(\sigma^2 g_x \times \sigma^2 g_y)}}$$

Where,

$Cov_{gxy}$ = Genotypic covariance between the trait x and trait y

$\sigma^2 g_x$ = Genotypic variance of the trait x

$\sigma^2 g_y$ = Genotypic variance of the trait y

Similarly,

$$\text{Phenotypic correlation } r_{pxy} = \frac{Cov_{pxy}}{\sqrt{(\sigma^2_{px} \times \sigma^2_{py})}}$$

Where,

$Cov_{px\,y}$ = Phenotypic covariance between the trait x and y

$\sigma^2_{px}$ = Phenotypic variance of the trait x

$\sigma^2_{py}$ = Phenotypic variance of the trait y

### 3.12.7 Path coefficient analysis

Path co-efficient analysis was done according to the procedure employed by Dewey and Lu (1959) also quoted in Singh and Chaudhary (1985) and Dabholkar (1992), using simple correlation values. In path analysis, the correlation coefficient 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 x1, x2 and x3 yield y, a set of simultaneous equations (three equations in this example) is required to be formulated as shown below:

$$r_{yx1} = P_{yx1} + P_{yx2}r_{x1x2} + P_{yx3}r_{x1x3}$$

$$r_{yx2} = P_{yx1}r_{x1x2} + P_{yx2} + P_{yx3}r_{x2x3}$$

$$r_{yx3} = P_{yx1}r_{x1x3} + P_{yx2}r_{x2x3} + P_{yx3}$$

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

Total correlation, say between x1 and y is thus partitioned as follows:

$P_{yx1}$ = The direct effect of x1 on y.

$P_{yx2}r_{x1x2}$ = The indirect effect of x1 via x2 on y.

$P_{yx3}r_{x1x3}$ = The indirect effect of x1 via x3 on y.

After calculating the direct and indirect effect of the characters, residual effect (R) was calculated by using the formula given below (Singh and Chaudhary, 1985):

$$P^2_{RY} = 1- \sum P_{iy} \, . \, riy$$

Where,

$P^2_{RY}$ = $(R^2)$; and hence residual effect, $R = (P^2_{RY})^{½}$

$P_{iy}$ = Direct effect of the character on yield

riy = Correlation of the character with yield.

### 3.12.8 Estimation of genetic diversity

Genetic diversity was estimated following Mahalanobis's (1936) generalized distance ($D^2$). Selection of parents in hybridization program 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 (1977) 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. For univariate analysis of variance, analysis was done individually and least of significance was done by F-Test (Pense and Shukhatme, 1978). 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 and Excel program.

### 3.12.8.1 Principal component analysis (PCA)

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

### 3.12.8.2 Principal coordinate analysis (PCO)

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

### 3.12.8.3 Canonical vector analysis (CVA)

The canonical vector analysis computes a linear combination of original variability that maximize the ratio in between group to within group variation to be finding out and thereby giving functions of the original variability that can be used to discriminate between groups. Finally, a series of orthogonal

transformations sequentially maximizing the ratio among groups within the group variations.

### 3.12.8.4 Average intra-cluster distances

The average intra-cluster distances for each cluster was calculated by taking possible $D^2$ values within the member of a cluster obtained from the Principal Coordinate Analysis (PCO). The formula used was $D^2/n$, where $D^2$ is the sum of distances between all possible combinations (n) of the genotype included in the cluster. The square root of the average $D^2$ values represents the distances (D) within cluster.

### 3.12.8.5 Clustering

To divide the genotypes of the study into some number of mutually exclusive groups clustering were done using non-hierarchical classification. Starting from some initial classification of the genotypes into required groups, the algorithm repeatedly transfers genotypes from one group to another so long as such transfers improve the criterion, the algorithm switches to a second stage which examine the effect of swapping two genotypes of different classes and so on.

# CHAPTER IV

# RESULTS AND DISCUSSION

The present experiment was carried out with twenty genotypes of red amaranth *(Amaranthus cruentus* L.) to assess the characterization and genetic diversity analysis among yield and its component traits of red amaranth. The results of the experiment are presented under the following headings.

## 4.1 Mean, range, analysis of variance and genetic parameters

The results are pertained to analysis of variance (ANOVA), range, grand mean, CV%, mean performance, genotypic and phenotypic variance, genotypic co-efficient of variation (GCV), phenotypic co-efficient of variation (PCV), heritability in broad sense ($h^2b$) and expected genetic advance in percent of mean (GA) for all the 6 traits are furnished in Table 2 to Table 4. Genotypic and phenotypic co-efficient of variation is shown in Table 4; heritability and genetic advance as percent of mean is also represented in Table 4. Out of the 6 traits studied, plant height, number of leaves plant$^{-1}$, average leaf length plant$^{-1}$ and average leaf area plant$^{-1}$ were considered as growth attributing characters. Average stem diameter plant$^{-1}$ and yield plant$^{-1}$ (fresh weight) were considered as reproductive traits. The analysis of variance indicated that significantly higher amount of variability among the genotypes for the growth and yield parameters. The phenotypic expression of the plant characters is mainly controlled by the genetic makeup of the plant and environment. Further, the genetic variance of any quantitative trait is composed of additive variance (heritable) and non-additive variance which include dominance and epistasis (non-allelic) interaction. Therefore, it becomes necessary to partition the observed phenotypic variability into its heritable and non-heritable components with suitable parameters such as genotypic and phenotypic co-efficient of variation, heritability and genetic advance. The character wise details of this variability of the genotypes are discussed below:

**Table 2. Mean performance for 6 different characters in 20 genotypes of red amaranth (*Amaranthus cruentus*)**

| Genotype | PH | NLP | ALLP | ALAP | ASDP | YPP |
|---|---|---|---|---|---|---|
| G1 | 17.90 | 8.67 | 3.63 | 88.16 | 8.72 | 27.21 |
| G2 | 16.43 | 8.33 | 3.47 | 70.77 | 7.70 | 25.35 |
| G3 | 21.37 | 9.33 | 4.10 | 120.67 | 9.65 | 28.80 |
| G4 | 22.60 | 9.67 | 4.30 | 139.61 | 9.87 | 29.93 |
| G5 | 19.03 | 9.00 | 3.87 | 96.84 | 8.83 | 27.64 |
| G6 | 19.90 | 9.00 | 3.93 | 103.53 | 9.10 | 27.92 |
| G7 | 25.07 | 10.33 | 4.67 | 154.59 | 10.19 | 30.44 |
| G8 | 14.97 | 7.00 | 3.23 | 51.85 | 6.19 | 22.53 |
| G9 | 16.97 | 8.67 | 3.60 | 78.84 | 8.17 | 26.71 |
| G10 | 16.83 | 8.67 | 3.57 | 74.84 | 7.83 | 25.73 |
| G11 | 14.87 | 6.33 | 3.03 | 44.86 | 6.36 | 20.45 |
| G12 | 17.63 | 8.67 | 3.63 | 82.31 | 8.45 | 27.04 |
| G13 | 26.87 | 10.67 | 4.70 | 181.53 | 9.99 | 30.82 |
| G14 | 15.33 | 7.33 | 3.27 | 59.17 | 6.59 | 23.73 |
| G15 | 26.43 | 11.33 | 4.90 | 185.75 | 10.12 | 31.19 |
| G16 | 20.43 | 9.33 | 3.93 | 108.74 | 9.47 | 28.40 |
| G17 | 16.27 | 8.33 | 3.40 | 67.54 | 7.32 | 25.18 |
| G18 | 15.57 | 8.00 | 3.37 | 66.16 | 7.01 | 24.83 |
| G19 | 14.70 | 6.67 | 3.13 | 48.23 | 6.75 | 20.78 |
| G20 | 15.33 | 8.00 | 3.30 | 62.93 | 6.79 | 24.01 |
| Range | 14.70-26.87 | 6.33-11.33 | 3.03-4.90 | 44.86-185.75 | 6.19-10.19 | 20.45-31.19 |
| Mean | 18.73 | 8.67 | 3.75 | 94.35 | 8.25 | 26.43 |
| SD | 3.909 | 1.280 | 0.543 | 42.37 | 1.367 | 3.131 |
| SE(±) | 0.820 | 0.832 | 0.412 | 32.279 | 0.044 | 0.148 |
| CV(%) | 11.64 | 8.78 | 6.44 | 13.37 | 7.92 | 10.84 |

PH = Plant height (cm), NLP = Number of leaves plant$^{-1}$, ALLP = Average leaf length plant$^{-1}$ (cm), ALAP = Average leaf area plant$^{-1}$ (cm$^2$), ASDP = Average stem diameter plant$^{-1}$ (mm), YPP = Yield plant$^{-1}$ (fresh weight) (g)

### 4.1.1 Plant height (cm)

The variability for plant height was high, as reflected by its wide range from 14.70 cm to 26.87 cm with mean value of 18.73 cm (Table 2). The maximum plant height was observed by the genotype G13 (26.87 cm) followed by G15 (26.43 cm) and the minimum was in G19 (14.70 cm) (Table 2). The co-efficient of variation of this trait (plant height) was 11.64%. The plant height exhibited high genotypic co-efficient of variation (GCV) (20.65%) and phenotypic co-efficient of variation (PCV) (21.33%) (Table 4 and Figure 1). The phenotypic co-efficient of variation was higher than the genotypic co-efficient of variation which suggested that environment had a significant role on the expression of this trait. Hiremath (2005) also found high PCV and GCV, for plant height of *Amaranthus sp.* The magnitude of heritability estimates for plant height was high (93.68%) with low genetic advance (7.71%) along with high genetic advance over percent mean (41.16%) (Table 4 and Figure 2) indicating apparent variation was due to genotypes. So, selection based on this trait would be effective. This result also has the agreement with the findings of Singh *et al*. (2005). Joshi *et al*. (1986) reported that heritability estimates and expected genetic advance were high for plant height. Hiremath (2005) found high heritability and genetic advance in percent of mean (GAM) for plant height. Kusuma *et al.* (2007) also found high heritability and moderate GAM for plant height in grain amaranth.

**Table 3. Analysis of variance for different characters in red amaranth genotypes**

| Parameters | Mean sum of square | | |
|---|---|---|---|
| | Replication<br>df = (r-1) = 2 | Genotype<br>df = (G-1) = 19 | Error<br>df = (r-1)(G-1) = 38 |
| PH | 1.400 | 45.843* | 1.009 |
| NLP | 1.267 | 4.912** | 1.039 |
| ALLP | 0.296 | $0.884^{NS}$ | 0.255 |
| ALAP | 1943.95 | 5384.67* | 1562.87 |
| ASDP | 0.019 | 5.610** | 0.003 |
| YPP | 0.079 | 29.413* | 0.033 |

PH = Plant height (cm), NLP = Number of leaves plant$^{-1}$, ALLP = Average leaf length plant$^{-1}$ (cm), ALAP = Average leaf area plant$^{-1}$ (cm$^2$), ASDP = Average stem diameter plant$^{-1}$ (mm), YPP = Yield plant$^{-1}$ (fresh weight) (g)

NS = Non-significant * = Significant at 5% level ** = Significant at 1% level

**Table 4. Estimation of genetic parameters in 6 characters of 20 red amaranth genotypes**

| Parameters | $\sigma^2p$ | $\sigma^2g$ | $\sigma^2e$ | PCV | GCV | $h^2b$ | GA (5%) | GA(%) mean |
|---|---|---|---|---|---|---|---|---|
| PH | 15.95 | 14.94 | 1.01 | 21.33 | 20.65 | 93.68 | 7.71 | 41.16 |
| NLP | 2.33 | 1.29 | 1.04 | 17.61 | 13.11 | 55.42 | 1.74 | 20.11 |
| ALLP | 0.47 | 0.21 | 0.26 | 18.17 | 12.21 | 45.19 | 0.64 | 16.91 |
| ALAP | 2836.80 | 1273.93 | 1562.87 | 56.45 | 37.83 | 44.91 | 49.27 | 52.22 |
| ASDP | 1.87 | 1.87 | 0.003 | 16.57 | 16.56 | 99.85 | 2.81 | 34.09 |
| YPP | 9.83 | 9.79 | 0.033 | 11.86 | 11.84 | 99.67 | 6.44 | 24.35 |

PH = Plant height (cm), NLP = Number of leaves plant$^{-1}$, ALLP = Average leaf length plant$^{-1}$ (cm), ALAP = Average leaf area plant$^{-1}$ (cm$^2$), ASDP = Average stem diameter plant$^{-1}$ (mm), YPP = Yield plant$^{-1}$ (fresh weight) (g), $\sigma^2p$ = Phenotypic variance, $\sigma^2g$ = Genotypic variance, $\sigma^2e$ = Environmental variance, PCV = Phenotypic Co-efficient of Variation, GCV = Genotypic Co-efficient of Variation, $h^2b$ = Heritability, GA = Genetic advanced, GA(%) mean = Genetic advance in percent of mean

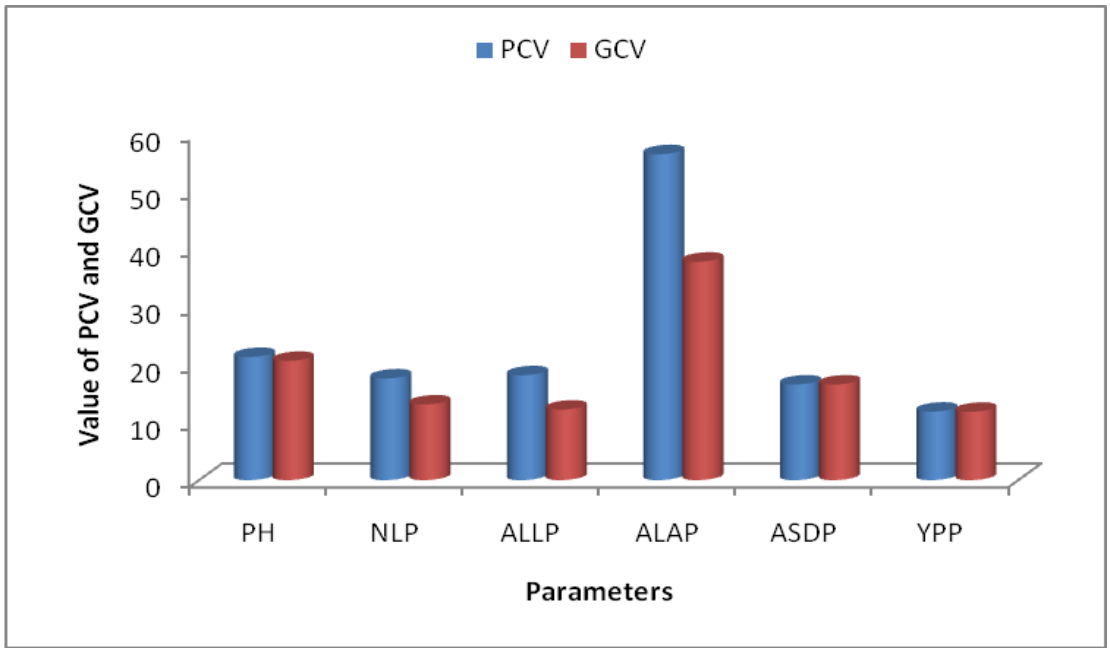


**Figure 1. Genotypic and phenotypic co-efficient of variation in red amaranth (*Amaranthus cruentus*).**

PH = Plant height (cm), NLP = Number of leaves plant$^{-1}$, ALLP = Average leaf length plant$^{-1}$ (cm), ALAP = Average leaf area plant$^{-1}$ (cm$^2$), ASDP = Average stem diameter plant$^{-1}$ (mm), YPP = Yield plant$^{-1}$ (fresh weight) (g)

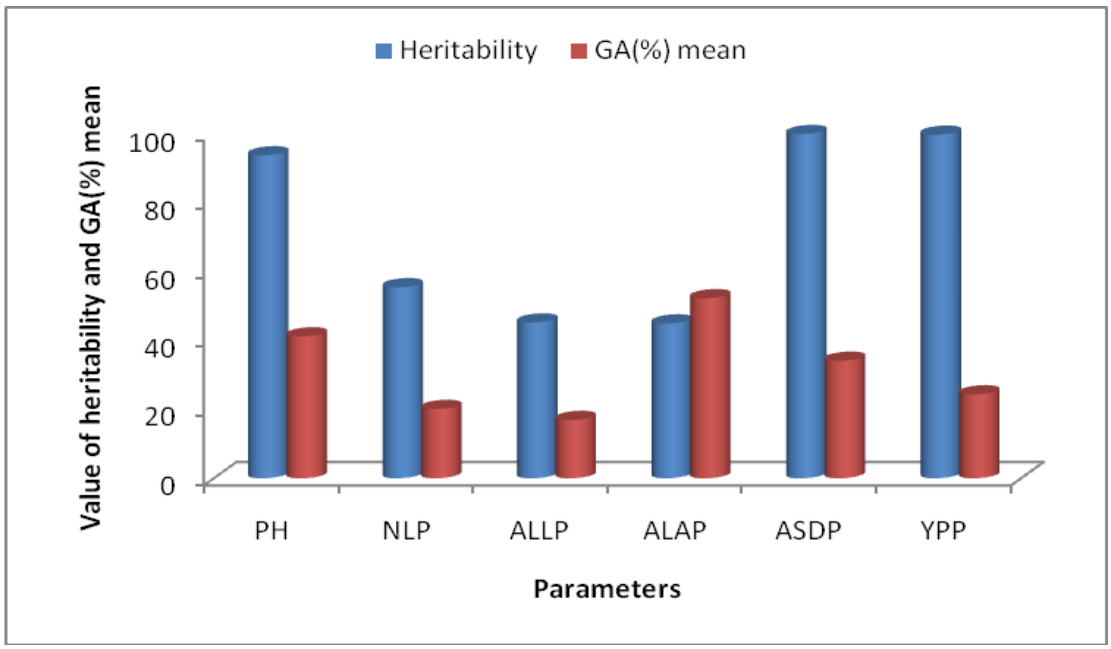


**Figure 2. Heritability and genetic advance over mean in red amaranth (*Amaranthus cruentus*)**

PH = Plant height (cm), NLP = Number of leaves plant$^{-1}$, ALLP = Average leaf length plant$^{-1}$ (cm), ALAP = Average leaf area plant$^{-1}$ (cm$^2$), ASDP = Average stem diameter plant$^{-1}$ (mm), YPP = Yield plant$^{-1}$ (fresh weight) (g)

### 4.1.2 Number of leaves plant$^{-1}$

Number of leaves plant$^{-1}$ among the genotypes was ranged from 6.33 to 11.33 with mean value of 8.67 (Table 2). The maximum number of leaves plant$^{-1}$ was observed by the genotype G15 (11.33) whereas the minimum was in G11 (6.33) (Table 2). The co-efficient of variation of the number of leaves plant$^{-1}$ was 8.78% (Table 2). The number of leaves plant$^{-1}$ exhibited moderate GCV (13.11%) and PCV (17.61%) (Table 4 and Figure 1). The phenotypic co-efficient of variation was much higher than the genotypic co-efficient of variation which suggested that environment had a significant role on the expression of this trait. High to moderate GCV and PCV values for number of leaves per plant was observed by Chattopadhyay *et al.* (2013) in grain amaranth. Similar result was also observed by Anuja and Mohideen (2007). Medium heritability for number of leaves plant$^{-1}$ (55.42%) was found with low genetic advance (1.74%) along with high genetic advance over percent mean (20.11%) (Table 4 and Figure 2). High heritability coupled with high genetic advance expressed in percentage of mean for number of leaves per plant was also observed by Tejaswini *et al.* (2017) indicating that these traits were mainly governed by additive gene action and response for further improvement of these traits. Yogendra *et al.* (2018) recorded high estimates of genetic advance as percentage of mean for number of leaves per plant.

### 4.1.3 Average leaf length plant$^{-1}$ (cm)

The average leaf length plant$^{-1}$ was ranged from 3.03 cm to 4.90 cm with mean value of 3.75 cm (Table 2). The maximum average leaf length was observed by the genotype G15 (4.90 cm) followed by G13 (4.70 cm) and G7 (4.67 cm) and the minimum was in G11 (3.03 cm) (Table 2). The co-efficient of variation of this trait (leaf length) was 6.44% (Table 2). The average leaf length plant$^{-1}$ exhibited moderate GCV (12.21%) and PCV (18.17%) (Table 4 and Figure 1). The phenotypic co-efficient of variation was much higher than the genotypic co-efficient of variation which suggested that environment had a significant

role on the expression of this trait. The similar results were also observed by Yadav *et al*. (2014) and Tejaswini *et al*. (2017) for leaf length. Medium heritability (45.19%) coupled with low genetic advance (0.64) along with moderate genetic advance over percent mean (16.91%) was noticed (Table 4 and Figure 2). Sudhir and Singh (2000) reported high heritability coupled with high genetic advance for leaf size. Tejaswini *et al.* (2017) found high heritability coupled with high genetic advance expressed in percentage of mean for leaf length. Yogendra *et al.* (2018) also found similar result with the present study.

### 4.1.4 Average leaf area plant$^{-1}$ (cm$^2$)

The values for average leaf area plant$^{-1}$ ranged from 44.86 (G11) to 185.75 cm$^2$ (G15) with mean value of 94.35 cm$^2$ (Table 2). The co-efficient of variation (CV) of this trait (leaf area) was 13.37% (Table 2). High estimates of GCV (37.83%) and PCV (56.45%) were found (Table 4 and Figure 1). The phenotypic co-efficient of variation was much higher than the genotypic co-efficient of variation which suggested that environment had a significant role on the expression of this trait. Anuja and Mohideen (2007), Ramesh *et al*. (2013) and Panda *et al*. (2017) also found similar result with the present study in terms of leaf area. Medium heritability (44.91%) coupled with high genetic advance (49.27%) along with high genetic advance as percent mean (52.22%) was observed for the trait (leaf area) (Table 4 and Figure 2). Tejaswini *et al.* (2017) observed high heritability coupled with high genetic advance expressed in percentage of mean for leaf area index indicating that these traits were mainly governed by additive gene action and response for further improvement of these traits.

### 4.1.5 Average stem diameter plant$^{-1}$ (mm)

The values for average stem diameter plant$^{-1}$ ranged from 6.19 to 10.19 mm with mean value of 8.25 mm (Table 2). The maximum average stem diameter plant$^{-1}$ was observed by the genotype G7 (10.19) whereas the minimum was in

G8 (6.19) (Table 2). The co-efficient of variation (CV) of stem diameter was 7.92% (Table 2). Moderate estimates of GCV (16.56%) and PCV (16.57%) were found (Table 4 and Figure 1). There was small difference between GCV and PCV. The phenotypic co-efficient of variation was little higher than the genotypic co-efficient of variation indicating that the apparent variation not only due to genotypes but also due to the influence of environment. The result obtained from the present study was similar with the study by Akaneme and Ani (2013) and Tejaswini *et al.* (2017). High heritability (99.85%) coupled with low genetic advance (2.81%) along with high genetic advance as percent mean (34.09%) was observed for stem diameter (Table 4 and Figure 2). Singh *et al*. (2005) reported that genetic advance was moderate for stem diameter. Lohithaswa and Nagaraj (1996) were reported that moderate heritability with moderate genetic advance for stem diameter. Tejaswini *et al.* (2017) found high estimates of PCV and GCV for stem diameter. High heritability coupled with high genetic advance expressed in percentage of mean for stem diameter, were also observed by Tejaswini *et al.* (2017).

### 4.1.6 Yield plant$^{-1}$ (fresh weight) (g)

The mean value for yield plant$^{-1}$ (fresh weight) was 26.43 g which ranged from 20.45 g (G11) to 31.19 g (G15) and the co-efficient of variation was 10.84% (Table 2). Moderate estimates of GCV (11.84%) and PCV (11.86%) was observed (Table 4 and Figure 1). The phenotypic co-efficient of variation was little higher than the genotypic co-efficient of variation indicating that the apparent variation not only due to genotypes but also due to the influence of environment. Moderate GCV and PCV were also observed by Hasan *et al*. (2013) and Buhroy *et al*. (2017) for fresh weight plant$^{-1}$. The high heritability (99.67%) coupled with low genetic advance (6.44%) and high genetic advance as percent of mean (24.35%) was noticed for this trait (Table 4 and Figure 2) which indicating that these traits were mainly governed by additive gene action and response for further improvement of these traits.

## 4.2 Correlation

The genotypic and phenotypic correlation studies were carried out to know the nature of relationship existing between yield and their component characters and are presented in the Tables 5 and 6 respectively. It is necessary to have the estimates of correlation of yield with other characters for which the genotype could be assessed visually. The phenotypic and genotypic correlation reveals the extent of association between different characters, it helps to base selection procedure to a required balance, when two opposite desirable characters affecting the principal characters are being selected. A positive correlation occurs due to coupling phase of linkage and negative correlation arises due to repulsion phase of linkage of genes controlling different traits. No correlation indicates that genes concerned are located far apart on the same chromosome or they are located on different chromosomes. Yield being a complex character is governed by a large number of genes. The influence of each character on yield could be known through correlation studies with a view to determine the extent and nature of relationships prevailing among yield and yield attributing characters. Yield is a complex character controlled by a large number of contributing characters and their interactions. A study of correlation between different quantitative characters provides an idea of association that could be effectively exploited to formulate selection strategies for improving yield components. For any effective selection program, it would be desirable to consider the relative magnitude of association of various characters with yield.

### 4.2.1 Genotypic correlation

The data pertaining to the genotypic correlation co-efficient for different characters of red amaranth genotypes are presented in Table 5.

**Table 5. Genotypic correlation co-efficient among different pairs of yield and yield contributing characters for different genotype of red amaranth**

| Characters | NLP | ALLP | ALAP | ASDP | YPP |
|---|---|---|---|---|---|
| PH | -0.754** | 0.907** | 0.880** | -0.632* | -0.676** |
| NLP | | -0.888** | 0.873* | 0.747** | 0.807** |
| ALLP | | | 0.870** | 0.804** | 0.862** |
| ALAP | | | | 0.798** | 0.835** |
| ASDP | | | | | 0.660* |

PH = Plant height (cm), NLP = Number of leaves plant$^{-1}$, ALLP = Average leaf length plant$^{-1}$ (cm), ALAP = Average leaf area plant$^{-1}$ (cm$^2$), ASDP = Average stem diameter plant$^{-1}$ (mm), YPP = Yield plant$^{-1}$ (fresh weight) (g)

#### 4.2.1.1 Plant height (cm)

Plant height showed highly significant and negative correlation with yield plant$^{-1}$ (fresh weight) (G = 0.676). Highly significant negative correlation between plant height and yield plant$^{-1}$ (fresh weight) at genotypic level was also observed by Ahammed *et al.* (2012). Significant positive associations between plant height and other characters indicate that the traits were governed by similar gene and simultaneous improvement would be effective while negative associations between plant height and other characters indicate that the traits were governed by different gene and simultaneous improvement would not be effective. It exhibited significant and negative correlation with number of leaves plant$^{-1}$ (G = -0.754) and average stem diameter plant$^{-1}$ (G = -0.632) but it showed significant and positive correlation with average leaf length plant$^{-1}$ (G = 0.907) and average leaf area plant$^{-1}$ (G = 0.880). Khurana *et al.* (2013) also concluded that plant height was positively correlated with leaf length, number of leaves per plant, leaf area index at genotypic level.

#### 4.2.1.2 Number of leaves plant$^{-1}$

Number of leaves plant$^{-1}$ showed significant and positive correlation with yield plant$^{-1}$ (fresh weight) (G = 0.807). Ahammed *et al.* (2012) also found highly significant positive correlation between leaves per plant and yield per plant at genotypic level. Similar result was also observed by Shankar *et al.* (2012). This result indicated that if number of leaves plant$^{-1}$ increases then yield plant$^{-1}$ also increases. This result also indicates that the traits were governed by similar gene and simultaneous improvement would be effective. Number of leaves plant$^{-1}$ also showed significant and positive correlation with average leaf area plant$^{-1}$ (G = 0.873) and average stem diameter plant$^{-1}$ (G = 0.747). Khurana *et al.* (2013) also found number of leaves per plant was positively correlated with plant height, leaf length and leaf area index at genotypic level.

#### 4.2.1.3 Average leaf length plant$^{-1}$ (cm)

Highly significant and positive correlation of average leaf area plant$^{-1}$ was recorded with yield plant$^{-1}$ (fresh weight) (G = 0.862). This result suggests that yield plant$^{-1}$ of red amaranth (fresh weight) increases when average leaf length plant$^{-1}$ increases. Khurana *et al.* (2013) concluded that leaf length was positively correlated with total green yield at genotypic level. Average leaf length plant$^{-1}$ also exhibited significant and positive correlation with average leaf area plant$^{-1}$ (G = 0.870,) and average stem diameter plant$^{-1}$ (G = 0.804). Khurana *et al.* (2013) also found leaf length was positively correlated with plant height, number of leaves per plant and leaf area index at genotypic level.

#### 4.2.1.4 Average leaf area plant$^{-1}$ (cm$^2$)

A significant and positive correlation of average leaf area plant$^{-1}$ was recorded with yield plant$^{-1}$ (fresh weight) (G = 0.835). This result suggests that yield plant$^{-1}$ of red amaranth is increased when average leaf area plant$^{-1}$ is increased. This result also suggested that the traits were governed by similar gene and simultaneous improvement would be effective. Similar result was also observed by Khurana *et al.* (2013) and found that total green yield exhibited highly significant and positive correlation with leaf area index both at genotypic level. Average leaf area plant$^{-1}$ also exhibited significant and positive correlation with average stem diameter plant$^{-1}$ (G = 0.798). Leaf area index was also positively correlated with plant height, leaf length, number of leaves per plant and total green yield at genotypic level reported by Khurana *et al.* (2013).

#### 4.2.1.5 Average stem diameter plant$^{-1}$ (mm)

Average stem diameter plant$^{-1}$ showed highly significant and positive correlation with yield plant$^{-1}$ (fresh weight) (G = 0.660). This result indicated that when average stem diameter plant$^{-1}$ increases then yield plant$^{-1}$ (fresh weight) also increases. Ahammed *et al.* (2012) studied the correlation in amaranthus and found that stem diameter exhibited highly significant positive

correlation with yield per plant at genotypic level. Similar result was also observed by Hasan *et al.* (2013).

### 4.2.2 Phenotypic correlation

The data pertaining to the phenotypic correlation co-efficient for different characters of red amaranth genotypes are presented in Table 6.

#### 4.2.2.1 Plant height (cm)

Plant height showed significant and negative interaction with yield plant$^{-1}$ (fresh weight) (P = -0.644). Significant negative correlation between plant height and yield plant$^{-1}$ (fresh weight) at phenotypic level was also observed by Ahammed *et al.* (2012). Significant negative associations between plant height and other characters indicate that the traits were governed by different gene and simultaneous improvement would not be effective. It exhibited significant and negative interaction with number of leaves plant$^{-1}$ (P = -0.481) and average stem diameter plant$^{-1}$ (P = -0.601) but significant and positive interaction with average leaf length plant$^{-1}$ (P = 0.452), average leaf area plant$^{-1}$ (P = 0.468). Khurana *et al.* (2013) reported that plant height was positively correlated with leaf length, number of leaves per plant, leaf area index at phenotypic level.

#### 4.2.2.2 Number of leaves plant$^{-1}$

Number of leaves plant$^{-1}$ showed highly significant and positive correlation with yield plant$^{-1}$ (fresh weight) (P = 0.528). This result indicated that if number of leaves plant$^{-1}$ increases then yield plant$^{-1}$ also increases. Ahammed *et al.* (2012) also found highly significant positive correlation between no. of leaves per plant and yield per plant at phenotypic level. Number of leaves plant$^{-1}$ also showed significant and positive correlation with average leaf area plant$^{-1}$ (P = 0.409) and average stem diameter plant$^{-1}$ (P = 0.478) but negatively correlated with average leaf length plant$^{-1}$ (P = -0.435). Khurana *et al.* (2013) also found number of leaves per plant was positively correlated with plant height, leaf length and leaf area index at phenotypic level. Significant positive

associations among number of leaves plant$^{-1}$ and other characters indicate that the traits were governed by similar gene and simultaneous improvement would be effective.

#### 4.2.2.3 Average leaf length plant$^{-1}$ (cm)

Highly significant and positive correlation of average leaf length plant$^{-1}$ was recorded with yield plant$^{-1}$ (fresh weight) (P = 0.472). This result suggests that yield plant$^{-1}$ (fresh weight) of red amaranth increases when average leaf length plant$^{-1}$ is increased. Khurana *et al.* (2013) concluded that leaf length was positively correlated with total green yield at phenotypic level. Average leaf length plant$^{-1}$ also exhibited significant and positive correlation with average leaf area plant$^{-1}$ (P = 0.529) average stem diameter plant$^{-1}$ (P = 0.451). Khurana *et al.* (2013) also found leaf length was positively correlated with plant height, number of leaves per plant and leaf area index at phenotypic level.

#### 4.2.2.4 Average leaf area plant$^{-1}$ (cm$^2$)

Highly significant and positive correlation of average leaf area plant$^{-1}$ was recorded with yield plant$^{-1}$ (fresh weight) (P = 0.455). This result suggests that yield plant$^{-1}$ (fresh weight) of red amaranth increases when average leaf area plant$^{-1}$ is increased. Similar result was also observed by Khurana *et al.* (2013) and found that total green yield exhibited highly significant and positive correlation with leaf area index both at phenotypic level. Average leaf area plant$^{-1}$ also exhibited significant and positive correlation with average stem diameter plant$^{-1}$ (P = 0.439). Leaf area index was also positively correlated with plant height, leaf length, number of leaves per plant and total green yield at phenotypic level reported by Khurana *et al.* (2013). Here, significant and positive associations between leaf area and other characters were observed and these results indicated that the traits were governed by similar gene and simultaneous improvement would be effective.

**Table 6. Phenotypic correlation co-efficient among different pairs of yield and yield contributing characters for different genotype of red amaranth**

| Characters | NLP | ALLP | ALAP | ASDP | YPP |
|---|---|---|---|---|---|
| PH | -0.481** | 0.452** | 0.468** | -0.601* | -0.644* |
| NLP | | -0.435** | 0.409* | 0.478** | 0.528** |
| ALLP | | | 0.529** | 0.451** | 0.472** |
| ALAP | | | | 0.439* | 0.455** |
| ASDP | | | | | 0.657* |

PH = Plant height (cm), NLP = Number of leaves plant$^{-1}$, ALLP = Average leaf length plant$^{-1}$ (cm), ALAP = Average leaf area plant$^{-1}$ (cm$^2$), ASDP = Average stem diameter plant$^{-1}$ (mm), YPP = Yield plant$^{-1}$ (fresh weight) (g)

### 4.2.2.5 Average stem diameter plant$^{-1}$ (mm)

Average stem diameter plant$^{-1}$ showed significant and positive correlation with yield plant$^{-1}$ (fresh weight) (P = 0.657). This result indicated that when average stem diameter plant$^{-1}$ increases then yield plant$^{-1}$ (fresh weight) also increases. Ahammed *et al.* (2012) studied the correlation in amaranthus and found that stem diameter exhibited highly significant positive correlation with yield per plant at phenotypic level. Similar result was also observed by Hasan *et al.* (2013).

## 4.3 Path co-efficient analysis

The result of path co-efficient analysis gives relative contribution of different characters towards the yield, by partitioning the correlation co-efficient into direct and indirect effect of a selected trait and its indirect effect through other characters were computed and presented in Table 7. The path co-efficient technique developed by Wright (1921) helps in estimating direct and indirect contribution of various components in building up the total correlation towards yield. Based on these studies the quantum importance of individual characters is marked to facilitate the selection program for better gains. Vegetative yield per hectare was considered as a resultant (dependent) variable and plant height, number of leaves plant$^{-1}$, leaf length plant$^{-1}$, leaf area plant$^{-1}$, stem diameter plant$^{-1}$, fresh weight plant$^{-1}$ and dry weight plant$^{-1}$ were causal (independent) variables.

### 4.3.1 Plant height (cm)

Path analysis revealed that plant height had negative direct effect (-0.391) on yield plant$^{-1}$ (fresh weight). It had negative indirect effect on number of leaves plant$^{-1}$ (-0.103), average leaf length plant$^{-1}$ (-0.030) and average stem diameter plant$^{-1}$ (-0.456) (Table 7). Among the 6 characters, plant height showed negative and direct effect on yield plant$^{-1}$ (fresh weight). Similar results were obtained by Varalakshmi and Devaraju (2010), Hasan *et al.* (2013),

Chattopadhyay *et al.* (2013), Sarker *et al.* (2015), Buhroy *et al.* (2017) and Jangde *et al.* (2017). Plant height had positive indirect effect on average leaf area plant$^{-1}$ (0.035) (Table 7).

### 4.3.2 Number of leaves plant$^{-1}$

Number of leaves plant$^{-1}$ had positive direct effect (0.131) on yield plant$^{-1}$ (fresh weight). While it had indirect positive effect on average leaf area plant$^{-1}$ (0.032) and average stem diameter plant$^{-1}$ (0.394) in Table 7. The trait had negative indirect effect via plant height (-0.305) and average leaf length plant$^{-1}$ (-0.029). But Shankar *et al.* (2012) found using path analysis in grain amaranth that yield per plot had a significant positive correlation with number of leaves per plant.

### 4.3.3 Average leaf length plant$^{-1}$ (cm)

Average leaf length plant$^{-1}$ had positive and significant association with yield plant$^{-1}$ (fresh weight) and had negative direct effect (-0.040) on yield plant$^{-1}$ (Table 7). While it had negative indirect effect on plant height (-0.294), number of leaves plant$^{-1}$ (-0.097) and average stem diameter plant$^{-1}$ (0.380). The trait also showed indirect positive effect on average leaf area plant$^{-1}$ (0.038). Regarding the present study, average leaf length plant$^{-1}$ had negative and significant direct effect on yield plant$^{-1}$ (fresh weight), but Varalakshmi and Reddy (1994) found that leaf length had positive and significant association with total yield per plant and had positive direct effect on total yield per plant. The negative association of the trait was mainly because of its indirect and negative effect of plant height and number of leaves plant$^{-1}$.

### 4.3.4 Average leaf area plant$^{-1}$ (cm$^2$)

Path analysis revealed that average leaf area plant$^{-1}$ had positive direct effect (0.046) on yield plant$^{-1}$ (fresh weight). It had negative indirect effect on plant height (-0.300), number of leaves plant$^{-1}$ (-0.093) and average leaf length plant$^{-1}$ (-0.033) (Table 7). Average leaf length plant$^{-1}$ had positive indirect effect on

average stem diameter plant$^{-1}$ (0.374). Average leaf area plant$^{-1}$ made a significant positive correlation with seed yield (0.046) which result indicated that if average leaf area plant$^{-1}$ increases than yield plant$^{-1}$ increases. Path analysis conducted by Kendre *et al.* (2013) revealed that the stem diameter exerted highest direct effect over yield followed by leaf area and number of leaves plant$^{-1}$ while plant height exhibited the negative direct effect on yield.

### 4.3.5 Average stem diameter plant$^{-1}$ (mm)

Average stem diameter plant$^{-1}$ had positive association with yield plant$^{-1}$ (fresh weight) and had positive direct effect (0.506) on yield plant$^{-1}$ while it had positive indirect effect via number of leaves plant$^{-1}$ (0.102) and average leaf area plant$^{-1}$ (0.034) in Table 7. It also had indirect negative effect on plant height (-0.352) and average leaf length plant$^{-1}$ (-0.030). The positive association of the trait was mainly because of its indirect and positive effect of number of leaves plant$^{-1}$ and average leaf area plant$^{-1}$.

**Table 7. Path co-efficient analysis showing Direct (bold) and indirect effects of different characters on yield of red amaranth**

| Characters | PH | NLP | ALLP | ALAP | ASDP | Genotypic correlation with yield |
|---|---|---|---|---|---|---|
| PH | **-0.391** | -0.103 | -0.030 | 0.035 | -0.456 | -0.676** |
| NLP | -0.305 | **0.131** | -0.029 | 0.032 | 0.394 | 0.807** |
| ALLP | -0.294 | -0.097 | **-0.040** | 0.038 | -0.380 | 0.862** |
| ALAP | -0.300 | -0.093 | -0.033 | **0.046** | 0.374 | 0.835** |
| ASDP | -0.352 | 0.102 | -0.030 | 0.034 | **0.506** | 0.660* |

Residual Effect (R) = 0.04137

- Bold figures denotes direct effect

**, * Correlation is significant at the 0.01 and 0.05 level, respectively

PH = Plant height (cm), NLP = Number of leaves plant$^{-1}$, ALLP = Average leaf length plant$^{-1}$ (cm), ALAP = Average leaf area plant$^{-1}$ (cm$^2$), ASDP = Average stem diameter plant$^{-1}$ (mm), YPP = Yield plant$^{-1}$ (fresh weight) (g)

## 4.4 Genetic diversity analysis

Generally diverse plants are expected to give higher hybrid vigour (Harrington, 1940). The importance of genetic diversity in the improvement of a crop has been stressed in both self and cross pollinated crop (Griffing and Lindstrom, 1954). Hence it is necessary to study the genetic divergence among the existing varieties and germplasm collection for identification of parents for the hybridization program. The information on genetic divergence of various yield and quality contributing traits would be the most useful in planning of the breeding program. Twenty red amaranth (*Amaranthus cruentus*) genotypes were evaluated for six characters to study the divergence and the data obtained was subjected to $D^2$ analysis. The genetic diversity of *Amaranthus cruentus* L. genotypes are presented in Table 8 to 11 and Figure 3.

### 4.4.1 Principal component analysis (PCA)

The PCA gives Eigen values of principal component axes of coordination of genotypes with the first axes totally accounted for the variation among the genotypes, whereas three of these Eigen values above unity accounted for 99.60% (Table 8). The first principal component accounted for 95.70% of the total variation while principal components two and three accounted for 2.70% and 1.20%, respectively. The first two principal axes accounted for 98.40% of the total variation among the characters describing 20 red amaranth (*Amaranthus cruentus* L.). genotypes.

### 4.4.2 Contribution of traits towards divergence of the genotypes

The character contributing maximum to the divergence were given greater emphasis for deciding on the cluster for the purpose of further selection and choice of parents for hybridization (Jagadev *et al*., 1991). The latent vectors (I and and II) obtained from principal component analysis (PCA). The important characters responsible for genetic divergence in the axis of differentiation in vector I were plant height (0.225), number of leaves plant$^{-1}$ (0.018), average leaf length plant$^{-1}$ (0.001) and average leaf area plant$^{-1}$ (0.01) (Table 9). In

vector-2 the important characters responsible for genetic divergence were plant height (0.467), number of leaves plant$^{-1}$ (0.030), average leaf length plant$^{-1}$ (0.047), average leaf area plant$^{-1}$ (0.016), average stem diameter plant$^{-1}$ (0.462) and yield plant$^{-1}$ (0.413). Negative value in vectors determined the lower contribution of genetic divergence like average stem diameter plant$^{-1}$ (-0.354) and yield plant$^{-1}$ (-0.326) in vector I. In the role of yield plant$^{-1}$ (fresh weight) in both vectors was important components for genetic divergence in these materials.

**Table 8. Eigen values and percentage of variation in respect of 8 characters in red amaranth genotypes**

| Principal component axis | Eigen values | % of total variation accounted for | Cumulative percent |
|---|---|---|---|
| I | 5.74 | 95.70 | 95.70 |
| II | 0.164 | 2.70 | 98.40 |
| III | 0.074 | 1.20 | 99.60 |
| IV | 0.013 | 0.20 | 99.90 |
| V | 0.006 | 0.10 | 100.00 |
| VI | 0.002 | 0.00 | 100.00 |

Table 9. Relative contribution of 6 characters towards divergence of the genotypes

| Characters | Vector-I | Vector-II |
|---|---|---|
| PH | 0.225 | 0.467 |
| NLP | 0.018 | 0.030 |
| ALLP | 0.001 | 0.047 |
| ALAP | 0.010 | 0.016 |
| ASDP | -0.354 | 0.462 |
| YPP | -0.326 | 0.413 |

PH = Plant height (cm), NLP = Number of leaves plant$^{-1}$, ALLP = Average leaf length plant$^{-1}$ (cm), ALAP = Average leaf area plant$^{-1}$ (cm$^2$), ASDP = Average stem diameter plant$^{-1}$ (mm), YPP = Yield plant$^{-1}$ (fresh weight) (g)

### 4.4.3 Non-hierarchical clustering

Twenty red amaranth (*Amaranthus cruentus* L.) genotypes were grouped into five different clusters as nonhierarchical clustering (Table 10). These results confirmed the clustering pattern of the genotypes obtained through principal component analysis. Hiremath (2005) studied the genetic diversity among 144 grain amaranth *(Amaranthus spp.)* genotypes and were grouped into five clusters based on the $D^2$ values. Pandey (2009) used 26 genotypes and were grouped eleven clusters based on the $D^2$ values. Chattopadhyay *et al.* (2013) studied genetic divergence of vegetable amaranthuhs. Among 11 genotypes, based on $D^2$ values the genotypes were grouped into two clusters. Among 54 genotypes of grain amaranth, Tiwari (2018) grouped 8 clusters based on $D^2$ values. Under the present study, cluster I had the highest number of genotypes (7) followed by II which had 5 genotypes. On the other hand, Cluster III and IV had lowest number of genotypes (2) whereas Cluster IV had 4 genotypes (Table 10). According to the cluster means (Table 11), cluster IV showed better performance in case of plant height (26.65 cm), number of leaves $plant^{-1}$ (11.00), average leaf length $plant^{-1}$ (4.80 cm), average leaf area $plant^{-1}$ (183.64 $cm^2$), average stem diameter $plant^{-1}$ (10.06 mm) and yield $plant^{-1}$ (fresh weight) (31.00 g). It indicated the genotype of this cluster could be used for future hybridization program for higher yield $plant^1$. The genotypes included in cluster II had lowest plant height (15.04), number of leaves $plant^{-1}$ (7.07), average leaf length $plant^{-1}$ (3.19 cm), average leaf area $plant^{-1}$ (53.41 $cm^2$), average stem diameter $plant^{-1}$ (6.53 mm) and yield $plant^{-1}$ (fresh weight) (22.30 g). It indicated the genotype of this cluster composed of low yielding genotypes. This clearly suggested that the genotypes found in any of these pairs of clusters were highly divergent. Hazra *et al*. (2004) and Pandey and Singh (2011) also found high and low yielding genotypes in different clusters. Regarding cluster mean of III and V for 6 characters of red amaranth (*Amaranthus cruentus*), it indicated intermediate results which can be considered as medium yielding genotypes for future hybridization program.

**Table 10. Distribution of 20 red amaranth genotypes in five different clusters**

| Cluster | Total no. of line | Genotype Number | Genotype Designation |
|---|---|---|---|
| I | 7 | 1, 2, 9, 10, 12, 17, 18 | BD-2925, BD-2928, BD-2956, BD-2957, BD-2961, BD-9790, BD-9795 |
| II | 5 | 8, 11, 14, 19, 20 | BD-2947, BD-2958, BD-7400, BD-9806, BD-9815 |
| III | 2 | 4, 7 | BD-2934, BD-2946 |
| IV | 2 | 13, 15 | BD-2964, BD-7406 |
| V | 4 | 3, 5, 6, 16 | BD-2930, BD-2941, BD-2942, BD-9004 |

**Table 11. Cluster means for 6 characters of 20 red amaranth genotypes**

| Characters | Cluster | | | | |
|---|---|---|---|---|---|
| | I | II | III | IV | V |
| PH | 16.80 | 15.04 | 23.83 | 26.65 | 20.18 |
| NLP | 8.48 | 7.07 | 10.00 | 11.00 | 9.17 |
| ALLP | 3.52 | 3.19 | 4.48 | 4.80 | 3.96 |
| ALAP | 75.52 | 53.41 | 147.10 | 183.64 | 107.45 |
| ASDP | 7.89 | 6.53 | 10.03 | 10.06 | 9.26 |
| YPP | 26.01 | 22.30 | 30.18 | 31.00 | 28.19 |

PH = Plant height (cm), NLP = Number of leaves plant$^{-1}$, ALLP = Average leaf length plant$^{-1}$ (cm), ALAP = Average leaf area plant$^{-1}$ (cm$^2$), ASDP = Average stem diameter plant$^{-1}$ (mm), YPP = Yield plant$^{-1}$ (fresh weight) (g)

### 4.4.4 Canonical Variate Analysis (CVA)

The quantification of genetic diversity through biometrical procedures such as Mahalanobis's $D^2$ statistics canonical variate Analysis (CVA) have made it possible to choose genetically diverse parents for a successful hybridization program. $D^2$ statistic developed by Mahalanobis (1936) provides a measure of magnitude for divergence between two genotypes under comparison. Grouping of genotypes based on $D^2$ analysis will be useful in choosing suitable parental lines for heterosis breeding. Canonical Variate Analysis (CVA) was done to compute the inter-cluster distances. The intra and inter-cluster distance ($D^2$) values were shown in Table 12. In this experiment, the inter-cluster distances were higher than the intra-cluster distances thus indicating broader genetic diversity among the genotypes of different groups. Islam (1995) carried out on experiment on amaranth (*Amaranthus tricalor*) and obtained larger inter-cluster distances than the intra cluster distances in a multivariate analysis.

The highest inter-cluster distance was observed between clusters II and IV (131.154), followed by between cluster I and IV (108.744), II and III (94.553), IV and V (76.552) and I and III (72.103). In contrast, the lowest inter-cluster distance was observed between cluster I and II (22.574) and this distance increased gradually between cluster I and V (32.220) and cluster III and IV (36.672) (Table 12). However, the maximum inter-cluster distance indicating genotypes from these two clusters, if involved in hybridization may produce a wide spectrum of segregating population. Similar reports were also made by Bansal *et al*. (1999) and Singh *et al*. (1996), Zhang *et al*. (1987) reported that the greater genetic distances implying higher heterosis than those with similar genetic distances.

On the other hand, the maximum intra-cluster distance was found in cluster II (3.152), while the minimum distance was found in cluster IV (1.018). The different multivariate analysis was superimposed in Figure 3 from which it could be concluded that different multivariate techniques supplemented and confirmed one another.

**Table 12. Average intra and inter-cluster distances ($D^2$) for 20 red amaranth genotypes**

| Cluster | I | II | III | IV | V |
|---|---|---|---|---|---|
| I | **2.036** | 22.574 | 72.103 | 108.744 | 32.220 |
| II | | **3.152** | 94.553 | 131.154 | 54.713 |
| III | | | **1.023** | 36.672 | 39.892 |
| IV | | | | **1.018** | 76.552 |
| V | | | | | **2.109** |

*Bold figures denotes intra-cluster distance

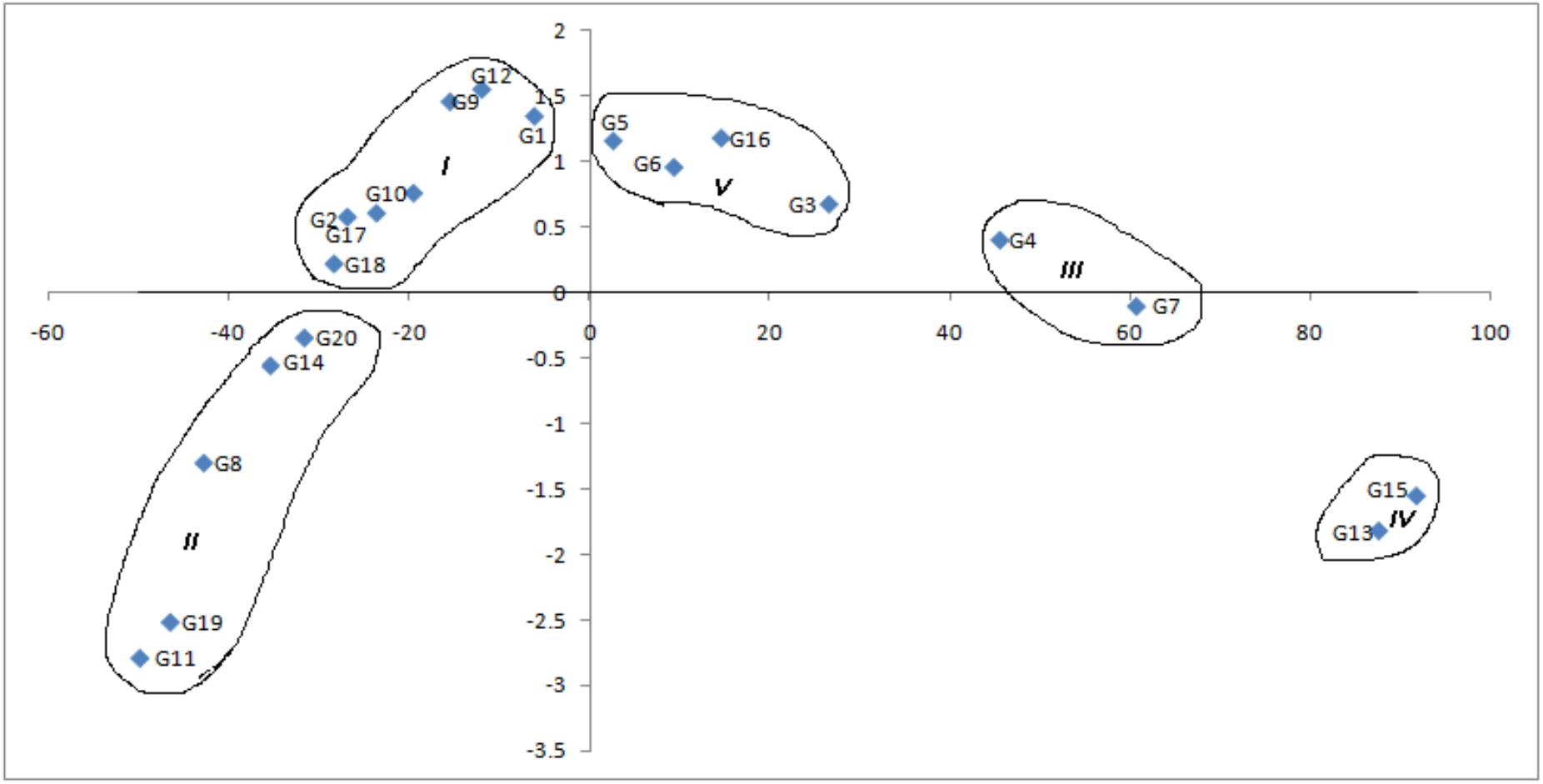


**Figure 3. Clustering (5 clusters) of 20 red amaranth genotypes regarding scattered distribution on principal component score**

A two-dimensional scatter diagram was constructed using principal component (PC) score (Z1-Z2) (Appendix IV) where PC1 as X-axis and PC2 as Y-axis, showing in the relative position (Figure 3). According to scatter diagram all the genotypes were apparently distributed into five clusters. It is assumed that the maximum amount of heterosis will be manifested in cross combination involving the genotypes belonging to most divergent clusters. Furthermore, for a practical plant breeder, the objective is to achieve high-level production in addition to high heterosis. In the present study the maximum distance existence between cluster II and IV. Main and Bahl (1989) reported that the parents separated by $D^2$ values showed higher heterosis.

Keeping this in view, it appears that the crosses between the genotypes belonging cluster II with cluster IV, cluster I with cluster IV, cluster II with cluster III, cluster IV with cluster V and cluster I with cluster III might produce high heterosis in respect of higher leaf area and fresh yield per plant. Also the crosses between genotypes from cluster II with cluster IV might produce high level of segregating population. So the genotypes belonging to cluster IV, cluster III, cluster V, cluster I and cluster II have been selected for future hybridization program.

### 4.4.5 Selection of parents for future hybridization

Selection of genetically diverse parents is the principal task for any plant breeding activities. Therefore, considering the magnitude of genetic distance, contribution of character towards divergence, magnitude of cluster mean and agronomic performance; the genotype G15 (BD-7406) for higher yield $ha^{-1}$, number of leaves $plant^{-1}$, leaf length $plant^{-1}$, leaf area $plant^{-1}$, fresh weight $plant^{-1}$ and dry weight $plant^{-1}$ followed by G13 (BD-2964), G7 (BD-2946), G4 (BD-2934) and the genotypes G13 (BD-2964) for plant height followed by G15 (BD-7406), G7 (BD-2946) and the genotype G7 (BD-2946) for stem diameter $plant^{-1}$ followed by G15 (BD-7406), G13 (BD-2964) might be considered for future hybridization.

Top four genotypes *viz*. G15 (BD-7406), G13 (BD-2964), G7 (BD-2946) and G4 (BD-2934) were identified as best genotypes with respect to foliage yield per plot. Therefore, these genotypes could be considered as suitable genotypes for efficient hybridization for increasing productivity of red amaranth in the future and these genotypes can be further assessed for their stability across environment and season. Involving of such diverse lines in crossing program could produce desirable segregants.

Divergence study revealed that, highest inter cluster mean for fresh weight per plant was observed between cluster IV and cluster III. Hence, the crosses between the genotypes of these clusters can be tried for improvement of yield. Considering group distance and other agronomic performance, genotypes G15 (BD-7406) and G13 (BD-2964) in cluster IV and genotypes G7 (BD-2946) and G4 (BD-2934) in cluster III could be considered suitable genotypes for efficient hybridization in future.

Based on quantitative data, the potentiality of the red amaranth genotypes with respect to foliage yield and its attributing characters and the genetically divergent genotypes was identified in the present study have wider applicability in planning the future breeding programs for increasing productivity of red amaranth.

# CHAPTER V

# SUMMARY AND CONCLUSION

An investigation entitled “characterization and genetic diversity analysis of red amaranth *(Amaranthus cruentus* L.)” for yield and its components was carried out to estimate the nature and extent of genetic variability, the degree of association, path analysis and amount of diversity for twenty red amaranth genotypes. The present study was undertaken at the Sher-e-Bangla Agricultural University Farm, Dhaka during November to December 2020. Seeds were sown in the main field in Randomized Complete Block Design (RCBD) with three replications. Data on various plant characters such as, plant height (cm), number of leaves plant$^{-1}$, average leaf length plant$^{-1}$ (cm), average leaf area plant$^{-1}$ (cm$^2$), average stem diameter plant$^{-1}$ (mm) and yield plant$^{-1}$ (fresh weight) (g) were recorded.

Analysis of variance revealed highly significant difference among genotypes for most of the characters studied. The tallest plant was recorded in G13 (BD-2964) and the shortest plant was recorded in G19 (BD-9806). The highest number of leaves plant$^{-1}$, average leaf length plant$^{-1}$, average leaf area plant$^{-1}$ and yield plant$^{-1}$ (fresh weight) were recorded in G15 (BD-7406) and the lowest for the respected parameters were recorded in G11 (BD-2958). But the highest average stem diameter plant$^{-1}$ was recorded in G7 (BD-2946) whereas the lowest was recorded in G8 (BD-2947).

The phenotypic co-efficient of variation was higher than genotypic co-efficient of variation for all the traits. High genotypic co-efficient of variation (GCV) and phenotypic co-efficient variation (PCV) were observed for plant height and average leaf area plant$^{-1}$. It indicated existence of broad genetic base, which would be useful for further selection. Moderate GCV and PCV were observed for number of leaves plant$^{-1}$, average leaf length plant$^{-1}$, average stem diameter plant$^{-1}$ and yield plant$^{-1}$ (fresh weight).

The high estimates of heritability coupled with higher values of genetic advance as percent mean (GAM) were observed for the parameters like plant height, average stem diameter plant$^{-1}$ and yield plant$^{-1}$ (fresh weight) which indicates the predominance of additive gene action. Moderate heritability coupled with high GAM was observed for number of leaves plant$^{-1}$, average leaf length plant$^{-1}$ and average leaf area plant$^{-1}$.

A narrow difference between the genotypic and phenotypic correlation coefficients was observed for various traits in the present findings and this indicated the lesser influence of environment in the expression of these traits and presence of strong inherent association among the traits. Yield plant$^{-1}$ (fresh weight) was positively and significantly correlated with all the studied parameters *viz*. number of leaves plant$^{-1}$, average leaf length plant$^{-1}$, average leaf area plant$^{-1}$ and average stem diameter plant$^{-1}$ except plant height both at phenotypic and genotypic level. In general, most of the characters showed higher genotypic correlation co-efficient than the corresponding phenotypic correlation co-efficient suggesting a strong inherent association between the characters under study and suppressive effect of the environment modified the phenotypic expression of these characters by reducing phenotypic correlation values.

Path analysis studies revealed that among the traits, number of leaves plant$^{-1}$, average leaf area plant$^{-1}$ and average stem diameter plant$^{-1}$ exhibited significant positive association with yield plant$^{-1}$ (fresh weight) which showed true association with high direct effect. The direct selection in these traits would be rewarding for improvement in the vegetative yield. However, parameters like plant height and average leaf length plant$^{-1}$ had direct negative effect on vegetative yield ha$^{-1}$.

Genetic diversity among red amaranth genotypes was performed through Principal Component Analysis (PCA), Cluster Analysis, Canonical Variate Analysis (CVA). The first three principal component axes accounted for

99.60% variation towards the divergence. From genetic divergence studies using $D^2$ statistics, 20 red amaranth genotypes were grouped into five distinct clusters. The cluster-I was the largest cluster having 7 genotypes followed by cluster-II with 5 genotypes, cluster-V with 4 genotypes, cluster-III and cluster-IV included 2 genotypes each. Based on distance between clusters, *i.e.,* inter cluster distances, the maximum divergence was observed between cluster II and cluster IV (131.154) having 5 and 2 genotypes respectively, followed by cluster I and cluster IV (108.744) having 7 and 2 genotypes respectively indicating genotypes from these two clusters, if involved in hybridization may produce a wide spectrum of segregating population whereas the lowest inter-cluster distance was observed between cluster I and cluster II (22.574) having 7 and 5 genotypes respectively. Among the five clusters, cluster II with five genotypes showed maximum intra cluster distance (3.152) while the minimum (1.018) was found for cluster IV with 2 genotypes. The intra cluster distance for cluster I (2.036) with 7 genotypes, cluster V with 4 genotypes (2.109) and cluster III (1.023) with 2 genotypes were recorded. Maximum intra cluster distance indicated that genotypes included in cluster II are very diverse. Therefore, crossing between the genotypes cluster II with cluster IV, cluster II with cluster III, cluster I with cluster IV, and cluster I with cluster III might produce high heterosis in respect of yield plant$^{-1}$ (fresh weight). Also the crosses between genotypes from cluster II with cluster IV might produce high level of segregating population. So, the genotypes belonging to cluster II, cluster IV, cluster III, cluster I and cluster V have been selected for future hybridization program.

## CONCLUSIONS

Considering the magnitude of genetic distance, contribution of character towards divergence, magnitude of cluster means and agronomic performance the genotypes G15 (BD-7406) for yield plant$^{-1}$ (fresh weight), number of leaves plant$^{-1}$, average leaf length plant$^{-1}$ and average leaf area plant$^{-1}$ and the genotypes G13 (BD-2964) for higher plant height and the genotype G7 (BD-2946) for higher average stem diameter plant$^{-1}$ might be considered for future hybridization. Therefore, considering diversity pattern and other agronomic performance, lines G15 (BD-7406), G13 (BD-2964), G7 (BD-2946) and G4 (BD-2934) could be considered as suitable genotypes for efficient hybridization in future.

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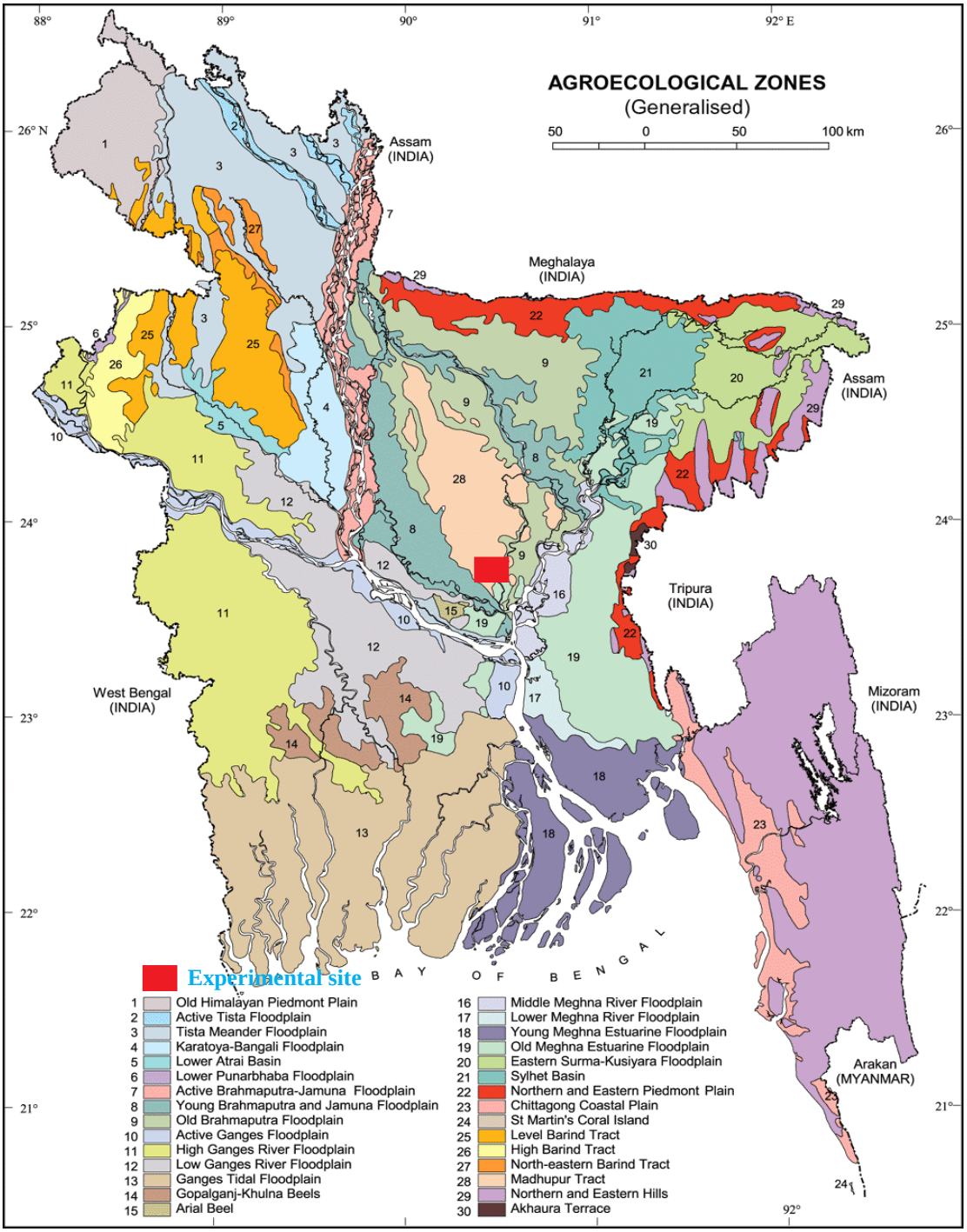
## Appendix I. Map showing the experimental site under the study



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

**A. Physical composition of the soil**

| Soil separates | % | Methods employed |
|---|---|---|
| Sand | 36.90 | Hydrometer method (Day, 1965) |
| Silt | 26.40 | Do |
| Clay | 36.66 | Do |
| Texture class | Clay loam | Do |

**B. Chemical composition of the soil**

| Sl. No. | Soil characteristics | Analytical data | Methods employed |
|---|---|---|---|
| 1 | Organic carbon (%) | 0.82 | Walkley, 1947 |
| 2 | Total N (kg/ha) | 1790.00 | Bremner and Mulvaney, 1982 |
| 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 (kg/ha) | 69.00 | Olsen and Dean, 1965 |
| 7 | Exchangeable K (kg/ha) | 89.50 | Pratt, 1965 |
| 8 | Available S (ppm) | 16.00 | Hunter, 1984 |
| 9 | pH (1:2.5 soil to water) | 5.55 | Jackson, 1958 |
| 10 | CEC | 11.23 | Chapman, 1965 |

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

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

| Month | Air temperature (°c) | | Relative humidity (%) | Rainfall (mm) (total) | Sunshine (hr) |
|---|---|---|---|---|---|
| | **Maximum** | **Minimum** | | | |
| November, 2020 | 34.7 | 18.0 | 77 | 227 | 5.8 |
| December, 2020 | 32.4 | 16.3 | 69 | 0 | 7.9 |

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

**Appendix IV. Principal component score (Z1-Z2) for 20 red amaranth genotypes**

| Genotype no. | PC1 | PC2 |
|---|---|---|
| G1 | -6.134 | 1.490 |
| G2 | -23.717 | 0.675 |
| G3 | 26.622 | 0.798 |
| G4 | 45.628 | 0.411 |
| G5 | 2.632 | 1.294 |
| G6 | 9.383 | 1.109 |
| G7 | 60.790 | -0.140 |
| G8 | -42.944 | -1.432 |
| G9 | -15.534 | 1.489 |
| G10 | -19.597 | 0.827 |
| G11 | -50.065 | -2.961 |
| G12 | -11.989 | 1.670 |
| G13 | 87.719 | -1.966 |
| G14 | -35.530 | -0.641 |
| G15 | 91.922 | -1.701 |
| G16 | 14.661 | 1.352 |
| G17 | -26.968 | 0.585 |
| G18 | -28.448 | 0.212 |
| G19 | -46.687 | -2.682 |
| G20 | -31.747 | -0.389 |