GENETIC DIVERGENCE STUDIES IN AMARANTHUS

THESIS

Submitted to
Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola
in partial fulfilment of the requirements
for the Degree of

MASTER OF SCIENCE
IN
HORTICULTURE
(VEGETABLE SCIENCE)

By
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DECLARATION OF STUDENT

I hereby declare that the experimental work and its interpretation in the thesis entitled **"GENETIC DIVERGENCE STUDIES IN AMARANTHUS"** or part thereof has neither been submitted for any other degree or diploma of any University, nor the data have been derived from any thesis / publication of any University or scientific organization. The source of materials used and all assistance received during the course of investigation have been duly acknowledged.

Place : Akola
Date : 16 / 6 /2015

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CERTIFICATE

This is to certify that thesis entitled **"GENETIC DIVERGENCE STUDIES IN AMARANTHUS"** submitted in partial fulfillment of the requirement for the degree of **"Master of Science in Horticulture (Vegetable Science)"** of Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola is a record of bonafide research work carried out by **Markand Mohini Sanjayrao** under my guidance and supervision.

The subject of the thesis has been approved by the Student's Advisory Committee.

Place : Akola
Date : 16 / 6 /2015

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(D) Abbreviations

% - Percentage
/ - Per
^{0}B - Degree brix
^{0}C - Degree Celsius
acre^{-1} - Per acre
Anon. - Anonymous
B:C ratio - Benefit Cost ratio
CD at 5% - Critical difference c.f. Cited from
cm - Centimeter
Cv. - Cultivar
DAP - Days after planting
DAS - Days after storage
DAT - Days after transplanting
day^{-1} - Per day
e.g. - Exampli gratia (for example)
et al. - et alia (and others)
etc. - Etcertera
Fig. - Figure
g - gram (s)
ha^{-1} - per hectare
hr - Hours
HW - Hand weeding
i.e. - that is
kg - Kilogram
m^2 - Square meter
Max. - Maximum
Mg - Milligram
Min. - Minimum
ml - Milli litre
MW - Meteorological week
No. - Number
NS - Non Significant
Plant^{-1} - Per plant
Plot^{-1} - Per plot
ppm - Parts per million
q - Quintal
RH - Relative humidity
Rs. - Rupees
SE(m)± - Standard mean error
Sig. - Significant
t - tons
viz., - Vide licet (namely)

(E) Glossary

Additive gene effect : Effect of different polygenes affecting a quantitative character being cumulative or additive in nature. It refers to straight line function of polygenes.

Additive variance : Average effect of alleles on all segregating loci. It results when there is lack of dominance.

Analysis of covariance : A statistical procedure that splits the covariation of two variables into different components.

Analysis of variance : A statistical procedure that splits the total variation into different components.

Broad sense heritability : The ratio of genotypic variance to the phenotypic variance.

Caducous : Non-persistent conditions of different plant parts which are shed within the life cycle of the plant e.g. sepals falling off as flower opens in okra.

Correlation : The degree of qualitative associationship among different variables of attributes.

Correlation analysis : The statistical analysis to find out the degree of relationship and the direction of relationship between two variable.

Correlation coefficient : A statistical measures of degree of the relationship between two or more series of variable.

Co-variance : The sum of the products of deviation of two or more correlated variables from their means divided by the number of degrees of freedom.

Genetic advance : A genetic parameter which depicts the improvement in performance of selected lines over the original population, used to predict the effect of selection.

Genetic shift : The change in genetic make up of varieties breed for a particular environment if grown over long period in areas outside their adaptation.

Genetic variability : A measure of variation in population that is due to genotype which can be studied by using different genetic parameters like, genotypic coefficient of variation, heritability, genetic advance, etc.

Genotype : The genetic constitution i.e. gene make up of an organism.

Genotypic variance : Component of total variance due to genetic difference among the genotype.

Germplasm : A collection of genotype of an organism.

Heritability : The proportion of total phenotypic variation that is due to genotype.

Narrow sense heritability : The ratio of additive genetic variance to phenotypic i.e. total variance.

Oligogenes : Genes having large individual effect qualitative characters which show distinct classes are governed by these genes.

Partial correlation coefficient : The correlation between two series of variables independent of the accompanying variation due to other variables.

Path coefficient : Statistical analysis, which provides an effective means of entangling direct and indirect cause of association and at the same time measures the relative importance of each causal factors.

Phenotype : The observed characters of an individual without reference to its genetic nature.

Phenotypic variance : The phenotypic variation of metric traits among the genotype i.e. total variance which is described due to sum total effect of genotypic variance and environmental variance.

Pleiotropy : The phenomenon of single major gene affecting more than one characters.

Polygenes : A series of multiple genes with small and cumulative effect of which produce continuous variation in the phenotypes, quantitative characters are governed by these genes.

Range : The difference between the largest and smallest item of the series.
Regression coefficient : A coefficient that gives the rate of change in one dependent variable per unit rate of change in the independent variables.

Selection : It aims at isolating the desirable ones from the mixture of numerous genotypes in the population.

Simple correlation coefficient : The total correlation between two series of variables.

Variance : A measure of variability which is the average of the square of deviation of the observations from the mean of a sample drawn from a population.

Variation : Occurance of difference among individual of the same species, sub species, etc. for one or more traits.

Yield component : The component or attribute which finally make up or control yield of any crop.

(F) Thesis Abstract

a) **Title of the thesis** : GENETIC DIVERGENCE STUDIES IN AMARANTHUS

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ABSTRACT

The present investigation entitled "Genetic divergence studies in Amaranthus" was carried out during summer season of the year 2014-2015 at College of Horticulture, Dr. PDKV, Akola. The study was undertaken on twenty five genotypes of amaranthus using randomized block design with three replications.

Sowing of different genotypes of amaranthus was done on 15 February 2014 with line sowing at distance of 10 x 10 cm between lines.

The material used in study having significant variation. D^2 statistic grouped the 25 genotypes under study into 8 clusters. Cluster I possessed maximum number of genotypes 16 (Ic-42271, Ic-42316-8, Ic-42292, Ic-42273-2, Ic-42331, Ic-42343-6, Ic-42296, Ic-42308, Ic-42275, Ec-146547, Ec-59440-1, Ec-170316, Arka Arunima, Ic-42268, Arka Saguna, Ic-42317) as well as highest intra cluster distance (374.19).

The maximum inter cluster distance was observed between cluster IV and cluster VIII (3331.81). The present contribution of characters towards the divergence was observed in characters days to harvest and leaf yield per plot.

Thus the genotypes (Ec-23638) from cluster IV and (OVAT-Sel-1) cluster VIII and the genotypes Krishna, Krishnashri and Arun from cluster V and genotypes Ic-345798 from cluster VI useful in heterosis breeding programme as well as in recombination breeding programme for obtaining desirable segregants.

CHAPTER I

INTRODUCTION

1.1 Background information

Vegetable are defined as the edible herbaceous plant or plant part consumed as raw or after cooking vegetables are rich source of vitamins and minerals. Vegetable play an important role in human diet by providing nutritious compounds like carbohydrates, proteins, fats, vitamins and minerals, etc. Which are essential constitute of balanced diet (Gopalkrishnan, 2007) which includes 125 g of green leafy vegetables, 100g of roots and tubers and 75 g other vegetables (Meena and Kumar, 2005).

Now India has emerged as the 2nd largest producer of vegetable after China in world. India's contribution in area, production and productivity of vegetable is 8495 ha, 146555 MT and 17.3 MT/ha respectively (Anonymous, 2011). In Maharashtra, area, production and productivity of vegetable is 611.0 hectare, 7504.0MT/ha, 12.3 MT/ ha respectively (Anonymous, 2011).

Among the vegetable amaranthus has unique place because of fast growing nature with extremely high yield potential, less susceptible to soil born diseases, easy for cultivation, suitable for both home garden and commercial cultivation. Being tropical and warm season crop. Amaranthus can be grown in summer and rainy season in India. Amaranthus leaves and succulent stems contain high levels of vitamins, including β-carotene (precursor of vitamins A), vitamin B6 , vitamin C, and dietary minerals such as calcium (350-400 mg/100g), iron (38mg/100g), magnesium, phosphorus, potassium, zinc, copper and manganese (Makus and Davis, 1984; Susan and Anne, 1988). Amaranthus is short- duration crop gives quick response to manures and fertilizers, high yield, easiness in cultivation and availability of diverse types suited to specific agro-climatic situation make it a favorite crop of farmers to fit in any cropping systems. Both leafy and grain type play important role to combat malnutrition of poor people (Gopalakrishnan, 2007).

1.2 Importance of study

Amaranthus (*Amaranthus tricolor* L.) is the most common grown leafy vegetable in Kerla and Tamilnadu. It is said to be native of India. It has 16 pairs chromosome number (2n=32). The genus *Amaranthus* belongs to the family Amaranthaceae. The genus contain about 60 species and three main species that appear to be superior for use as vegetable are A. *cruentus*, A. *dubius* and A. *tricolor* (Daloz and Munger, 1980). Major species found in India are as four cultivated *A. tricolor,* tristis, blitum and dubius and two are wild *viz., A. viridis, A. spinosus* (Gopalakrishnan, 2007).

Considering the importance of amaranthus as a vegetable and its adaptability to arid drought conditions, there is a prime need for its improvement. Breeding varieties suited to specific agro- ecological conditions for vegetable purpose is urgently needed for various parts of India. Though amaranthus has been under cultivation in small patches for vegetable purpose its potentiality is not fully exploited. Therefore, there is a need for identification or development of amaranthus genotypes suited for vegetable fodder, leafy purpose. This calls for an evaluation of local or related genotypes to know the variability and divergence. With limited variability nothing can be achieved and the breeder will have to enrich the germplasm or genotypes or can resort to create greater variability through hybridization, mutation and polyploidy breeding.

Character association study does not reveal the direct and indirect contribution of individual character towards yield. In order to have clear picture of yield components for effective selection programme, it would be desirable to consider the relative magnitude of various characters contributing towards yield. On the basis of these studies, the quantum importance of individual characters is marked to facilitate the selection programme in amaranthus.

Generally diverse germplasm are expected to give high hybrid vigour (Harrigngton, 1940) and hence, it necessitates the study of genetic divergence among the existing varieties and genotypes for the identification of parents for hybridization programme. The information on genetic divergence of various traits particularly of those that contribute to yield and quality would be of most useful in planning the breeding programme. D^2 statistics developed by Mahalanobis (1936) provides a measure of magnitude for divergence between two genotypes under comparison. Grouping of genotypes based on D^2 analysis will be useful in choosing suitable parental lines for heterosis breeding. Therefore the present investigation on "Genetic divergence studies in Amaranthus" was undertaken with following objective.

1.3 Objectives of study

1. To estimate the degree of genetic divergence among the amaranthus genotype.
2. To identify genetically divergent parents for their exploitation in further breeding programme.

1.4 Hypothesis

The collection and procurement of genotypes from various places are very difficult without help of nodal agency of germplasm collection within country i.e. National Bureau of Plant Genetic Resources (NBPGR) New Delhi, Indian Institute of Horticulture Research (IIHR) Banglore and Kerla Agriculture University (KAU) Kerla.

The study of genetic divergence among the existing varieties and genotypes for the identification of parents for hybridization programme. The information on genetic divergence of various traits particularly of those that contribute to yield and quality would be of most useful in planning the breeding program.

1.5 Scope and Limitations

New generation is becoming diet and health conscious day by day, so amaranthus is one of the best option to them as it is rich source of nutrients and energy. Therefore, it is very essential to increase the production on large scale to fulfill the need.

There is a huge potential for these rapidly maturing crops that fit into multiple cropping systems. These species can play a special role in relieving protein malnutrition because they have higher lysine content than other cereals. Thus, amaranthus is a prime candidate for cultivation by the small farmers of the less developed countries where protein deficiencies are often major nutritional problems (Khashoo and Subrahmanyam, 1983).

Amaranthus is unique due to its easy cultivation, low growing period, high production per unit area, response very favorably to fertilizers and organic matter, low cost of production; grow in adverse climatic condition, mostly free from pest and diseases during their growing period.

Among these, there are some factors, which are responsible for limited production of amaranthus.

- It has very less shelf life i.e. only 4 hrs.
- Being highly nutritious, but has sour taste, so less demand in though market.
- Amaranthus has received very less attention as far as crop improvement is concerned.

Genetic diversity is one of the key factors for the improvement of many crop plants including amaranthus. . The determination of genetic diversity of germplasm will maximize the probability of transgressive segregation and increase the probability that unrelated accessions contribute with positive alleles at different loci. Among various tools available for assessing the genetic variability and relatedness among crop genetic resources, morphological characterization is the first step in the description and organization of germplasm of any crop.

CHAPTER II

REVIEW OF LITERATURE

Genetic diversity arises due to geographical separation or due to genetic barriers to cross ability. One of the potent techniques of measuring genetic divergence is D^2 statistics proposed by Mahalanobis (1928), which measures the degree of diversification and determines the relative proportion of each component character to the total divergence. Genetic diversity plays an important role in plant breeding because crossing between diverse strains gives a greater heterosis than those between closely related strains.

Mahalanobis (1928) developed D^2 statistic which provides a measure of magnitude of divergence between any two individuals under study. This technique is in the form of a generalized distance, which considers the variation produced by any characters. Mahalanobis also pointed out that D^2 would remain constant when samples were drawn from two different populations irrespective of the size of representative sample. This indicates that D^2 provided a measure of actual magnitude of divergence between two individuals under comparison.

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

Joshi *et al.* (1992) recorded the potential of *Amaranthus* and *Chenopodium* species as grain and leaf vegetable crops, particularly in India, is assessed, with attention being paid to the germplasm collections, evaluation and breeding work carried out, crop production technology, nutritive value, and local and domestic uses.

Mathur (1992) observed, genetic diversity in 50 genotypes of *T. foenum-graecum* collected from 4 different agroclimatic zones of India was estimated using Mahalanobis'D^2 value. There were significant differences between the genotypes for all the 10 characters studied. The genotypes were grouped in 15 clusters using multivariate analysis. The pattern of distribution of genotypes from different geographical regions into various clusters was random, suggesting that geographical distribution is not the factor responsible for genetic diversity.

Pan *et al.* (1992) studied the genetic divergence in Amaranthus and observed that clusters were highly divergent from each other. The genotypes in clusters 4 and 7 were the least divergent at the intercluster level. Clustering pattern was not associated with geographic distribution. Cluster 7 had low mean values for days to first clipping and leaf-stem ratio and high mean values for diameter of stem, length of lamina and internode, and total yield. Cluster 3 had the highest mean value for width of lamina and number of clippings. Cluster 6 had the highest mean values for days to flowering and duration of harvest. About 87% of the genetic diversity present in the 45 genotypes occurred in the first 2 canonical roots. Duration of harvest and total yield accounted for most of the variation present.

Joshi and Rana (1995) evaluated, 20 diverse genotypes for 10 different yield contributing components for to study of divergence. On the basis of D^2 analysis, the genotypes were grouped into 9 clusters. These clusters were heterogeneous for geographical origin of the genotypes. Popping size contributed the greatest divergence (65.48%)

followed by protein content (18.62%). Genotypes of cluster II showed the highest grain yield, inflorescence length, spikelets/spike, leaf length and number of leaves

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

Haas *et al.* (1997) recorded, genetic differences between and within populations of *Amaranthus retroflexus*, using genomic DNA from 11 *A. retroflexus* and 2 *A. hybridus* populations. The populations originated from France, Germany, Hungary, Turkey, Israel and the West Bank. Genetic diversity between populations was detected with 7 RAPD markers, selected from 20 arbitrary primers. Three RAPD markers were used to study differences between single plants. Polymorphic banding patterns were detected between all populations. The polymorphisms were used to calculate genetic distances between populations and to analyse their relationship. Genetic differences were found between single plant in one population.

Revanappa and Madalgeri (1997) studied variability among 40 *Amaranthus* genotypes collected from Tamil Nadu and Karnataka and significant differences were observed. Phenotypic coefficients of variability (PCV) were higher than genotypic coefficients of variability (GCV) for all the characters studied. PCV and GCV were maximum for leaf:stem ratio, number of leaves and fresh weight of leaves and minimum for stem girth.

Kole and Mishra (2002) conducted experiment on genetic divergence using Mahalanobis's D^2 statistic for yield and eight component characters in 20 genotypes of fenugreek. The genotypes were grouped into four clusters of which cluster I was the largest with 15 genotypes and clusters III and IV were monogenotypic. Seeds per pod, 100-seed weight, grain yield, straw yield and branches per plant were the major characters contributing towards divergence.

Shukla and Singh (2002) concluded that an experiment was conducted in Lucknow, Uttar Pradesh, India to assess the genetic diversity of 66 amaranth genotypes for agronomic traits, *viz.*, days to flower and maturity, plant height, stem diameter, number of branches, nodes and inflorescences per plant, inflorescence length, leaf size, number of spikelets per spikes, and grain yield per plant. A wide range of variation for days to flower (44.33-75.33 days) and days to maturity (123.5-160.0 days), plant height (31.67-125.33 cm), number of branches (4.33-19.67), nodes (4.83-32.10) and inflorescences (15.5-213.00) per plant, inflorescence length (10.00-39.00 cm), number of spikelets per spike (1.00-5.00), leaf size (11.20-144.79 cm^2) and grain yield was observed. Days to flower contributed the maximum towards genetic divergence followed by plant height and number of nodes per plant. The genotypes were grouped into 9 clusters. Cluster VIII had the maximum grain yield, days to maturity and plant height, and was next to the highest leaf size. Cluster III had the highest number of inflorescence per plant and was next to the highest grain yield. The grain yield in different clusters was greatly influenced by plant height, number of inflorescence and nodes per plant, number of spikelets per spike, and leaf size. Among the different traits, the days to flower had the maximum contribution towards divergence followed by plant height, number of nodes per plant and leaf size.

Verma *et al.* (2002) reported that, sixty-eight genotypes of grain amaranth (*Amaranthus hypochondriacus*) were grouped into 9 clusters. The clustering pattern revealed that the genetic diversity might not be related to the geographical diversity. The average intercluster distance was maximum between clusters VIII and IX, followed by VI and VIII, II and VIII, and V and IX, indicating that these groups of genotypes were highly divergent from each other. The genotypes in these cluster revealed substantial differences in the means for the 4 traits studied. Genotypes IC-95453, IC-35746, IC-35634 and IC-35778 were important for a breeder for exploiting their potential in breeding programme.

Kole *et al.* (2003) carried out divergence studies in 15 genotypes of fenugreek following D^2 analysis resulted in the formation of four different clusters showing considerable amount of genetic diversity among the genotypes. The genotypes collected from the same geographical region were grouped into different clusters which might be due to human selection and or genetic draft. Cluster-I had maximum number of nine genotypes, while cluster-IV was monogenotypic. The intra-cluster distance was maximum in cluster-III and the inter-cluster distance was maximum in-between clusters-II and III. Maximum contribution to genetic divergence was observe because of the character viz. Pods per plant, straw yield, test weight, days from flowering to maturity and grains per pod. Based on the genetic divergence, the relative contribution of characters in determining seed yield and *per se* performance of the genotypes, the cross combinations RMT-143 x UM-301, UM-301 x Local, UM-118 x Local, UM-302 x Local, UM-118 x UM-34, UM-302 x UM-32 and UM-304 x UM-118 are suggested.

Rani and Veeraragavathatham (2003) Fifty-seven lines of amaranthus (*Amaranthus* spp.) were evaluated. The phenotypic and genotypic variability expressed as coefficients over mean (PCV and GCV, respectively) were the highest for green yield per plant (84.66 and 81.53%), followed by stem weight per plant (76.04 and 75.08%), leaf weight per plant (58.77 and 55.70%) and leaf number (57.22 and 54.69%). Heritability estimates were computed for the various characters and ranged from 73.33 to 97.00%. High heritability coupled with high genetic advance was obtained for green yield per plant (92.56 and 161.36%), stem weight per plant (97.00 and 152.40%), leaf number per plant (91.31 and 107.65%) and leaf weight per plant (89.94 and 108.77%), followed by the other traits such as plant height (85.93 and 44.37%), leaf length (82.68 and 47.80%), leaf breadth (74.26 and 45.72%) and stem girth (73.33 and 47.87%), which suggested additive gene effects controlling these traits.

Banerjee and Kole (2004) studied, genetic divergence among 22 genotypes of fenugreek (*Trigónella foenum-graecum*) for 8 quantitative characters using Mahalanobis D^2 statistics. The genotypes were grouped into 6 clusters. Cluster I consisted of the maximum number of 13 genotypes, followed by clusters II and III with 4 and 2 genotypes, respectively. Three clusters were monogenotypic. Clustering pattern of genotypes was not related to geographical differentiation. Inter-cluster distance was highest between clusters III and VI and lowest between clusters II and VI, while intra-cluster distance was highest in cluster III. Plant height, pods per plant, days to flowering and test weight were the major forces for divergence

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

Kamble *et al.* (2005) analysed, genetic divergence among 50 genotypes of Amaranthus collected from different geographic regions in India. Considerable variation among genotypes for all ten metric characters were observed. Statistical analysis exhibited adequate genetic diversity among genotypes which were grouped into 11 clusters of which six were solitary and the remaining 5 clusters consisted of 2 to 20 genotypes. No parallelism was observed between geographic diversity and genetic diversity. Other traits such as height, number of spikelets and leaf area per plant appeared as the major sources of diversity.

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

Anuja and Mohideen (2006) determined, the genetic diversity in 100 amaranthus germplasm including *Amaranthus tricolor, A. blitum* and *A. dubius* by using the Mahalanobis D^2 analysis. The genotypes grouped into 10 clusters. The types collected from the same eco-geographical origin were scattered in different clusters, although grouping of types from different eco-geographic regions in one cluster was also observed. Cluster IX and X showed high genetic divergence, hence crossing between types from these 2 clusters may results in the development of useful progenies. Among the different characters, the number of leaves and leaf area contributed the to the highest genetic divergence.

Jain *et al.* (2006) evaluated, thirty-six genotypes of fenugreek (*T. foenum-graecum*) for genetic divergence following D^2 analysis. The genotypes were grouped into 6 clusters. Among the 10 characters, fat content had the greatest effect (70.3%) on the total divergence, followed by plant height (8.6%).

Kalpande *et al.* (2007) studied genetic divergence in 61 genoyupes of grain amaranth in this study the genoyupes were grouped into 10 clusters . Cluster I accompanied highest number of genotypes (23) followed by cluster II with 17 genotypes, cluster III with seven genotypes, cluster IV with six genotypes, cluster V and VI with two genotypes each whereas, clusters VII, VIII, IX, and X were with solitary genotype. Inter cluster distance was maximum between clusters III and X followed by clusters III and IV, Clusters II and VII. While, minimum inter cluster distance was observed between clusters V and X.

Kusuma *et al.* (2007) assessed, genetic divergence among sixty-four grain amaranth genotype by using Mahalanobis D^2 statistic. The genotypes were grouped into eleven clusters, which revealed wide diversity in the experimental material. Panicle fresh weight contributed maximum towards genetic divergence. The maximum inter cluster distance was observed between cluster III and XI followed by cluster VII and XI, cluster II and III. The highly diverse clusters could serve as potential sources of the accessions for their use in hybridization programme.

Pandey (2009) evaluated 26 accessions of grain amaranths (*Amaranthus hypochondriacus*), to determine genetic divergence in yield and yield components Based on D^2 analysis, the accessions were grouped into 11 clusters. Clusters I, II and III had 7, 4 and 3 accessions, respectively; clusters VII, VIII, IX and X had only one accession each. The accessions in cluster V exhibited the greatest divergence, closely followed by those in clusters IV and I. Maximum and minimum divergence were observed between clusters VIII and XI, and between clusters II and VII, respectively.

Swami *et al.* (2010) studied the genetic divergence in fenugreek , for 12 characters by evaluating 20 genotype of fenugreek in two crop seasons. On the basis of divergence analysis these genotypes were grouped in 9 clusters. The inter-cluster distances were greater than intra-cluster distance revealing considerable amount of genetic diversity among the genotypes studied. Selection of superior genotype from these clusters may throw good recombinants during hybridization programme.

Branches per plant, 100-seed weight and harvest index seemed promising to contribute to higher seed yield.

Prashantha and Nagaraja (2011) recorded that ,wide range of PCV and GCV were observed for harvest index, seed yield plant^{-1}, number of branches plant^{-1}, dry weight of stem and dry weight of panicle. The per cent mean genetic advance was high for number of leaves, number of branches, panicle fresh weight and number of spikelets panicle^{-1}. Higher heritability coupled with high genetic advance was observed for number of leaves, number of branches, number of spikelets panicle^{-1}, dry weight of panicle, fresh weight of stem, harvest index and seed yield plant^{-1}. Following Mahalanobis (1936) D^2 statistics genotypes were grouped into 10 clusters. Seed yield plant^{-1}, fresh weight of stem, number of leaves, number of branches, days to maturity, panicle length, fresh weight of panicle and dry weight of panicle were identified as potential variability which can be used as parameters while selecting diverse parents in the hybridization programme for yield improvement.

Erum *et al.* (2012) recorded that, in the present study different species (*Amaranthus hypochondriacus* & *A. tricolor*) of amaranthus were collected from different agro-ecological zones of Pakistan and compared for their phenotypic and nutritional traits. The 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.

Akther *et al.* (2013) concluded an experiment to identify the extent of genetic divergence that exist for the yield and yield contributing characters of seventeen genotypes of amaranth using Mahalanobis D^2 analysis. Analysis of variance showed significant difference among the genotypes for most of the characters studied. The genotypes under study fell into 4 clusters. The distribution pattern indicated that the maximum number of genotypes (6) was included in cluster (IV) followed by cluster III (5) and cluster II (5), and the minimum number was in cluster I (1). The inter cluster distance in most of the cases was higher than the intra cluster distance, which indicated wider genetic diversity among the accessions of different groups. The highest inter cluster distance was observed between IV and I, followed by the distance between cluster II and I showing wide diversity among the groups. The lowest inter-cluster distance was observed between clusters III and II suggesting a close relationship among the genotypes of these two clusters. The highest intra-cluster distance was observed for the cluster IV and the lowest for the cluster I. The positive values of vector I and vector 2 for stem weight and weight of leaf indicated that these two characters had the highest contribution towards the divergence among the stem amaranths. The genotypes of stem amaranth from cluster I and cluster IV may be selected as parents in future hybridization program.

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 which in fact demonstrated the presence of additive gene effects. The correlation studies revealed strong positive association of yield with leaf weight, stem weight, stem diameter, dry weight with rind, and dry weight without rind.

The relationship was non-significant and negative at 1st flowering. The result of path analysis indicated that stem weight had maximum direct effect on marketable yield followed by leaf weight, leaf number and dry weight without rind.

Venkatesh *et al.* (2014) studied, 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 indicating scope for improvement of the traits of interest through hybridization and selection.

CHAPTER III

MATERIAL AND METHODS

The present investigation "Genetic divergence studies in Amaranthus (*Amaranthus* spp.)" were carried out at Department of Horticulture, Dr, Panjabrao Deshmukh Krishi Vidyapeeth, Akola during summer season of the year 2014.

3.1 Material

The material under study was constituted of 25 genotypes of Amaranthus (*Amaranhus* spp.) comparising *A. tricolor, A. cruentus* and *A. hypocondriacus.* Which were collected from National Bureau of Plant Genetic Resources (NBPGR), Regional Station, Shimla, Himachal Pradesh, Indian Institute of Horticulture Research (IIHR), Banglore and Kerala Agriculture University (KAU), Kerla. The genotype under study listed with their sources in Table 1.

Table 1. Name of the genotype under study

Sr. No.	Name of Genotype	Source
1	T_1 - Arka Arunima	IIHR, Indian Institute of Horticulture Research, Banglore
2	T_2 - Ic- 42331	NBPGR, Regional Station, Shimla, Himachal Pradesh
3	T_3 - Ic-345798	NBPGR, Regional Station, Shimla, Himachal Pradesh
4	T_4 - Ec- 23638	NBPGR, Regional Station, Shimla, Himachal Pradesh
5	T_5 - Ic- 42296	NBPGR, Regional Station, Shimla, Himachal Pradesh
6	T_6 - Ic- 42271	NBPGR, Regional Station, Shimla, Himachal Pradesh
7	T_7 - Ic- 42343-6	NBPGR, Regional Station, Shimla, Himachal Pradesh
8	T_8 - Ic- 42316-8	NBPGR, Regional Station, Shimla, Himachal Pradesh
9	T_9 - Ec- 146547	NBPGR, Regional Station, Shimla, Himachal Pradesh
10	T_{10} - Ic- 42268	NBPGR, Regional Station, Shimla, Himachal Pradesh

11	T_{11} - Ec- 59440-1	NBPGR, Regional Station, Shimla, Himachal Pradesh
12	T_{12} - Ic- 42275	NBPGR, Regional Station, Shimla, Himachal Pradesh
13	T_{13} - Ic- 42308	NBPGR, Regional Station, Shimla, Himachal Pradesh
14	T_{14} - Ic- 42273-2	NBPGR, Regional Station, Shimla, Himachal Pradesh
15	T_{15} - Ec- 328878	NBPGR, Regional Station, Shimla, Himachal Pradesh
16	T_{16} - Ec- 170316	NBPGR, Regional Station, Shimla, Himachal Pradesh
17	T_{17} - Ic- 42317	NBPGR, Regional Station, Shimla, Himachal Pradesh
18	T_{18} - Ic-42308-1	NBPGR, Regional Station, Shimla, Himachal Pradesh
19	T_{19} - Ic- 42292	NBPGR, Regional Station, Shimla, Himachal Pradesh
20	T_{20} - OVAT-Sel-1	NBPGR, Regional Station, Shimla, Himachal Pradesh
21	T_{21} - Arka Suguna	IIHR, Indian Institute of Horticulture Research, Banglore
22	T_{22} - Krishna	Kerla Agriculture University, Kerla
23	T_{23} - Krishnashri	Kerla Agriculture University, Kerla
24	T_{24} - Renushri	Kerla Agriculture University, Kerla
25	T_{25} - Arun	Kerla Agriculture University, Kerla

3.1.1 Experimental site

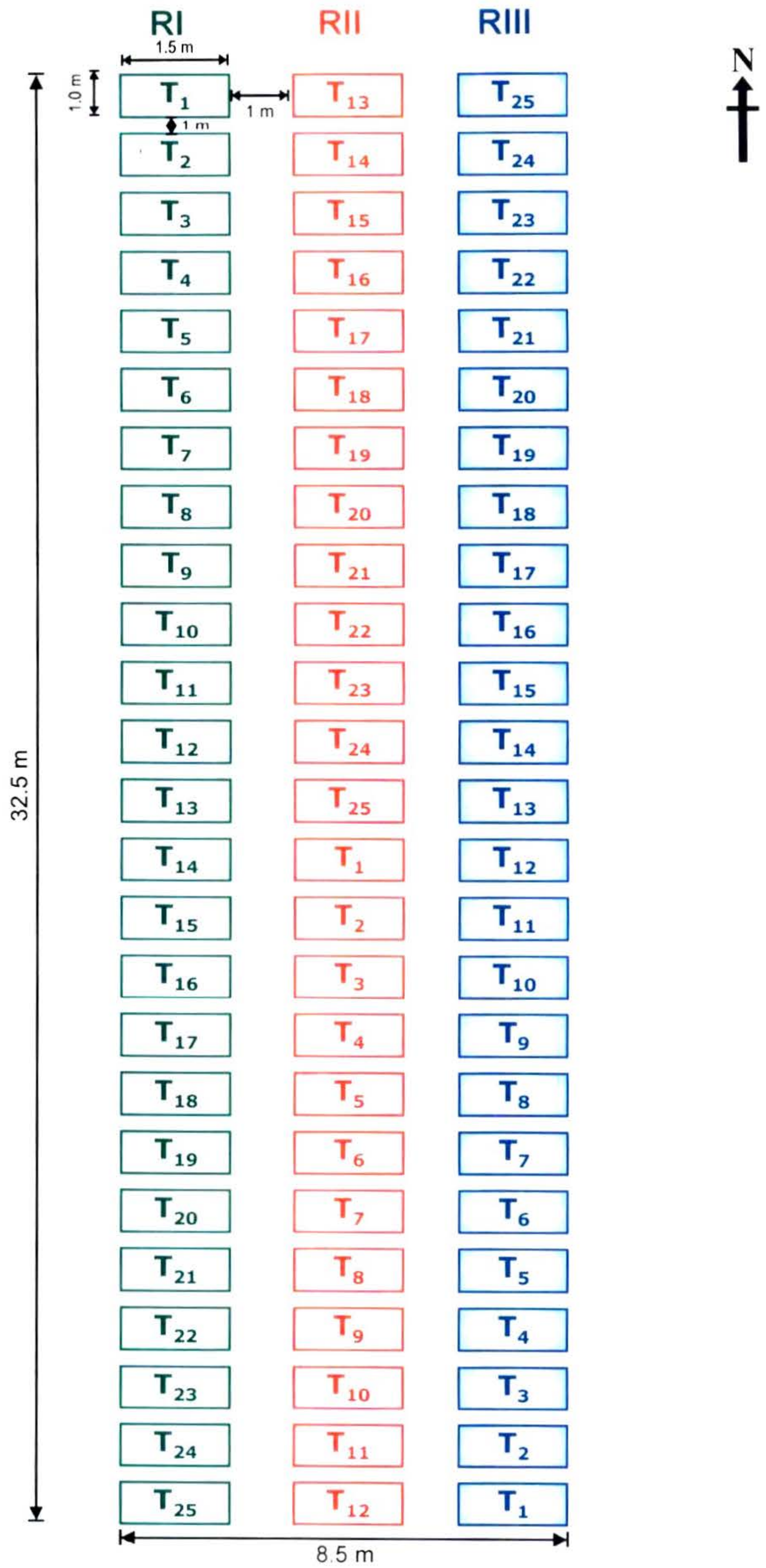
The experiment on amaranthus was laid out in the Plot No. 10 of the College of Horticulture, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola. The plot were well leveled and uniform.

3.1.2 Soil

The plot was medium black with clay soil, well leveled and uniform in topography with appropriate drainage.

3.1.3 Climate

Akola comes under tropical belt and is situated at attitude 307.4 meters above mean sea level. The geographical situation is 20.42^0 N latitude,77.02^0 E longitude. Mansoon arrives in the month of June and extends up to October.



Design : Randomized Block Design (RBD)
Treatments : 25
Replications : 3

Fig. 1. Plan of layout

Plate 1. General view of experimental plot

3.2 Details of Layout

1) Experimental design : Randomized Block Design (RBD)
2) Number of replication : Three (3)
3) Number of treatments (genotypes) : Twenty five (25)
4) Spacing : 10 cm between lines
5) Net plot size : 1 m x 1.5 m
6) Sowing time : 15th February 2014

3.2.1 Planting

Seeds were sown in a line and line to line distance was 10 cm recommended doses (75:100:80 kg/ha) of manure as and when fertilizer were applied. Irrigation and other cultural operations were undertaken as and 3 to 4 days interval when required.

3.3 Observations

Observations on various characters were recorded on five competitive randomly selected plants for each genotype and were averaged to represent treatment means of the replication.

A. Growth Parameters

3.3.1 Plant Height (cm)

The height of the plant were recorded from the ground level to the growing point of the main stem was at 25 days after sowing (DAS) and the mean were expressed in centimeter.

3.3.2 Number of leaves per plant

The total number of leaves per plant were counted from randomly selected plants and the mean expressed in number.

3.3.3 Length of leaf (cm)

The length of the leaf from petiole to tip was taken at harvesting stage and the mean expressed in centimeters.

3.3.4 Width of leaf (cm)

The width of leaf was taken at harvesting stage from five randomly selected plant and the mean expressed in centimeters.

3.3.5 Leaf area (cm^2)

Mature developed leaves from five randomly selected plant of amaranthus plants were selected and measured the leaf area by graph paper.

3.3.6 Petiole length (cm)

The length of the petiole from the bottom to its tip at 25 DAS was recorded from five randomly selected plant and expressed in centimeters.

3.3.7 Diameter of stem (cm)

At harvesting stage diameter of stem were measured by vernier caliper.

3.3.8 Leaf/ stem ratio

The harvested plants were divided into leaves and stems and weighed separately. The leaf – stem ratio was calculated by dividing the weight of leaves by the weight of stems.

B) Leaf Yield Parameters

3.3.9 Days to harvesting

Harvesting time were different from the genotype to genotype. It started from days to 33 days after sowing.

3.3.10 Leaf yield /plot (g)

The yield per plot were estimated for the cropped area based on the yield per plant and expressed in grams.

3.3.11 Leaf yield /ha (q)

The yield per hectare were estimated for the cropped area based on the yield per plot and expressed in tons.

C) Quality Parameters

3.3.12 Chlorophyll Index (%)

At the time of harvesting fully developed, mature leaves of amaranthus plant were selected and took a reading of chlorophyll index by the use of chlorophyll index meter.

3.4 Statistical Analysis

The mean values for each character over two replications were subjected to the following statistical analysis.

1. Analysis of variance
2. Estimation of genetic divergence using Mahalanobis's D^2 analysis.

3.4.1 Analysis of variance

The differences among genotypes for different characters were tested for significance by using analysis of variance technique on the basis of model proposed by Panse and Sukhatme (1961).

$$Y_{ij} = \mu + g_i + \gamma_j + e_{ij}$$

where,

Y_{ij} = Phenotypic observation on 'i'th genotype in 'j'th replication.

μ = General mean

g_i = Effect of i^{th} genotype

γ_j = Effect of j^{th} replication

e_{ij} = Random error associated with i^{th} genotype and j^{th} replication.

The analysis of variance for each character was carried out as follows:

Source of variation	Degree of freedom	Sum of squares	Mean sum of squares	F ratio
Replication	(r-1)	RSS	Mr	Mr/Me
Genotypes	(g-1)	GSS	Mg	Mg/Me
Error	(r-1) (g-1)	ESS	Me	-
Total	(rg-1)	TSS		

Where,

r = Number of replications
g = Number of genotypes
Mr = Mean sum of squares due to replications
Mg = Mean sum of squares due to genotypes
Me = Mean sum of squares due to error.

3.4.2 Genetic Divergence

The data collected on different characters was analyzed by Mahalanobis's Generalized distance (D^2).

Mahalanobis (1928) D^2 statistic was used for assessing the genetic divergence between different populations. The D^2 analysis was carried out using the data recorded on germplasms. Mahalanobis generalized distance (D^2) between any two populations is given by the formula

$$D^2=\sum\lambda^{ij}\sigma^i\sigma^j$$

Where,

D^2 = Square of generalized distance∑
λ^{ij} = Reciprocal of the common dispersal index
σi = $\mu i1 - \mu i2$
σ^j = $\mu j1 - \mu j2$
μ = General mean

Since the formula for computation requires inversion of higher order Determinants, transformation of the original correlated un standardized character mean (Xs) to standardize uncorrelated variable

(Ys) was done to simplify the computational procedure. The D^2 values were obtained as the corresponding uncorrelated (Ys) values of any two uncorrelated genotypes (Rao, 1952).

Clustering D^2 values

All the n (n-1)/2D^2 values were clustered using Toucher's method (Rao, 1952).

3.4.2.1 Mahalanobis's Generalized distance (D^2)

Genetic diversity among genotypes was estimated using D^2 statistic given by Mahalanobis (1936).

3.4.2.1.1 Test of significance

Variances were calculated for all the twelve characters and test of significance was done. Analysis of covariance for the character pairs was estimated on the basis of mean values (Panse and Sukhatme, 1961). After testing the differences among genotypes for each of the character, a simultaneous test of significance of differences between the mean values of a number of correlated variables with regard to the pooled effect of 11 characters was carried out using 'V' statistic, which in turn utilized Wilk's 'Λ' criterion. The sum of squares and sum of products of error and error plus Variety Variance, Covariance matrix were used for this purpose. The estimation of Λ (Wilk's criterion) was done using the following relationship:

$$'\Lambda' = \frac{(E)}{(E+D)}$$

Where,

(E) = Determinant of error matrix

(E + V) = Determinant of error + varieties matrix

The significance of 'Λ' was tested by

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

Where,

m = n - (P + q + 1)/2 with pq degree of freedom

n = Degrees of freedom of error + varieties
p = Number of characters
q = Number of genotypes – 1
$\log_e \Lambda = 2.3407 \log_{10} \Lambda$

3.4.2.1.2 Transformation of correlated variables

Transformation was done using pivotal condensation method. Transformation of correlated variables into standardized uncorrelated ones was done before working out the D^2 values because computation of D^2 values reduced to simple enumeration of differences in mean values of various characters of the two genotypes i.e., Σd_i^2.

3.4.2.1.3 Computation of D^2 values

The D^2 value between 'i^th' and 'j^th' genotypes for 'p' characters was calculated as

$$D_{ij} = p\Sigma_{t=1} (\overline{Y_{it}} - \overline{Y_{jt}})^2$$

Where,

$\overline{Y_{it}}$ = Uncorrelated mean value of 'ith' genotype for 't' character
$\overline{Y_{jt}}$ = Uncorrelated mean value of 'jth' genotype for 't' character
D_{ij} = D^2 value between 'ith' and 'jth' genotypes

3.4.2.1.4 Testing the significance of D^2 values

The D^2 values obtained for a pair of genotypes was taken as the calculated value of χ^2 and tested against the tabulated χ^2 at 'p' degree of freedom where 'p' is the number of characters considered.

3.4.2.1.5 Determination of group constellations (or) clusters

Grouping of genotypes into different clusters was done by using Tocher's method as described by Rao (1952). The criterion used in clustering by the method was that any two variables belonging to the same cluster should at least, on an average show a smaller D^2 values of the combinations of each genotype arranged in increasing (ascending) order of their magnitudes in a tabular form as described by Singh and Choudhary (1977).

To start with two populations having the smallest distance from each other were considered, to which a third population is having to smaller D^2 value from the first two populations was added. Similarly, the nearest next fourth population was considered and this procedure was continued. At certain stage when it was felt that after adding a particular population, there was an abrupt increase in the average D^2, that population was not considered for including in that cluster. The groups of the first cluster were then omitted and the rest were treated in similar way. This process was continued till all the populations were included into one or the other cluster. After the formation of the cluster, the average inter and intra cluster divergence (distances) were calculated.

3.4.2.1.6 Average intra-cluster distance

For the measurement of intra cluster distance, the formula used was

$$\text{Square of intra cluster distance} = \frac{\sum Di^2}{N}$$

Where,
$\sum Di^2$ = Sum of distances between all possible combinations of the entries included in the cluster
N = Number of all possible combinations

3.4.2.1.7 Average inter- cluster distance

Clusters are taken one by one and their distance from other clusters was calculated. The distance between two clusters was the sum of the product of number of genotypes in both the clusters under consideration.

$$\text{Square of inter-cluster distance} = \frac{\sum Dij^{2}}{ninj}$$

Where,
$\sum$Dij2 = Sum of distances between all possible combinations (ninj) of the entries included in the cluster
ni = Number of entries in the cluster i
nj = Number of entries in the cluster j

3.4.2.1.8 Cluster diagram

The clusters and their mutual relationship were presented diagrammatically. The square root of average D^2, which was an approximate measure of divergence between groups, had been used to denote the distance.

3.4.2.1.9 Contribution of individual characters towards divergence

In all the combinations, each cluster was ranked on the basis of their combination towards divergence between two entries ($d_i = Y_{it} - Y_{jt}$). Rank one is given to the highest mean difference and rank 'p' to the lowest difference, where 'p' is the total number of characters. Percentage contribution of each character (X) towards genetic divergence was calculated using formula:

$$X = \frac{N}{M} \times 100$$

Where,
N = Number of genotype combinations where the character was ranked first
M = All possible combinations of number of genotypic pairs.

CHAPTER IV

RESULTS AND DISCUSSION

The observations recorded for various growth characters, quantitative characters and qualitative characters on 25 genotypes of vegetable amaranthus from the field experiment conducted on genetic diversity studies were compiled, tabulated and analyzed following the standard procedure as per the experimental design and other statistical techniques. The present investigation on "Genetic divergence Studies in Amaranthus" was undertaken on twenty five genotypes of amaranthus with following objectives.

1. To estimate the degree of genetic divergence among the amaranthus genotypes.
2. To identify genetically divergent parents for their exploitation in further breeding programme.

The data collected for twelve characters on five competitive plants each from 25 genotypes were subjected to the different statistical analysis the results obtained are presented and discussed under the following sub-heads.

4.1 Analysis of variance

4.2 Genetic divergence studies

  4.2.1 Divergence analysis

  4.2.2 Grouping of genotypes into clusters

  4.2.3 Intra-and inter-cluster average D^2 values

  4.2.4 Average intra and inter cluster distance

  4.2.5 Contribution of different characters towards divergence

  4.2.6 Cluster-wise mean values of characters

4.1 Analysis of Variance

The analysis of variance of all the 12 quantitative characters observed in the present study on different 25 vegetable amaranthus genotypes was carried out to test the significance of differences among the genotypes investigated. The mean sums of squares of all the characters are presented in (Table 2). Analysis of variance revealed that the treatments under study (genotypes) differed significantly from each other even at 1% level of probability for all the characters studied, exhibiting wide variation in the material investigated.

Table 2. Analysis of variance for various characters in vegetable Amaranthus genotype

Sr. No.	Characters	Mean squares		
		Replication	Genotype	Error
		(2)	(24)	(48)
1.	Plant height (cm)	0.35	19.99**	0.11
2.	No. of leaves per plant	0.17	6.32**	0.09
3.	Leaf length (cm)	0.10	5.41**	0.09
4.	Leaf width (cm)	0.11	0.11**	0.05
5.	Leaf area (cm^2)	6.06	56.99**	3.95
6.	Petiole length (cm)	0.09	0.50**	0.05
7.	Diameter of stem (cm)	0.00	0.01**	0.00
8.	Leaf per stem ratio	0.06	0.18**	0.03
9.	Days to harvest	7.84	13.97**	2.96
10.	Chlorophyll content (%)	9.42	48.03**	3.46
11.	Leaf yield per plot (kg)	0.16	6.39**	0.13
12.	Leaf yield per hectare (q)	759.33	28463.08**	574.21

*, ** significant at 5% and 1% level, respectively

Table 2(a). Variety Mean

Source of variation	Df	Mean square	F ratio	Probability
Varieties	24	2.6236E06	9.999E03	0.000000***
Error	47	6.5965E-12		
Total	71	8.8686E05		

4.2.1 Divergence analysis

Estimation of the degree of divergence between biological populations and computation of the relevant contribution of different components to the total divergence is done completely by Mahalanobis's generalized distance estimated through D^2 statistic. During any hybridization programme, the selection of parents using D^2 statistic provides the required potential parents, which are under study with respect to an array of characters. With the selection of genotypes, based on their genetic distance and yield potential, breeder can formulate an appropriate crossing programme for the desired crop improvement.

4.2.2 Grouping of genotypes into various clusters

The twenty five genotypes of amaranthus assessed in the present study were classified into various clusters based on the degree of divergence and similarity among them. These genotypes differed widely and classified into eight distinct clusters (Table 3 and Fig. 2). The cluster-I possessed maximum (16) number of genotypes. The cluster-V included five (3) genotypes, while the another clusters-II, III, IV, VI, VII and VIII accommodated Eight genotypes single pair of genotypes, respectively.

Table 3. Clustering pattern of 25 genotypes of amaranthus based on D^2 analysis

Clusters	Number of genotypes	Name of genotypes*
I	16	Ic-42271, Ic-42316-8, Ic- 42292, Ic- 42273-2, Ic-42331, Ic- 42343-6, Ic- 42296, Ic- 42308, Ic-42275, Ec- 146547, Ec- 59440-1, Ec-170316, Arka arunima, Ic- 42268, Arka saguna, Ic- 42317
II	1	Ec- 328878
III	1	Renushri
IV	1	Ec- 23638
V	3	Krishna, Krishnashri, Arun.
VI	1	Ic- 345798
VII	1	Ic- 42308-1
VIII	1	Ovat - sel -1

4.2.3 Intra- and inter-cluster average D^2 values

The average intra and inter-cluster D^2 values for eight clusters as per the procedure suggested by Singh and Chaudhary (1977) are presented in (Table 4 and Fig. 3) below. The maximum intra-cluster distance was observed for cluster-I (374.19), followed by the cluster-V (257.81) and cluster-II, cluster-III, cluster-IV, cluster VI, cluster VII and cluster-VIII were (0.00). Based on distance between clusters (inter-cluster), the maximum divergence was observed between cluster IV and cluster VIII (3331.81), followed by cluster V and VI (3192.74), cluster III and cluster VI (2876.00), cluster VII and cluster VIII (2605.73), cluster VI and cluster VIII (2424.31), cluster VI and VII (2335.69), followed by cluster IV and cluster V (1970.24), cluster II and cluster IV (1857.59), cluster II and cluster VII (1737.44), cluster III and cluster VIII (1712.42), cluster II and cluster III (1513.50), cluster I and cluster VIII (1503.23), cluster IV and cluster VI (1448.16), cluster III and cluster IV (1850.80), cluster V and

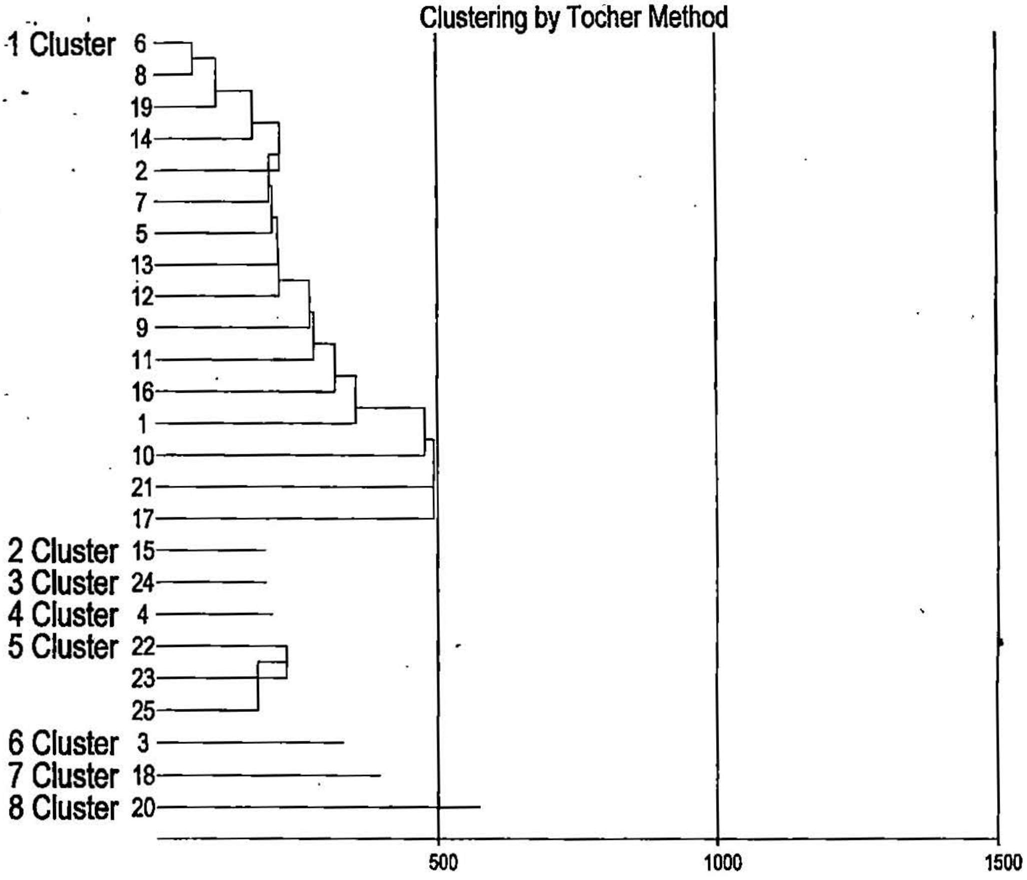


Fig. 2. Clustering pattern of 25 genotypes of Amaranthus based on D^2 analysis

cluster VIII (1277.19) cluster II and cluster V (1250.57), cluster I and cluster V (1205.12),cluster V and cluster VII (1090.45), cluster I and cluster III (1034.77), cluster I and cluster VI (913.16), cluster II and cluster VI (887.63), cluster II and cluster VI (887.45), cluster I and cluster VII (818.63), cluster III and cluster VII (792.05), cluster I and cluster IV (702.50), cluster I and cluster II (609.16), cluster II and cluster VIII (573.53) and least inter cluster distance found between cluster IV and cluster VII (471.96), cluster III and cluster V (449.35).

Table 4. Average intra and inter cluster distance

Cluster	I	II	III	IV	V	VI	VII	VIII
I	374.19	609.16	1034.77	702.50	1205.12	913.16	818.63	1503.23
II		0.00	1513.50	1857.59	1250.57	887.45	1737.44	573.53
III			0.00	1350.80	449.35	2876.00	792.05	1712.42
IV				0.00	1970.24	1448.16	471.96	3331.81
V					257.81	3192.74	1090.45	1277.19
VI						0.00	2335.69	2424.31
VII							0.00	2605.73
VIII								0.00

4.2.4 Contribution of different characters towards divergence

The per cent contribution of each character towards divergence, as per the Tocher's Method, has been presented in (Table 5) below. It was observed that Days to harvest (53.33 %) towards divergence followed by leaf yield per plot (kg) (19.67 %), plant height (12.00 %), no. of leaves per plant 8.00 %), leaf length (2.67 %), chlorophyll content (%) (1.67%) yield per hectare (q) (1.33%), leaf per stem ratio (1.00 %), leaf area (0.33%), that order, respectively. Three characters had no contribution.

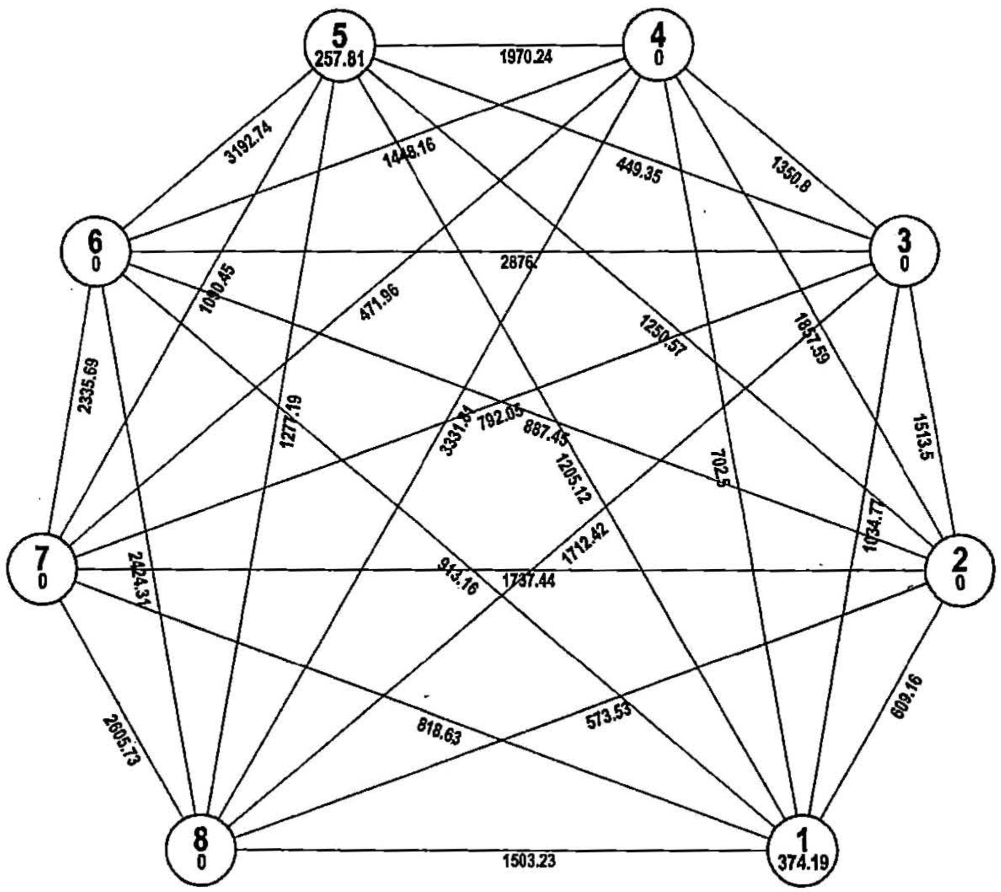


Fig. 3. Cluster diagram showing average intra- and inter-cluster D^2 values of genotypes

(Not to the Scale)

Table 5. Per cent contribution of individual characters toward total divergence of twenty five genotypes of vegetable amaranthus

Sr. No.	Characters	Number of times ranked R	Contribution towards divergence (%) and rank standing
1	Plant height (cm)	36	12.00
2	No. of leaves per plant	24	8.00
3	Leaf length (cm)	8	2.67
4	Leaf width (cm)	0	0.00
5	Leaf area (cm^2)	1	0.33
6	Petiole length (cm)	0	0.00
7	Diameter of stem (cm)	0	0.00
8	Leaf per stem ratio	3	1.00
9	Days to harvest	160	53.33
10	Chlorophyll content (%)	5	1.67
11	Leaf yield per plot (kg)	59	19.67
12	Leaf yield per hectare (q)	4	1.33

4.2.5 Cluster-wise mean values of characters

Cluster means were calculated in all clusters for all 12 characters and presented in Table 6.

a) Plant height

The maximum cluster mean for plant height was recorded in cluster VI (18.32 cm) followed by cluster I (14.90 cm) and the minimum cluster mean values for plant height was recorded in cluster VIII (7.28 cm).

b) Number of leaves per plant

The lowest cluster mean was observed for number of leaves per plant in cluster II (8.57) and the highest was observed in cluster III (13.43).

Table 6. Cluster mean table

Sr. No.	Plant height	No. of leaves	Leaf length	Leaf width	Leaf area	Petiole length	Diameter of system	Leaf per stem ratio	Days to harvest	Chlorop-hyll content	Yield per plot	Yield per ha
Cluster1	14.90	10.40	7.16	3.00	23.56	2.42	0.52	2.10	26.21	29.90	5.56	369.46
Cluster2	12.52	8.57	7.07	3.19	26.21	1.87	0.55	1.91	24.00	32.00	4.00	266.63
Cluster3	12.45	13.43	5.50	3.14	26.47	2.89	0.43	2.62	31.00	31.00	2.50	166.63
Cluster4	17.53	12.60	9.10	2.99	20.10	2.58	0.46	2.10	26.33	29.12	6.70	446.70
Cluster5	11.37	9.38	5.00	2.99	24.27	2.26	0.40	1.91	29.11	31.69	3.00	199.99
Cluster6	18.32	9.40	8.30	3.02	27.10	3.01	0.68	2.41	24.00	35.00	6.84	457.17
Cluster7	12.38	11.33	7.33	3.25	33.93	2.84	0.41	2.26	29.00	30.00	6.43	422.10
Cluster8	7.28	9.37	3.63	2.95	11.47	2.66	0.54	2.26	25.00	23.74	3.80	253.30

c) Leaf length

The lowest cluster mean was observed for leaf length in cluster VIII (3.63 cm) and the highest was observed in cluster IV (9.10 cm) followed by cluster VI (8.30 cm).

d) Leaf width

The lowest cluster mean was observed for leaf length in cluster VIII and cluster V same (2.99 cm) and the highest was observed in cluster VII (3.25 cm) followed by cluster II (3.19 cm).

e) Leaf area

The lowest cluster mean was observed for leaf length in cluster VIII (11.47 cm^2) and the highest was observed in cluster VII (33.93 cm^2) followed by cluster VI (27.10 cm^2).

f) Petiole length

The lowest cluster mean was observed for leaf length in cluster II (1.87 cm) and the highest was observed in cluster VI (3.01 cm) followed by cluster VI (2.89 cm).

g) Diameter of stem

The lowest cluster mean was observed for leaf length in cluster V (0.40 cm) and the highest was observed in cluster VI (0.68 cm) followed by cluster II (0.55 cm).

h) Leaf per stem ratio

The lowest cluster mean was observed for leaf length in cluster II and cluster V are same (1.91) and the highest was observed in cluster III (2.62) followed by cluster VI (2.41)

Plate 2. The genotypes of *Amaranthus* spp. used for divergence study

i) Days to harvest

The lowest cluster mean was observed for leaf length in cluster II and cluster VI (24.00) and the highest was observed in cluster III (31.00) followed by cluster VII (29.00).

j) Chlorophyll content

The lowest cluster mean was observed for leaf length in cluster VIII (23.74 %) and the highest was observed in cluster VI (35.00 %) followed by cluster II (32.00 %).

k) Yield per plot (kg)

The lowest cluster mean was observed for leaf length in cluster III (2.50 kg) and the highest was observed in cluster VI (6.84 kg) followed by cluster VI (6.70 kg).

l) Yield per hectare (q)

The lowest cluster mean was observed for leaf length in cluster III (166.63 q) and the highest was observed in cluster VI (457.17 q) followed by cluster IV (446.70 q).

Discussion

Genetic divergence

C

The success of a breeding programme depends upon the selection of parents. It has been found that the progenies derived from crossing divergent parents give divergent and useful progenies. The D^2 analysis proposed by Mahalanobis (1928) has been reported to be an effective tool to assess the genetic divergence. Such an analysis eventually helps to choose desirable parents for recombination breeding and thus results in the development of superior varieties.

Quantification of genetic diversity existing within and between groups of germplasm is important and particularly useful in proper choice of parents for realizing higher heterosis and obtaining useful recombinants. D^2 Statistics is a unique method for disseminating populations considering a set of parameters together rather than interring from indices based upon morphological similarities: eco-geographical diversity and phylogenetic relationships.

Genetic diversity analysis

Creation of variability and selection within, leading to diverse genotypes is the common protocol that a conventional plant breeder follows. Genetic relationship among genotypes thus generated can be measured by similarity or dissimilarity of any number of quantitative characters assuming that the differences between characters of genotypes ultimately reflect in the divergence of genotypes. In heterosis breeding programs the diversity of parents is always emphasized upon. More diverse the parents within a responsible range, better the chances of improving economic traits under consideration in the resulting offspring. However, it is a difficult task for the breeder to select the most suitable and genetically divergence parents, unless one is provided with necessary information about genetic variability and genetic diversity present in the available germplasm.

Generally, geographical diversity was considered and taken as a measure of genetic diversity when no scientific tools were available. However, this was an inferential criterion and may not be used for discrimination among the populations occupying ecologically marginal habits. The multivariate analysis, using Mahalanobis's D statistic, provides a useful statistical tool for measuring the genetic diversity in a given population with respect to the characters considered together. Further the problem of selecting diverse parents for hybridization programme can be narrowed, if one can identify the characters responsible for the discrimination between populations.

The data collected on twelve yield and growth characters from twenty five genotypes were subjected to multivariate analysis and genetic divergence was estimated using Mahalanobis's D statistic. The magnitude of D values suggested that there was considerable variability in the material studied, which leads to genetic diversity.

The evaluation of variability in germplasm is very vital for any varietal improvement and hybrid development programme. Greater the variability among the germplasm, better the chance for further upgrading of the crop. The crosses involving diverse parents within compatible range are anticipated to produce more heterotic hybrids and greater extent of transgressive segregants in subsequent generations. In the present research efforts were made through systematic experimentation to study the genetic diversity. In any crop improvement programme, genetic diversity plays an important role. In fact, it is an essential pre-requisite while initiating hybridization programme because the choice of potential and diverse parents determines the success of such programme and will serve the purpose of desirable combining genes so as to obtain superior recombination's.

The choice of parents is generally done on the basis of performance. However, several methods of multivariate analysis have been found to be useful in selecting parents for hybridization. among these methods, Mahalanobis D^2 statistics has been one of the reasonable test in estimation of genetic diversity. Assessment of genetic diversity by use of D^2 statistics is useful in choosing parents for any breeding objectives.

Therefore the present investigation was undertaken on 25 genotypes of amaranthus with the following objectives.

1. To estimate the degree of genetic divergence among the amaranthus genotypes.
2. To identify genetically divergent parents for their exploitation for their exploitation in further breeding programme.

Genetic diversity

Assessment of divergence in the germplasm is essential to know the spectrum of diversity so that improvement in crop yield can be normally attained through involvement of the genetically diverse parents in breeding programmes. Mahalanobis's D^2 statistics has been used to quantify the genetic divergence between the genotypes and to identify diverse parents for crossing. This also helps to relate Clustering pattern with the geographical origin. This technique has been employed widely to resolve divergence at inter varietal, species and subspecies levels in classifying problems in crop plants. In plant breeding, genetic diversity plays an important role because hybrids between lines of diverse origin, generally display a greater heterosis than those between closely related plants. The magnitude of D^2 values confirmed that there was considerable amount of diversity in the experimental material evaluated. Cluster-I contained highest number of genotypes i.e. 16 and Cluster.–II, III, IV, VI, VII, VIII had lowest number of genotypes i.e. only one genotype. Cluster V contained three genotypes. Moreover, certain genotypes probably having same pedigree were merged into different Clusters. This indicated there was no association between clustering pattern and eco-geographical distribution of genotypes. The formation of solitary clusters may be due to total isolation preventing the gene flow or intensive human selection for diverse adaptive complexes. Among the 8 clusters, cluster I with 16 genotypes showed maximum intra-cluster diversity (D^2=374.19)).

Selection of genotypes is recommended from the clusters showing higher inter cluster distance (Cluster IV and VIII i.e. D^2=3331.81) also with higher leaf yield as parents in recombination breeding programmes for obtaining desirable segregants.

The percent contribution of each character towards divergence, as per the Tocher's Method, has been presented in Table 5. It was observed that Days to harvest (53.33 %) towards divergence followed by leaf yield per plot (kg) (19.67 %), plant height (12.00 %), no. of leaves per plant 8.00 %), leaf length (2.67 %), chlorophyll content (%) (1.67%) yield per hectare (q) (1.33%), leaf per stem ratio (1.00 %), leaf area (0.33%), that order, respectively. Three characters had no contribution. The most important character contributing to divergence followed by other responsible traits like plant height, number of leaves per plant, green yield per plant, leaf length, leaf width, result were supported by Anuja and Mohideen (2006), Rani and Veeraragavathatham (2003) and Hasan *et al.* (2013).

Overall study of cluster mean for all characters but Tocher's method indicated that cluster VI (18.32 cm) show highest plant height. Highest cluster, mean value for leaf length cluster IV (9.10 cm). For leaf width the maximum cluster mean in cluster VII (3.25 cm). Leaf area highest cluster mean was observed in cluster VII (33.93 cm^2). Petiole length the highest cluster mean was observed in cluster VI (3.01cm). For diameter of stem, the maximum diameter was estimated in cluster VI

(0.68 cm) In case of leaf per stem ratio, the maximum value recorded in cluster III (2.62). For the trait Days to harvest, the maximum in cluster III (31.00). For chlorophyll content cluster VI (35.00%) produced maximum.

Therefore, if the parents are selected on the basis of above characters, they sure expected to be genetically diverse and can be used in hybridization programme for improvement of these traits in desirable direction. Quantification of genetic diversity existing within and between groups of germplasm is important and particularly useful in proper choice of parents for realizing higher heterosis and obtaining useful recombinants. D^2 Statistics is a unique method for disseminating populations considering a set of parameters together rather than interring from indices based upon morphological similarities eco-geographical diversity and phytogenetic relationships.

The germplasm is the reservoir of genetic diversity which is basic requirement for successful breeding programme. In Plant breeding, assessment of genetic diversity in breeding material is of paramount importance because crosses affected between lines of diverse origin generally display greater heterosis and generate more useful recombinations than crosses made between closely related lines.

The D^2 technique (Mahalanobis, 1936) helps in the identification of of genetically divergent parents. Rao (1952) suggested the application of this technique for the assessment of genetic diversity in plant breeding. It also measures the degree of divergence and determines relative proportion of each component character in the total divergence.

In the present study, 25 genotypes of amaranthus were evaluated and D^2 analysis was carried out to study the genetic divergence among these genotypes for 12 important characters. The results revealed the presence of wide genetic diversity for all characters studied. Further 25 genotypes were grouped into eight distinct Clusters by Tocher's method.

Generalized distance

Based on D^2 values 25 genotypes were grouped into 8 clusters by treating estimated D^2 values as the square of the generalized distance. Cluster I was the largest cluster having 16 genotypes followed by cluster V with 3 genotype and cluster II, cluster III, cluster IV, cluster VI, cluster VII, cluster VIII with one genotype each.

The formation of solitary clusters may be due to total isolation preventing the gene flow or intensive human selection for diverse adaptive complexes. Among the 8 clusters, cluster I with 16 genotypes showed maximum intra-cluster diversity (D^2=374.19)).

Selection of genotypes is recommended from the clusters showing higher inter cluster distance (Cluster IV and VIII i.e. D^2=3331.81) also with higher leaf yield as parents in recombination breeding programmes for obtaining desirable segregants.

On the basis of clustering pattern of 25 genotypes of amaranthus it can be concluded that cluster II (Ec-328878), cluster III (Renushri), cluster IV (Ec- 23638), cluster VI (Ic- 345798), cluster VII (Ic-42308-1), and cluster VIII (OVAT-Sel-1) all these have single in cluster no similarities with other genotypes for that these can be useful in further breeding programme.

CHAPTER V

SUMMARY AND CONCLUSIONS

The principle objective of the present investigation was to study and highlight genetic diversity present in the amaranthus germplasm collection, to know the association between different quantitative characters. The study was undertaken during summer season 2014. The material was grown in the field following completely randomized block design (RBD). The inter character association were also carried out to know the association of different characters with yield attributing characters and among themselves. The 25 amaranthus genotypes were subjected to D^2 Statistics to access the genetic divergence. The salient findings of the investigation are summarized here under.

The genetic divergence studies using D2 statistics helped in grouping 25 amaranthus genotypes into 8 distinct clusters. Among the 8 clusters, cluster I with 16 genotypes showed maximum intra-cluster diversity (D^2=374.19) followed by cluster V intra-cluster diversity (D^2=257.81) Whereas cluster II and cluster III cluster IV, cluster, cluster VI, cluster VII, cluster VIII had no intra-cluster distance as it possessed only one genotype.

The maximum intra-cluster distance was observed for cluster-I (374.19), followed by the cluster-v (257.81) and cluster-II, cluster-III, cluster-IV, cluster VI, cluster VII and cluster-VIII were (0.00). Based on distance between clusters (inter-cluster), the maximum divergence was observed between cluster IV and cluster VIII (3331.81), followed by cluster V and VI (3192.74), cluster III and cluster VI (2876.00), cluster VII and cluster VIII (2605.73), cluster VI and cluster VIII (2424.31), cluster VI and VII (2335.69), followed by cluster IV and cluster V (1970.24), cluster II and cluster IV (1857.59), cluster II and cluster VII (1737.44), cluster III and cluster VIII (1712.42), cluster II and cluster III (1513.50) , cluster I and cluster VIII (1503.23) ,cluster IV and cluster VI (1448.16) ,cluster III and cluster IV (1350.80), cluster V and cluster VIII (1277.19) c;luster II and cluster V (1250.57), cluster I and cluster V (1205.12),cluster V and cluster VII (1090.45), cluster I and cluster III (1034.77), cluster I and cluster VI (913.16), cluster II and cluster VI (887.63), cluster II nad cluster VI (887.45), cluster I and cluster VII (818.63), cluster III and cluster VII (792.05), cluster I and cluster IV (702.50), cluster I and cluster II (609.16), cluster II and cluster VIII (573.53),cluster IV and cluster VII (471.96) and least inter cluster distance found between cluster III and cluster V (449.35).

Selection of genotype is recommended from the cluster showing highest inter cluster distance i.e. cluster IV and cluster VIII (3331.81) and cluster V and cluster VI (3192.74) also with higher leaf yield as a parents can be used in heterosis breeding programme as well as in recombination breeding programme for obtaining desirable segregants.

The per cent contribution of each character towards divergence, as per the Tocher's Method, has been presented in (Table 5) below. It was observed that Days to harvest (53.33 %) towards divergence followed by leaf yield per plot (kg) (19.67 %), plant height (12.00 %), no. of leaves per plant 8.00 %), leaf length (2.67 %), chlorophyll content (%) (1.67%) yield per hectare (q) (1.33%), leaf per stem ratio (1.00 %), leaf area (0.33%), that order, respectively. three characters had no contribution.

Conclusion

From the finding of present investigation it can be concluded that the material used in study have significant variation.

D2 statistic grouped the 25 genotypes under study into 8 clusters. Cluster I possessed maximum number of genotypes (16) as well as highest intra cluster distance (374.19).

The maximum inter cluster distance was observed between cluster IV and cluster VIII (3331.81).

The present contribution of characters towards the divergence was observed in characters days to harvest and leaf yield per plot.

Thus, the genotypes (Ec-23638) from cluster IV and (OVAT-Sel-1) cluster VIII and the genotypes Krishna, Krishnashri and Arun from cluster V and genotypes Ic-345798 from cluster VI useful in heterosis breeding programme as well as in recombination breeding programme for obtaining desirable segregants.

CHAPTER IV

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APPENDIX I

Weekly Weather data for the year 2014 recorded at Meteorological Observatory, Department of Agronomy, Dr. PDKV, Akola

Actual 2014
Normal : 1971-2010

Weeks	Dates	T MAX (°C)		T MIN (°C)		BSH (hrs)		WS (km/hr)		RH I (%)		RH II (%)		Evap. (mm)		RF (mm)		CRF (mm)	Rainy Days	
		N	A	N	A	N	A	N	A	N	A	N	A	N	A	N	A		N	A
1	1-7 Jan	28.8	29.0	11.0	13.0	8.2	4.8	4.4	1.0	71	80	31	31	4.2	4.4	2.8	0.0	0.0	0.2	0.0
2	8-14	29.3	28.5	11.7	13.9	8.3	4.6	4.4	2.3	71	80	30	34	4.4	3.7	3.3	0.0	0.0	0.2	0.0
3	15-21	30.0	29.2	12.0	15.8	8.6	3.4	4.5	2.0	68	76	28	33	4.9	4.7	0.7	0.4	0.4	0.1	0.0
4	22-28	30.6	28.9	12.0	14.5	8.8	3.3	4.6	1.9	65	81	26	31	5.2	4.2	0.9	0.0	0.4	0.1	0.0
5	29-4 Feb	31.0	30.0	12.6	11.0	8.8	8.4	4.9	1.7	62	59	25	16	5.5	5.2	3.0	0.0	0.4	0.2	0.0
6	5-11	31.4	31.9	12.7	14.0	8.8	7.6	5.0	1.7	59	60	23	20	5.9	5.3	3.7	0.0	0.4	0.3	0.0
7	12-18	32.7	29.4	14.4	12.7	9.0	7.4	5.4	2.3	55	64	22	24	6.6	6.7	0.1	0.0	0.4	0.0	0.0
8	19-25	33.4	31.7	14.5	16.2	9.1	5.9	5.7	2.0	54	64	21	29	7.3	6.2	2.5	2.0	2.4	0.2	0.0
9	26-4 Mar	35.0	30.2	15.7	15.3	9.5	7.5	6.1	2.8	50	76	18	25	8.2	5.7	4.1	34.7	37.1	0.3	3.0
10	5-11	35.9	28.9	17.3	16.5	9.2	6.0	6.1	3.1	46	83	20	29	8.8	4.4	5.2	8.6	45.7	0.3	2.0
11	12-18	37.0	35.3	18.1	18.9	9.1	8.7	6.3	2.2	45	70	18	16	9.2	6.5	2.4	7.9	53.6	0.3	1.0
12	19-25	38.4	37.8	19.3	20.0	9.2	8.7	6.4	2.8	39	43	15	11	10.4	9.7	0.6	0.0	53.6	0.1	0.0
13	26-1 Apr	39.0	39.8	20.4	23.7	9.2	8.0	6.9	2.8	37	35	15	11	11.2	9.5	2.2	0.0	53.6	0.2	0.0
14	2-8 Apr	40.0	39.9	21.7	22.2	9.4	8.0	7.3	3.1	37	30	14	9	11.7	10.2	1.0	0.0	53.6	0.1	0.0
15	9-15	40.8	39.3	23.1	21.8	9.5	7.5	8.4	3.5	35	38	14	10	12.9	10.6	0.4	0.0	53.6	0.1	0.0
16	16-22	41.6	40.4	24.1	23.8	9.7	8.2	8.6	3.5	36	52	14	22	13.9	10.7	0.5	4.2	57.8	0.1	1.0
17	23-29	42.3	41.5	25.4	24.2	9.8	8.7	9.0	3.8	37	38	15	11	14.7	12.7	0.5	0.0	57.8	0.1	0.0
18	30- 6 May	42.6	42.6	26.6	25.5	9.4	8.3	10.5	3.2	39	38	15	11	15.5	11.7	0.8	6.4	64.2	0.1	1.0
19	7-13	42.6	39.3	27.1	25.8	9.7	6.6	12.2	6.4	42	56	17	21	16.2	10.8	1.3	0.8	65.0	0.1	0.0
20	14-20	42.5	41.2	27.7	26.5	9.4	7.5	14.2	5.1	47	46	19	21	16.8	11.7	2.8	0.0	65.0	0.4	0.0
21	21-27	42.1	43.3	27.8	27.2	9.5	7.2	15.1	6.7	50	47	20	16	16.9	13.1	3.8	3.2	68.2	0.4	0.0
22	28-3 Jun	41.7	43.6	27.8	28.3	9.4	8.3	15.2	7.1	53	48	23	21	16.2	11.8	6.3	4.5	72.7	0.4	1.0
23	4-10	40.2	43.0	26.9	29.6	8.4	6.5	15.2	10.9	62	49	30	26	14.0	16.6	16.8	0.0	72.7	1.0	0.0
24	11-17	38.0	39.3	25.7	25.3	7.1	8.5	13.4	10.4	69	66	40	28	11.1	13.2	43.6	22.5	95.2	1.7	2.0
25	18-24	35.5	37.2	25.0	26.8	5.8	4.7	14.2	14.6	74	63	48	31	9.2	14.3	43.5	1.5	96.7	2.0	0.0
26	25-1 Jul	33.8	38.2	24.3	26.8	4.8	5.2	12.8	15.0	80	61	55	31	7.4	14.3	43.4	1.7	98.4	2.2	0.0
27	2-8	33.2	36.4	24.0	26.3	4.8	4.1	12.0	12.5	81	74	58	44	6.5	11.9	39.4	1.4	99.8	2.2	0.0
28	9-15	32.3	35.1	23.8	24.7	3.8	2.8	11.2	10.0	83	84	60	51	5.5	6.8	42.8	48.6	148.4	2.5	1.0
29	16-22	31.9	30.7	23.6	23.9	4.0	1.5	10.4	8.8	84	88	63	70	5.2	3.8	52.8	45.8	194.2	2.4	6.0
30	23-29	31.3	28.2	23.3	22.6	4.0	1.2	10.8	11.4	86	90	64	68	4.8	4.7	43.4	194.2	388.4	2.6	3.0
31	30-5 Aug	30.9	31.6	23.3	24.2	3.5	3.2	10.6	7.6	86	89	67	66	4.6	6.0	49.6	16.4	404.8	2.4	1.0
32	6-12	29.9	32.2	23.0	23.6	3.2	5.9	10.9	11.9	88	87	70	48	4.1	8.3	61.0	13.7	418.5	2.8	2.0
33	13-19	30.4	33.6	23.0	23.6	4.0	6.9	12.4	9.5	87	89	67	46	4.5	7.1	35.9	6.9	425.4	2.0	2.0
34	20-26	30.4	33.8	22.8	23.6	4.1	5.6	11.9	1.9	87	92	67	57	4.3	4.1	42.5	28.9	454.3	1.9	4.0
35	27-2 Sep	30.5	29.1	22.7	22.4	4.2	2.1	9.3	4.1	87	94	66	81	4.6	5.0	42.4	73.6	527.9	2.1	5.0
36	3-9	31.0	28.8	22.5	22.7	5.3	3.3	8.6	8.7	87	93	62	65	5.3	7.0	33.6	109.2	637.1	1.5	3.0
37	10-16	32.1	30.3	22.4	22.6	6.6	4.2	8.0	7.3	85	68	57	65	5.1	5.7	22.0	0.7	637.8	1.1	0.0
38	17-23	32.9	32.5	22.4	23.1	6.8	6.0	5.4	6.4	84	90	55	56	5.2	5.2	23.7	0.5	638.3	1.4	0.0
39	24-30	33.5	34.5	22.1	20.7	7.3	8.5	5.1	1.0	84	81	50	37	5.0	4.2	24.4	2.0	640.3	1.4	0.0
40	1-7 Oct	33.7	36.5	21.2	21.1	7.6	7.4	4.8	1.4	82	73	47	29	5.4	5.2	23.4	0.0	640.3	1.1	0.0
41	8-14	34.0	36.8	19.8	20.9	8.1	5.6	4.5	1.7	78	66	40	26	5.3	5.4	13.1	0.0	640.3	0.7	0.0
42	15-21	33.7	34.5	18.3	21.8	8.2	5.6	4.6	1.4	76	76	37	37	5.3	5.6	6.1	0.0	640.3	0.4	0.0
43	22-28	33.1	31.9	16.8	18.0	8.3	4.3	4.4	1.1	74	77	34	37	5.3	4.0	7.6	0.0	640.3	0.4	0.0
44	29-4 Nov	32.7	33.8	16.0	15.9	8.4	7.9	4.1	1.3	73	68	32	21	5.3	4.7	2.3	0.0	640.3	0.2	0.0
45	5-11	32.3	33.5	15.2	16.6	8.4	6.5	3.9	1.4	71	69	32	28	5.1	5.2	3.0	0.0	640.3	0.2	0.0
46	12-18	31.6	30.0	14.6	20.4	8.3	3.2	3.9	2.2	73	87	32	46	4.8	3.5	5.3	20.1	660.4	0.2	2.0
47	19-25	31.0	31.7	13.3	12.9	8.4	7.4	3.7	0.9	72	72	30	16	4.6	4.2	7.7	0.0	660.4	0.3	0.0
48	26-2 Dec	30.5	32.2	12.8	12.4	8.4	7.2	3.6	0.6	71	75	32	15	4.4	3.6	5.5	0.0	660.4	0.3	0.0
49	3-9	30.0	30.8	11.9	10.9	8.4	8.3	3.8	0.9	71	73	30	18	4.3	4.4	1.0	0.0	660.4	0.1	0.0
50	10-16	29.6	29.5	10.9	14.4	8.4	4.7	3.6	1.5	71	74	28	33	4.2	4.6	0.8	0.9	661.3	0.1	0.0
51	17-23	29.5	26.4	10.8	6.9	8.5	8.3	3.8	1.6	70	71	29	16	4.1	5.0	0.9	0.0	661.3	0.1	0.0
52	24-31	29.1	28.6	11.1	8.3	8.3	8.6	4.5	1.5	71	69	30	16	4.2	5.2	2.6	0.0	661.3	0.2	0.0
TOTAL RF January to Dec																	661.3			40
Total RF June to Dec																	593.1			32