“GENETIC DIVERSITY STUDIES IN GRAIN AMARANTHUS
[*Amaranthus hypochondriacus* (L.)]’’

BY

KALE BALU HARIBHAU

(Reg. No. 2017A09MB)

DEPARTMENT OF AGRICULTURAL BOTANY

(GENETICS AND PLANT BREEDING)

COLLEGE OF AGRICULTURE, BADNAPUR, DIST. JALNA

VASANTRAO NAIK MARATHWADA KRISHI VIDYAPEETH,

PARBHANI 431 402 (M.S.), INDIA

2019

"GENETIC DIVERSITY STUDIES IN GRAIN AMARANTHUS [*Amaranthus hypochondriacus* (L.)]''

DISSERTATION

Submitted to the

Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani

in partial fulfilment of the

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IN

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2019

CANDIDATE'S DECLARATION

I hereby declare that this dissertation
Or part thereof has not been
Previously submitted by me
For a degree of any
University or
Institute

Place: BADNAPUR

(Kale B. H.)
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Date: 31/05/2019

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CERTIFICATE - I

This is to certify that the dissertation entitled **"Genetic Diversity Studies in Grain Amaranthus [*Amaranthus hypochondriacus* (L.)]"** submitted by Shri. **KALE BALU HARIBHAU (Reg. No. 2017A09MB)** to the College of Agriculture, Badnapur in partial fulfillment of the requirement for the degree of **MASTER OF SCIENCE (AGRICULTURE)** in the subject of **AGRICULTURAL BOTANY** (**GENETICS AND PLANT BREEDING)** is record of original and bonafide research work carried out by him under my guidance and supervision. It is of sufficiently high standard to warrant its presentation for the award of the said degree

I also certify that the dissertation or part there of has not been previously submitted for a degree of any university. The assistance and help rendered during the course of investigation and sources of literature have been duly acknowledged.

Place: BADNAPUR
Date: 31 / 05 /2019

(Dr. S. B. Sarode)
Research Guide and Chairman
Advisory Committee

CERTIFICATE – II

This is to certify that the dissertation entitled **"Genetic Diversity Studies in Grain Amaranthus [*Amaranthus hypochondriacus* (L.)]"** submitted by Shri. **KALE BALU HARIBHAU** to the College of Agriculture, Badnapur in partial fulfillment of the requirement for the degree of **MASTER OF SCIENCE (Agriculture)** in the subject of **AGRICULTURAL BOTANY (GENETICS AND PLANT BREEDING)** has been approved by the student's advisory ccommittee after viva-voce examination in collaboration with the external examiner.

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Place: Badnapur ***(Kale B.H.)***

Date: 31/05/2019 ***Reg. No. 2017A09MB***

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Abbreviations

/	-	Per
bs (h^2)	-	Broad sense
C.D.	-	Critical differences
Cm	-	Centimeter
d. f.	-	Degree of freedom
e.g.	-	Exampli gratia (For example)
EDTA	-	Ethylene diamine tetra acetic acid
et al.	-	Et alia (and others)
etc.	-	Et cetra
Fig.	-	Figure
g	-	gram
GCV	-	Genotypic coefficient of variation
NaOH	-	Sodium hydroxide
H_3BO_3		Boric acid
i.e.	-	That is
J.	-	Journal
Kg	-	Kilogram
Mm	-	Milimeter
M	-	Million
M / ha	-	Million per hectare
m^2	-	Square meter
Mg	-	miligram
MS	-	Mean square
Mse	-	Error mean squares
MT	-	Metric Tonnes
PCV	-	Phenotypic coefficient of variation
q/ha	-	Quintals per hectare
Sci.	-	Science
SE	-	Standard Error
SE(d)	-	Standard error of difference
SE(m) ±	-	Stanadard error of mean
Sr. No.	-	Serial number
Unpub.	-	Unpublished
Viz.,	-	Videlicet (namely)
Vs	-	Versus
Wt	-	Weight
%	-	Per cent
Σ	-	Standard deviation
Σ	-	Summation

Introduction

CHAPTER-I

INTRODUCTION

Grain Amaranthus [*Amaranthus hypochondriacus* (L.)] also known as Rajgira or pigweed or Ramdanna belongs to family *Amaranthaceae* trib *Amarantheae* Subfamily Amaranthoideae Suborder Chenopodiineae Goosefoot family Chenopodiaceae. It is a self pollinated, tetraploid (2n = 36) crop. Grain Amaranthus (*Amaranthus hypochondriacus* L.) are important pseudocereals that are widely cultivated in India in the sub-Himalayan ranges and in the Nilgiri Hills of South India. Amaranthus are one of the oldest food crops in the new world. It is an ancient food crop reported to have been cultivated in Mexico. Amongst the three pseudo cereals (chenopods – *Chenopodium* spp., buckwheat, *Fagopyrum* spp. and amaranth – *Amaranthus* spp.) grain amaranthus are the most important. The crop is native to the Ethiopian highlands of Central Africa and was introduced into Indian sub continent approximately 3000 years ago. The long history of cultivation of grain amaranthus in India under diverse agro-climatic conditions and the associated human and natural selection has resulted in generation of large variability giving India the status of secondary centre of diversity. The first advance estimation area, production and productivity in Maharashtra *Kharif* 2017-2018 total area 0.864 lakh ha, production 0.932 lakh tones and productivity 1078 kg/ha (Directorate of Agriculuture, Government of Maharashtra).

Amaranth having its origin in America and Europe, is being cultivated as a grain for 8000 years ago. Earlier Amaranth species were grown as the principle grain crop by the Aztecs, synonyms such as "mystical grains of the Aztecs," "super grain of the Aztecs," and the "golden grain of the Gods", used to describe nutritious amaranth grain. In India, grain amaranth is grown from tropical lowlands to 3500 m height in the Himalayas. Amaranth was a major grain crop in the pre conquest Aztec empire. Pale seeded amaranth were also being grown in Germany during 16^{th} century, India and Ceylon in 18^{th} century, the Himalayas in 19^{th} century and interior China and eastern Siberia in the late 19^{th} century.

In India amaranth is cultivated in Jammu and Kashmir, Himachal Pradesh, Uttarakhand, Sikkim, Assam, Meghalaya, Arunachal Pradesh, Nagaland,

Tripura, Jharkhand, Chattisgarh, Maharashtra, Gujrat, Orissa, Karnataka, Kerala and Tamil Nadu both in hills and plains. The exact information about the statistics on area and production in India is lacking. However, as a grain crop it is estimated to be grown in about 40-50 thousands ha. Hand harvested yields have been as high as 4000 kg/ha in Montana and 6000 kg/ha in Peru, between 2500 and 3300 kg/ha in southwest Germany, between 2100 and 2700 kg/ha in Slovak Republic and 1200 kg/ha in India.

Amaranth, a C_4 plant, is one of a few dicots in which the first product of photosynthesis is a four carbon compound. The combination of anatomical features in amaranth and C_4 metabolism, results in increased efficiency to use CO_2 under a wide range of both temperature and moisture stress environments. This contributes to the plant's wide geographic adaptability to diverse environmental conditions.

Amaranthus hypochondriacus is the predominant grain amaranth cultivated in North America. Similar to the other two grain amaranths *A. hypochondriacus* genotypes have white seeds, but there are several exceptions with dark seeds. One particular case is a genotype from Southern Mexico that was selected for dark seeds for a special traditional dish.

Amaranth is more correctly termed as "pseudo grain". The amaranth is highly edible by gluten intolerant individuals as it contains no gluten. Both grain and leaf types require little fuel to cook and are utilized as food by humans and animals. Amaranth species are receiving a great deal of attention in developing countries as a means to fight protein malnutrition due to the presence of high seed protein (about 16 %) which is much higher than most of the common grains except soybeans. The seed protein contains a balanced amino acid composition with high lysine content ranging from 0.73 to 0.84 % of total protein content. The "protein complement" of amaranth grain is very near to the levels recommended by FAO/WHO.

The main virtue of the seed lies in its high protein (8-22%) and with 6% lysine content which ranges from 0.73 to 0.84% of amaranth’s total protein content, and sulphur containing amino acids (4.4%) which are deficient in other grain crops, it also contains minerals (3%), vitamins (1.5%) and easily digestible carbohydrates (62%) and is considered as one of the best source of an anti oxidant called squalene. In addition to proteins, dietary fiber and lipids, calcium, iron, magnesium, phosphorus, copper, manganese cobalt, chromium, iodine, selenium,

zinc, molybdenum and sodium like other cereals which are also required by the human body in very small quantities (generally less than 100 µg/ day)

The achievement in plant breeding programme largely depend upon the genetic variability available in breeding population and the efficiency of selection technique. The importance of genetic diversity in plant breeding is obvious from results obtained in different crops. The recognition and measurement of such diversity, its nature and magnitude are beneficial, perhaps crucial to any breeding programme. This is particularly important in a crop like amaranthus where hybridization is difficult, there being limited scope for making large number of crosses by random mating and hence, the information regarding the nature of genetic diversity of the parents to be used in the hybridization, is of peramount importance to amaranthus breeder.

The D^2 statistic is useful tool to assess the genetic divergence among population. It also provides a quantitative measure of association between geographic and genetic diversity based on generalized distance (Mahalanobis, 1936). Analysis and utilization of available genetic diversity is a short-term strategy for developing improved cultivars for meeting immediate requirement of the farmers and the end users. The present study was undertaken with the following objectives to identify diverse genotypes with good yield potential.

The original concept of correlation was given by Galton (1889). Path analysis is done with the main purpose of understanding the direct and indirect contribution of different characters towards grain yield. The direct contribution of each component to the yield and the indirect effects and its association with other characters cannot be differentiated by simple correlations. It was first developed and described by Wright (1921) as a tool in genetic analysis for deriving the direct and indirect effects of any set of variables themselves related to one another. Later it was employed for crop improvement by Dewey and Lu, (1959).

Keeping the above aspects in consideration the present investigation entitled **"Genetic diversity studies in Grain Amaranthus [*Amaranthus hypochondriacus* (L.)]"** was undertaken during *Kharif* 2018 on the experimental

field of Department of Agriculture Botany, College of Agriculture, Badnapur with following objective.

1. To study the genetic variability in Amaranthus.

2. To study the correlation and path analysis in Amarnthus.

Review of Literature

CHAPTER-II

REVIEW OF LITERTURE

A comprehensive review of literature is an essential part of any scientific investigation. Review of literature is always necessary to compare the present findings with the previous studies undertaken by the research workers.

The literature pertaining to the present investigation entitled "Genetic diversity studies in Grain Amaranthus [*Amaranthus hypochondriacus* (L.)]" has been reviewed under following different aspects.

1) To study the genetic variability in Amaranthus.

2) To study the correlation and path analysis in Amaranthus.

1) Genetic variability in Amaranthus.

Arunachalam and Bandyopadhyay (1984) devised method to delineate parental divergence into four divergence clases (D.C). To take into account the variable magnitude of variation in parental divergence, the mean (m) and standard deviation (s) of the values of intra and inter cluster divergence (D) were calculated.

Pawar (1995) observed higher estimation of GCV and PCV for number of branches per plant followed by grain yield per plant and leaf area per plant in grain amaranthus.

Joshi (1986) in the study of twenty genotypes of *A.hypochondriacus* observed wide variability for height, number of leaves per plant, leaf length and width, inflorescence length, number of spikelets per plant, days to maturity and 1000 seed weight. Heritability estimates and expected genetic advance were high for 1000 seed weight, inflorescence length and height.

Arntz *et al*. (1998) to assess the contributions of individual growth traits to reproduction, we calculated covariances between standardized traits and relative fitness (selection differ- entials), and compared selection between the two bio- types. However, the reproductive biomass of the photosynthetic mutants was significantly reduced compared to the wild type. In the competitive environment, the wild type

achieved greater fitness because, while similar in size to the mutants, at any given size it produced more reproductive biomass.

Pandey (2003) reviewed three different aspects in grain amaranthus research for its genetic improvement, including (i) the study on plant genetic structure and function to develop suitable plant type, (ii) the analysis of genetic structure for different plant characters and formulation of rational breeding approach and (iii) the restructuring of plants (such as *A. hypochondriacus*) by polyploidy as well as by interspecific hybridization to generate genetic variation and new gene combinations.

Shukla *et al*. (2005) evaluated 29 strains of vegetable amaranth (*A. tricolor*). The data were recorded for plant height (cm), stem diameter (cm), branches/plant, leaves/plant, leaf size (cm), and protein content (mg/100 mg) in each cutting separately. Foliage yield (kg) was recorded on plot basis comprising 4 cuttings. The highest foliage yield per plot was recorded for strain AV-38, followed by AV-23 and AV-31. In general, protein content was high in the 2^{nd} cutting in all strains. The heritability estimates were in general high for all the characters in all the cuttings and ranged from 74.87% to 93.33%. Genetic advance was maximum for foliage yield (42.50%), followed by leaf size (31.02%) and stem diameter (21.13%).

Shukla *et al. (*2006) reported the proximate mineral composition in 30 strains of *A. tricolor* along with some suggestions for qualitative improvement of the foliage yield with reference to minerals. Our study showed that vegetable amaranth is a rich source of minerals like calcium (1.7±0.04 g/100 g), iron (1233.8±50.02 mg/kg), and zinc (791.7±28.98 mg/kg). The heritability estimates were high for most of the traits, with potassium and calcium showing high values, while comparatively lower values were recorded for magnesium and nickel. Nickel was the only mineral that showed positive correlation with all the minerals, as well as with leaf size and foliage yield. Zinc showed strong positive relationship with iron (0.66) and manganese (0.74), and was the only mineral exhibiting significant positive association with foliage yield.

Tui Roy and Satyesh Chandra Roy (2008) the present investigation was conducted to elucidate the interrelationship among various agronomic and quality traits and their direct and indirect effect on foliage yield in 39 distinct cultivars of

vegetable amaranth (*A. tricolor*). Among the agronomic traits, plant height and number of inflorescence exhibited significant positive association with foliage yield, while chlorophyll a, chlorophyll b, carotenoid, fiber and ascorbic acid were positively correlated with foliage yield. Chlorophyll a and chlorophyll b exhibited significant positive association with carotenoid, fiber and ascorbic acid. Ascorbic acid was positively correlated with fiber and carotenoid. Protein was associated with plant height, branches per plant and 500 seed weight. Chlorophyll a, carotenoid and inflorescence length revealed high positive direct effect on foliage yield, while branches per plant, leaf size, seed yield, chlorophyll b, moisture content and ascorbic acid showed negative path coefficient with foliage yield.

Pan *et al.* (2008) that estimates of heritability and genetic advance are useful in determining the influence of environment in expression of the characters and the extent to which improvement is possible after selection (Robinson *et al.,* 1949). Correlation between yield and its components and their relative contribution to yield will be of great value in improving the efficiency of selection.

Shukla *et al.* (2010) conducted investigation to elucidate the interrelationship among various agronomic and quality traits and their direct and indirect effect on foliage yield in 39 distinct cultivars of vegetable amaranth (*A. tricolor*). Among the agronomic traits, plant height and number of inflorescence exhibited significant positive association with foliage yield, while chlorophyll a, chlorophyll b, carotenoid, fiber and ascorbic acid were positively correlated with foliage yield. Chlorophyll a and chlorophyll b exhibited significant positive association with carotenoid, fiber and ascorbic acid. Ascorbic acid was positively correlated with fiber and carotenoid. Protein was associated with plant height, branches per plant and 500 seed weight. Chlorophyll a, carotenoid and inflorescence length revealed high positive direct effect on foliage yield, while branches plant, leaf size, seed yield, chlorophyll b, moisture content and ascorbic acid showed negative path coefficient with foliage yield.

Chottopadhyay *et al*. (2013) seven genotypes of green mustard (*Brassca juncea*). The direct and indirect effects on leaf yield have also been studied. High heritability with high genetic advance as percent of mean was registered for plant height, vitamin C content and yield per plant (g) which in fact demonstrated the

presence of additive gene effects. The correlation studies revealed strong positive association of yield with Leaf area index (LAI), dry matter yield, number of leaves per plant at genotypic level, whereas at phenotypic level only dry matter yield showed a significant positive correlation. The result of path analysis indicated that dry matter yield had maximum direct effect on yield per plant followed by vitamin C content, total chlorophyll content and leaf length.

Akaneme and Ani (2013) in their study observed that analyses of variance revealed highly significant differences ($P<0.001$) for leaf width, hypocotyls length, days to 50% flowering, 500 seed weight ($P<0.01$) and leaf length ($P<0.05$). The range, coefficient of variability, phenotypic and genotypic coefficients of variability also revealed high variability for each of the quantitative traits. The highest broad sense heritability (h2b), GCV, PCV and GA were obtained for days to 50% flowering which was also positively correlated with leaf length and stem diameter.

Upadhyay and Maurya (2013) revealed that interrelationship among direct and indirect influence of component characters of yield is important in detecting the correlated response to directional selection, and in the detection of traits as useful markers. The present investigation is carried out with the aim to elucidate the genetic association among different agronomic traits in vegetable amaranthus by correlation and path coefficient analysis.

Venkatesh *et al.* (2013) evaluated during *Kharif*- 2011 one hundred germplasm accessions of grain amaranth for assessing the genetic variability present in the material for grain yield and yield related traits. Analysis of variance revealed significant differences among the genotypes for all the characters studied. High PCV and GCV was observed for stem girth, plant height, panicle length and grain yield per plant. On the other hand, low PCV and GCV were observed for days to maturity and grain protein content. All the traits studied exhibited high heritability. High genetic advance as per cent of 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.

Gajdosova *et al.* (2014) selected two genotypes of *Amaranthus sp.* have been selected –*Amaranthus cruentus* "Ficha" and hybrid "K–433" .The seeds were treated with 175 Gy. During the period of the project duration (10 December 1998–19 May 2003) the M1 - M5 generations were established. The phenological observations were performed during all vegetation periods and selection on desired traits was done. The negative plants were removed from the field. The weight of seeds per plant and weight of 1000 seeds (WTS) was recorded and statistically evaluated. Finally, as seed progeny of M4 generation, 48 samples of *A. cruentus* (irradiated) with WTS 0.87g and 18 samples of K–433 (irradiated) with WTS 0.75g were selected and used for establishment of M5 generation. In several samples of *A. cruentus*, the WTS reached 0.9–1.0g and in K–433 0.8–0.9g with an obvious tendency to stabilization of this trait when comparing them with the mother plants of the previous generation.

Sarkar *et al.* (2014) in study aimed to evaluate genotypic variability in 30 vegetable amaranth genotypes for nutrient composition, antioxidant content, and 12 yield contributing traits. High mean value, high range of variability and high genotypic variance were observed for all the traits except content of Ca, protein and betacarotenoid. Close differences between genotypic and phenotypic variances and genotypic and phenotypic coefficient of variations were observed for all the traits. Considering all genetic parameters, selection based on contents of potassium, manganese, and ascorbic acid, plant height, leaves/plant, diameter of stem base, fiber content, leaf area and foliage yield/plot seemed to be effective for the improvement of vegetable amaranth. Foliage yield had significant positive correlation with plant height, leaves per plant, diameter of stem base, fiber content and leaf area. Nutrient content and antioxidant traits exhibited interesting results, i.e., had insignificant genotypic correlations with foliage yield and most of the studied traits indicating that selection with these traits might be possible without compromising any yield loss.

Enoch *et al.* (2014) conducted research on amaranth species *A. blitum, A. caudatus, A. cruentus, A. dubius, A. hypochondriacus, A. spinosus, A. thunbergii, A. tricolor,* and *A. viridis*. Research and development opportunities on nutritive and nutraceutical properties, production and commercialization, taxonomic evaluation and breeding perspectives were explored.

Yadav *et al.* (2014) recorded estimates for the characters like leaf blade width, lateral spikelet length and grain yield per plant which showed high GCV and PCV

values. Genotypic coefficient of variation for different characters ranged from 11.60 to 42.73%. The highest GCV was recorded with grain yield per plant (42.73%). High heritability exhibited for all the characters studied ranged from 97.81 to 99.98%. The estimates of heritability were observed to be high in magnitude for days to 80 % maturity, days to 50 % flowering, leaf blade width, inflorescence length and plant height. At genotypic level, seed yield per plant showed highly significant positive correlation with days to 80% maturity (rg = 0.696) and plant height (rg = 0.403) and significant positive correlation with days to 50% flowering (rg = 0.338). Inflorescence length had significant positive correlation with lateral spikelet length.

Sammour *et al*. (2014) in an experiment aimed at identifing genetic variability and assesing the evolutionary relationships between 24 accessions of eight *Amaranthus* species, based on the morphological features of the basic chromosome numbers and numerical characterization of the karyotypes using total chromosome length (TCL), mean chromosome length (MCL) and mean centromeric index (MCI). The basic chromosome numbers were analyzedn cytologically by Feulgen staining. They were 16 for all the studied accessions, except some accessions belong to *A. powellii* and *A. palmeria* which exhibited n=17. The karyotypes of the studied accessions had a predominance of metacentric chromosomes with some accessions characterized by subtelocentric chromosomes. The karyptype analysis showed a variation in the karyotype of the accessions of the same species. The variation may be considered of adaptive significance. Cluster analysis showed *A. hybridus* and *A. powelli* as a progenitor of amaranthus species. The obtained data indicated that *A. powelli* could be considered the most advanced species, since it has the smallest chromosome length.

Mobina and Jagatpati (2015) in their study selected six accessions namely (i) IC 95609, (ii) IC 35482, (iii) IC 120617, (iv) IC 35626, (v) IC 9559 & (vi) IC 95589 out of fifteen accessions. The phenotypic variations were observed and exhibited in this context following proper statistical model. The aims and objects of this experimentation was to highlight the phenotypic as well as genotypic significance, component of variances, heritability (in broad sense), genetic advance of each accession over this particular location.

Gueco *et al.* (2016) the diversity in the morphological characters of 18 accessions of amaranth germplasm collection. A total of 34 characters comprising 22 qualitative and 12 quantitative data were observed. Based on Shannon-Weaver Diversity Index, 17 characters (50%) were found to have high diversity (>0.67) while two characters were invariant. Using Gower's coefficient at 0.7 r2, five clusters were generated from all the morphological characters. Following the taxonomic key, 4 species *A. spinosus, A.gracilis, A. hybridus,* and *A. tricolor* were identified in the 18 accessions used in the study. The results of the taxonomic identification and cluster analysis agree with each other.

Ishwar Singh Diwan *et al*. (2017) studied 10 germplasm of amaranthus. The analysis of variance indicated that the mean sum of square due to genotypes were highly significant for all the sixteen characters. The highest leaf yield kg per plot was recorded in genotype 2012/AMVAR- 4 followed by 2012/AMVAR-7 (17.41 kg/plot), CG Amaranthus-1 (17.36 kg/plot). Moderate estimates of phenotypic and genotypic coefficient of variation for almost all traits except leaf weight show the high genotypic and phenotypic variation indicated that there was high variability offering ample scope for selection of desired variability. Heritability along with genetic advance as percent of mean for all the tested characters indicated that these characters were under additive gene action and there were excellent chances of effective selection for improvement of these traits. Highly significant and positive correlation with leaf yield was observed with plant height, plant weight, stem girth and seed yield, whereas leaf length and petiole length showed negative association with green yield.

Tejaswini *et al.* (2017) evaluated a set of 27 genotypes comprising of 25 germplasm lines and two checks of amaranthus (*Amaranthus tricolor.* L). The analysis of variance revealed highly significant differences among the genotypes for all the 19 characters. On the basis of mean performance of the genotypes, five genotypes *viz*., IC-522214, IC-536718, IC-536712, IC-536699 and IC-536728 were identified as promising genotypes with reference to the characters *viz.*, leaf length, leaf width, leaf area index, leaf weight per plant, total foliage yield per plant, total chlorophyll content, protein content, ascorbic acid, moisture content, iron content and folic acid.

Panda *et al.* (2017) evaluated twelve genotypes of amaranthus were subjected to evaluation for 13 quantitative traits namely as plant height, number of nodes per plant, number of leaves per plant, number of inflorescence per plant, stem girth, leaf length, leaf breadth, petiole length, leaf area, stem weight, leaf weight, leaf: stem ratio and yield per plant. The results of the investigation revealed a wide range of variation for all the characters. Presence of minimum difference between phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for all the characters indicated that the phenotypes were true to the 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 materials evaluated.

2) Genetic divergence in Amaranthus

The sum total of genes present in the genotypes is called germplasm. The study of genotype diversity and the information of core subsets are important activities in the conservation, evaluation and utilization of genetic resources (Brown, 1989).

Morphological similarity, eco-geographic diversity, phylogenetical relationship, Mahalanobis D^2 statistics etc were the few earlier methods used for discriminating divergent populations, which are reinforced by more scientific and advanced biometric techniques *viz.*, multivariate analysis based on principal component analysis, agglomerative cluster analysis.

Fatocum (1985) studied 40 accessions from twelve countries using cluster analysis of principal component analysis. Accessions formed six groups. The cluster analysis revealed that leaf length, leaf dry weight per plant and total above ground dry matter yield per plant were the most important characters in formulating the clusters.

Kamble (2000) studied genetic divergence in fifty genotypes of grain amaranthus. He observed adequate diversity among the genotypes with D^2 values ranging from 7.13 to 14758.63. On the basis of D^2 values, the fifty genotypes studied were grouped into eleven clusters. Clustering pattern of these genotypes did not necessarily follow the geographical distribution.

Shukla and Singh (2002) studied genetic divergence in 66 strains of grain amaranthus. The 66 strains were grouped in nine clusters depending upon the genetic constitution of strains. The cluster VIII had maximum grain yield, days to maturity, plant height, inflorescence per plant and highest leaf size.

Kanthaswamy (2006) studied genetic divergence in 74 amaranthus genotypes from different localities using D^2. The genotypes were grouped in 12 clusters, with cluster I having 52 genotypes. Intracluster distance was highest between cluster XI and XII. Based on the mean performance of genotypes, genetic distance of clustering pattern, it was concluded that hybridization between genotypes from cluster XI and XII will produce highly heterotic hybrids.

Pandey (2009) evaluated twenty six accessions of grain Amaranths (*Amaranthus hypochondriacus*), including both indigenous and exotic introductions. Based on D^2 analysis, the accessions were grouped into eleven clusters. Clusters I, II, and III had seven, four, and three accessions, respectively; clusters VII, VIII, IX and X had only one accession in each case. 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 pattern of clustering did not show any relationship with geographic origin.

Pandey and Singh (2010) evaluated twenty six accessions of grain Amaranth (*Amaranthus hypochondriacus* L.) Chlorophyll a, chlorophyll b, total chlorophyll and phenol content showed significantly higher values for all the accessions. Leaf protein content was noted significant in four accessions, namely AG-67/1 (3.152 mg g-1), AG-21 (2.452 mg g-1), AG-306 (2.101 mg g-1) and AG-1175 (2.101 mg g-1). Using Euclidean cluster analysis 26 accessions were distributed in 3 clusters (at 9.0 euclidean distance) of which cluster I contained maximum (13) accessions, cluster II (10) and cluster III (3) accessions. Biochemical characters had no significant genetic association with grain yield plant-1 which revealed that biochemical traits can be improved without altering grain yield. Cluster I and III were found more diverse than others and therefore can be used for developing recombinants.

Erum *et al.* (2012) in UPGMA cluster, analysis grouped the 13 amaranthus genotypes into two major clusters, I and II, differentiating the ornamental amaranthus cultivars from edible. However, comparative view of the cluster showed that the *Amaranthus hypochondriacus* were closest to the China variety than to the *Amaranthus tricolor* according to their morphological characters. Optimal level of carbohydrates, fats, proteins and moisture contents were observed in 7033 (192.7 mg/ml), 7051(30.68 %) and 7033 (102.7 µg/ml) and 7034 (16 %) respectively, of Gonar, Northern Area and AJK of Pakistan.

Hailu *et al*. (2015) evaluated 36 accessions of *Amaranthus spp*. were evaluated Analysis of variance revealed that there was a significant difference ($p< 0.01$) among thirty six germplasm accessions for all the characters studied except for thousand seed weight which was non significant ($p>0.05$). The analysis based on D^2 statistics classified the 36 genotypes in to six clusters, which makes them moderately divergent and maximum distance between clusters III and I (2467).

Adhikary and Pratt (2015) in the investigation on genetic variability and genetic divergence with respect to yield component traits estimated using 105 germplasm. A high phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was observed for all the traits except for, chlorophyll content (SPAD chlorophyll meter reading), panicle width and 1000 seed weight. Heritability estimates were high for all the characters studied. High genetic advance as per cent mean (GAM) was registered for most of the traits except for 50 per cent flowering, 1000 seed weight and days to maturity. 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.

Lokeshkumar and Murthy (2017) Grain amaranth is a protein rich psuedocereal, assumes an important position in terms of quality breeding activities. Systematic characterization, evaluation and utilization of the potential germplasm in the crop are prerequisite to any crop improvement. The investigation on genetic variability and genetic divergence with respect to yield component traits estimated

using 105 germplasm during *Kharif* 2013 at University of Agricultural Sciences, Bengaluru. A high phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was observed for all the traits except for, chlorophyll content (SPAD chlorophyll meter reading), panicle width and 1000 seed weight. Heritability estimates were high for all the characters studied. High genetic advance as per cent mean (GAM) was registered for most of the traits except for 50 per cent flowering, 1000 seed weight and days to maturity. 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.

3) To study the correlation and path analysis in Amaranthus.

Lerner (1958) stressed the importance of correlation of the various characters with yield. Genotypic correlation coefficient provides a measure of genotypic association between characters and gives an indication of more useful characters. The main genetic cause of such correlation is paleographic, which refers to manyfold effects of gene (Falconer, 1981). Genotypic correlation provides basic information to breeders in understanding the nature of the species with which they work.

Grafius (1964) has pointed out that it would be more meaningful if the structure of yield were provided through its components rather than per se performance. For improving yield through breeding, it is necessary to study these yield components, their interrelationship with yield and their direct and indirect contributions.

Hauptil and Jain (1977) in a comparative study between three weedy and four domesticated grain amaranth species observed that allocation of biomass to seed production is positively correlated with seed yield for domesticated, but not for weedy types. Upon more elaborate partitioning, the per cent of biomass as seeds were found strongly and negatively correlated which indicated a direct antagonism between stem and seed production

Panday (1979) reported that the harvest index of *Amaranthus hypochondriacus* had the strong correlation with the yield followed by pollen fertility. He further noticed negative correlation of number of days to flowering and length of panicle with the yield.

Hauptil and Jain (1980) reported that in *Amaranthus cruentus*, late maturity, tallness and yield were positively correlated with each other but were negatively correlated with harvest index. Earlyness and lower seed yield appeared to be unfavorable character association in grain amaranth.

Pandey (1981) studied the genetic association in *A.hypochondriacus*. The data indicated that the genotypic correlations, in general, were higher than the corresponding phenotypic correlations because of the modifying effect of environment on the association of characters at the genic level. Grain yield had high positive correlation with number of days to flowering, plant height, number of days to maturity, harvest index and pollen fertility. Grain yield had moderate positive correlation with length of the panicle, number of panicles per plant and negative correlation with grains per panicle and 1000 grain weight.

Naidu *et al.* (1982) revealed that positive correlation was observed in all the species of grain amaranth between the mean nitrate reductase activity and grain yield and total dry matter accumulation at harvest; leaf nitrate reductase activity with total reduced nitrogen per plant; leaf of grain protein with the nitrate reductase activities; leaf protinase activity and percentage of protein in grain; root growth and total reduced nitrogen per plant and nitrate reductase activity.

Mohideen *et al*. (1983) observed higher yields in long duration lanky growth habit with shy branching grain Amaranth types and also reported negative relationship of branch with plant height.

Espindola and Gandarillas (1985) in results on a study conducted on correlations between yield and contributing characters in Quinoa revealed positive phenotypic correlations between yield and stem diameter. Path coefficient analysis

revealed the importance of panicle length, stem diameter, 1000 seed weight as yield contributing characters.

Maruthi *et al*. (1987) in character association studies in Grain Amaranth (*Amaranthus spp*.) indicated significant positive phenotypic and genotypic correlation of number of branches per plant, stem girth, dry weight of inflorescence with yield. Grain yield showed negative genotypic correlation with days to 50% flowering, days to maturity and length of inflorescence. Number of nodes per plant and length of inflorescence exhibited negative direct effect on yield. Dry weight of inflorescence had positive and high direct effect on seed yield. Plant height and inflorescence length also showed considerable direct effect on seed yield.

Agong and Ayiecho (1992) reported high positive association of head weight with seed yield per plant. Plant height also had significant association with seed yield. Head weight and head length had significant correlation with other traits in grain amaranth (*Amaranthus sps.).*

Gowda *et al*. (1999) reported positive correlation of grain yield with plant height, dry weight per plant, panicle length and panicle weight and negative correlation with leaf number, days to 50% flowering and 1000 seed weight in Grain Amaranth.

Patgar (2003) stated that genotypic and phenotypic association of grain yield was positive and significant with panicle fresh weight, panicle length, number of spikes per panicle, dry weight of panicle, dry weight of stem and harvest index. Panicle fresh weight had high direct positive effect on seed yield per plant. Positive but direct effects of panicle fresh weight was exerted through number of spikes per panicle, dry weight of stem and harvest index.

Shukla and Singh (2003) investigated path analysis in grain Amaranth (*Amaranthus spp.)* revealed highest direct effect of leaf size towards grain yield followed by plant height. Indirect positive effects of plant height via days to flowering on grain yield. But inflorescence length, leaf size and number of spikes per panicle showed negative direct effect on grain yield.

Shukla and Singh (2003) evaluated sixty-six genotypes of *Amaranthus* spp. At phenotypic level, grain yield per plant showed a significant positive association with plant height and leaf size; plant height with number of primary branches per plant, number of spikelets per spike, number of nodes/plant and leaf size; number of spikelets/spike with no. of nodes per plant and leaf size; and number of nodes per plant with leaf size. The grain yield/plant was found to be positively and significantly associated with plant height (0.572), number of inflorescence per plant (0.475), number of spikelets per spike (0.45) and leaf size (0.530), which indicated that selection for these traits, would lead to an improvement in yield.

Kusuma *et a*l. (2007) in studies on character association and formulation of selection indices in Grain Amaranth was carried out in which they evaluated 64 accessions of Grain Amaranth (*Amaranthus spp*.) for quantitative traits and noticed that genotypic correlations were slightly higher than the phenotypic correlations. Seed yield exhibited significant and positive association with panicle fresh weight, panicle length, number of spikes per panicle, dry weight of panicle, dry weight of stem and harvest index. These characters also recorded high heritability and genetic advance. The selection indices revealed that relative efficiency was greater for the minimum character combination of panicle fresh weight plus panicle, length plus panicle dry weight. Selection based on these characters would enhance the yield potential in Grain Amaranth.

Aruna (2010) evaluated six genotypes of vegetable amaranthus and thirty F1 hybrids were involved to estimate the correlation and path analysis. The correlation coefficient between yield of greens with weight of leaves was highest both at genotypic level and at phenotypic level. Path analysis indicated that weight of leaves and weight of stem had higher and direct contribution to the yield.

Shukla *et al.* (2010) conducted experiment to elucidate the interrelationship among various agronomic and quality traits and their direct and indirect effect on foliage yield in 39 distinct cultivars of vegetable amaranth (*A. tricolor*). Among the agronomic traits, plant height and number of inflorescence exhibited significant positive association with foliage yield, while chlorophyll a, chlorophyll b, carotenoid, fiber and ascorbic acid were positively correlated with foliage yield. Chlorophyll a

and chlorophyll b exhibited significant positive association with carotenoid, fiber and ascorbic acid. Ascorbic acid was positively correlated with fiber and carotenoid. Protein was associated with plant height, branches per plant and 500 seed weight. Chlorophyll a, carotenoid and inflorescence length revealed high positive direct effect on foliage yield, while branches per plant, leaf size, seed yield, chlorophyll b, moisture content and ascorbic acid showed negative path coefficient with foliage yield. Suitable traits have been marked out to enhance foliage yield in vegetable amaranth.

Ravindra Babu *et al*. (2012) carried out experiment to study the correlation and path analysis in twenty one popular hybrids of rice (*Oryza sativa* L.). Character association of the yield attributing traits revealed significantly positive association of grain yield per plant with number of productive tillers per plant. Hence, selection for these traits can improve yield. Path coefficient analysis revealed that panicle length and number of productive tillers per plant exhibited positive direct effect on yield. Among these characters, number of productive tillers per plant possessed both positive association and high direct effects. Hence, selection for this character could bring improvement in yield and yield components.

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

Srivastava and Roy (2012) in genetic diversity analysis studied relationships among 12 cultivated and wild *Amaranthus spp.* were using protein and RAPD

markers. High level of genetic diversity was common within species contrary to genetic uniformity within most accessions. On average, the polymorphism reached 42.60% among the cultivars but raised to 46.88% in the wild counterpart. The seed protein content varied in the 11.80-17% range and seeds of amaranth proved highly nutritive. The SDS-PAGE analysis indicated that such proteins in case of amaranths were highly heterogenous with 8-18 bands. Based on the electrophoretic mobility, such bands were assigned four zones (A, B, C and D). The RAPD analyses of *Amaranthus spp.* are further substantiated by the seed protein profile, indicating that a combination of such approaches can offer relatively reliable parameters to unravel genetic diversity.

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 direct and indirect effects of marketable yield were also evaluated. High heritability with high genetic advance as percent of mean was registered for number of leaf, leaf weight and marketable yield followed by leaf weight, leaf number and dry weight without rind.

Upadhyay and Maurya (2013) revealed that interrelationship among direct and indirect influence of component characters of yield is important in detecting the correlated response to directional selection, and in the detection of traits as useful markers. The present investigation is carried out with the aim to elucidate the genetic association among different agronomic traits in vegetable amaranthus by correlation and path coefficient analysis.

Sarker *et al.* (2014) in study aimed to evaluate genotypic variability in 30 vegetable amaranth genotypes for nutrient composition, antioxidant content, and 12 yield contributing traits. High mean value, high range of variability and high genotypic variance were observed for all the traits except content of Ca, protein and betacarotenoid. Close differences between genotypic and phenotypic variances and genotypic and phenotypic coefficient of variations were observed for all the traits. Based on mean, range, genetic parameters, correlation coefficient and path coefficient values, direct selection through three traits, i.e., fiber content, leaf area and diameter of stem base would significantly improve the foliage yield of vegetable amaranth. On the other hand, concomitant selection based on high nutrient and antioxidant content

and high foliage yield would be effective selection method for improvement of vegetable amaranth.

Patial *et al.* (2014) evaluated twenty-two genotypes of amaranth (*Amaranthus spp.*) evaluated for 12 quantitative traits. Path coefficient analysis was carried out using correlation coefficients to know the yield-contributing traits having true associations with seed yield. The low differences between the phenotypic and genotypic coefficients of variations indicated low environmental influences on the expression of the traits studied. High heritability coupled with high genetic advance for yield/day to maturity, yield per day to seed fill, harvest index, panicle girth and seed yield/plant was observed. All the 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.

Venkatesh *et al.* (2014) evaluated one hundred genotypes of grain amaranth to estimate correlation and path coefficients among 10 quantitative traits including grain yield in grain amaranth. At the phenotypic level, stem girth, number of leaves per plant, plant height, panicle length and seed weight exhibited significant positive correlation with grain yield. While, its association with panicle width was negative and significant. Path co-efficient analysis revealed maximum positive direct effect of number of leaves per plant (0.575) on grain yield followed by seed weight (0.234), panicle length (0.221) and plant height (0.124).

Sarker *et al.* (2015) investigated twenty five vegetable amaranth genotypes for antioxidant vitamins and minerals composition. Significant Mean Sum of Square revealed a wide range of genotypic variability among traits. Considering genetic parameter six traits i e., Fe, Zn, Mn, ascorbic acid, number of leaves plant and foliage yield would be selected for the improvement of vegetable amaranth genotypes under study. However, correlation study revealed that selection based on Fe, Mn, ascorbic acid and number of leaves per plant could lead to increase the foliage yield of vegetable amaranth strains. Insignificant genotypic correlations between foliage yield with most of the antioxidant vitamins and minerals traits indicating that selection for

high vitamins and minerals content might be possible without compromising yield loss. Based on mean, genetic parameters and correlation coefficient values, five vegetable amaranth genotypes.

Oduwaye *et al*. (2016) evaluated eighteen *Amaranthus cruentus* and 11 *Amaranthus hypochondriacus* genotypes were evaluated. Higher genotypic coefficient of variability, heritability estimates, and genetic advance was observed for the traits at Abeokuta (more wet) than Ibadan (more dry) conditions. Grain yield had positive association with the traits at the two locations except the number of leaves and inflorescence length. Inflorescence length was positively associated with grain yield at Abeokuta and negatively associated at Ibadan. Path analysis indicated simultaneous improvement of grain yield with petiole length and leaf length at Abeokuta but with petiole length and leaf area at Ibadan.

Ahmed and Mohammad (2017) tested one hundred recombinant inbred lines (RILs) derived from four F4 populations of Flue Cured Virginia (FCV) tobacco to identify effective selection indices. Experimental material was planted at two locations *i.e.* Mardan (E-1, E-3 and E-5) and Mansehra (E-2, E-4 and E-6) using alpha lattice design with three replicates during 2012/13, 2013/14 and 2014/15. Heritability in broad sense was generally low for all traits except nicotine and reducing sugar. Days to flowering was the most environment responsive trait and its heritability fluctuated between 0.22 and 0.91. Plant height was significantly associated with yield at phenotypic level only. Yield exhibited significantly negative phenotypic correlation with days to flowering. Similarly, yield was positively correlated with leaves per plant, green leaves weight per plot, cured leaves weight per plot and grade index at both phenotypic and genotypic level. Based on findings of the present study, selection among RILs would be more effective on the basis of nicotine, reducing sugar, leaves per plant, green leaves weight, cured leaves weight and grade index.

Tejaswini *et al*. (2017) carried out correlation and path coefficient analysis with 19 yield and yield attributing characters in 27 genotypes of vegetable amaranth .Highly significant and positive correlation with foliage yield was observed with plant height at 30 and 60 DAS, stem diameter at 60 and 90 DAS, stem weight per plant, leaf length, leaf width, leaf area index, leaf weight per plant and leaf stem ratio at 30, 60

and 90 DAS, total chlorophyll content, protein content, ascorbic acid, moisture content and folic acid, whereas number of branches at 30, 60 and 90 DAS and number of leaves at 60 and 90 DAS showed negative association with foliage yield. Path coefficient analysis revealed that the characters like plant height (60 DAS), leaf weight per plant (30, 60 and 90 DAS), protein content had high to moderate positive direct effect on foliage yield per plant and these traits recorded significant, positive correlation with foliage yield per plant.

Jangde *et al*. (2017) in the experiment comprising twenty three genotypes of amaranthus. Analysis of variance revealed that mean sum of squares due to genotypes was highly significant for all characters. Correlation coefficient correlation studies revealed 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 significant positive correlation with Total Chlorophyll at both phenotypic and genotypic levels. It also showed significant negative correlation with Chlorophyll b at genotypic level only. Chlorophyll b showed significant positive correlation with Total Chlorophyll at both phenotypic and genotypic levels. Path coefficient analysis revealed that fresh stem weight (1.100) and number of leaves per plant (0.014) showed the highest positive direct effect on leaf yield, whereas direct negative effect on leaf yield *viz*. Plant height (-0.071) for quantitative characters.

Buhroy *et al*. (2017) carried out experiment to study the magnitude of genetic variability, correlation and path coefficient among 20 traits in ten amaranthus accessions belonging to *Amaranthus tricolor*. Comparison of genotypic co-efficient of variation (GCV) and phenotypic co-efficient variation (PCV) for different traits indicated that the values of PCV were higher as compared to GCV due to the influence of environment. High GCV and PCV were observed for leaf length, leaf breadth, stem weight, seed yield per plant and anthocyanin content. Significant and positive correlation of green yield per plant with plant height, stem girth, number of leaves per plant, number of branches per plant, leaf length, leaf breadth, ascorbic acid and crude fibre content was observed. Path analysis revealed that the number of branches per plant exerted the highest direct effect on green yield per plant and was indirectly influenced through days to flower appearance, stem girth, number of leaves per plant, leaf length and leaf breadth**.**

Oduwaye *et al.* (2017) evaluated thirty-eight genotypes of amaranth were evaluated to determine genetic variation and selection indices for foliar yield in the crop. Significant ($p < 0.05$) difference was observed among the genotypes for the traits evaluated. Specific leaf area, fresh leaf, stem and root weights and leaf dry matter had high phenotypic and genotypic coefficient of variations, heritability estimates and genetic advance. Leaf dry matter had significant genotypic correlation coefficients with specific leaf area (-0.70), fresh leaf weight (0.59), fresh root weight (0.60) and biomass weight (0.39). Biomass weight (10.72) and leaf area (0.56) had positive direct effect on leaf dry matter was revealed for. Co-heritability between leaf dry matter and other traits varied from 0.94 (harvest index) to 1.29 (leaf area) which revealed simultaneous inheritance between the traits.

Tiwari *et al*. (2018) evaluated 54 genotypes including four checks viz., Annapurna, Durga, PRA-2 and PRA-3. Genetic variability and genetic divergence was studied for characters viz., days to 50% flowering, days to maturity, plant height, inflorescence length, spikelet length, number of spikelets per plant, stem thickness, 1000 seed weight and seed yield per plant. Analysis of variance reviled that differences among the entries were highly significant for days to 50% flowering, days to maturity, plant height (cm), inflorescence length (cm), spikelet length (cm), number of spikelets per plant, stem thickness (mm) and non significant for 1000 seed weight (g) and seed yield per plant (g). Adjusted mean for earliest flowering (63.20 days) and maturity (128.00 days) minimum in Durga. 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). Using the Non-hierarchical Euclidean cluster analysis, the 54 genotypes were group 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 in temperate conditions mid hills of Uttarakhand.

Salej Sood *et al*. (2018) evaluated fourty eight grain amaranth accessions were evaluated in augmented block design along with 4 checks for 10 quantitative traits in two growing seasons and the grain samples of 52 along with three additional checks

were analyzed for nutritional parameters. Adjusted mean values of quantitative traits for each year and mean values of nutritional traits were used for correlation and multivariate analysis. Grain yield per plant was significantly positively associated with plant height (0.459, 0.574), leaf length (0.615, 0.321), and petiole length (0.726, 0.381) during both the years. Wide range of variation was also observed for iron (66.67-83.19 ppm) and zinc content (28.47-42.98 ppm). The accessions identified for nutritional traits could be used in breeding programme for the improvement of nutritional traits in adapted varieties.

Sagar *et al*. (2018) study reported that foliage yield per plant was significantly and positively correlated with stem girth, number of leaves per plant, number of branches per plant, spike length, number of spikes per plant at both phenotypic and genotypic level. Yield per plant was also positively and significantly correlated with leaf area only at genotypic level. Negative and significant correlation was also found for calcium and iron content of leaves with foliage yield per plant at both phenotypic and genotypic level whereas, hypocotyl length exhibited negative and significant association with foliage yield per plant only at genotypic level.

Bhargava *et al*. (2019) evaluated the foliage yield potential in 13 germplasm lines of Chenopodium album for 3 successive cuttings. Correlations among foliage yield and its contributing traits, along with path analysis was also worked out. Foliage yield was maximum for *C. album* IC 107297, followed by *C. album* H.P. and *C. album, Amaranth tricolor*. Significant negative association was observed between leaves/plant and foliage yield at genotypic level in all the cuttings (I^{st} cutting: -0.472*; II^{nd} cutting: -0.414*; III^{rd} cutting: -0.480*) as well as on pooled basis (-.591**). Protein content negatively affected foliage yield in all the cuttings. Fibre content had high negative value of direct path for pooled data but positively influenced foliage yield indirectly via leaves/plant, stem diameter, chlorophyll a, chlorophyll b and protein content. Ascorbic acid positively affected yield in I^{st} cutting as well as on pooled basis. Leaf size had high positive direct effect and significant positive association with foliage yield that indicates a true relationship between these traits. Leaf size also indirectly affected foliage yield in a positive direction through majority of other traits. Thus, direct selection for leaf size should be exercised to bring about improvement in foliage yield in *C. album*.

Materials and Methods

CHAPTER-III

MATERIALS AND METHODS

The present investigation entitled “Genetic diversity studies in Grain Amaranthus” [*Amaranthus hypochondriacus* (L.)]” was undertaken during *Kharif*, 2018 in randomized block design with 150 genotypes was carried out at Section of Agricultural Botany, College of Agriculture, Badnapur. The details of material and methods used for this investigation are given below.

3.1 Materials

3.1.1 Experimental field

The field experiment was conducted on Agricultural Botany farm, College of Agriculture, Badnapur. Experimental material comprises of 150 germplasm lines received from NBPGR, Akola grown in two replication with randomized block design during *Kharif*, 2018. The genotypes used for study are mentioned in following table 3.1. Recommended agronomic practice followed as per the requirement of crop. Plant protection measures were taken as per requirement. The details of material given below,

Table-3.1 List of grain Amaranthus germplasm lines

SN	**Acc. Nos.**	SN	**Acc. Nos.**	SN	**Acc. Nos.**	SN	**Acc. Nos.**
1	IC35421	41	IC35498	81	IC35574	121	IC35710
2	IC35424	42	IC35499	82	IC35576	122	IC35711
3	IC35427	43	IC35500	83	IC35580	123	IC35713
4	IC35429	44	IC35501	84	IC35590	124	IC35714
5	IC35431	45	IC35502	85	IC35594	125	IC35716
6	IC35433	46	IC35503	86	IC35596	126	IC35719
7	IC35434	47	IC35404	87	IC35598	127	IC35720
8	IC35435	48	IC35505	88	GA2	128	IC35721
9	IC35436	49	IC-35506	89	IC35601	129	IC35722
10	IC35438	50	IC35514	90	IC35603	130	IC35726
11	IC35439	51	IC-35515	91	IC35606	131	IC35727
12	IC35440	52	IC35521	92	IC35607	132	IC35729
13	IC35441	53	IC35524	93	IC35609	133	IC35731
14	IC35442	54	IC35530	94	IC35611	134	IC35732
15	IC35445	55	IC35533	95	IC35613	135	IC35736
16	IC35449	56	IC35534	96	IC35614	136	IC35741
17	IC35450	57	IC-35537	97	IC35616	137	IC35742
18	IC35451	58	IC-35540	98	IC35618	138	IC35747
19	IC35452	59	IC-35541	99	IC35635	139	IC35749
20	IC35453	60	IC-35542	100	IC35641	140	IC35753
21	IC53459	61	IC-35543	101	IC35651	141	IC35754
22	IC35460	62	IC-35544	102	IC35652	142	IC35770
23	IC35462	63	IC35545	103	IC35666	143	IC35771
24	IC35463	64	IC35546	104	Suvarna	144	IC35774
25	IC35470	65	IC35548	105	IC35668	145	IC35783
26	IC35471	66	IC35550	106	IC35679	146	IC41985
27	IC35476	67	IC-35553	107	IC35681	147	IC41988
28	IC35479	68	IC35554	108	IC35682	148	IC41989
29	IC35480	69	IC35555	109	IC35686	149	IC81706
30	IC35481	70	IC35557	110	IC35687	150	IC81707
31	IC35483	71	IC35558	111	IC35688		
32	IC35484	72	IC35559	112	IC35689		
33	IC35488	73	IC35561	113	IC35694		
34	IC35491	74	IC35562	114	IC35701		
35	IC35492	75	IC35563	115	IC35702		
36	IC35493	76	IC35564	116	IC35703		
37	IC35494	77	IC35567	117	IC35706		
38	IC35495	78	IC35568	118	IC35707		
39	GA1	79	IC35569	119	IC35708		
40	IC35497	80	IC35571	120	IC35709		

3.2 Experimental Methods

3.2.1 Experimental details

One hundred fifty germplasm lines of Amaranthus including were sown during *Kharif*, 2018 in randomized block design with two replications at experimental field Section of Agricultural Botany. College of Agriculture, Badnapur. The experimental details were as below,

1) Design : RBD
2) Number of Replication : Two
3) Treatments : 150
4) Plot size : One row of 3 mt length
5) Spacing : 45 cm x 15 cm
6) Fertilizer dose : 50:40:25 NPK (Kg/ha)
7) Season : *Kharif* 2018
8) Locations : College of Agriculture, Badnapur.

3.3 Observations recorded

Random plants from each line in each replication were selected for recording observations. The following observations were recorded on the plants from each genotype at different growth stages of crop and average values per plant were worked out.

3.3.1 Days to 50 per cent flowering

Plant population was counted in which there was complete opening of florets among 50 per cent population of the each plot and the date on which this condition was observed from date of sowing recorded as days to 50 per cent flowering observation in all two replications.

3.3.2 Plant height (cm)

Plant height was recorded from ground level to tip of plant in centimeter at maturity on selected observational plants.

3.3..3 Number of primary branches per plant

This observation was recorded by counting the total number of effective branches from basal portion of the plant on five randomly selected plants.

3.3.4 Number of secondery branches per plant

This observation was recorded by counting the total number of effective sub branches of primary branches of the plant on five randomly selected plants.

3.3.5 Stem diameter (cm)

The diameter of stem was recorded in centimeter .

3.3.6 Inflorescence length (cm)

Length of inflorescence was measured from each observational plant in centimeter.

3.3.7 Days to maturity

. Number of days required from sowing till the physiological maturity of the inflorescence on the observational plot was considered as days to maturity.

3.3.8 1000 seed weight (g)

One thousand seed were counted and took weight in electronic balance.

3.3.9 Seed yield per plant (g)

Random plants from each replication were harvested separately, dried in the sun for fifteen days and then threshed and weight of individual plant were recorded in gram.

3.3.10 Protein content (%)

Protein content from seeds of selected five plants was recorded in percent by Microkjeldahl method.

3.4 Statistical analysis

3.4.1 Assessment of variability

a. Analysis of variance

The data collected on individual characters were subjected to the method of analysis of variance commonly applicable to the randomized block design (Panse and Sukhatme, 1967).

$$Y_{ij} = \mu + G_i + R_j + E_{ij}$$

Where,

i = 1, 2…....G

j = 1, 2……..R

Y_{ij} = Observation on i^{th}genotype in j^{th} replication

μ = General mean

G_i = Effect of i^{th}genotype

R_j = Effect of j^{th}replication

E_{ij} = Random error associated with Y_{ij} observation

ANOVA Table:

Source	**Degree of Freedom**	**Mean of sum**	**expected Mean sum of squares**
Replication	r-1	RMS	$б^2_e + {}_g б^2_r$
Treatment	g-1	GMS	$б^2_e + {}_r б^2_g$
Error	(r-1)(g-1)	EMS	$б^2_e$

Where,

r = Number of replications

g = Number of genotypes

$б^2_r$ = Variance due to replications

$б^2_g$ = Variance due to genotypes and

$б^2_e$ = Variance due to error

The genotype mean square (GMS) was tested against error mean square (EMS) by 'F' test for $n_1 = (g-1)$ and $n_2 = (r-1)(g-1)$ degrees of freedom, where, g = number of genotypes and r = number of replications. The characters showing significant differences were subjected to further analysis.

Estimation of S.E. and C.D.

$$\text{S.E. of mean (S.Em)} = \sqrt{\sigma^2_{e/r}}$$

$$\text{C.D.} = t \text{ at error d.f.} \times \text{S.E.m} \sqrt{2}$$

b. Estimation of mean and range

The mean values for each character were worked out by dividing the total by corresponding number of observations:

$$\overline{X} = \frac{1}{n} \left(\sum_{i=1}^{n} X_i\right)$$

Where,

$\overline{X}$ = Mean of character

$\sum X_i$ = Total of all the observations for character

N = Number of observations

The lowest and highest values of mean of each character represented the range.

c. Estimation of components of variation

The phenotypic and genotypic variances were calculated using the respective mean squares from variance table (Johnson *et al.* 1955) as below.

Environmental variance (σ^2_e) = EMS

$$\text{Genotypic variance } (\sigma^2_g) = \frac{GMS - EMS}{r}$$

$$\text{Phenotypic variance } (\sigma^2_p) = \sigma^2_g + \sigma^2_e$$

Where,

GMS = Genotypic mean sum of square

EMS = Error mean sum of squares

r = Number of replications

d. Estimation of coefficient of variation

The genotypic and phenotypic coefficients of variation were calculated by using following formulae given by Burton, (1952).

i) Genotypic coefficient of variation (GCV)

$$GCV\ (\%) = \frac{\sigma^2_g}{\overline{X}} \times 100$$

Where,

σ^2_g = Genotypic variance and,

$\overline{X}$ = Mean of character

ii) Phenotypic coefficient of variation (PCV)

$$PCV\ (\%) = \frac{\sigma^2_p}{\overline{X}} \times 100$$

Where,

σ^2_p = Phenotypic variance and,

$\overline{X}$ = Mean of character

GCV and PCV estimates were classified as Low : < 10 per cent, Medium: 10 to 20 per cent and High: > 20 per cent.

e. Estimation of heritability (b.s.)

Heritability in broad sense was estimated for various characters as suggested by Hanson *et al.* (1956).

$$h^2 = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,

h^2 = Heritability

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

The high, medium and low heritability estimates were classified on the basis of values given by Robinson (1966).

Low heritability = < 10 %

Moderate heritability = 10-30 %

High heritability = > 30 %

f. Genetic advance (G.A.)

Genetic advance (at 5 % selection intensity) was calculated using the formula given by Allard (1960).

i) Genetic advance (G.A.)

$$G.A. = k \times \frac{\sigma^2_g}{\sigma^2_p} \times \sqrt{\sigma^2_p}$$

Where,

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

k = Selection differential (at 5 % selection = 2.06)

ii) G.A. as percentage of means (GAM)

$$GAM = \frac{GA}{\overline{X}} \times 100$$

Where,

G.A. = Genetic advance

$\overline{X}$ = Character mean

GA (As percentage of mean) was classified as

Low : 10 per cent

Medium : 10 to 20 per cent s

High : > 20 per cent

3.4.2 Genetic divergence

D^2 analysis

The analysis of divergence was carried out by D^2 statistics proposed by Mahalanobis (1928) as described by Rao (1952). Analysis of variance for the individual character was worked out as per randomized block design analysis to test the significances of differences among the genotypes. The characters exhibited significant differences so all were used for further analysis of D^2 statistics. The analysis of covariance for character pair based on plant average was carried out (Cochran and Cox, 1957).

a. Wilk's criteria

After testing differences among populations for characters, a simultaneous test of significance of difference between the mean value of number of correlated variables with regard to pooled effect of nine characters considered together was carried out using Wilk's criteria 'Λ' (Wilks, 1932) which was estimated using the relationship.

$$\Lambda = \frac{|E|}{|E + V|}$$

Where,

$|E|$ = The determinant of experimental error sum of squares and sum of products matrix

$|E + V|$ = The determinant of experimental error sum of squares and sum of products plus population sum of squares and product matrix

The significance of Wilk's criteria (Λ) was tested by χ^2 as,

$\chi^2_{pq} = V = -m.\log_e(\Lambda)$

Where,

$$m = n - \frac{(p+q+1)}{2}$$

$n = N_1 + \ldots\ldots\ldots + N_{k-1}$ (Total number of observations-1)

p = Number of significant characters

q = k-1 (Number of genotypes -1)

K = Number of genotypes

b. Mahalanobis's generalized distance (D^2)

The generalized distance between any two populations is defined as:

$$D^2 = D^2 = \sum\sum \lambda_{ij}\delta_i\delta j$$

Where,

λij = Reciprocal matrix to the common dispersion matrix

δ_i = Difference between mean value of the two populations for the i^{th} character.

σj = Difference between mean value of the two populations for the j^{th} character.

This quantity is estimated by D^2 statistic (Majumdar and Rao, 1958) as:

$D^2 = \Sigma$ Sij

Where,

$S_{ij,}$ $\delta_{i,}$ δj are the sample estimates of $\lambda_{ij,}$ δ_i and δj respectively, since this formula for computation requires inversion of tenth order determinant and then evaluation of 10 (10+1) terms, whose sum is D^2.

c. Computation of D^2 values

For each combination, D^2 was calculated. Thus total 80 (79)/2 = 3160 number of D^2 values were worked out.

d. Determination of population constellation

No rules can be laid down for the finding the clusters, because cluster is not well defined term. The only criteria appears to be that, any two groups belonging to same cluster should be at least, on an average show a smaller D^2 value than those belonging to two differents.

The simple method suggested by Tocher (Rao, 1952) for cluster formation is to start with two closely related groups and find third group which has a smaller average D^2 value from the first two. Similarly, the fourth group is chosen to have smaller average D^2 values from the first three and so an. While proceeding further from cluster formation, it at any stage, the average D^2 value of the group appears to be high than those already listed, then this group does not fit in that format group and taken outside of that cluster.

The genotypes included in first cluster are then omitted and the rest are treated similarly to form next cluster.

e. Average intra-cluster distances

The intra cluster distances were calculated as,

$$\frac{\Sigma Di^2}{n}$$

Where,

ΣDi^2 = Sum of distances between all possible combinations

n = Number of genotypes included in a cluster

f. Average inter-cluster distances

The procedure followed for calculating inter-cluster distances was first to measure the distance between cluster-I and cluster-II, between cluster-I and cluster-III, and between cluster-I and cluster-IV and so on. Likewise the clusters were taken one by one and the distances between other clusters were calculated. The average inter-cluster distances were they calculated as,

$$\frac{\Sigma Di^2}{(ni.nj)}$$

Where,

ni = Number of genotypes in cluster 'i'

nj = Number of genotypes in cluster 'j'

g. Cluster diagram

The intra and inter-cluster distances (D values) were obtained by taking square root of average D^2 values of respective groups.

With the help of D^2 values between the clusters, a diagram showing the relationship between different populations was drawn.

3.4.3 Correlations

Analysis of covariance was carried out by taking two characters at a time. The genotypic co-variance was calculated as per Johnson *et al.* (1955) as below:

Source	Degree of Freedom	Sum of squares	Mean sum of squares	Expectation of mean sum of squares
Replications	(r-1)	RP	RMP	$COVe_{1.2+\ g}COVr_{1.2}$
Genotypes	(g-1)	GP	GMP	$COVe_{1.2\ +\ r}COV_{g1.2}$
Error	(r-1) (g-1)	EP	EMP	$COVe_{1.2}$

Environmental covariance (COV. $e_{1.2}$) = EMP

$$\text{Genotypic covariance (COV. } g_{1.2}) = \frac{GMP - EMP}{r}$$

Phenotypic covariance (COV. $p_{1.2}$) = (COV. $g_{1.2}$) + (COV. $e_{1.2}$)

Where,

GMP = Genotypic mean sum of product

EMP = Error mean sum of product

r = Replication

Appropriate variances and co-variances were used for calculating phenotypic and genotypic correlation coefficients (Johnson *et al.,* 1955).

The phenotypic correlation coefficient (r_p) was calculated as:

$$r_{p1.2} = \frac{COV._{p1.2}}{\sqrt{(\sigma^2_{p1}).(\sigma^2_{p2})}}$$

Where,

$r_{p1.2}$ = Phenotypic correlation coefficient between character 1 and 2

$COV._{p1.2}$ = Phenotypic covariance between character 1 and 2.

σ^2_{p1}, σ^2_{p2} = Phenotypic variance of character 1 and 2 respectively.

The significance of the phenotypic correlation coefficient was tested by referring to Fisher and Yates (1943). The genotypic correlation coefficient (rg) was calculated as:

$$r_{g1.2} = \frac{COV._{g1.2}}{\sqrt{(\sigma^2_{g1}).(\sigma^2_{g2})}}$$

Where,

$r_{g1.2}$ = Genotypic correlation coefficient between character 1 and 2

$COV._{g1.2}$ = Genotypic covariance between character 1 and 2

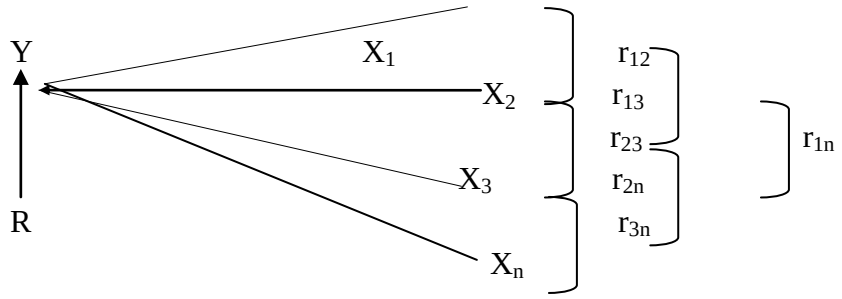
σ^2_{g1}, σ^2_{g} = Genotypic variance of character 1 and 2 respectively.

The significance of correlation coefficients was tested from the statistical table of correlation coefficient at 1 and 5 per cent level of significance (Snedcor and Cochran, 1967).

3.4.4 Path coefficient analysis

To establish a cause and effect relationship the first step used was to partition genotypic and phenotypic correlation coefficient into direct and indirect effects by path analysis as suggested by Dewey and Lu (1959) and developed by Wright (1921).

The second step in path analysis is to prepare path diagram based on cause and effect relationship. In the present study, path diagram was prepared by taking yield as the effect i.e. function of various components like X_1, X_2, X_3 and these component showed following type of association with each other.



In path diagram the yield is the result of X_1, X_2, X_3 ……..Xn and some other undefined factors designated by R. The double arrow lines indicated mutual association as measured by correlation coefficient. The single arrow represents direct influence as measured by path coefficient P_{ij}.

Path coefficients were obtained by solving a set of simultaneous equation of the form as per Dewey and Lu (1959).

$$r_{ny} = P_{ny} + r_{n2} P_{2y} + r_{n3} P_{3y} + \ldots\ldots\ldots\ldots\ldots$$

Where,

r_{ny} = represents the correlation between one component and yield

P_{ny} = represents path coefficient between that character and yield

r_{n2} = represents correlation between that character and each of the other components in turn.

Matrix A Matrix B C

$$\begin{pmatrix} r_{1y} \\ r_{2y} \\ r_{ny} \end{pmatrix} = \begin{pmatrix} r_{11} & r_{12} & r_{13} \ldots\ldots\ldots r_{1n} \\ r_{21} & r_{22} & r_{23} \ldots\ldots\ldots r_{2n} \\ r_{n1} & r_{n2} & r_{n3} \ldots\ldots\ldots 1 \end{pmatrix} \begin{pmatrix} P_{1y} \\ P_{2y} \\ P_{ny} \end{pmatrix}$$

Where,

r_{12} = r_{21} and so on

r_{1y} = Correlation between one component character and seed yield

The ‘B’ matrix was inverted $[B]^{-1}$ and path coefficients (Pij) were obtained as,

i.e. $Pij = (B)^{-1}.A$

The indirect effects of a particular character through other characters were obtained by multiplication of direct paths and particular correlation between these characters separately.

Indirect effects = $r_{ij} \times p_{iy}$

Where,

i = 1 to 9

j = 1 to 9

P_{iy} = P_{1y}, P_{2y}, ……, P_{ny}

Path coefficient (P_{ij}), correlation coefficient (r_{ij}) and residual factors (R) were diagrammatically presented. The residual factor i.e. variation in yield unaccounted for by these associations was calculated with the following formula:

Residual factor (R) = $(1 - R^2)$

Where,

$R^2 = P_{1y} r_{1y} + P_{2y} r_{2y} + \ldots\ldots\ldots\ldots\ldots + P_{ny} r_{ny}$

P_{1y}, P_{2y}, ……,P_{ny} = Direct path values

r_{1y}, $r_{2y,}$ r_{ny} = Correlation coefficient.

Result

CHAPTER - IV

RESULTS

The present investigation was undertaken with 150 germplasm lines of grain Amaranthus [*Amaranthus hypochondriacus* (L.)]". The objective of experiment was to study genetic variability, correlation and path analysis of ten traits in Amaranthus.

They ten characters studied were subjected to analysis for various quantitative characters have been presented under the following major headings

4.1 Analysis of variance

4.2 Mean performance

4.3 Genetic variability

4.4 Genetic diversity

4.5 Correlation

4.6 Path analysis

4.1 Analysis of variance

The variation among genotypes were highly significant for day to 50 % flowering, plant height (cm), number of primary branches per plant, number of secondery branches per plant , stem diameter (cm), Inflorescence length (cm), days to maturity, thousand grain weight, seed yield per plant (gm) and protein content (%) (Table No 4.1)

Table. 4.1. Analysis of variance for ten characters in grain Amaranthus.

Sr. No.	Characters	Mean sum of squares		
		Replication (d.f. 1)	**Genotype** (d.f. 149)	**Error** (d.f. 149)
1	Days to 50% flowering	8.003**	50.00***	0.81
2	Plant height (cm)	0.75	836.74***	3.60
3	Number of primary branches per plant	3.00*	7.37***	0.58
4	Number of secondary branches per plant	0.213	12.58***	0.522
5	Stem diameter (cm)	0.34	0.37***	0.140
6	Inflorescence length (cm)	2.083	138.08***	0.66
7	Days to maturity	1.20	320.58***	4.57
8	Thousand grain weight (g)	0.027	0.349***	0.032
9	Seed yield per plant (g)	7.363*	54.17***	1.27
10	Protein content (%)	5.16**	17.81***	0.49

* -Significant at 5 % level of significance

**- Signi1ficant at 1 % level of significance

Table 4.2. Mean performance of ten quantitative characters in 150 germplasm lines in Amaranthus.

SN	Name of Germplasm /Genotype	Days to 50 % flowering	Plant height (cm)	Number of primary branches per plant	Number of secondary branches per plant	Stem diameter (cm)	Inflorescence length (cm)	Days to maturity	Thousand grain weight (g)	Seed yield per plant (g)	Protein content (%)
1	IC-35421	50	147.5	3.5	4.5	0.7	27.5	87	2.35	9	8
2	IC-35424	53	158.5	3.5	5.5	1.2	27.5	88	2.35	11	8.0
3	IC-35427	57	163	4.5	5.5	0.8	28.5	97	2.55	9	6.9
4	IC-35429	56	167	5.5	6.5	0.7	30.5	98	2.65	9	7.9
5	IC-35431	51	154	3.5	4.5	0.8	30.5	100	2.35	11	8
6	IC-35433	55	157	3.5	7.5	0.6	31.5	99	2.55	9	8.0
7	IC-35434	53	186	3.5	4.5	0.9	33.5	102	2.25	11	8.0
8	IC-35435	57	155.5	3.5	4.5	0.7	35.5	109	2.45	14	7.9
9	IC-35436	53	159.5	5.5	5.5	0.8	32.5	106	2.85	9	8.1
10	IC-35438	50	175.5	2.5	6.5	1.1	34.5	111	2.75	11	9.4
11	IC-35439	65	173.5	3.5	5.5	1.2	32.5	104	2.10	14	8.1
12	IC-35440	63	184.5	4.5	5.5	1.3	38.5	92	2.10	13	9

SN	Name of Germplasm /Genotype	Days to 50 % flowering	Plant height (cm)	Number of primary branches per plant	Number of secondary branches per plant	Stem diameter (cm)	Inflorescence length (cm)	Days to maturity	Thousand grain weight (g)	Seed yield per plant (g)	Protein content (%)
13	IC-35441	65	175	3.5	4.5	0.8	36.5	95.5	2.12	8	9.1
14	IC-35442	67	192	3.5	7.5	1.4	34.5	105	2.85	12.5	8.8
15	IC-35445	68	195.5	6.5	4.5	1.2	39.5	103	1.13	14.5	7
16	IC-35449	64	152	3.5	5.5	1.2	33.5	102	1.14	8	7.2
17	IC-35450	57	156.5	7.5	4.5	1.5	36.5	99	1.105	9.5	7.6
18	IC-35451	61	191	3.5	5.5	1.3	39.5	97	1.155	9	7.1
19	IC-35452	53	185.5	5.5	5	1.5	40.5	108	1.165	8	7.1
20	IC35453	50	152.5	4.5	7.5	1.7	41.5	104	1.125	6.5	7.1
21	IC-53459	59	175	5.5	5.5	1.5	41.5	101	2.15	7	7.1
22	IC-35460	57	153	3.5	5.5	1.7	43.5	108	2.05	10	8.1
23	IC-35462	57	174.5	4.5	4.5	1.5	42.5	93	2.195	10.5	7.9
24	IC-35463	57	161.5	8.5	6.5	1.4	44.5	94	2.215	9.5	8.9
25	IC-35470	61	186.5	3.5	7.5	1.1	42.5	98	2.235	7.5	8.8

SN	Name of Germplasm /Genotype	Days to 50 % flowering	Plant height (cm)	Number of primary branches per plant	Number of secondary branches per plant	Stem diameter (cm)	Inflorescence length (cm)	Days to maturity	Thousand grain weight (g)	Seed yield per plant (g)	Protein content (%)
26	IC-35471	66	170.5	5.5	6.5	1.3	47	110	2.5	6	9.8
27	IC-35476	61	178	2.5	5.5	1.6	38.5	109	2.45	8.5	9.2
28	IC-35479	66	179	5.5	7.5	1.7	44.5	99	2.5	11	8.0
29	IC-35480	63	160	3.5	6.5	1.5	45.5	97	2.235	9	7.6
30	IC-35481	60	156	3.5	7.5	1.4	46.5	98	2.195	14.5	9
31	IC-35483	62	153	5.5	5.5	1.0	47.5	104	2.21	10	9.8
32	IC-35484	66	198	3.5	7.5	1.3	40.5	97	2.85	10.5	9.6
33	IC-35488	67	167	5.5	6.5	1.5	41.5	99	2.245	9.5	9.6
34	IC-35491	65	187	3.5	7	0.9	44.5	96	2.85	15.5	9.7
35	IC-35492	68	155.5	3.5	4.5	0.7	46.5	86	2.75	8.5	9.8
36	IC-35493	54	166	5.5	6.5	0.7	48.5	119	2.15	7.5	8.8
37	IC-35494	51	187	4.5	6.5	0.8	43.5	108	2.05	6.5	9.7
38	IC-35495	66	164	2.5	4.5	1.0	48.5	105	3.745	5.5	7.0

SN	Name of Germplasm /Genotype	Days to 50 % flowering	Plant height (cm)	Number of primary branches per plant	Number of secondary branches per plant	Stem diameter (cm)	Inflorescence length (cm)	Days to maturity	Thousand grain weight (g)	Seed yield per plant (g)	Protein content (%)
39	GA1	67	129.5	9.5	15.5	1.7	48.5	145	2.285	27.5	15.5
40	IC-35497	68	178	8.5	7.5	1.7	37.5	109	2.305	5.5	12.1
41	IC-35498	66	183	6.5	7.5	1.9	49.5	98	2.325	7.5	10.6
42	IC-35499	65	187	7.5	6.5	1.6	40.5	84	2.345	6.5	15.3
43	IC-35500	57	197	7.5	5.5	1.2	41.5	92	2.85	9.5	14.6
44	IC-35501	60.5	175.5	7.5	8.5	1.5	47.5	98	2.75	10.5	10.0
45	IC-35502	69	156	8	6.5	1.6	37.5	92	2.105	9.5	10.6
46	IC-35503	60	166	5.5	6.5	1.9	28.5	93	2.5	7.5	12.6
47	IC-35404	67	167	6.5	7.5	1.3	40.5	95	2.115	8.5	14.6
48	IC-35505	61	180.5	5.5	5.5	0.7	42.5	100	1.625	9.5	7.6
49	IC-35506	66	156	4.5	8.5	0.8	35.5	95	1.655	9.5	14.6
50	IC-35514	67	172	6.5	7.5	0.6	43.5	94	2.35	10.5	9.6
51	IC-35515	64	177.5	3.5	6.5	0.8	25.5	95	2.5	7.5	12.6

SN	Name of Germplasm /Genotype	Days to 50 % flowering	Plant height (cm)	Number of primary branches per plant	Number of secondary branches per plant	Stem diameter (cm)	Inflorescence length (cm)	Days to maturity	Thousand grain weight (g)	Seed yield per plant (g)	Protein content (%)
52	IC-35521	63	198	3.5	8.5	0.7	33.5	94	2.275	8.5	7.7
53	IC35524	53	194	4.5	7.5	0.9	35.5	105	2.295	12.5	9.3
54	IC-35530	57	192	5.5	7.5	0.9	38.5	84	2.235	18.5	9.4
55	IC-35533	54	190.5	7.5	7.5	1.1	34.5	95	2.85	7.5	8.1
56	IC-35534	56	153	7.5	5.5	0.8	28.5	96	2.305	7.5	9.3
57	IC-35537	53	186.5	4.5	7.5	1.2	40.5	105	2.205	8.5	8.2
58	IC-35540	64	178.5	8.5	8.5	1.3	27.5	102	2.295	9.5	9.4
59	IC-35541	59	172	8.5	9.5	0.7	31.5	96	2.345	5.5	8.0
60	IC-35542	60	186.5	7.5	8.5	1.3	39.5	106	2.285	8.5	9.3
61	IC-35543	62	174	7.5	8.5	0.9	29.5	106	2.345	8.5	9.6
62	IC-35544	58	162	8.5	9.5	3.8	33.5	101	2.305	7.5	10.6
63	IC-35545	66	176	7.5	8.5	0.7	37.5	98	2.345	11.5	7.9
64	IC-35546	66	190.5	5.5	7.5	1.05	38.5	91	2.395	9.5	13.9

SN	Name of Germplasm /Genotype	Days to 50 % flowering	Plant height (cm)	Number of primary branches per plant	Number of secondary branches per plant	Stem diameter (cm)	Inflorescence length (cm)	Days to maturity	Thousand grain weight (g)	Seed yield per plant (g)	Protein content (%)
65	IC-35548	58	179.5	5.5	7.5	0.6	37.5	105	2.285	9.5	13.6
66	IC-35550	67	153.5	6.5	8.5	1.3	47.5	94	2.335	17.5	12
67	IC-35553	65	154	5.5	9.5	1.2	30.5	104	2.395	6.5	9.6
68	IC-35554	59	152.5	6.5	8.5	0.7	18.5	96	2.405	8.5	14.8
69	IC-35555	61	152	5.5	9.5	0.6	40.5	109	2.52	10.5	14.7
70	IC-35557	63	153	7.5	10.5	0.95	26.5	106	2.465	7.5	8.4
71	IC-35558	60	190.5	8.5	10.5	1.05	30.5	97	2.525	10.5	8.7
72	IC-35559	59	198	8.5	7.5	0.65	33.5	94	2.515	9.5	11.0
73	IC-35561	62	187.5	6.5	6.5	1.05	24.5	98	2.535	9.5	9
74	IC-35562	65	152	5.5	9.5	0.65	26.5	94	2.535	11.5	12.2
75	IC-35563	62	190.5	6.5	10.5	0.85	38.5	92	2.525	8.5	15.2
76	IC-35564	54	163.5	5.5	11.5	1.15	31.5	108	2.545	9.5	13.4
77	IC-35567	65	188.5	7.5	11.5	0.85	33.5	112	2.515	8.5	14.0

SN	Name of Germplasm /Genotype	Days to 50 % flowering	Plant height (cm)	Number of primary branches per plant	Number of secondary branches per plant	Stem diameter (cm)	Inflorescence length (cm)	Days to maturity	Thousand grain weight (g)	Seed yield per plant (g)	Protein content (%)
78	IC-35568	67	192	8.5	9.5	1.1	35.5	116	2.5	10.5	12.6
79	IC-35569	59	155	8.5	8.5	1.3	37.5	89	2.105	12.5	11.7
80	IC-35571	63	156	7.5	9.5	1.0	26.5	92	2.135	7.5	9.4
81	IC-35574	60	154.5	7.5	11.5	1.2	29.5	93	2.175	9.5	15
82	IC-35576	51	195.5	8.5	8.5	1.5	30.5	116	2.225	10.5	10.1
83	IC-35580	50	199.5	6.5	7.5	1.3	34.5	106	2.185	10.5	15.1
84	IC-35590	53	154.5	8.5	9.5	1.2	32.5	106	2.545	17.5	9.0
85	IC-35594	62	177	8.5	10.5	1.5	33.5	103	2.5	22.5	14.8
86	IC-35596	68	119.5	6.5	9.5	1.8	39.5	111	2.54	25.5	9.2
87	IC-35598	53	162	7.5	9.5	0.9	31.5	106	3.5	19.5	9.6
88	GA2	68	119.5	10.5	14.5	1.8	61.5	128	2.495	28.5	14.5
89	IC-35601	54	162.5	4.5	8.5	0.7	37.5	93	2.5	12.5	10.0
90	IC-35603	55	166	4.5	10.5	0.8	39.5	94	2.75	13.5	7.4

SN	Name of Germplasm /Genotype	Days to 50 % flowering	Plant height (cm)	Number of primary branches per plant	Number of secondary branches per plant	Stem diameter (cm)	Inflorescence length (cm)	Days to maturity	Thousand grain weight (g)	Seed yield per plant (g)	Protein content (%)
91	IC-35606	67	196.5	8.5	10.5	0.9	38.5	92	2.115	11.5	8.2
92	IC-35607	62	156	7.5	11.5	1.0	41.5	117	2.595	9.5	10.1
93	IC-35609	67	199.5	9.5	11.5	1.2	42.5	118	2.595	15.5	14.2
94	IC-35611	63	199	7.5	8.5	1.4	44.5	100	2.435	14.5	10.7
95	IC-35613	63	176	6.5	9.5	1.2	43.5	96	2.455	9.5	6.3
96	IC-35614	65	198.5	4.5	11.5	1.3	45.5	119	2.475	12.5	15.5
97	IC-35616	57	199	6.5	12.5	1.7	48.5	118	2.595	10.5	14.1
98	IC-35618	62	151.5	4.5	10.5	1.1	49.5	97	2.615	16.5	9.9
99	IC-35635	65	148.5	2.5	11.5	1.6	47.5	119	2.595	17.5	12.9
100	IC-35641	67	190	3.5	10.5	1.6	50.5	118	2.635	19.5	13.8
101	IC-35651	61	194.5	4.5	9.5	1.3	45.5	88	2.225	21.5	13.6
102	IC-35652	63	196.5	8.5	8.5	1.7	47.5	91	2.665	22.5	15.2
103	IC-35666	59	192.5	7.5	10.5	1.8	48.5	98	4	18.5	10.2

SN	Name of Germplasm /Genotype	Days to 50 % flowering	Plant height (cm)	Number of primary branches per plant	Number of secondary branches per plant	Stem diameter (cm)	Inflorescence length (cm)	Days to maturity	Thousand grain weight (g)	Seed yield per plant (g)	Protein content (%)
104	Suvarna	66	112.5	10.5	13.5	1.8	57	145	2.665	28.5	15.5
105	IC-35668	64	198.5	6.5	6.5	1.4	46.5	112	2.645	21.5	15.1
106	IC-35679	60	197.5	3.5	7.5	1.7	57.5	113	2.675	17.5	15.0
107	IC-35681	62	193.5	8.5	12.5	1.3	51.5	94	2.695	22.5	15.0
108	IC-35682	57	191.5	6.5	11.5	1.9	32.5	120	2.575	19.5	10.6
109	IC-35686	63	190.5	4.5	9.5	1.9	39.5	124	2.595	14	15.1
110	IC-35687	67	196	3.5	11.5	0.6	41.5	114	2.85	19	13.8
111	IC-35688	60	153.5	5.5	11.5	0.8	25.5	97	2.765	13	8.3
112	IC-35689	66	198.5	7.5	12.5	1.9	26.5	111	2.725	14.5	15.0
113	IC-35694	59	189.5	5.5	11.5	1.4	32.5	110	2.715	13.5	14.8
114	IC-35701	62	200.5	6.5	9.5	1.2	46.5	108	2.705	16.5	14.9
115	IC-35702	58	199.5	5.5	8.5	1.9	44.5	105	2.715	12.5	14.6
116	IC-35703	61	144.5	4.5	12.5	1.1	32.5	114	2.735	27.5	15.7

SN	Name of Germplasm /Genotype	Days to 50 % flowering	Plant height (cm)	Number of primary branches per plant	Number of secondary branches per plant	Stem diameter (cm)	Inflorescence length (cm)	Days to maturity	Thousand grain weight (g)	Seed yield per plant (g)	Protein content (%)
117	IC-35706	58	188.5	7.5	12.5	1.2	33.5	112	2.665	18.5	12.6
118	IC-35707	60	164.5	5.5	8.5	1.1	29.5	108	2.675	18	7.6
119	IC-35708	61	143.5	4.5	10.5	1.4	48.5	117	2.695	17.5	8.2
120	IC-35709	67	202.5	6.5	10.5	0.6	35.5	128	2.735	20	14.8
121	IC-35710	67	203.5	7.5	9.5	0.9	45.5	124	2.715	15	14.7
122	IC-35711	65	203.5	6.5	10.5	1.3	43	134	2.755	14.5	15.0
123	IC-35713	57	205.5	5.5	11.5	1.4	29.5	134	2.735	16.5	15
124	IC-35714	55	165.5	6	12.5	1.3	45.5	115	2.745	14.5	14.8
125	IC-35716	66	177.5	8.5	12.5	1.2	47.5	122	2.775	11.5	14.5
126	IC-35719	58	194.5	6.5	10.5	1.1	48.5	117	2.85	14	15.2
127	IC-35720	57	206.5	8.5	9.5	1.7	41	118	2.635	11	14.7
128	IC-35721	63	165.5	4.5	8.5	1.8	41.5	122	2.185	12	15.3
129	IC-35722	60	151.5	8.5	9.5	1.2	32.5	124	2.105	21	13.3

SN	Name of Germplasm /Genotype	Days to 50 % flowering	Plant height (cm)	Number of primary branches per plant	Number of secondary branches per plant	Stem diameter (cm)	Inflorescence length (cm)	Days to maturity	Thousand grain weight (g)	Seed yield per plant (g)	Protein content (%)
130	IC-35726	59	203.5	8.5	11.5	0.7	41.5	120	2.15	11.5	15.2
131	IC-35727	57	169.5	7.5	8.5	0.6	43.5	120	2.85	13.5	13.7
132	IC-35729	58	172.5	4.5	7.5	0.8	45.5	123	2.875	13.5	14.8
133	IC-35731	66	207.5	5.5	9.5	0.8	49.5	120	2.275	18.5	15.0
134	IC-35732	60	174.5	6.5	8.5	1.0	46.5	127	2.785	19	14.8
135	IC-35736	66	199.5	7.5	11.5	1.7	57	121	2.805	17	15
136	IC-35741	65	200.5	9.5	12.5	1.2	55	122	2.815	18	14.6
137	IC-35742	66	163.5	5.5	6.5	1.5	54	123	2.805	17	14.7
138	IC-35747	64	208.5	7.5	7.5	1.0	64	119	2.845	18	14.8
139	IC-35749	68	198.5	6.5	5.5	0.7	53	123	2.845	20	14.8
140	IC-35753	63	201.5	8.5	8.5	1.8	57	125	2.875	22	13.6

SN	Name of Germplasm /Genotype	Days to 50 % flowering	Plant height (cm)	Number of primary branches per plant	Number of secondary branches per plant	Stem diameter (cm)	Inflorescence length (cm)	Days to maturity	Thousand grain weight (g)	Seed yield per plant (g)	Protein content (%)
141	IC-35754	63	205.5	5.5	7.5	1.9	51.5	118	2.895	20.5	14.7
142	IC-35770	74	162	6.5	9.5	1	46	123	2.905	16	14.6
143	IC-35771	66	183.5	7.5	9.5	1.8	49	121	2.975	12	14.6
144	IC-35774	66	193.5	8.5	12.5	1.7	49	127	2.95	12	12.6
145	IC-35783	57	200.5	8.5	12.5	1.3	48	121	2.865	12.5	14.6
146	IC-41985	60	202.5	7.5	10.5	1.7	43	122	2.785	13	13.6
147	IC-41988	58	204.5	9.5	13.5	1.2	45	125	2.805	13	13.6
148	IC-41989	65	201.5	8.5	13.5	1.3	44	124	2.825	17	14.7
149	IC-81706	59	203.5	9.5	9.5	1.4	48	126	2.845	21	13.6
150	IC-81707	62	206.5	7.5	13.5	1.9	46	124	2.845	25	15.5

Table 4.2.contd….

SN	Name of Germplasm/Genotype	Days to 50 % flowering	Plant height (cm)	Number of primary branches per plant	Number of secondary branches per plant	Stem diameter (cm)	Inflorescence length (cm)	Days to maturity	Thousand grain weight (g)	Seed yield per plant (g)	Protein content (%)
	Mean	61.53	177.0633	6.16	8.64	1.2727	40.1567	107.2633	2.4739	12.9833	11.4951
	C.V. %	1.4676	1.0729	12.4047	8.3627	29.4728	2.0341	1.9935	7.2838	8.7007	6.113
	S.E. +/-	0.6385	1.3433	0.5403	0.5109	0.2652	0.5776	1.512	0.1274	0.7988	0.4969
	C.D. 5%	1.7843	3.7539	1.5099	1.4277	0.7412	1.6141	4.2254	0.3561	2.2322	1.3885

4.2 Mean performance and the range of variability

The mean values of the genotypes for different characters studied are given in Table 4.2, while the estimates of variability parameters are given in Table 4.3

4.2.1 Days to 50 per cent flowering

The variation in days to 50 per cent flowering ranged between 49 to 74 days. Genotype IC-35421 flowered in 49 days while highest days 74 were taken by IC-35770. Seventy six genotypes were late in flowering than the mean flowering of genotypes 61 days.

4.2.2 Plant height (cm)

The variation in plant height ranged between 112.5 to 208.5 cm. The plant height was maximum in case of IC-35747 while it was minimum in case of suvarna. The value recorded for maximum height was 208.5 cm while minimum height was 112.5cm. Seventy eight genotypes were recorded highest plant height than mean value 177.0.

4.2.3 Number of primary branches per plant

The number of primary branches per plant ranged from 2.5 to 10.5 with general mean of 3.78. The genotype IC-35438 recorded lowest 2.5 number of primary branches, while highest 15.5 primary branches in suvarna. Seventy seven genotypes had highest primary branches per plant than general mean value 6.16.

4.2.4 Number of secondary branches per plant

The number of secondary branches per plant ranged from 4.5 to 15.5. Genotype IC-35421 showed lowest 4.5 while highest 15.5 in GA1. Sixty three genotypes recorded more secondary branches per plant than the mean. Mean value for this character was 8.64.

4.2.5 Stem diameter (cm)

The stem diameter ranged from 0.6 to 3.8 cm. The lowest stem diameter was recorded in genotype IC35727 while the highest was recorded for the genotype IC35544. Sixty nine genotypes were recorded highest stem diameter than mean value 1.27 cm.

4.2.6 Inflorescence length (cm)

The inflorescence length ranged from 18.5 to 64 cm. The lowest inflorescence length was recorded in genotype IC35554 while the highest was recorded in genotype IC55747. Seventy eight genotypes recorded highest inflorescence length than mean value 40.15 cm.

.4.2.7 Days to maturity

The variation in days to maturity ranged between 84 to 145 days. Genotype IC35499 matured in least number of days (84) while suvarna matured very late (145 days). Mean value for this character was 107 days and sixty seven genotypes were late matured than mean value.

4.2.8 1000 grain weight (g)

The variation in thousand grain weight ranged between 1.10g to 4.0g. The lowest thousand grain weight was recorded by IC35569 while the highest was recorded by IC35666. Seventy four genotypes had more thousand grain weight than mean value 2.47 g.

4.2.9 Seed yield /plant (g)

The variation seed yield per plant ranged between 5.5g to 28.5g. The lowest seed yield per plant was recorded by genotype IC35497 while the highest was recorded by genotype suvarna. Sixty two genotypes recorded more seed yield per plant than mean value 12.98 g.

4.2.10 Protein content (%)

The variation for protein content (%) ranged between 6.3 to 15.7(%). The lowest protein content (%) was recorded in case of IC-35611 (10.7%) while maximum in case of IC35703 (15.7%) and the mean value for this character was 11.4(%).

Table 4.3. Estimates of variability parameters for ten characters in grain Amaranthus

Sr. No.	Name of the characters	Range	Mean	σ^2g	σ^2p	σ^2e	GCV (%)	PCV (%)	h^2 (b.s.) (%)	G.A.	G.A. as % of mean
1.	Days to 50% flowering	49 -74	61.53	24.59	25.41	0.81	8.06	8.19	96.8	10.05	16.33
2.	Plant height (cm)	112.5-208.5	177.06	416.56	420.17	3.60	11.52	11.57	99.1	41.86	23.64
3.	Number of primary branches per plant	2.5-10.5	6.16	416.56	3.97	0.58	29.90	32.37	85.3	3.50	56.90
4.	Number of secondary branches per plant	4.5-15.5	8.64	6.03	6.55	0.52	28.42	29.62	92.0	4.85	56.17
5.	Stem diameter (cm)	0.6-3.8	1.27	0.11	0.25	0.14	27.06	40.01	45.8	0.48	37.71
6.	Inflorescence length (cm)	18.5-64	40.15	68.70	69.37	0.66	20.64	20.74	99.0	16.99	42.31
7.	Days to maturity	84-145	107.26	158.00	162.58	4.57	11.71	11.88	97.2	25.52	42.31
8.	Thousand grain weight (g)	1.105-4	2.47	0.15	0.19	0.03	16.10	17.67	83.0	0.74	30.22
9.	Seed yield per plant (g)	5.5-28.5	12.98	26.44	27.72	1.27	39.61	40.55	95.4	10.34	79.69
10	Protein content (%)	6.31-15.7	11.49	8.66	9.15	0.49	25.60	26.32	94.6	5.89	51.29

4.3 variability and genetic parameters

The estimates of variability (Genotypic and Phenotypic coefficients of variation), heritability (broad sense), genetic advance and genetic advance as per cent of mean for ten characters in one hundred fifty genotypes of grain Amaranthus were presented in Table 4.3.

4.3.1 Genetic variability

The phenotypic variance is greater than the genotypic variance in phenotypic variance highest for plant height (420.17) followed by days to maturity (163), inflorescence length (69.37), seed yield per plant (27.72), days to 50 % flowering (25.41), protein content (9.15), number of secondary branches per plant (6.55), number of primary branches per plant (3.97), thousand grain weight (0.19) and stem diameter (0.25).

At genotypic level plant height (416.56) followed by number of primary branches per plant (416.56), days to maturity (158), inflorescence length (68.7), seed yield per plant (26.44), days to 50 percent flowering (24.59), protein content (8.66), number of secondary branches per plant (6.03), stem diameter (0.11) and thousand grain weight (0.15).

4.3.2 Genotypic and phenotypic coefficients of variation

GCV and PCV values were categorized as low (0-10%), moderate (10-20%) and high (20% and above).

Genotypic coefficient of variation (GCV) was highest for seed yield per plant (39.61%) followed by number of primary branches per plant (29.9%), number of secondary branches per plant (28.45%), stem diameter (27.06%), protein content (25.6%), inflorescence length (20.64%), thousand grain weight (16.1%), days to maturity (11.71%), plant height (11.52%), days to 50 percent flowering (8.06%).

The maximum phenotypic coefficient of variation was recorded for seed yield per plant (40.55%) followed by stem diameter (40.01%), number of primary branches per plant (32.37%), number of secondary branches per plant (29.62%), protein content (26.32) , inflorescence length (20.74%), thousand grain weight (17.67%), days to maturity (11.88%), plant height (11.57%), days to 50 percent flowering (8.19%).

In general, the magnitude of phenotypic coefficient of variation was higher than the genotypic coefficient of variation.

4.3.2 Heritability and genetic advance

Maximum heritability was observed for plant height (99.1%) followed inflorescence length (99%), days to maturity (97.2 %), days to 50% flowering (96.8%), seed yield per plant (95.4%), protein content (94.6%), number of secondary branches per plant (92%), number of primary branches per plant (85.3%), thousand grain weight (83%), stem diameter (45.8%), High heritability (> 70 %) was observed in most of the characters studied.

The estimates of Genetic Advance ranged from 0.74 to 41.86 with the highest estimate in case of number of plant height (41.86%) followed by days to maturity (25.52%), inflorescence length (16.99%), seed yield per plant (10.34%), days to 50% flowering (10.05%), protein content (5.89%), number of secondary branches per plant (4.85%), number of primary branches per plant (3.5%), thousand grain weight (0.74%) and stem diameter (0.48%).

Genetic advance as per cent of mean ranged from 16.33 to 79.69 per cent. seed yield per plant (79.69%) recorded highest genetic advance as per cent mean followed by number of primary branches per plant (56.9%), number of secondary branches per plant (56.17 %), protein content (51.29%), days to maturity (42.31%), inflorescence length (42.31%), stem diameter (37.71%), thousand grain weight (30.22%), plant height (23.64%) and days to 50% flowering (16.33%).

4.4 Genetic divergence

4.4.1 Mahalanobis's generalized distance (D^2)

Wilk's criterion showed significant differences between the genotypes for the pooled effect of the ten characters studied. Hence, further analysis was done to calculate D^2 values for all the possible pairs of comparison among one hundred fifty genotypes. The calculated D^2 values ranged from 22.49 to 2366.48.

The mean values of one hundred fifty genotypes $[(X_1)-(X_2)]$ were transformed into standardized uncorrelated mean values $[(Y_1)-(Y_2)]$. The D^2 values were computed for all the possible 150(149-1)/2= 11,175 pairs of genotypes.

4.4.2 Clustering pattern of the genotypes

The clustering pattern obtained on the basis of magnitude of D^2 values studied, are presented in Table 4.4.

These one hundred fifty genotypes were grouped into twelve clusters. The cluster II was with the highest number of genotypes (62) followed by cluster I (33), clusters VI (25), cluster VI (16) , IX (3), X (3) and cluster III, V, VII, VIII, XI, XII had single genotype .

4.4.3 Intra and inter cluster divergence

The average intra and inter cluster D^2 and D values are presented in Table 4.5 and Table 4.6.

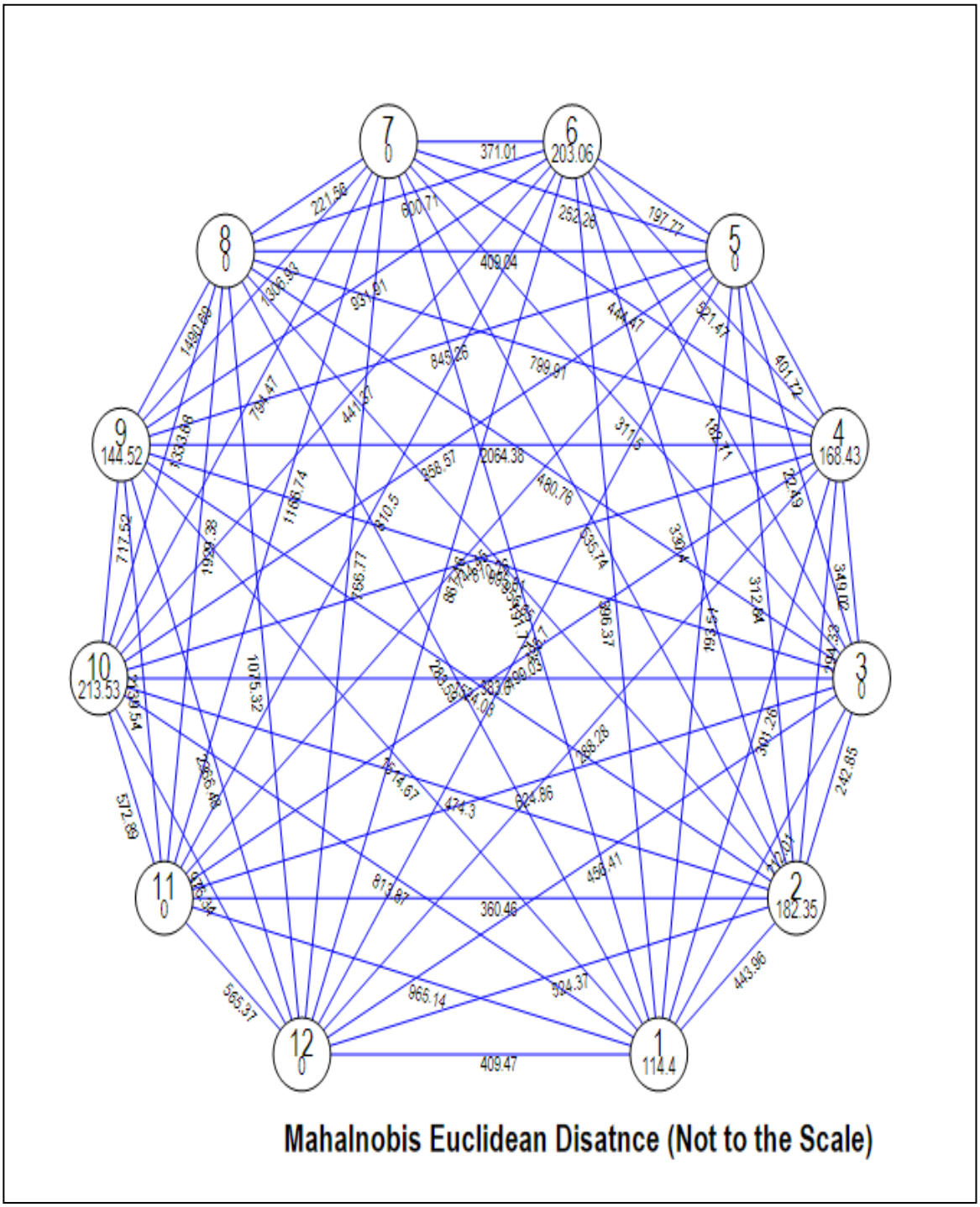
The intra cluster distance (D) range from 4.74 to 48.64. The maximum inter cluster distance (D = 48.64) was observed between cluster XII and IX cluster, followed by cluster XI and IX (D = 46.25), cluster XI and cluster IV (D = 45.43), cluster IX and cluster VIII (D = 43.92), cluster IX and cluster II (D = 39.03). The minimum inter cluster distance (D = 4.74) was between IX and VII.

At inter cluster level, cluster XII and IX had the highest value which was followed by cluster XI and IX.

Table. 4.4. Composition of one hundred fifty grain Amaranthus genotypes into different clusters by Tocher's method.

Cluster No.	No. of genotypes	Genotypes included in the cluster
I	33	IC-35616, IC-35783, IC-35719, IC-41988, IC-41985, IC-35726, IC-35720, IC-35701, IC-35702, IC-35614, IC-41989, IC-35710, IC-35609, IC-35711, IC-81706, IC-35731, IC-25668, IC-35754, IC-35774, IC-81707, IC-35687, IC-35682, IC-35611, IC-35771, IC-35641, IC-35749, IC-35716, IC-35741, IC-35736, IC-35753, IC-35779, IC-35491, IC-35652.
II	62	IC-35427, IC-35429, IC-35433, IC-35436, IC-35534, IC-35424, IC-35431, IC-35421, IC-35435, IC-35601, IC-35438, IC-35564, IC-35590, IC-35707, IC-35598, IC-35688, IC-35544, IC-35403, IC-35574, IC-35571, IC-35557, IC-35553, IC-35562, IC-35541, IC-35543, IC-35439, IC-35450, IC-35449, IC-35589, IC-35603, IC-35548, IC-35476, IC-35506, IC-35441, IC-35459, IC-35434,IC-35462, IC-35440, IC-35445, IC-35537, IC-35502, IC-35488, IC-35440, IC-35552, IC-35505, IC-35533, IC-35524, IC-35452, IC-35404, IC-35470, IC-35497, IC-35613, IC-35555, IC-35463, IC-35514, IC-35480, IC-35607, IC-35460, IC-35494, IC-35479, IC-35727, IC-35721, IC-25594, IC-35501.
III	1	IC-35729
IV	25	IC-35567, IC-35568, IC-35694, IC-35706, IC-35682, IC-35558, IC-35442, IC-35559, IC-35563, IC-35546, IC-35521, IC-35484, IC-35606, IC-35451, IC-35445, IC-35500, IC-35499, IC-35530, IC-35561, IC-35515, IC-35580, IC-35576, IC-35689, IC-35709, IC-35651.
V	1	IC-35732.
VI	16	IC-35481, IC-35483, IC-35618, IC-35550, IC-35492, IC-35635, IC-35708, IC-35742, IC-35714, IC-35493, IC-35471, IC-35495, IC-35770, IC-35498, IC-35453, IC-35666.
VII	1	IC-35681.
VIII	1	IC-35747
IX	3	GA2, Suvarna, GA1
X	3	IC-35703, IC-35722, IC-35596
XI	1	IC-35554
XII	1	IC-35713

Fig.1. Cluster diagram in grain Amaranthus.



Mahalnobis Euclidean Disatnce (Not to the Scale)

Table. 4.5. Average intra and inter cluster D^2 values in grain Amaranthus.

Cluster No.	I	II	III	IV	V	VI	VII
I	114.40	443.96	212.01	301.26	193.51	396.37	191.71
II		182.35	242.85	294.33	312.84	330.40	535.74
III			0	349.02	22.49	182.71	311.50
IV				168.43	401.72	521.47	444.47
V					0	197.77	252.26
VI						203.06	371.01
VII							0
VIII							
IX							
X							
XI							
XII							

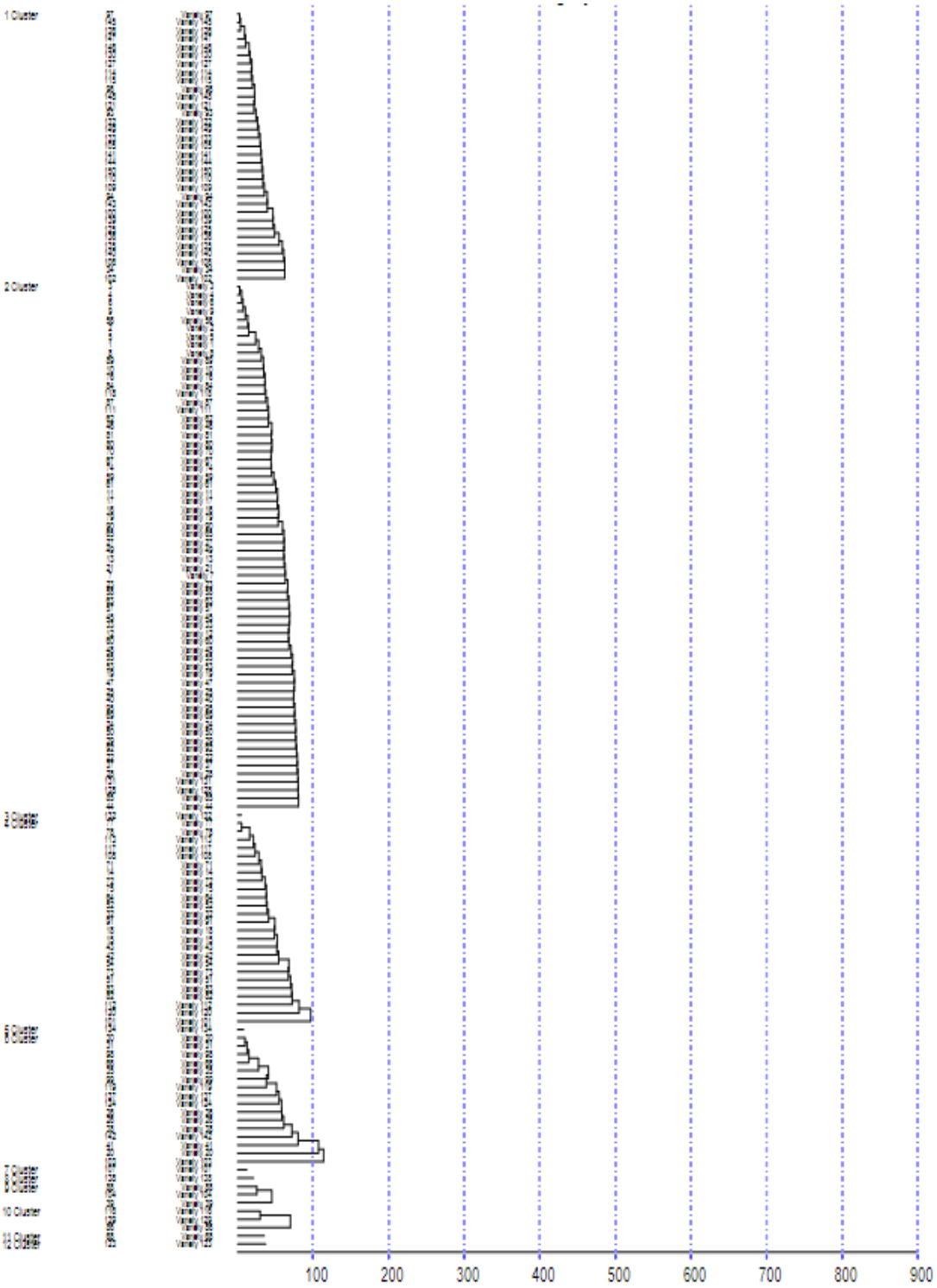
Table. 4.5. contd…

Cluster No.	VIII	IX	X	XI	XII
I	283.59	1514.67	813.87	965.14	409.47
II	956.65	1524.03	474.30	360.46	524.37
III	480.76	995.61	383.60	624.86	456.41
IV	799.91	2064.38	810.26	499.03	288.28
V	409.04	845.26	358.57	744.45	495.70
VI	600.71	931.91	441.37	810.50	867.46
VII	221.56	1306.93	794.47	1166.74	766.77
VIII	0	1490.69	1333.68	1929.38	1075.32
IX		144.52	717.52	2139.54	2366.48
X			213.53	572.89	976.34
XI				0	565.37
XII					0

Table. 4.6. Average intra and inter cluster distance (D) values in grain Amaranthus.

Cluster No.	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	10.69579	21.07036	14.56056	17.35684	13.91079	19.90904	13.84594	16.84013	38.91876	28.52841	31.0667	20.23537
II		13.5037	15.58365	17.15605	17.68728	18.17691	23.14606	30.92976	39.03883	21.77843	18.98578	22.89913
III			0.00	18.68208	4.742362	13.51703	17.64936	21.92624	31.55329	19.58571	24.9972	21.36375
IV				12.97806	20.04295	22.83572	21.08246	28.28268	45.43545	28.46507	22.33898	16.97881
V					0.00	14.06307	15.88269	20.22474	29.07336	18.93594	27.28461	22.26432
VI						14.24991	19.26162	24.50939	30.5272	21.00881	28.46928	29.45267
VII							0.00	14.88489	36.15149	28.18634	34.15758	27.69061
VIII								0.00	38.60945	36.51958	43.92471	32.79207
IX									12.02165	26.78656	46.25516	48.64648
X										14.61267	23.93512	31.24644
XI											0.00	23.77751
XII												0.00

Fig.2. Clustering of grain amaranthus genotypes by Tocher method.



4.4.4 Cluster means for different characters

The cluster mean for the ten characters are presented in Table 4.7 A considerable inter cluster variation was observed among the cluster means for the characters studied *viz.* day to 50 % flowering, plant height, number of primary branches per plant, number of secondary branches per plant, stem diameter (cm), inflorescence length (cm), days to maturity, thousand grain weight (g), seed yield per plant (g), protein content (%) .

The cluster mean for days to 50 per cent flowering varied from 57.50 (XII) to 67.50 days (IX). The cluster means for plant height ranged between 120.50 (IX) to 208.50 cm (VIII). The cluster mean for primary branches per plant ranged between 4.50 (III) to 10.17 (IX). The cluster mean for secondary branches per plant ranged from 7.50 (III) and (VIII) to 14.50 (cluster XI). The cluster mean for stem diameter ranged between 0.75 (XI) and 1.82 (IX). The cluster mean for inflorescence length was maximum in cluster (VIII) 64.00 and it was minimum in cluster (XI) 18.50. The cluster mean for days to maturity was maximum in cluster (IX) 139.83 and minimum in case of cluster (VII) 94.00. The cluster mean for thousand grain weight was maximum in cluster (III) 2.88 and it was minimum in cluster (II) 12.32. The cluster mean for seed yield per plant was maximum in cluster (IX) 28.17 and it was minimum in cluster (XI) 8.50. The cluster mean for protein content was minimum in cluster (II) 9.64 and it was maximum in cluster (IX) 15.17

Table 4.7. Cluster means of different characters to genetic diversity in grain Amaranthus.

SN	Days to 50 % flowering	Plant height (cm)	Number of primary branches per plant	Number of secondary branches per plant	Stem diameter (cm)	Inflorescence length (cm)	Days to maturity	Thousand grain weight (g)	Seed yield per plant (g)	Protein content (%)
I	63.42	198.48	6.95	10.21	1.44	47.32	118.14	2.72	16.08	14.32
II	59.63	167.54	5.74	7.51	1.19	35.86	101.15	2.32	10.25	9.64
III	58.50	172.50	4.50	7.50	0.85	45.50	123.50	2.88	13.50	14.84
IV	62.22	192..88	6.30	8.70	1.19	35.10	101.58	2.39	12.14	11.69
V	60.50	174.50	6.50	8.50	1.05	46.50	127.00	2.79	19.00	14.89
VI	63.03	161.31	5.03	8.13	1.34	47.66	107.16	2.61	12.56	10.61
VII	62.50	193.50	8.50	12.50	1.35	51.50	94.00	2.70	22.50	15.06
VIII	64.50	208.50	7.50	7.50	1.05	64.00	119.50	2.85	18.00	14.80
IX	67.50	120.50	10.17	14.50	1.82	55.67	139.83	2.48	28.17	15.17
X	63.50	138.50	6.50	10.50	1.42	34.83	116.50	2.46	24.67	12.78
XI	59.50	152.50	6.50	8.50	0.75	18.50	96.50	2.41	8.50	14.83
XII	57.50	205.50	5.50	11.50	1.45	29.50	134.00	2.74	16.50	15.00

The utility of D^2 analysis was enhanced by its application to estimate the relative contribution of the various plant characters to genetic divergence. The per cent contribution of ten characters studied, towards total divergence is presented in Table 4.8.

It was observed that, thousand grain weight (62.00%) contributed highest for divergence. It was followed by plant height (38.87%), number of primary branches per plant (38.00%), inflorescence length (34.72%), flag leaf sheath width (0.53%), finger length (0.53%), finger number per panicle (0.49%), stem diameter (12.00%), days to 50% flowering (9.12%), days to maturity (7.79%), seed yield per plant (4.64%), protein content (2.54%), number of secondary branches per plant (1.22%).

Table 4.8. Per cent contribution of different characters to genetic diversity in grain Amaranthus

Sr. No.	**Characters**	**No. of times appearing Ist in ranking**	**% contribution**
1.	Days to 50% flowering	1019	9.12
2.	Plant height (cm)	4344	38.87
3.	Number of primary branches per plant	42	38
4.	Number of secondary branches per plant	136	1.22
5.	Stem diameter (cm)	13	12
6.	Inflorescence length (cm)	3880	34.72
7.	Days to maturity	870	7.79
8.	Thousand grain weight (g)	69	62
9.	Seed yield per plant (g)	518	4.64
10.	Protein content (%)	284	2.54
	Total	11175	100.00

Table 4.9. Estimation of genotypic (above diagonal) correlation coefficients in Grain Amaranthus.

SN	Days to 50 % flowering	Plant height (cm)	Primary branches per plant	Secondary branches per plant	Stem diameter (cm)	Inflorescence length (cm)	Days to maturity	Thousand grain weight (g)
	1	2	3	4	5	6	7	8
1	**1.0000**	0.0454	0.1746**	0.2298**	0.1395*	0.3380**	0.1706**	0.1169
2		**1.0000**	0.1312*	0.0910	0.0525	0.1873**	0.1360*	0.2066**
3			**1.0000**	0.5448**	0.2672**	0.1459**	0.3102**	0.1515
4				**1.0000**	0.2379**	0.1858**	0.5394**	0.4038**
5					**1.0000**	0.3652**	0.2858**	0.0175
6						**1.0000**	0.4247**	0.2403**
7							**1.0000**	0.3169**
8								**1.0000**
9								
10								

***** Significant at 5 % and ****** Significant at 1 % level of probability or level of significance,

Table 4.9. contd…….

SN	Protein content (%)	Seed yield per plant (g)
	9	10
1	0.3049**	0.2358**
2	0.3126**	0.0097
3	0.3881**	0.2708**
4	0.5791**	0.5194**
5	0.2298**	0.2579**
6	0.3557**	0.4248**
7	0.5399**	0.5115**
8	0.3752**	0.3674**
9	**1.0000**	0.4883**
10		**1.0000**

***** Significant at 5 % and ****** Significant at 1 % level of probability or level of significance,

Table 4.10 Estimation of phenotypic (above diagonal) correlation coefficients in grain Amaranthus.

SN	Days to 50 % flowering	Plant height (cm)	Primary branches per plant	Secondary branches per plant	Stem diameter (cm)	Inflorescence length (cm)	Days to maturity	Thousand grain weight (g)
	1	2	3	4	5	6	7	8
1	**1.0000**	0.0415	0.1574**	0.2108**	0.1034	0.3298**	0.1649**	0.1088
2		**1.0000**	0.1231*	0.0848	0.0401	0.1871**	0.1352*	0.1861*
3			**1.0000**	0.4904**	0.1827**	0.1289*	0.2818**	0.1298
4				**1.0000**	0.1722**	0.1749**	0.5100**	0.3470**
5					**1.0000**	0.2400**	0.1856**	0.0076
6						**1.0000**	0.4182**	0.2202**
7							**1.0000**	0.2845**
8								**1.0000**
9								
10								

Table 4.10. contd…….

SN	Seed yield per plant	Protein content (%)
		10
1	0.2303**	0.2936**
2	0.0137	0.3013**
3	0.2416**	0.3472**
4	0.4809**	0.5462**
5	0.1799**	0.1600**
6	0.4113**	0.3442**
7	0.4960**	0.5168**
8	0.3181**	0.3435**
9	**1.0000**	0.4588**
10		**1.0000**

***** Significant at 5 % and ****** Significant at 1 % level of probability or level of significance,

4.5 Correlation studies

The correlation study was undertaken in 150 genotypes of grain Amaranthus in order to find out interrelation of different yield components at genotypic and phenotypic level. The genotypic and phenotypic correlation coefficient for ten characters as presented in Table 4.9 and 4.10 respectively.

4.5.1 Association of seed yield with its components

From Table 4.9, 4.10 and Fig. 3 reveals that, seed yield per plant had significant positive association with days to maturity (p= 0.4960; g= 0.5115), number of secondary branches per plant (p= 0.4809; g= 0.5194), inflorescence length (p= 0.4113; g= 0.4248), thousand grain weight (p= 0.3181; g= 0.3674), number of primary branches per plant (p= 0.2416; g= 0.2708), days to 50% flowering (p= 0.2303; g= 0.2358) and stem diameter (p= 0.1799; g= 0.2579).

4.5.2 Interrelationship of yield components

4.5.2.1 Days to 50% flowering

Days to 50% flowering showed significant and positive correlation at phenotypic and genotypic level with inflorescence length (p= 0.329; g= 0.3380), protein content (p= 0.2936; g= 0.3049), number of secondary branches per plant (p= 0.2108; g= 0.22980), days to maturity (p= 0.1649; g= 0.1706), and number of primary branches per plant (p= 0.1574; g= 0.1746).

4.5.2.2 Plant height

The character plant height had positively significant correlation at phenotypic and genotypic level with protein content (p= 0.3013; g= 0.3126), inflorescence length (p= 0.1871; g= 0.1873), thousand grain weight (p= 0.1861; g= 0.2066), days to maturity (p= 0.1352; g = 0.1360) and number of primary branches per plant (p= 0.1231; g= 0.1312).

4.5.2.3 Number of primary branches per plant with other character

The number of primary branches per plant showed significant positive correlation at phenotypic and genotypic level with number of secondary branches per plant (p= 0.4904; g = 0.5448), protein content (p= 0.3472; g= 0.3881), days to maturity (p= 0.2818; g= 0.3102), stem diameter (p= 01827; g= 0.26720), thousand grian weight (p= 0.1298; g = 0.1515) and inflorescence length (p= 0.1289; g= 0.1459).

Fig.3. Genotypical correlation in grain amaranthus.

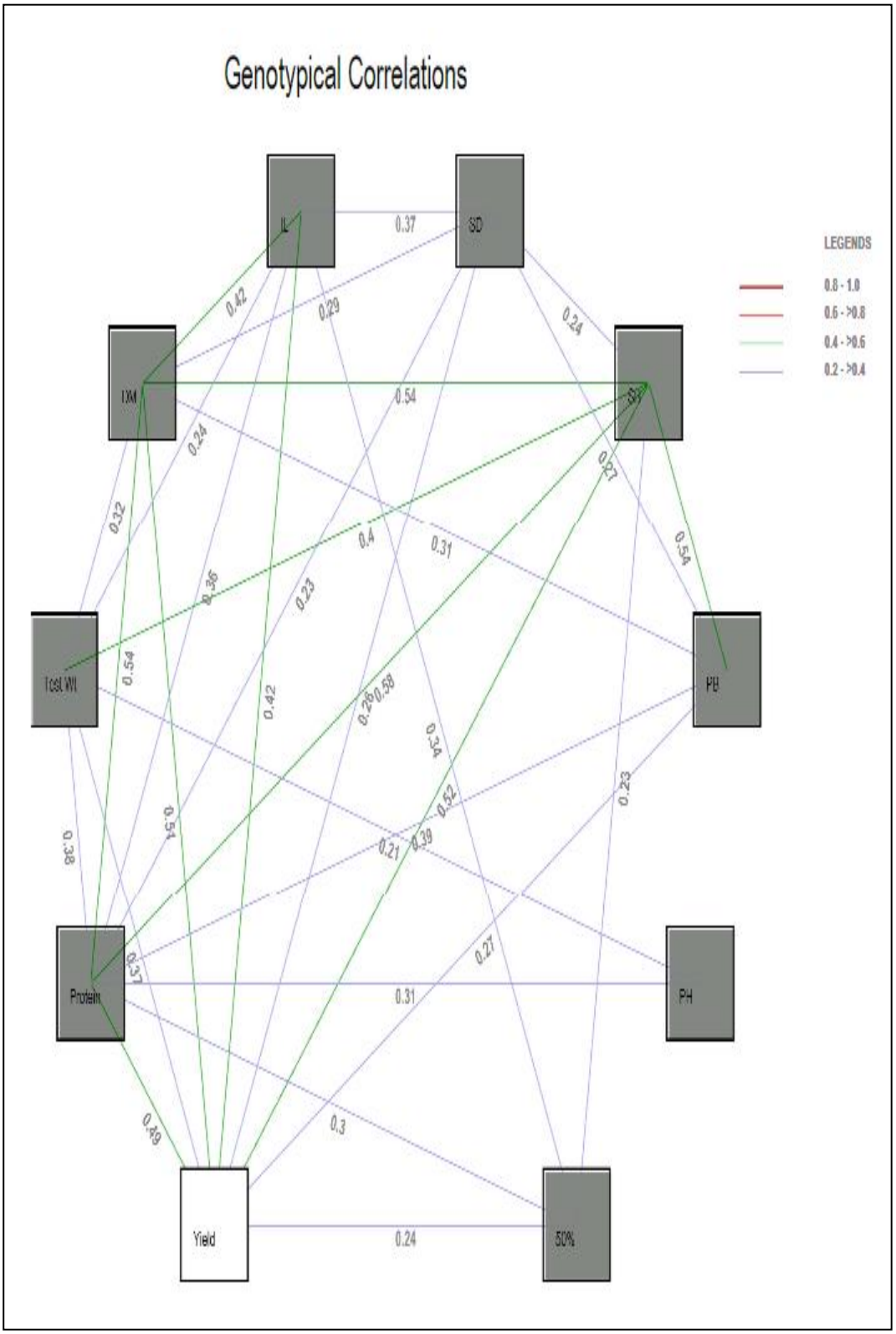
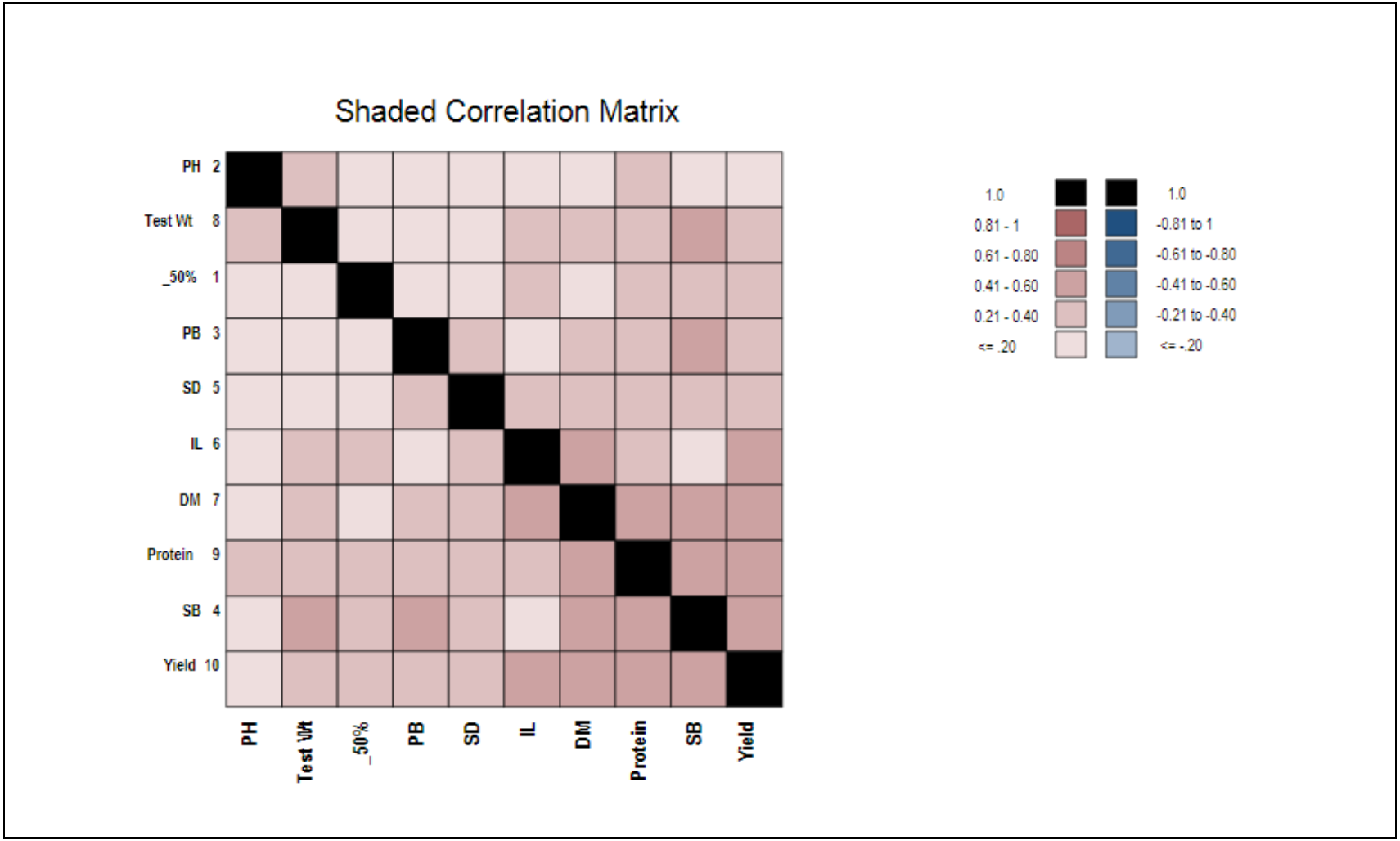


Fig.4. Shaded Correlation Matrix in grain Amaranthus.



4.5.2.4 Number of secondary braches per plant

The number of secondary branches per plant showed significant positive correlation at phenotypic and genotypic level with protein content (p= 0.5462; g= 0.5791), days to maturity (p= 0.5100; g= 0.5394), thousand grain weight (p= 0.3470; g= 0.4038), inflorescence length (p= 0.1749; g= 0.1858) and stem diameter (p= 0.1722; g= 0.2379).

4.5.2.5 Stem Diameter (cm)

The stem diameter showed highly significant positive correlation at phenotypic and genotypic level with inflorescence length (p= 0.2400; g= 0.3652), days to maturity (p= 0.1856; g= 0.2858) and protein content (p= 0.1600; g= 0.2298).

4.5.2.6 Inflorescence Length (cm)

The inflorescence length had significant positive correlation at phenotypic and phenotypic level with days to maturity (p= 0.4182; g= 0.4247), protein content (p= 0.3442; g= 35570) and thousand grain weight (p= 0.2202; g= 0.2403).

4.5.2.7 Days to maturity

The days to maturity had significant positive correlation at phenotypic and genotypic level with protein content (p= 0.5168; g= 0.5399) and thousand grain weight (p= 0.2845; g= 0.3169).

4.5.2.8 Thousand grain weight (gm)

The thousand grain weight had significant positive correlation at phenotypic and genotypic level with protein content (p= 0.3435; g= 0.3752).

4.5.2.9 Protein content (%)

The stem diameter showed highly significant positive correlation at phenotypic and genotypic level with thousand grain weight (p= 0.4545; g= 0.4400) and stem diameter (p= 0.2465; g= 0.2329)**.**

Table. 4.11. Direct and indirect effect of ten causal variables on seed yield in Grain Amaranthus.

SN	Days to 50 % flowering	Plant height (cm)	Primary branches per plant	Secondary branches per plant	Stem diameter (cm)	Inflorescence length (cm)	Days to maturity	Thousand grain weight (g)
	1	2	3	4	5	6	7	8
1	**0.0100**	0.0005	0.0017	0.0023	0.0014	0.0034	0.0017	0.0012
2		**-0.1575**	-0.0207	-0.0143	-0.0083	-0.0295	-0.0214	-0.0325
3			**-0.0312**	-0.0170	-0.0083	-0.0045	-0.0097	-0.0047
4				**0.2606**	0.0620	0.0484	0.1405	0.1052
5					**0.0391**	0.0143	0.0112	0.0007
6						**0.2348**	0.0997	0.0564
7							**0.1570**	0.0498
8								**0.1273**
9								
10								

Table. 4.11.contd…….

SN	Protein content(%)	correlation with seed yield/plant(g)
	9	10
1	0.0031	0.2358
2	-0.0492	0.0097
3	-0.0121	0.2708
4	0.1509	0.5194
5	0.0090	0.2579
6	0.0835	0.4248
7	0.0848	0.5115
8	0.0478	03674
9	**0.1707**	0.4883

Residual effect = 0.7850, Underlined figures indicate direct effect.

*, ** indicates significant at 5 and 1 % level of significant respective

4.6 Genotypic path coefficient analysis

To find out the direct and indirect contribution from each of the characters towards seed yield per plant, path coefficient analysis was carried out. The genotypic correlation coefficients being more important are only partitioned to direct and indirect effects which are presented in Table 4.11.

4.6.1 Days to 50 per cent flowering

Days to 50 per cent flowering expressed positive direct effect (0.0100) on seed yield per plant. It had negative indirect effect through, plant height (-0.0071), number of primary branches per plant (-0.0054). While positive indirect effect through number of secondary branches per plant (0.0599), stem diameter (0.0054), inflorescence length (0.0794), days to maturity (0.0268), thousand grain weigh t(0.0149), protein content (0.0520). The total genotypic correlation with seed yield per plant was positive and significant (0.02358).

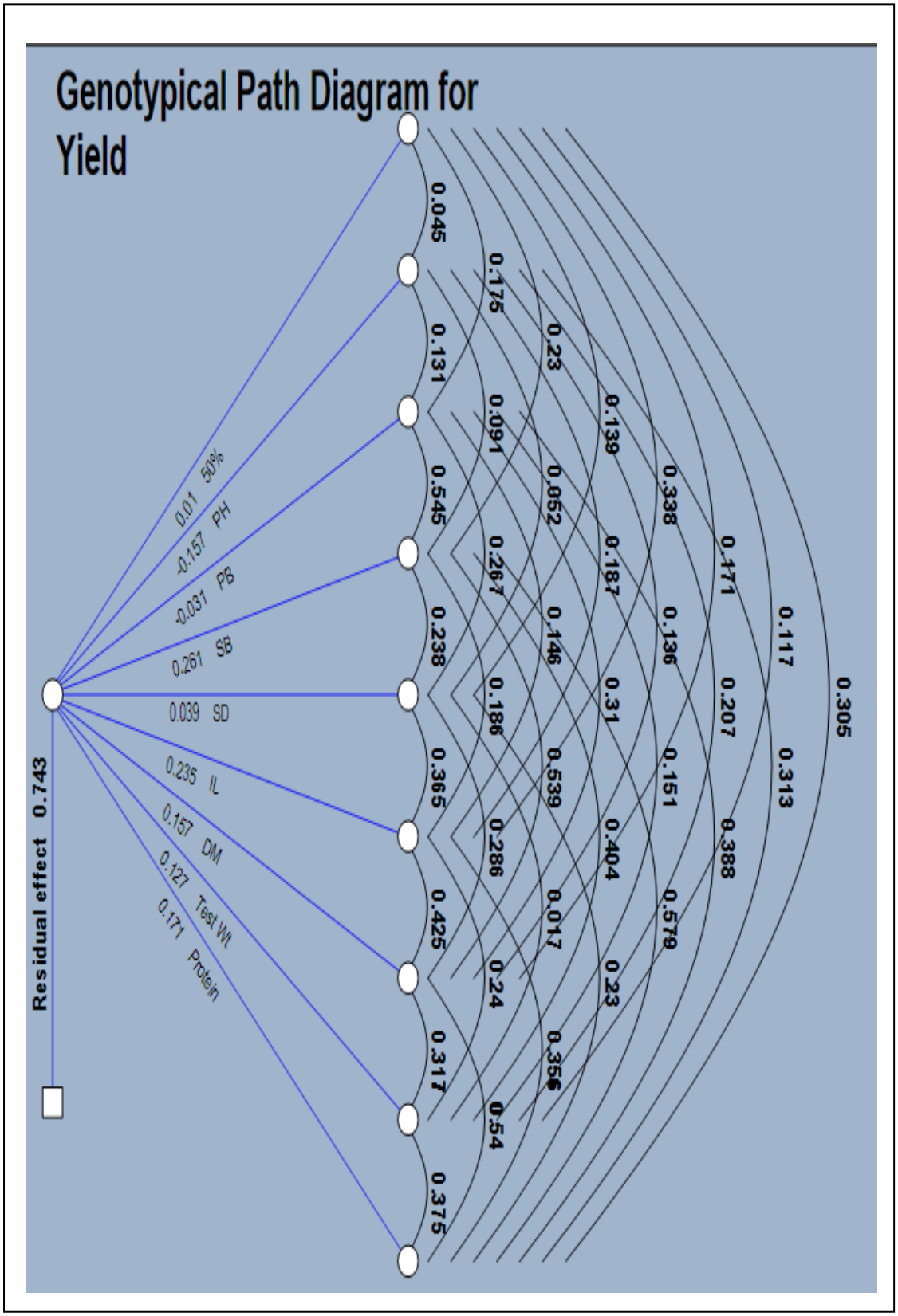
4.6.2 Plant height (cm)

Plant height showed negative direct effect (-0.1575) on seed yield per plant. It had positive indirect effects through characters *via.*, Days to 50 % flowering (0.0005), number of secondary branches per plant (0.0237), stem diameter (0.0020), inflorescence length (0.0440), days to maturity (0.0214), thousand grain weight (0.0263), protein content (0.0533) and negative indirect effect through number of primary branches per plant (-0.0041). Thus the total genotypic correlation with seed yield per plant was negative and non-significant (0.0097).

4.6.3 Number of primary branches per plant

Primary branches per plant showed negative direct effect (-0.0312) on seed yield per plant. It had positive indirect effect through characters *via.*, days to 50% flowering (0.0017), number of secondary branches per plant (0.1419), stem diameter (0.0104)), inflorescence length (0.0343), days to maturity (0.0487), thousand grain weight (0.0193), protein content (0.0662) and negative indirect effect *via*. plant height (-0.0207), number of primary branches per plant (-0.0312). Thus, leading to negative and non-significant correlation with seed yield per plant (0.2708).

Fig.5 Genotypical path diagram for seed yield per plant (g) in grain Amaranthus.



4.6.4 Number of secondary branches per plant

Number of secondary branches per plant showed positive direct effect (0.2606) on seed yield per plant. It had positive indirect effect through characters *via.,* days to 50% flowering (0.0023), stem diameter (0.0093), inflorescence length (0.0436), days to maturity (0.0847), thousand grain weight (0.0514), protein content (0.0988) and negative indirect effect *via.,* plant height (-0.0143), number of primary branches per plant (-0.0170). Thus the total genotypic correlation with seed yield per plant was positive and significant (0.5194).

4.6.5 Stem diameter (cm)

Stem diameter showed positive direct effect on seed yield per plant (0.0391). It showed positive indirect effect of characters day to 50% flowering (0.0014), number of secondary branches per plant (0.0620), inflorescence length (0.0858), days to maturity (0.0449), thousand grain weight (0.0022) and protein content (0.0392). Negative indirect effect through characters *viz.* plant height (-0.0083) and number of primary branches per plant (-0.0083). The total genotypic correlation with seed yield per plant was positive and significant (0.2579).

4.6.6 Inflorescence length (cm)

Inflorescence length showed positive and direct effect correlation with seed yield per plant (0.2348). It had positive indirect effect of characters day to 50% flowering (0.0034), number of secondary branches per plant (0.0484), stem diameter (0.0143), days to maturity (0.0667), thousand grain weight (0.0306), protein content (0.0607). It is having negative indirect effect through characters *viz.,* plant height (-0.0295), number of primary branches per plant (-0.0045). The total genotypic correlation with seed yield per plant was positive and significant (0.4248).

4.6.7 Days to maturity

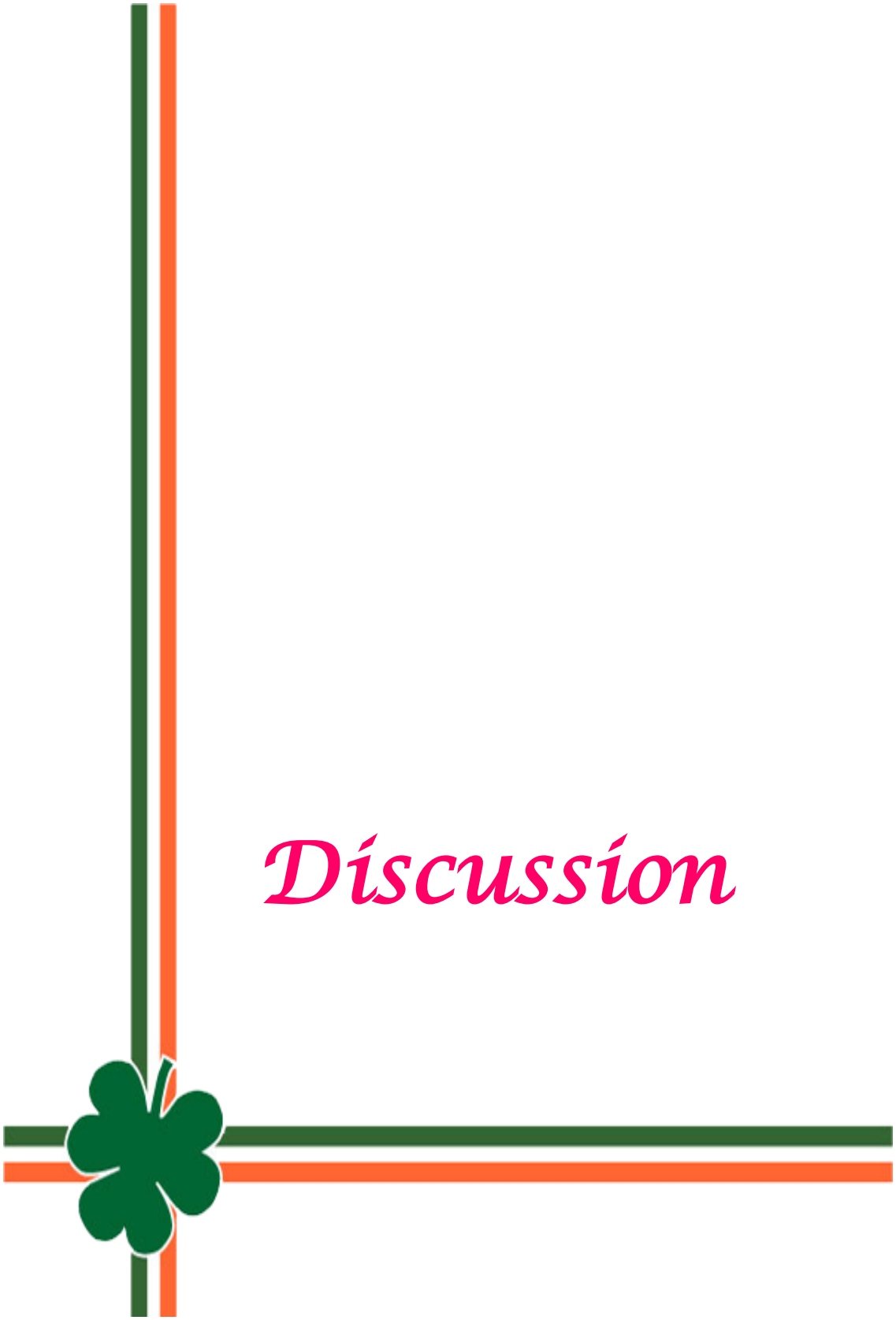
Days to maturity showed positive direct effect on seed yield (0.1570). It showed negative indirect effect through plant height (-0.0214), number of primary branches per plant (-0.0097). Positive indirect effect through characters *viz,* days to 50% flowering (0.0017), number of secondary branches per plant (0.1405), stem diameter (0.0112), inflorescence length (0.0997), thousand grain weight (0.0404), protein content (0.0921). The total genotypic correlation with seed yield per plant was positive and significant (0.5115).

4.6.8 Thousand grain weight (g)

Thousand grain weight showed positive direct effect on seed yield (0.1273). It showed negative indirect effect through plant height (-0.0325), number of primary branches per plant (-00047). Positive indirect effect days to 50% flowering (0.0012), number of secondary branches per plant (0.1052), stem diameter (0.0007), inflorescence length (0.0564), days to maturity (0.0498), protein content (0.0640). The total genotypic correlation with seed yield per plant was positive and significant (0.3674).

4.6.9 Protein content (%)

Protein content showed positive direct effect on seed yield (0.1707). It showed negative indirect effect through days to plant height (-0.0492), number of primary branches per plant (-0.0121) and positive indirect effect days to 50% flowering (0.0031), number of secondary branches per plant (0.1509), stem diameter (0.0090), inflorescence length (0.0835), days to maturity (0.848), thousand grain weight (0.0478). The total genotypic correlation with seed yield per plant was positive and significant (0.4883).



Discussion

CHAPTER - V

DISCUSSION

Genetic variability and diversity are important pre requisites for success of any breeding programme and selection of elite genotypes. The genotypic and phenotypic coefficients of variation are the simple measures to assess the extent of variability present in a population for a particular character. Heritability on the other hand suggests the relative role of genetic factors in expression of phenotypes (Falconer, 1989). It also acts as an index of inheritance of a particular character to its off spring. Genetic advance on the other hand measures the expected genetic gain from the selection applied in a population. Heritability along with genetic advance gives the best efficiency of selection. The study of correlations provides the inter relationships among the quantitative traits which facilitates the choice of suitable breeding method for improvement of crop. The D^2 statistics suggested by Mahalanobis (1936) and Tocher's method described by Rao (1952) help to select the genetically diverse genotypes for hybridization programme.

In the present investigation entitled "Genetic diversity studies in Grain Amaranthus [*Amaranthus hypochondriacus* (L.)]" attempts were made to study the variability, correlation and path analysis for 10 different quantitative characters among 150 genotypes.

The results obtained on these aspects are presented in chapter four and are discussed in this chapter under appropriate headings.

5.1 Mean performance

Mean is used for the measurement of all types of parameters. It is useful in comparing varieties or advanced generation breeding materials. Mean helps in reduction of huge individual observations in to a small and meaningful data. The mean performance of the genotypes for different characters studied is presented in Table 4.2

4.2.1 Days to 50 per cent flowering

The variation in days to 50 per cent flowering ranged between 49 to 74 days. Genotype IC-35421 flowered in 50 days while highest 74 days were taken by IC-35770. Seventy six genotypes were late in flowering than the mean flowering of genotypes (61) days. Similar results were obtained by Akaneme and Ani (2013).

4.2.2 Plant height (cm)

The variation in plant height ranged between 112.5 to 208.5cm.The plant height was maximum in case of IC-35747 while it was minimum in Suvarna. The value recorded for maximum height was 208.5 cm while minimum height was 112.5cm. Seventy eight genotype recorded highest plant height than mean value 177.0. Similar results were obtained by Panda (2017).

4.2.3 Number of primary branches per plant

The number of primary branches per plant ranged from 2.5 to 10.5 with general mean of 3.78.Genotype IC-35438 showed lowest (2.5) while highest (10.5) number of primary branches per plant in Suvarna. Seventy seven genotypes were highest primary branches per plant than general mean value 6.16. Similar results were obtained by Ahammed *et al.* (2012).

4.2.4 Number of secondary branches per plant

The number of secondary branches per plant ranged from 4.5-15.5. Genotype IC-35421 recorded lowest (4.5) while highest (15.5) in GA1. Sixty three genotypes recorded more secondary branches per plant than the mean. Mean value for this character was 8.64. Similar results were obtained by Pawar (1995).

4.2.5 Stem diameter (cm)

The stem diameter ranged from 0.6 to 3.8 cm. The lowest stem diameter was recorded for the genotype IC35727 while the highest was recorded by the genotype IC35544. Sixty nine genotypes were highest stem diameter than mean value 1.27cm. Similar results were obtained by Venkatesh *et al.* (2013).

4.2.6 Inflorescence length (cm)

The inflorescence length ranged from 18.5 to 64 cm. The lowest inflorescence length was recorded for the genotype IC35554 while the highest was recorded by the genotype IC55747. Seventy eight genotypes were highest inflorescence length than mean value 40.15 cm. Similar results were obtained by Joshi (1986).

4.2.7 Days to maturity

The variation in days to maturity ranged between 84 to 145 days. Genotype IC35499 matured in least number of days (84) while Suvarna matured very late (145 days). Mean value for this character was 107 days and sixty seven genotypes

were late matured than mean value. Similar results were obtained by Yadav *et al. (*2014).

4.2.8 1000 grain weight (g)

The variation in thousand grain weight ranged between 1.10 to 4 g. The lowest thousand grain weight was recorded for the genotype IC35450 while the highest was recorded for the genotype IC35666. Seventy four genotypes were more thousand grain weight than mean value 2.47g. Similar results were obtained by Akaneme and Ani (2013).

4.2.9 Seed yield /plant (g)

The variation seed yield per plant ranged between 5.5 to 28.5 gm. The lowest seed yield per plant was recorded by genotype IC35497 while the highest was recorded by genotype Suvarna. Sixty two genotypes were more seed yield per plant than mean value 12.98. Similar results were obtained by Venkatesh *et al. (*2013).

4.2.10 Protein content (%)

The variation for protein content (%) ranged between 6.3 to 15.7 (%). The lowest protein content (%) was recorded in case of IC-35613 while maximum in case of IC-35703 and the mean value for this character was 11.49(%). Similar results were obtained by Venkatesh *et al. (*2013).

5.2.1 Range of variability

Wide range of variability was observed for majority of yield contributing characters. Range of variation on the basis of mean was more for traits viz. plant height, days to maturity, inflorescence length, seed yield per plant, days to 50 % flowering, protein content, number of secondary branches per plant, number of primary branches per plant, thousand seed weight and stem diameter. This indicates that these parameters can be effectively used as selection criteria of the genotype.

Estimates of phenotypic variance are higher than the genotypic variance in all characters. High genotypic variances and phenotypic variances were observed for plant height, days to 50 % flowering and 1000 seed weight. This suggests that the less influence of environment hence we can make effective selection of genotypes in breeding. Similar results observed by Akaneme and Ani (2013) in grain Amaranthus.

5.2.2 Genotypic and phenotypic coefficient of variation

In the present investigation the phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the traits this indicates that there is small effect of environment on characters and selection may be effective. Although range can provide a preliminary idea about the variability, coefficient of variation is reliable, as it is independent of unit measurement. The extent of variability as measured by GCV and PCV also gives information regarding relative amount of variation in different populations. The GCV and PCV showed wide variation for most of the characters. As expected the PCV was invariably higher than GCV for all the characters. GCV and PCV values were categorized as low (0-10%), moderate (10-20) and high (20% and above). The value for GCV ranged from 8.06 to 39.61 per cent.

The highest value of GCV and PCV were recorded for characters seed yield per plant and number of branches per plant indicating presence of large variability among the genotypes and the possibilities of improvement of these traits through selection. Similar observations were observed by Pawar (1995), Venkatesh *et al.*, (2013) and Yadav *et al.* (2014). Similar observations were observed for days to 50 per cent by Akaneme and Ani (2013), for stem diameter by Vekatesh *et al.* (2013), for inflorescence length by Joshi (1986), Venkatesh *et al.* (2013) and Yadav *et al.* (2014), for character 1000 seed weight by Joshi (1986) and Akaneme and Ani (2013), for days to maturity by Joshi (1986), for protein content by Venkatesh *et al.* (2013) and for plant height by Venkatesh *et al.* (2013).

The medium GCV and PCV observed for plant height and seed yield per plant indicated moderate genetic variability for these traits in the material. Similar results was recorded by Panda (2017). Moderate to low variability of these characters indicated the need for improvement of base population.

The low GCV and PCV was observed for days to maturity and protein content indicated low genetic variability for these traits in this material. Similar results was observed by Joshi *et al.* (1986).

5.2.3 Heritability and Genetic advance

Genotypic coefficient of variation alone does not indicate the proportion of total heritable variation. However, the heritability estimates are better indicator of heritable portion of the variation. The broad sense heritability includes the contribution of additive gene effects and allelic interaction due to dominance and allelic due to epistasis. Burton (1952) suggested that the genetic coefficient of variation and heritability estimates together give better idea about the amount of genetic advance expected through selection. Johnson *et al.* (1955) pointed out that in a selection programme, heritability values as well as genetic advance were more useful than heritability alone. The progress of any breeding programme is conditioned by the magnitude and the nature of genotypic and non-genotypic variation in the various characters since, most of the economic characters (e.g., yield) are complex in inheritance and are greatly influenced by various environmental conditions, the study of heritability and genetic advance is very useful in order to estimate the scope for improvement by selection. The heritability magnitude indicates the reliability with which the genotype will be recognized by its phenotype expression. According to them heritability is categorized like, less than 30% as low, 30-60% as moderate and more than 60% as high heritability.

In the present study, estimate of heritability ranged from 45.8% for stem diameter to 99.1 for plant height. High heritability was also exhibited by plant height (99.1%) followed by inflorescence length (99%), days to 50% flowering (96.8%), days to maturity (97.2%), seed yield per plant (95.4%), protein content (94.6%), number of secondary branches per plant (92%), number of primary branches per plant (85.3%) thousand grain weight (83%) and stem diameter (45.8) indicating scope for selection on the basis of heritable performance. Similar results were observed for thousand seed weight by Joshi (1986), for inflorescence length by Joshi (1986) and Yadav *et al.* (2014), for plant height by Joshi (1986) and Yadav *et al.* (2014), for days to 50 per cent flowering by Akaneme and Ani (2013) and Yadav *et al.* (2014), for stem diameter by Akaneme and Ani (2013) and Venkatesh *et al.* (2013), for character days to maturity by Yadav *et al.* (2014) and Patial *et al.* (2014), for seed yield per plant by Venkatesh (2013), Ahammad *et al.* (2012), Patial *et al.* (2014) and Panda (2017) and for character number of primary branches per plant Ahammad *et al.* (2012).

Heritability which is the heritable portion of phenotypic variance is a good index of transmission of characters from parents to offspring (Falconer, 1960).

Genetic advance as per cent of mean ranged from 16.33 to 79.69 per cent. Seed yield per plant (79.69%) recorded highest genetic advance as per cent mean followed by number of primary branches per plant (56.90%), number of primary branches per plant (56.17%), protein content (51.29%), inflorescence length (42.31%), stem diameter (37.71%), thousand grain weight (30.22%), days to maturity (23.79%), plant height (23.64%) and days to 50% flowering (16.33%) .

High genetic advance indicated that these characters are governed by additive genes and selection will be rewarding for improvement of these traits. Similar results were observed for thousand seed weight by Joshi (1986), for inflorescence length by Joshi (1986) and Venkatesh *et al.* (2013), for plant height by Joshi (1986) and Venkatesh *et al.* (2013), for 50 per cent flowering by Venkatesh *et al.* (2013), for stem diameter Venkatesh *et al.* (2013), for days to maturity by Yadav *et al.* (2014) and Patial *et al.* (2014) and for seed yield per plant by Venkatesh *et al.* (2013), Patial *et al.* (2014).

5.3 Genetic divergence

Genetic divergence, which is due to genetic factors, is the basis for heritable improvement. The plant breeders have always therefore, been fascinated by great amount of diversity in crop plants as could serve as raw material for crop improvement programme. The precise information about the genetic divergence is therefore, crucial for effective breeding programme. The genetically diverse parents are known to produce higher heterotic effects and consequently give desirable recombinants in the breeding material. Multivariate analysis as shown by Mahalanobis (1936), D^2 statistics is a measure that appraises the genetic variability quantitatively among a set of genotypes.

5.3.1. Diversity

The estimates of D^2 values ranged from 22.49 to 2366.48. This clearly indicates the presence of adequate diversity between genotypes studied.

5.3.2 Cluster formation

The aim of cluster formation and measuring inter and intra cluster divergence is to provide the basis for hybridization programme. The theoretical concept behind such grouping is that, the genotypes grouped into the same cluster presumably are less diverse from each other than those belonging to the different

clusters and will not give expected desired heterotic response and segregants in further generations.

Consequently breeding programme should be designed in such a way that, the parents are selected from different clusters with wider in genetic diversity in the genotypes. The crosses involving the parents with extreme divergence have also been reported to exhibit decrease in heterosis (Moll *et al.* 1965). Therefore, while selecting the parents by considering the genetic diversity, their performance and cluster mean for the characters also need due consideration in the crop improvement programme.

In the present investigation, the cluster II was with the highest number of genotypes (62) followed by cluster I (33), clusters VI (25), cluster VI (16), IX (3), X (3) and cluster III, V, VII, VIII, XI ,XII had single genotype. The cluster formation in grain amaranthus reported Shukla and Singh (2002).

The intra cluster distance (D) range from 4.74 to 48.64 The maximum inter cluster distance (D= 48.64) was observed between cluster XII and IX cluster, followed by cluster XI and IX (D= 46.25), cluster XI and cluster IV (D= 45.43), cluster IX and cluster VIII (D= 43.92), cluster IX and cluster II (D= 39.03) indicating that the genotypes falling in these clusters were highly divergent from each other implying large amount of diversity within and between groups, which could be exploited in breeding programmes. The minimum inter cluster distance (D= 4.74) was between IX and VII indicating that this cluster is less divergent. The cluster means revealed high variability among the clusters for the traits, the cluster mean for days to 50 per cent flowering varied from 54 (XI) to 78 days (I) and (II). The cluster means for plant height ranged between 102.70 (XI) to 135.80 cm (XIII). The cluster mean for productive tillers per plant ranged between 2.70 (X) to 4.50 (III). The cluster mean for flag leaf sheath length ranged from 8.69 (cluster X) to 12.55 (cluster III). The cluster mean for flag leaf sheath width ranged between 0.71 (cluster III) and 0.99 (cluster XIII).

The cluster mean for The cluster mean for days to 50 per cent flowering varied from 57.50 (XII) to 67.50 days (IX). The cluster means for plant height ranged between 120.50 (IX) to 208.50 cm (VIII). The cluster mean for primary branches per plant ranged between 4.50 (III) to 10.17 (IX). The cluster mean for secondary branches per plant ranged from 7.50 (III) and (VIII) to 14.50 (cluster XI).

The cluster mean for stem diameter ranged between 0.75 (XI) and 1.82 (IX). The cluster mean for inflorescence lenght was maximum in cluster (VIII) 64.00 and it was minimum in cluster (XI) 18.50. The cluster mean for days to maturity was maximum in cluster (IX) 139.83 and minimum in case of cluster (VII) 94.00. The cluster mean for thousand grain weight was maximum in cluster (III) 2.88 and it was minimum in cluster (II) 12.32. The cluster mean for seed yield per plant was maximum in cluster (IX) 28.17 and it was minimum in cluster (XI) 8.50. The cluster mean for protein content was minimum in cluster (II) 9.64 and it was maximum in cluster (IX) 15.17

It was observed that, thousand grain weight (62%) contributed highest for divergence. It was followed by plant height (38.87%), number of primary branches per plant (38%), inflorescence length (34.72%), flag leaf sheath width (0.53%), finger length (0.53%), finger number per panicle (0.49%), stem diameter (12 %), days to 50% flowering (9.12%), days to maturity (7.79%), seed yield per plant (4.64%), protein content (2.54%), number of secondary branches per plant (1.22%). Similar results were observed for protein by Erum *et al.* (2012) and Srivastava and Roy (2012).

5.4 Correlation studies

Correlated characters are of interest for three chief reasons, firstly in connection with the genetic cause of correlation through the linkage and pleiotropic action of genes, secondly in connection with the change brought about by selections. It is important to know, how the improvement of one character will cause simultaneous changes in other characters and thirdly in connection with natural selection (Falconer, 1960).

The value of correlation coefficient cannot be constant everywhere. It varies considerably according with kind of material handled, mode of observations taken, cultural practices followed and environmental conditions in which material is grown. Even though the material used is same, the environment including fertilization, plant population, cultural practices changes the value of correlation coefficient considerably. All correlations are greatest upon poorer soils and increased fertility tends to decrease the variability (Ramiah and Rao, 1953).

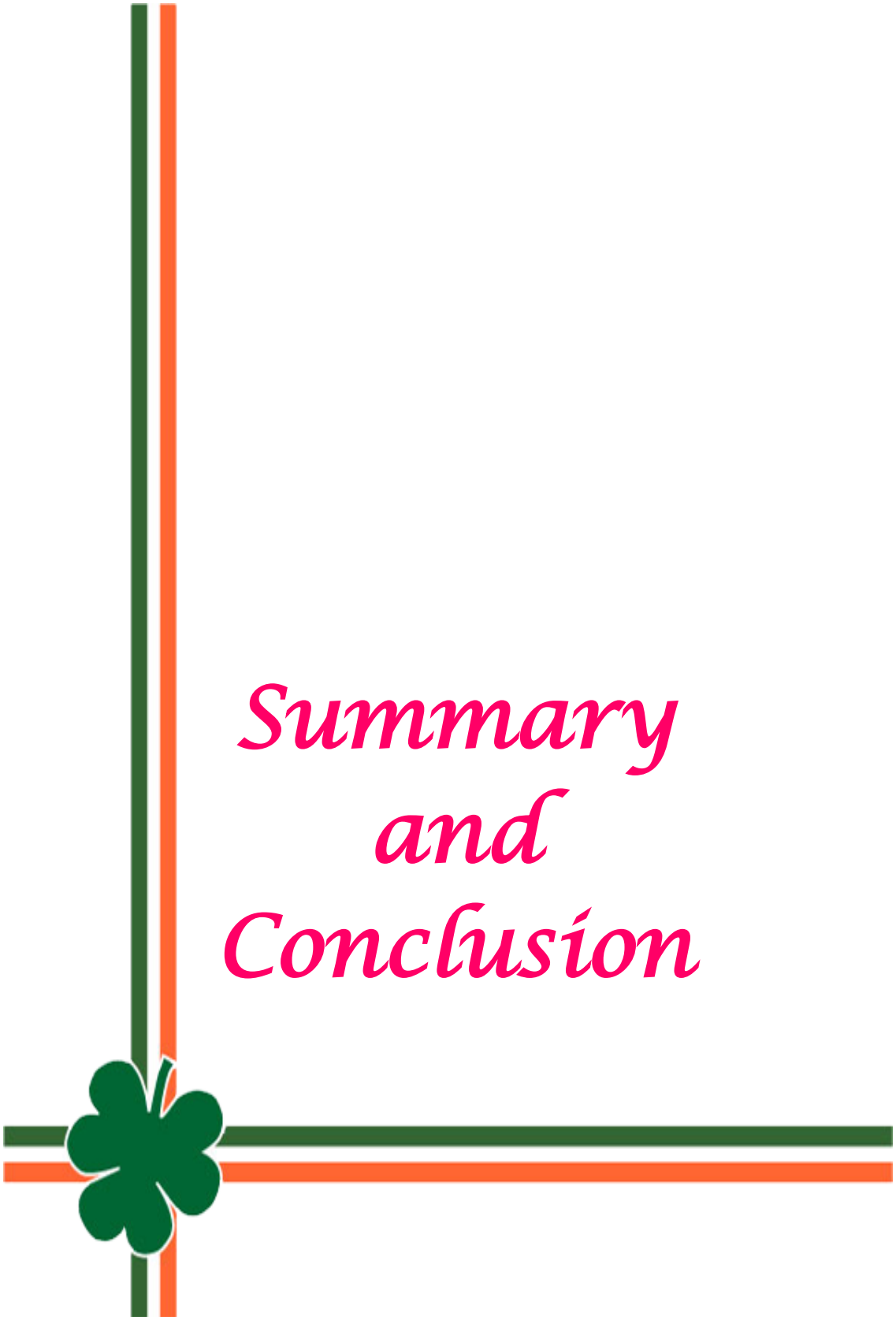
In present investigation, the genotypic correlation of seed yield per plant had significant positive association with days to 50% flowering, plant height, number of primary branches per plant, number of secondary branches per plant, stem diameter, inflorescence length, days to maturity, thousand grain weight, protein content is mainly because of increase in one or more of the above characters and selection of genotypes on the basis of these traits will be effective for yield improvement. Similar result were observed for inflorescence length by Pandey (1981), Gowda *et al.* (1999), Patgar (2003) and Venkatesh *et al. (*2014), for days to 50% flowering by Pandey (1981), for plant height Pandey (1981), Agong and Aylecho (1992), Gowda *et al.(*1992), Shukla and Singh (2003) and Venkatesh *et al. (*2014) for days to maturity Pandey (1981), for stem diameter by Espindola and Gandarillas (1985), Maruthi *et al. (*1987) and Ahammmed *et al*. (2012), for number of primary branches per plant Shukla and Singh (2003), thousand seed weight Venkatesh *et al.* (2014)

5.4.1 Path coefficient analysis

It provides basis for selection of superior genotypes from the diverse breeding population. Seed yield is the product of interaction of component traits. Apart from correlation studies, path coefficient analysis is important to obtain information about how the component characters influence the seed yield through each other.

It is evident from the data presented in Table 4.11 that positive direct effect on seed yield per plant were observed for days to 50% flowering, number of secondary branches per plant, stem diameter, inflorescence length, days to maturity, thousand grain weight, and protein content. These traits should be taken into consideration in breeding high yielding varieties in grain amaranthus through selection. Similar results were observed for plant height, number of branches per plant and 1000 seed weight by Shukla *et al*. (2010), for plant height and inflorescence length by Maruthi *et al*. (1987), for plant height Shukla and Singh (2003), for days to maturity by Patial *et al*. (2014), for protein content by Tejaswini *et al.* (2017).

Negative indirect effect on seed yield per plant was recorded by character inflorescence length Similar results were obtained by Shukla and singh (2003).



Summary and Conclusion

CHAPTER - VI

SUMMARY AND CONCLUSION

The present study entitled **"Genetic diversity studies in Grain Amaranthus [*Amaranthus hypochondriacus* (L.)]"**consisting of one hundred fifty germplasm of Grain Amaranthus was carried out with a view to study the genetic diversity, genetic parameters, character association, path coefficient analysis. The experiment was carried out in a randomized block design with two replications at the College of Agriculture Badnapur, Jalna, during *kharif* 2018.

Observations were recorded on five randomly selected plants for ten characters *viz.*, day to 50 % flowering, plant height, number of primary branches per plant, number of secondary branches per plant, stem diameter, inflorescence length, days to maturity, thousand grain weight (g), seed yield per plant (g) and protein content (%). Analysis of variance revealed significant differences for all the characters studied indicating the presence of considerable amount of variability. In the present study, high estimates of genotypic and phenotypic coefficient of variation were observed for protein content, seed yield per plant, inflorescence length, number of secondary branches per plant.

6.1 Variability and genetic parameters

The highest broad sense heritability was recorded for plant height (99.1%) followed inflorescence length (99%), days to maturity (97.2 %), days to 50% flowering (96.8%), seed yield per plant (95.4%), protein content (94.6%), number of secondary branches per plant (92%), number of primary branches per plant (85.3%), thousand grain weight (83%) and stem diameter (45.8%).

The highest genetic advance (79.69%) was noticed for the character seed yield per plant followed by number of primary branches per plant (56.9%), number of secondary branches per plant (56.17 %), protein content (51.29%) and days to maturity (42.31%). The remaining characters recorded low genetic advance.

6.2 Genetic divergence

The D^2 values showed adequate genetic diversity among the genotypes studied. On the basis of D^2 values all the genotypes were grouped into the twelve clusters with varying number of genotypes in the clusters. The clustering pattern of these genotypes does not follow the geographical distribution. The maximum genetic distance (D) of 48.64 was found between the clusters XII and cluster IX.

Cluster formation

The aim of cluster formation and measuring intra and inter cluster divergence is to provide the basis for selecting parents for hybridization programme. Crossing between the genotypes belonging to the same clusters will not give desired improvement hence; the parents selected for crossing should be from different clusters. Greater the divergence between the two clusters, wider is the genetic diversity in the genotypes. The crosses involving the parents with extreme divergence have also been reported to exhibit decrease in heterosis. Therefore, while selecting the parents by considering the genetic diversity, their performance and cluster mean for the characters also need due consideration in the crop improvement programme. In the present investigation, the cluster means for the ten characters studied are presented in Table 4.7.

The cluster mean for days to 50 per cent flowering varied from 57.50 (XII) to 67.50 days (IX). The cluster means for plant height ranged between 120.50 (IX) to 208.50 cm (VIII). The cluster mean for primary branches per plant ranged between 4.50 (III) to 10.17 (IX). The cluster mean for secondary branches per plant ranged from 7.50 (III) and (VIII) to 14.50 (cluster XI). The cluster mean for stem diameter ranged between 0.75 (XI) and 1.82 (IX). The cluster mean for inflorescence length was maximum in cluster (VIII) 64.00 and it was minimum in cluster (XI) 18.50. The cluster mean for days to maturity was maximum in cluster (IX) 139.83 and minimum in case of cluster (VII) 94.00. The cluster mean for thousand grain weight was maximum in cluster (III) 2.88 and it was minimum in cluster (II) 12.32. The cluster mean for seed yield per plant was maximum in cluster (IX) 28.17 and it was minimum in cluster (XI) 8.50. The cluster mean for protein content was minimum in cluster (II) 9.64 and it was maximum in cluster (IX) 15.17.

6.3 Correlation

Correlation studies at both genotypic and phenotypic levels were made to resolve the direction and magnitude of association among characters. It indicates that strong inherent association between various character studied and genotypic expression of correlation was comparatively less influenced by the environmental condition. The traits days to 50% flowering, plant height, number of primary branches per plant, number secondary branches per plant, stem diameter, inflorescence length, days to maturity, thousand grain weight and protein content exhibited significantly positive association with seed yield. This indicates the simultaneous improvement of these characters through selection.

6.4 Path coefficient analysis

The path coefficient analysis revealed that, thousand grain weight exerted the highest direct effect on seed yield followed by inflorescence length, protein content and number of secondary branches per plant.

CONCLUSION

On the basis of finding generated from the present investigation, following conclusion can be drawn, which may be considered for improvement in grain Amaranthus crop in future breeding programmes:

The wide range of genetic variability observed for most of the characters as evidenced by significant variances due to genotypes suggesting that, it could be helpful in isolation of better germplasm. The phenotypic coefficients of variation were slightly higher than genotypic coefficients of variation which suggest the influence role of environment in governing these traits. Similarly, the magnitude of GCV and PCV was observed high to moderate for the characters namely, for plant height and seed yield per plant indicated that selection of desired germplasm for these traits may be worthwhile for improving grain yield in future breeding programme.

The high heritability was recorded for plant height followed by inflorescence length, days to maturity, days to 50% flowering, seed yield per plant, protein content, number of secondary branches per plant, number of primary branches per plant, thousand grain weight and stem diameter.

Highest genetic advance as percentage of mean was observed for seed yield per plant followed by number of primary branches per plant, number of secondary branches per plant, protein content, days to maturity, inflorescence length, stem diameter, thousand grain weight, plant height and days to 50% flowering.

SUGGESTIONS FOR FUTURE RESEARCH WORK

On the basis of present study following suggestions could be drawn to plan out further improvement programme in selecting desirable genotypes in grain amaranthus.

1) The experiment should be repeated over the year to confirm the findings.

2) Genotypes having high genetic diversity and desirable performance identified in present investigation may be involved in future breeding programme.

3) The genotype identified as best general combiner for seed yield per plant should further be utilized in hybrid breeding programme.

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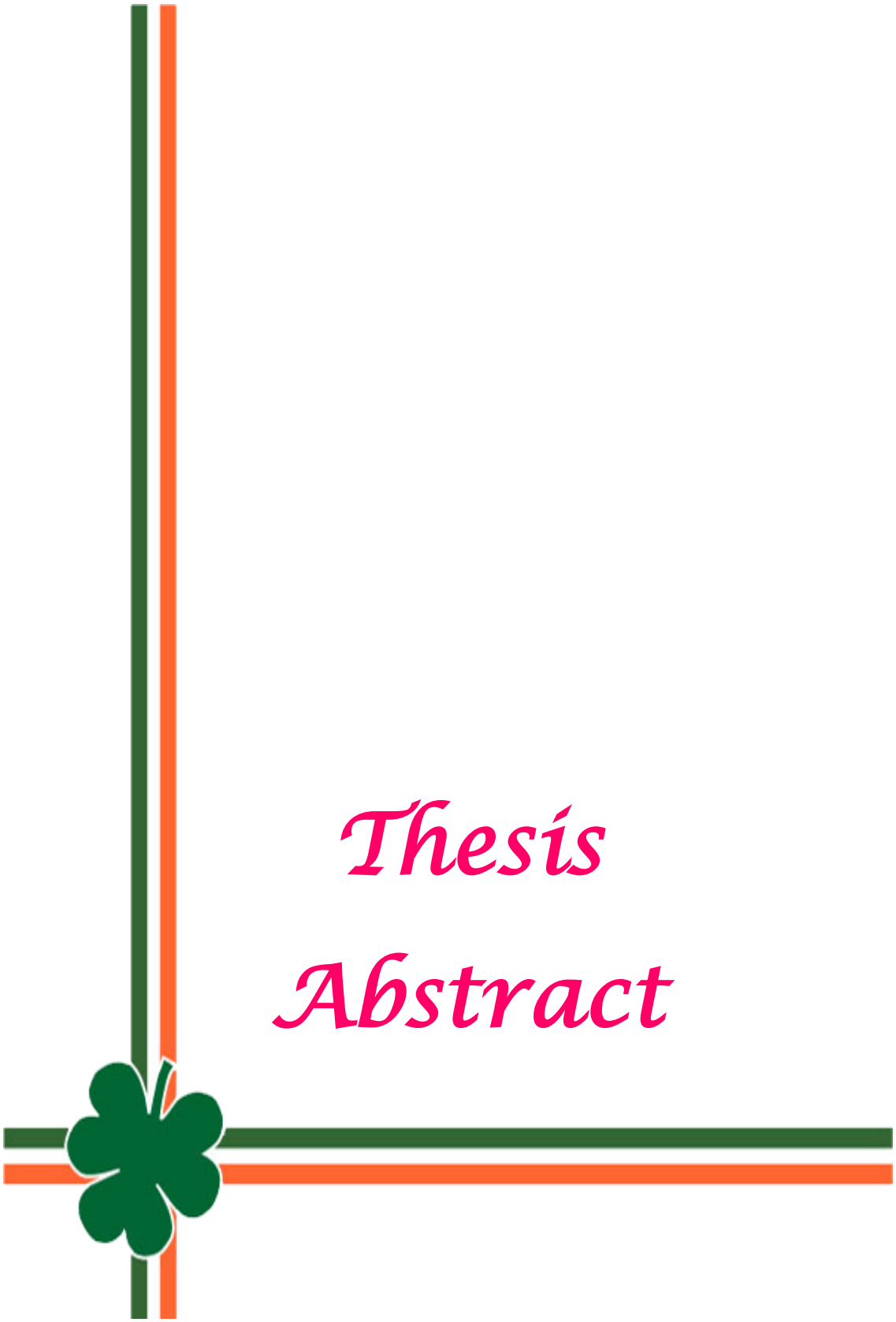

Thesis Abstract

THESIS ABSTRACT

a) Title of the Thesis	:	**"Genetic Diversity Studies in Grain Amaranthus [*Amaranthus hypochondriacus* (L.) .]"**
b) Name of student	:	Kale Balu Haribhau
c) Degree to be awarded	:	M.Sc. (Agriculture)
d) Year of award of degree	:	2019
e) Major subject	:	Genetics and Plant Breeding
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h) Signature of the student	:	(Kale B.H)
i) Name and address of Major Advisor	:	**S. B. Sarode** Assistant Professor, Department of Agricultural Botany, College of Agriculture, Badnapur.
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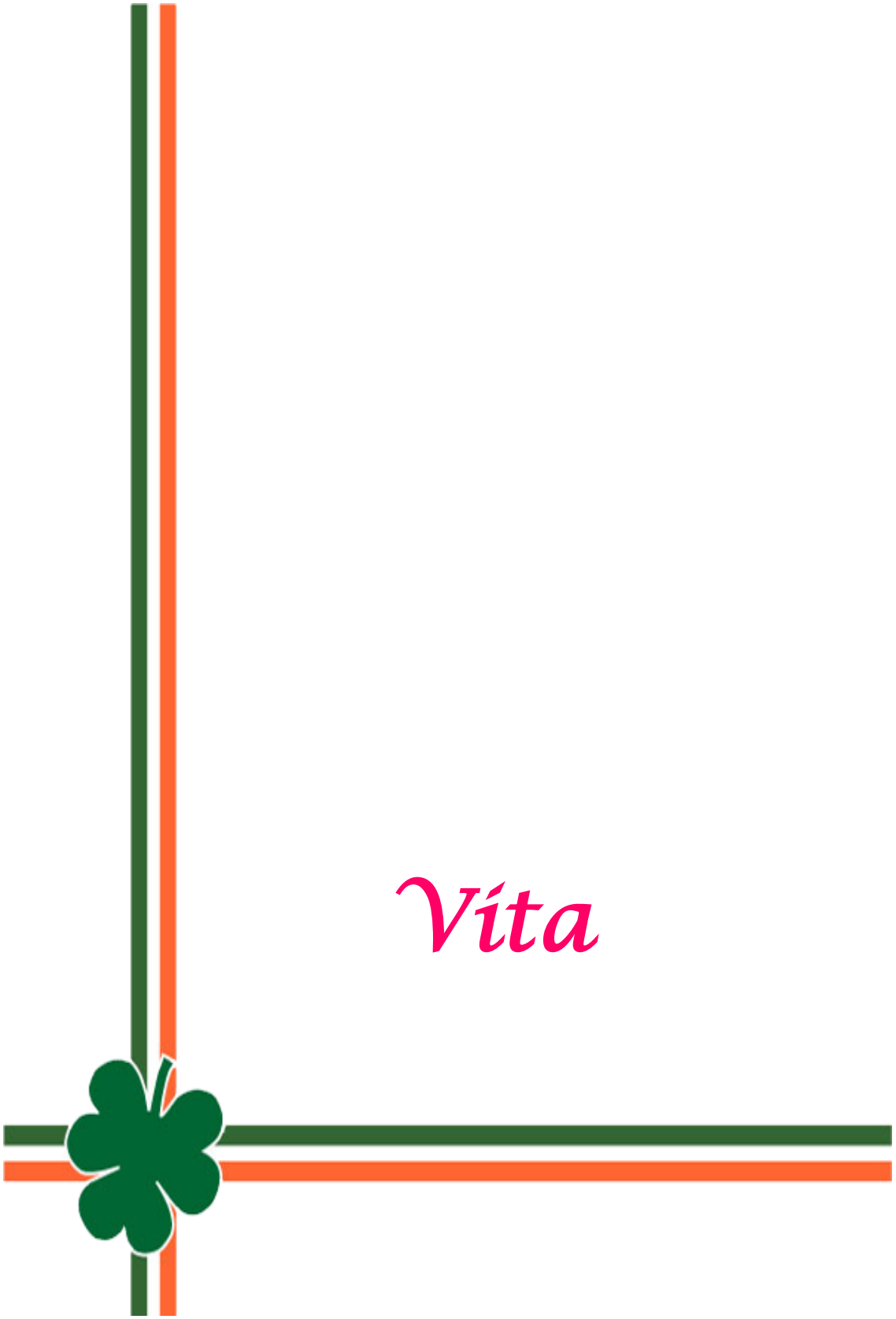
ABSTRACT

The exploration of genetically variable accession is the key source of germplasm conservation and potential breeding material for the future. Assesment of genetic diversity existing in and within germplasm groups for yield and its components to obtain superior recombinants which will help in understanding pattern of variation was performed utilizing the one hundred fifty germplasm and three standard checks of grain Amaranthus replicated twice. To study the nature and magnitude of genetic divergence using Mahalanobis (1936) D^2 statistics, genotypic and phenotypic variances, coefficient of variation, heritability, genetic advance, correlation coefficient and path coefficient were estimated and cluster analysis was performed. The data was recorded on ten traits. One hundred fifty genotypes were grouped into XII clusters. Clusters II was the largest with 62 genotypes. Maximum heritability was observed for plant height (99.1%) followed by inflorescence length (99%), days to maturity (97.2%), days to 50% flowering (96.8%), seed yield per plant (95.4%), protein content (94.6%), number of secondary branches per plant (92%), number of primary branches per plant (85.3%), thousand grain weight (83%) and stem diameter (45.8%). Genetic advance as per cent of mean ranged from 16.33 to 79.69. Seed yield per plant had significant positive association with days to 50% flowering, plant height , number of primary branches per plant, number of secondary branches per plant, stem diameter, inflorescence length, days to maturity, thousand grain weight , seed yield per plant and protein content . Positive direct effect on seed yield per plant were observed for days to 50 per cent flowering, number of secondary branches per plant, stem diameter, inflorescence length, days to maturity, thousand grain weight, seed yield per plant and protein content. These traits should be taken into consideration in breeding high yielding varieties in grain Amaranthus through selection.



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