GENETIC DIVERGENCE AND PATH ANALYSIS IN GRAIN AMARANTHUS (*Amaranthus hypochondriacus L.)*

By

ANIL KRISHNA KAMBLE
(Reg. No. 97015)

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A Thesis Submitted To The

**MAHATMA PHULE KRISHI VIDYAPEETH
RAHURI – 413722 DIST.- AHMEDNAGAR,
MAHARASHTRA STATE (INDIA)**

In partial fulfilment of the requirements for the degree

Of

MASTER OF SCIENCE (AGRICULTURE)

IN

CYTOGENETICS AND PLANT BREEDING

DEPARTMENT OF AGRICULTURAL BOTANY
POST GRADUATE INSTITUTE

**MAHATMA PHULE KRISHI VIDYAPEETH
RAHURI
DIST. AHMEDNAGAR. M.S. (INDIA)**

2000

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Approved by

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DEPARTMENT OF AGRICULTURAL BOTANY
POST GRADUATE INSTITUTE

MAHATMA PHULE KRISHI VIDYAPEETH
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2000

CANDIDATE'S DECLARATION

J *hereby dectare that this thesis or part*
thereof has not been submitted by me
or any other person to any other
"University or Institute
for (Degree or
(Diploma

Place : MPKV,Rahuri (A.K.Kamble)
Dated :14/OI/2000

Prof. A.H. SONONE,
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Maharashtra State (INDIA)

CERTIFICATE

This is to certify that the thesis entitled, **"GENETIC DIVERGENCE AND PATH ANALYSIS IN GRAIN AMARANTHUS** (A. *hypochondriacus* **L.)",** submitted to the faculty of Agriculture, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar, Maharashtra, in partial fulfilment of the requirements for the degree of **MASTER OF SCIENCE** (AGRICULTURE) in **CYTOGENETICS AND PLANT BREEDING,** embodies the results of a piece of *bona fide* research work carried out by **Mr. ANIL KRISHNA KAMBLE,** under my guidance and supervision and no part of the thesis has been submitted for any other degree, diploma or publication in any other form.

The assistance and help received during the course of this investigation have been duly acknowledged.

Place :MPKV, Rahuri (L.H.Sonone^
Dated : /01/2000. Research Guide

Dr. S.S. Kadam
Associate Dean,
Post Graduate Institute,
Mahatma Phule Krishi Vidyapeeth,
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Maharashtra State (INDIA)

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Place :MPKV, Rahuri (S.S. Kadam)

Date : -n/OV 2000.

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I am also thankful to Mr. Vishwanath Z. %adamfor type setting of this manuscript in a descent manner.

Place : MPKV, Rahuri (Kamble, A.K.)

Dated : 1 l\J 0 1 / 2000

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ABBREVIATIONS

B.S.	:	Broad sense
cm	:	Centimeter
C.D.	:	Critical difference
Cov.	:	Covariance
C.V.	:	Coefficient of variation
D.F.	:	Degrees of freedom
et ah	:	*et* alii (and others)
EMP	:	Error mean sum of products
g	:	Gram Cs)
GA	:	Genetic advance
GCV	:	Genotypic coefficient of variation
GMP	:	Genotypic mean sum of products
h^2	:	Heritability
^	:	Kilogram (s)
MSS	:	Mean sum of squares
N	:	Nitrogen
PCV	:	Phenotypic coefficient of variation
RBD	:	Randomised Block Design
S.E.	:	Standard error
viz	:	Videlicet (Namely)
62	:	Variance
/	:	Per
0/ /o	:	Per cent

ABSTRACT

GENETIC DIVERGENCE AND PATH ANALYSIS *IN* GRAIN AMARANTHUS *(A. hypochondriacus* L.)

By

A.K. Kamble

MASTER OF SCIENCE (AGRICULTURE)

Mahatma Phule Krishi Vidyapeeth,

Rahuri - 413 722

2000

Research Guide	:	Prof. A.H. Sonone
Department	:	Agricultural Botany
Major field	:	Cytogenetics and Plant Breeding

The investigation on "Genetic divergence and Path analysis in grain amaranthus *(A. hypochondriacus* L.)" was conducted to assess the genetic divergence among the genetic stocks of amaranthus and to study direct and indirect contribution of various components towards yield.

The data was collected on ten important yield components on fifty genotypes evaluated during *Kharif* 1997. Genotypic and phenotypic coefficients of variation were higher for grain yield per plant followed by number of spikelets per inflorescence, leaf area per plant, length of inflorescence, oil content, girth of inflorescence and plant height, while its estimate was the least for days to 50 per cent flowering. The heritability in broad sense was the highest for per cent grain oil content. High heritability associated with high genetic gain as per cent of mean were observed for grain yield per plant, numberof spikelets per inflorescence, leaf area per plant suggesting additive genetic control in their inheritance and scope for selection for improving these characters.

Leaf area per plant, number of spikelets per inflorescence, plant height at flowering, length of inflorescence, girth of inflorescence, oil content had significant positive correlation with grain yield. These characters also exhibited positive direct and indirect effects *via* number of other yield components suggesting their importance while selecting for improvement in grain yield.

The D^2 statistic showed that there was 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.

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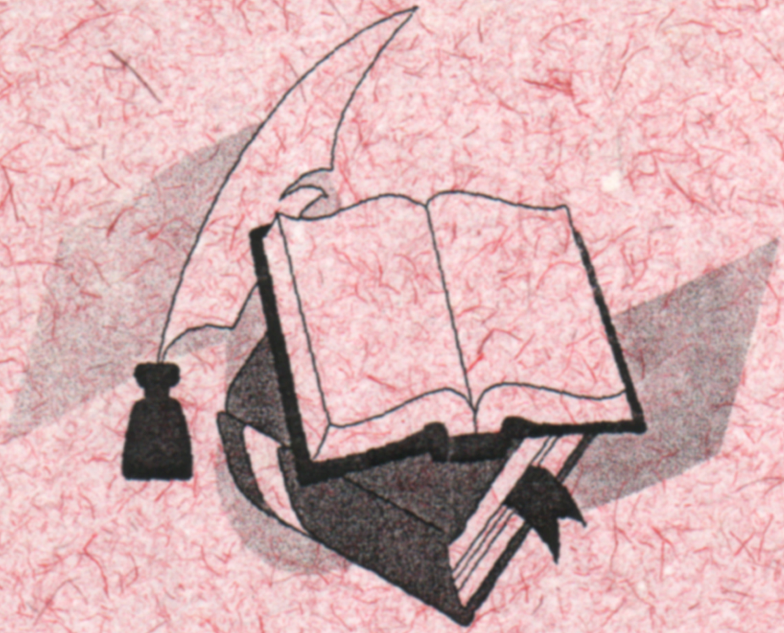

INTRODUCTION

1. INTRODUCTION

Grain amaranth is an ancient food crop reported to have been cultivated in Mexico. Although the plant is undoubtedly of an American origin, it is still not known as to when and how it was introduced into Asia in general and the Himalayas in particular. These have been under cultivation since ancient times in several countries of the world. The genus *Amaranthus* of annual coarse herbs, is distributed in temperate and tropical regions of the world (Sauer, 1967).

The crop is grown in India in the Sub-Himalayan ranges and in the Nilgiri hills of South India under the common name of ᵛrandaana' or "rajgeera' (Singh, 1961). In his earlier study, Sauer % (1950) had grouped grain amaranth species into four classes viz., *Amaranthus hypochondriacus* L., *A. cruentus* L., *A. caudatus* L. and *A. edulis.*

The family Amaranthaceae (Dicotyledons, Order - Caryophyllates) is composed of 60 genera and about 850 species. About 60 species have been recognized in this genus (Willis, 1973). Amaranthus is a dual purpose crop, used both for grains and greens.

Origin

India has been regarded as one of the two main centers of distribution of genus *amaranthus,* the other being tropical America. There seems to be no conclusive evidence as to correct origin of

Amaranthus species. Many investigators (De Candolle, 1883; Hooker, 1885; Ames, 1939; Vavilov, 1950 and Merril, 1950) believed that grain amaranthus have been cultivated in Southern Asia from time immemorial and originated there. De Candolle (1883) and Vavilov (1950) considered Indo-Burma region to be the center of origin of *A. cruentus* L. and *A. paniculatus.*

Botany and Cytological studies

Amaranthus is a dibasic genus with X = 16 and X = 17 chromosomes. Grant (1959) tabulated information on chromosome number of 30 species of *Amaranthus.* With the exception of one tetraploid species *A. dubius* (2n = 64), all the species have a diploid chromosome number of either 32 or 34.

Distribution in India and agronomic practices followed

In the Himalayas two grain species i.e. *A. hyipochondriacus* and *A. caudatus* are mostly grown and often intercropped with maize, finger millet, Italian millet, barnyard millet, french bean, soybean, black gram, horse gram and colocasia and sometimes in pure stand (Joshi, 1986). *A. cruentus* is of rare occur nee. Amaranthus cultivation is most wide spread in the mountain regions above 1500 m and extends upto 3000 m elevation in the hills of India. On the South Indian hills, the grain amaranthus is mostly mixed with ragi and rarely grown as pure crop (Anonymous, 1983).

In North Indian hills, the grain crop is planted at the break of monsoon and in South Indian hills, it is grown throughout the year. Amaranthus can be grown on a wide range of soils, however, sandy loam soil, slightly acidic in nature is preferred. The amaranth grain has been considered as sacred food. In Mexico and other South American countries, the seeds of amaranth have been offered to Gods.

Amranthus is not usually transplanted for grain crop. Irrigation is given just after broadcasting the seeds. The normal seed rate is between l.lto 1.5 kg/ha, however, it varies according to the method of sowing. Germination starts 5-6 days after first irrigation. The next irrigation is given after 15-20 days and subsequently at an interval of 10-15 days till the crop is 2.5 to 3 month old.

Joshi and Rana (1991) reported that there is mosaic disease caused by virus on these species. Its raw grains contain hepatoxic substances. The toxin is heat liable. In India, the plant is used as an application to scarofulous sores.

Grain amaranth has considerably high potential for grain yield. In the experiment conducted at the National Bureau of Plant Genetic Resources (NBPGR), Regional Station, Shimla, grain yield was upto 38 q/ha. Average grain yield of 22.5 q/ha has been reported from North West hills of India (Joshi, 1985).

Allemann *et al.* (1996) evaluated six amaranthus genotypes for productivity, taste and acceptability as the source of nutrition. *A. tricolor* and *A. hypochondriacus* had the best taste, significantly better than that of *A. cruentus* and one of the *A. hybridus* cultivars. *A. tricolor* had the best texture. The highest total yield was obtained from *A. hypochondriacus* (43 t/ha) and the lowest from *A. tricolor* (13 t/ha).

Nutritional quality

In general, grain amaranth is a nutritious pseudocereal yielding high amounts of energy, starch and proteins. In India amaranthus assumes special significance as they are consumed during the religious days of fast. At present, amaranthus has gained some importance in the plains of India especially in parts *of* Gujarat and Maharashtra.

It has been reported that the amaranthus grains have more nutritive value than common food grains. Subramaniam and Shrinivasan (1952) while working on vegetable proteins, observed that the seed of *A. emeritus* L., *A. hypochondriacus* L. contained 14.5 to 16 per cent crude protein. Mahajan (1998) analysed grains of amaranthus and observed 12.34 to 16.86 per cent crude protein. The crude fat ranged from 4.06 to 6.38 per cent, while crude fibre content varied from 2.90 to 4.34 per cent. The raw seed was found to contain 3.03 per cent cystine and 2.37 per cent methionine. Smith *et ah,* (1959) reported the amino acid composition (in percentage) of *A. hypochondriacus* as Arginine 14.7, Histidine 2.9, Isoleucine 6,9, Leucine 8.0, Lysine 8.2, Methionine 2.5, Phenylalanine 4.7, Threonine 4.3, Tryptophan 0.9 and Valine 6.0. Bersani and Gozzales (1987) estimated the grain protein content which varied from 12.5 to 16 per cent. The highest protein content was found in *A. caudatus.*

Dhan Prakash *et ah,* (1995) analysed various grain and vegetable species of amaranthus for vitamin C in leaves and oil content in seed. The vitamin C content in *A. cruentus* was 288 mg/100 gm fresh weight while in *A. hypochondriacus* it was 209 mg/100 gm fresh weight. The seed oil content in *A. hypochondriacus* lines varied from 4.4 to 13.2 per cent.

Giranko and Borodkin (1987) reported the amaranthus grains as the rich source of ascorbic acid (70.6 -109.9 mg/100 kg) and carotene (0.95 - 8.18 mg/100 gm).

The grains of amaranthus are consumed in various ways. Generally roasted and poped, boiled for gruel or stews or poped seed subjected to binding in sugar syrup for preparing cakes or ladoos. The stalks are reported to be used for fencing and roof construction. The tender stem of amaranthus are used as drum stick in making curry. Amaranthus as green leafy vegetable constitutes an excellent component of the diet in tropical countries, making it richer in minerals, vitamins and proteins. Amaranthus is one of the cheapest leafy vegetables available in the market and it could be rightly described as a poor man's vegetable.

Inspite of varied uses of amaranth the crop is not fully exploited for its potential, thus there is a need to improve and exploit the genetic potential of this crop through systematic assessment of variability, its utilization in hybridization programme by using proper selection criterion. The research work on genetic diversity and cause and effect relationship through path analysis in this crop is scanty and the situation calls for more detailed studies.

The main aim of plant breeder is to evolve superior varieties. Knowledge of genetic diversity helps in selection of parents in the breeding programme. The Mahalanobis's(1936) D^2 stafcsticsis a powerful tool for quantifying the divergence between two populations. It thus, gives better idea about the magnitude of divergence and is independent of size of sample and provides the basis for selection of parental lines for future breeding programme. Many studies based on this technique have indicated that geographical isolation is not necessarily related to genetic diversity.

Association among the characters influenced by a large number of genes is elaborated statistically by estimating correlation co-efficient which provides a measure of genotypk correlation between characters. The method of partitioning the correlation into the direct and indirect effects by Path Coefficient analysis suggested by Wright (1921) provides useful information on the relative merit of various traits in selection criteria.

The present investigation was therefore taken up on D^2 and path analysis with the following objectives.

To study the direct and indirect contribution of the components to grain yield.

To study the nature and magnitude of divergence among the genotypes of Amaranthus.

To study the efficiency of D^2 in formulating genetic clusters.

To provide basis for selection of parents for hybridization aiming at improvement for grain yield and its components.

Chapter Opener Page

REVIEW OF LITERATURE

2. REVIEW OF LITERATURE

An attempt has been made here to review the published literature on genetic diversity, variability, correlation and path analysis for some important traits in grain *Amaranthus* spp.

2.1 Origin, botany and cytological studies in amaranth

2.1.1 Origin of amaranth

Early botanists and explorers were struck by the excellent establishment and the wide spread distribution of grain amaranthus and some of their progenitors in Africa, Europe and particularly in Asia, so much so that they thought them to be indegenous in Asia. De Candolle (1886) and Vavilov (1951), Darlington (1963) believed that grain amaranthus like *Amaranthus cruentus* L. arose in the Indo-Burma region. However, based on the data from geographical, morphological, archeological, ethnobotanical and physiological studies Sauer (1950, 1967) concluded that the domestication of grain amaranthus began in America with the dawn of American-Indian agriculture and there is evidence for amaranth being one of the ancient (4800 BC) American crops. There is no valid evidence of the movement of crops by man between the old and the new world in pre-columbian times (Hutchinson, 1974).

2.1.2 Botany

The family Amaranthaceae (Dicotyledons, Order - Caryophyllates) is composed of 60 genera and about 850 species. They are all annual herbaceous plants with many species having tropical origin, but with adaptation to temperate climates as well. The genus *Amaranthiis* L. of Amaranthaceae is taxonomically a difficult group. Attempts of the classification and taxonomy of this genus have been made by Thellung (1914), Schinz (1934), Kowal (1954) and Sauer (1950,1955,1957,1967). Thellung (1914) and Schinz (1934) have recognised two sections such as *Amaranthotypes,* Dumort and *Bliotopsis* Dumort (Singh and Thomas, 1978). However, Kowal (1954) suggested a few changes such as removal of *A. spinosus* L. from section Amaranthotypes and its inclusion in the section Bliotopsis and creation of new section puncticulatae. His revision was based on a study of the morphology and anatomy of 21 *Amaranthus* species.

Sauer (1967) replaced section *Amaranthotypes* Dumort by section *Amaranthiis* Sauer. *Amaranthus* section includes most of the domesticated ornaments, all the grain and dye amaranth and common weeds. According to present rules of nomenclature, it must bear the same name as the genus since it includes the type of species *A. caudatus* L. (Sauer, 1967).

The Amaranth plant is monoecious, with cymes continuing above uppermost leaf to form large, compound terminal inflorescences, sepals and stamens 5 (or varying between 3-5), circumscissile utricle (indehiscent in occasional mutant and hybrid individuals). The monoecious habit, the dehiscent utricle allowing easy threshing and winnowing and large compound inflorescences producing enormous quantities of seed have made this section as the member of successful grain crops. Within the section, discontinuties between species are quite clear. The pigmentation and growth habits are usually used as important characters for identification of the taxa, which segregate and are extreamly plastic under different day length and environments. But some characters are constant such as shape and position of pistillate flower parts whose correlated discontinuties reveal genetically isolated species.

The basic unit of infloresence are little dichasial cymes, usually called glomerules, each ordinarily consisting of an initial staminate flower and an indefinite number of female flowers. The glomerules are crowded on a leafless axis to form complex inflorescences, technically thyrses, which are generally called spikes. In all the grain species each flower is subtended by a short pointed bract. The perianth consists of five free sepals, the male flowers characteristically have five stamens, the female has a single circumcissile utricle.

The main axis of inflorescence is usually branched. The length and number of these branches and their angle with the main axis determines the shape of inflorescence. The individual flower clusters develope along these in an alternate fashion. The first flower is terminal on the branch and at its base two branches develope the second and third flowers. Each of these flowers in turn is terminal and at its base develope the next two flowers, developement is uaually symmetrical upto the third or fourth series of flowers. At this time, the setting of the first seed usually slows down the growth and upsets the symmetry. UnpoUinated clusters may develope an exceptionally large number of flowers.

The monoecious species of grain amaranth, exhibit two types of arrangement of the staminate and pistillate flowers. These types are important because of their different breeding behaviour. In the first type, the first flower of each flower cluster is staminate and all secondary one are pistillate. There is only one staminate flower in each flower cluster of the inflorescence and this abscisses soon after shedding the pollen. All species, except *A. spinosus* L. are of this type.

In the second type, all the flowers of each cluster are of same sex but the clusters of pistillate flowers develope only in the axils of branches and at the base of the terminal inflorescence, where as the clusters of staminate flowers are borne terminally on the main axis and lateral branches. *A. spinosus* L. is of this type.

According to Pal and Khoshoo (1973), the monoecious habit together with predominant out breeding is an important feature of grain amaranth, which appears to have helped in their domestication. The presence of single male flower per glomerule and about 250 female flowers per inflorescence in grain amaranth has been of an advantage for their exploitation as grain. The presence of very large, closely set compound terminal inflorescence with many branches, held well above the leafy stems, have enabled greater grain yield although seed size has not improved. It yields about 500000 seeds/plant (Sauer, 1967).

2.1.3 Cytological studies

Darlington and Wylie (1955) reported the chromosome number in 13 species of *Amaranthus.* Grant (1959) has tabulated the information available on chromosome number of 30 species of *Amaranthus.* Pal (1964) reported chromosome compliment for four species of *Amaranthus* and one interspecific hybrid. The chromosome number of few important species are given below.

Species	Chromosome No.	Reference (s)
Amaranthus edulis Speg.	2n = 32	Covas (1950)
A. caudatus	2n = 32	Grant (1959), Takagi (1933), Murray (1940)
A. dubius	2n = 64	Grant (1959), Pal (1964)
A. hypochondriacus	2n = 32	Grant (1959), Murray (1940)
A. cruentus L.	2n = 34	Grant (1959)

It is seen from the above table that with exception of one tetraploid speices *A. dubius,* all the species so far examined have a diploid number of either 32 or 34 chromosomes.

In a recent study, Mallika (1988), reported that members of section *Blitopsis* had a basic chromosome compliment of 17, while section *Amaranthus* had 16 and 17. The polyploid nature of *A. dubius* has also been confirmed.

Greizerstein and Poggio (1992) studied the meiotic behaviour of six interspecific hybrids of Amaranthus. Hybrids between species with n = 16 chromosomes showed regular meiosis with 16 bivalents; they varied considerably in pollen viability (5 - 60 %) which suggested the existance of cryptic structural hybridity. The structural divergence between *A. quitensis* (2n = 32) and the grain species *A. caudatus* (2n = 32) and *A. hypochondriacus* (2n = 32) was higher than that observed between *A. quitensis* (2n = 32) and the wild species *A. hybridus* (2n = 32). Pollen viability of *A. hybridus* (2n = 32) x *A. quitensis* (2n = 32) hybrid was lower than that observed in its parents which suggested that there was some degree of reproductive isolation and consequently that they were not co-specific. The *A. cruentus* (2n = 34) x *A. quitensis* (2n = 32) hybrid showed 15 II + 1 HI in all cells. This supported the hypothesis that n = 17 had its origin in a n = 16 ancestor through primary trisomy.

In (1995), Greizerstein and Poggio studied the meiotic behaviour of 13 spontaneous Fi hybrids between *Amaranthus* spp. The hybrids between the species with n = 16 chromosomes had 16 bivalents but varied considerably in pollen stainability (0-55 %). These results suggested the existance of cryptic structural hybridity. The hybrids involving *A. cruentus* (n = 17) and speices with n = 16 *(A. caudatus* and *A. quitensis)* always formed 15 II + 1 III with very low pollen stainability (5-7 %). Further observations indicated that *Amaranthus* spp. are allotetraploids with basic numbers of X = 8 and

X = 9 but exhibit X = 16 and X = 17 as secondary basic numbers as demonstrated by the frequent presence of 8 II and 17 I in meiosis of the hybrid *A. spinosus* (n = 17) x *A.hybridus* (n = 16) and the occurance of secondary associations between bivalents in M I. Genomic formulae are proposed for each species on the basis of the meiotic behaviour of the hybrids studied.

2.2 Correlation and path coefficient analysis

/ The method of partitioning the correlation coefficients in to direct and indirect effects of the independent characters was outlined by Wright (1921). Dewey and Lu (1959) gave the detailed procedure for path analysis in the case of replicated trials, which was quite a different technique in eliminating the environmental variance.

2.2.1 Correlation and path analysis in Amaranth

Hauptli and Jain (1980) observed positive correlation of late maturity, tallness with yield in *A. cruentus.*

Rangaswami *et al.* (1980) observed that the genotypic correlation was higher than phenotypic correlations during April and July seasons in 1976. However, in respect of number of leaves per plant and weight of stem the relationship got reversed i.e. phenotypic correlation was higher than genotypic in April as compared to July sowing. The direct effect of length of stem on yield as shown by path analysis also was reversed in April season as compared to July season.

Mathai and Ramchandra (1981) studied correlation and causation effects in sixty seven genotypes of amaranthus. Girth of stem was positively correlated with height and yield. The major components that exerted maximum influence on yield-were grftkand plant height.

Kadar and Muthukrishnan (1979) observed highly significant positive correlations between yield of greens and stem weight, leaf weight, stem diameter, leaf length, plant height and leaf breadth.

Kadar and Muthukrishnan (1981) reported a highly significant negative correlation of leaf/stem ratio with yield of greens. Thus, the leaf/stem ratio deserved little importance as selection critierion in improvement of yield of greens in Amaranthus. Due to the negative association of leaf/stem ratio with yield, the high yielders had low leaf/stem ratio and *Vice versa.*

Pandey (1981a) studied the association of six varieties and their possible Fis and F2S in *A. hypochondriacus* L. at phenotypic and genotypic level. Grain yield showed positive correlation with number of panicles per plant, length of panicle and plant height for all generations.

Pandey (1981b) worked out path coefficients in *A. hypochondriacus* by evaluating ten characters. Plant height had the greatest direct effect on the number of panicles per plant, followed by days to maturity and grain yield per plant. Length of panicle associated with seed yield per plant, indicating that selection for heavier heads would result in higher grain yield.

Devadas *et al.* (1993) evaluated twelve red and eleven green leaf vegetable amaranth genotypes for various yield components. Red types tended to have broader and longer leaves and fewer branches. They also took longer to bolt and had more nodes and were taller at bolting than green types. Red types proved superior for leaf yield due to their ability to sustain a greater number of harvest.

Pawar (1995) reported significant positive correlation between number of branches per plant, length of inflorescence and girth of inflorescence with grain yield. These characters also exhibited positive direct and indirect effects via number of other yield components suggesting their importance while selecting for improvement in grain yield.

Batta *et al.* (1996) studied forage production of Amaranthus spp. on the Indian sub-continent. They reported high positive correlation of plant height with leaf area and suggested that due emphasis should be given to these traits.

^ Jamriska (1996) studied the correlation between the stand density, height, length of inflorescence and 1000 seed weight. A positive correlation between stand density, height and length of inflorescence was relatively the most stable and strongest.

Mahajan (1998) reported a significant correlation between nitrate reductase (NR) activity in leaves and grain protein content. He identified cultivars with higher protein and NR activity such as AG-114 and Rasana-2 could be used for breeding high protein grain genotypes.

2.3 Concept of genetic diversity

The concept of D^2 statisticsfor measuring the divergence between two populations was introduced by Mahalanobis (1936). D^2 statistic gives a result based on the magnitude of divergence and is independent of size of sample.

Mahalanobis *et al.* (1949) employed D^2 statistics in a detailed study of Anthropometric data of Uttar Pradesh classifying 23 groups into three major clusters. With Brahmin (B-cluster) at the top of Hindu social heirarchy comprising nine groups, the Artisan (A-cluster) in the middle consisting of four groups and the Trival (T-cluster) at the botton consisting of ten groups.

Moll *et al.* (1962) reported no relationship between geographical distribution and genetic diversity as reflected in heterosis between crosses in maize. Heterosis in maize appeared to be increased with the increased genetic divergence of the parental populations over a rather wide range of diversity.

Moll *et al.* (1965) observed that heterosis increased with increase in divergence among the parents within the restricted range but extreamly divergent crosses resulted in decreased heterosis.

According to Burnaby (1966) D^2 statistic is a sum of squares of differences between corresponding mean values of two sets of suitably weighted measurements.

Murty and Arunachalam (1966) stated that a change in the breeding structure could bring about a substantial change in character association and the patterns of distribution of genetic variability. Geographical distribution and genetic diversity could not be directly related in many of the crops examined by them. Genetic drift and selection in different environments may cause greater diversity than geographic diversity.

2.3.1 Genetic divergence and variability in Amaranth

Hauptli and Jain (1980) observed wide variation in flowering time, plant height, seed yield in *A. cruentus* L.

Rangaswamy *et ah,* (1980) studied genetic evaluation and path analysis in 19 different vegetable amaranth genotypes. The variation was high in length of stem and weight of plants followed by number of leaves. All the characters offered scope for selection in that order mentioned only, as inferred from estimates of H and GA.

Kadar and Muthukrishnan (1982) studied variability in germplasm of vegetable amaranthus (A. *tricolor* L.) under different seasons. The range, mean and coefficient of variation for different characters, were generally high and showed decrease in mansoon as compared to summer season. The genotypic coefficients of variation were high for weight of stem, leaf/stem ratio, yield of grains and weight of leaves. The heritability estimates were generally high for different traits studied. High heritability estimates associated with high genetic advance were obtained for weight of stem, leaf/stem ratio, yield of greens and weight of leaves, indicating the usefulness of phenotypic selection for these traits.

y Pandey (1982) in his work on genetics of agronomic traits in *A. hypochondriacus* reported the estimates of genetic variance and heritability for plant height, panicle length and pollen fertility revealed both additive and dominance variances in the expression of traits studied.

Hauptli (1984) partitioned the diversity for three amaranth species and revealed approximately equal variability within and between species components. In study of several quantitative traits in 15 selfed families from each of six diverse population, mean squares between populations were high and significant for all the traits implying high intra population diversity.

Vaidya (1984) evaluated ten land races of Amaranthus from two states of India in the green houses for genetic variation in quantitative and qualitative characters. He observed significant differences for quantitative characters among the populations. Differences in family variances were significant for all quantitative characters. Population fell into distinct regional groups with possible exceptions of two populations.

Fatocun (1985) studied 40 accessions from 12 countries using cluster analysis and principal component analysis. Accessions formed 6 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.

Joshi (1986) in the study of 20 genotypes of *A. hypochondriacus* observed wide variability for height, number of leaves per plant, leaf length and width, inflorescence length, number of spiklets 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.

/ Tilekar (1986) studied variability and diversity in 105 strains of *A. cruentus.* The estimates of GCV, PCV, heritability and GA revealed plant height and days to 50 per cent flowering as the most important characters for improvement. These strains were grouped into 20 clusters. Clustering pattern of the strains does not follow the geographic distribution.

Varalakshmi and *Rgddy* (1994) studied variability and correlations in 25 vegetable amaranthus lines during summer 1993. Information on variation, heritability and correlations was derived from the data on 12 leaf yield components. Variation, heritability and genetic advance were high for number of leaves, leaf weight, stem weight, leaf stem ratio and yield of greens per plant.

Goptsii and Voronkov (1994) studied diversity in various accessions (varieties and species) of amaranthus from Russia and USA. Particular attention was paid to the type of inflorescence that would give maximum seed yield. The accessions useful for high competitive ability were *A. hybridus* from Mali and *A. hypochondriacus* from Mexico. Two cycles of mass selection in an A. *hybridus* population gave a form that ripened 7-10 days earlier than the base population and equalled it in yield. Interspecific crosses were also useful in breeding, especially between *A. hybridus* and *A. cruentus.*

Joshi and Rana (1995) studied genetic divergence in 20 diverse genotypes grown during kharif 1991 and 1992. 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, infloresence length, spikelets/spike, leaf length and number of leaves.

^ Pawar (1995) collected the data on ten important yield components measured on fifty genotypes evaluated during Rabi-1993. The D^2 statistic showed that there was adequate diversity among the genotypes with D^2 values ranging from 6.84 to 1807.98. On the basis of D^2 values, the fifty genotypes studied, were grouped into sixteen clusters. Clustering pattern of these genotypes did not necessarily follow the geographical distribution. Using meteroglyph analysis, fifty genotypes were grouped into fourteen clusters.

z 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 fresh weight of plant, fresh weight of inflorescence, rachis/ inflorescence, grain yield followed by dry weight of stem, stem girth at collar region and plant height. High heritability coupled with moderate genetic advance was observed for plant height and days to 50 per cent 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 fresh weight of inflorescence, rachis/inflorescence and stem girth at collar region indicating the importance of both additive and non additive gene action for these characters.

x Okeno and Avftecbo (1996) studied electrophoretic variation of esterase (Est.) peroxidase (Per.), phosphoglucoisomerase (Pgi) and phosphoglucomutase (Pgm) in seven Amaranthus populations of A. *hypochondriacus, A. coudatus, A. emeritus, A tricolor* and *A. hybridus.* There was variation among the cultivars for Est banding pattern. Although heterozygosity was observed for some allozymes, homozygosity was prevalent for Est. Per and Pgm showed less variation with a high degree of homozygosity. All *A. hypochondriacus* population had similar alleles for Per and Pgm. Heterozygosity was noted for one Per isoenzyme in population of *A. caudatus.* One of the Pgi isoenzymes showed homozygosity, while for the other isoenzymes there was heterozygosity in all the cultivars except *A. tricolor* and *A. hybridus.*

/ Chan and €ao (1997) examined genetic diversity and relationships of 23 cultivated and wild Amaranthus species using both isoenzyme and RAPD markers. A total of 30 loci encoding 15 enzymes were resolved and all were polymorphic at the interspecific level. High levels of inter accessional genetic diversity were found within species, but genetic uniformity was observed within most accessions. The evolutionary relationships between grain amaranths and their putative ancestors were investigated, and both the RAPD and isoenzyme data sets supported a monophyletic origin of grain amaranthus, with A. *hybridus* as the common ancestor. A complementary approach using information from both isoenzymes and RAPDs was shown to generate more accurate estimates of genetic diversity, and of relationships within and among crop species and their wild relatives than either data set alone.

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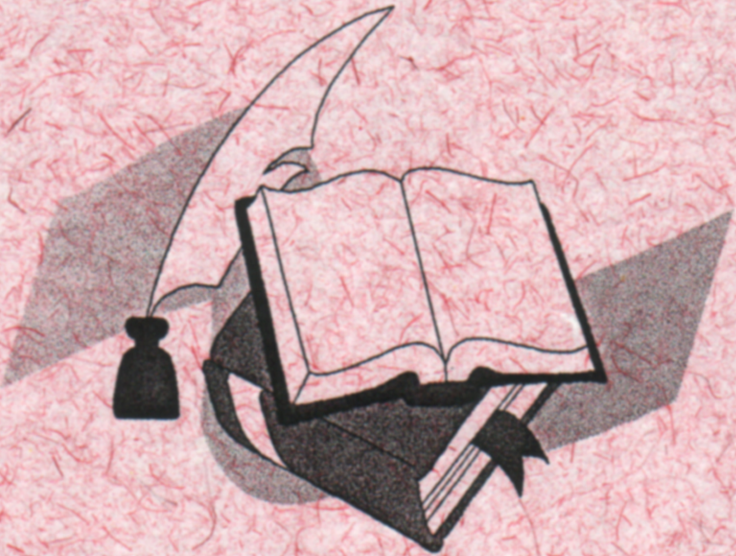

MATERIAL AND METHODS

3. MATERIAL AND METHODS

The present investigation on genetic divergence and path analysis for grain yield and its components in grain amaranthus (A. *hypochondriacus* L.) envisaged the studies on

1. Correlations
2. Path analysis
3. Genetic diversity by D^2 statistics

The details of the material used, methods adopted and statistical analysis followed during the course of this investigation are described below.

3.1 Experimental material

Fifty genotypes of grain Amaranthus originating from different geographical regions (Table 1) and showing phenotypic variability for different agronomic and yield characters were used. The seeds were supplied by the Plant Breeder, AICRP on under utilized and under exploited plants, M.P.K.V., Rahuri.

3.2 Experimental design

Fifty genotypes of Amaranthus were evaluated in a Randomised Block Design (RBD) with three replications during kharif, 1997 at the Post Graduate Institutional **farm** of the Department of Botany, Mahatma Phule Krishi Vidyapeeth, Rahuri, Maharashtra. Each genotype was evaluated in two rows of four meter length in each replication. j^s P ^C 7^

I* (Rahuri]* § "7^-^/382—

Table 1. List of genotypes with their origin used for study

Sr. No.	Genotype	Origin/source	Sr. No.	Genotype	Origin/source
1.	IC-1491	NBPGR, Akola	26.	IC-35526	Rajastan and M.P.
2.	IC-1493	——do——	27.	IC-35527	- - d o -
3.	IC-6646	——do——	28	IC-35532	——do——
4.	IC-21810	Madhya Pradesh	29.	IC-35544	——do——
5.	IC-21925	——do——	30.	IC-35556	——do——
6.	IC-21966	——do——	31.	IC-35580	——do——
7.	IC-32190	NBPGR, Akola	32.	IC-35588	——do —
8.	IC-32193	——do——	33.	IC-35589	——do——
9.	IC-32195	——do——	34.	IC-35625	——do——
10.	IC-35196	„ **-do——**	35.	IC-35633	- do——
11.	IC-35366	Gujarat	36.	IC-35634	——do——
12.	IC-35367	——*do*——	37.	IC-41991	NEH, Shillong
13.	IC-35385	——do —	38.	IC-81710	NBPGR, Akola
14.	IC-35397	——do——	39.	IC-93942	——do——
15.	IC-35402	——do——	40.	IC-93945	- do
16.	IC-35409	——do——	41.	IC-95254	Himachal Pradesh
17.	IC-35416	——do——	42.	IC-95266	——do——
18.	IC-35431	——do——	43.	IC-95381	——do——
19.	IC-35436	——do——	44.	IC-120618	Uttar Pradesh
20.	IC-35470	——do——	45.	IC-120626	——do——
21.	IC-35475	——do——	46.	IC-120661	„ **_do——**
22.	IC-35500	——do——	47.	RGAS 92-10-1	MPKV, Rahuri
23.	IC-35503	——do——	48.	GA-1	Gujarat
24.	IC-35524	Rajastan and M.P.	49.	Suvarna	Karnataka
25.	IC-35525	„ **_do——**	50.	Annapurna	Himachal Pradesh

The row to row spacing was 45 cm, while the plant to plant spacing was 15 cm. The crop was sown on medium black soil on 9th July, 1997, under vapsa condition after irrigation. A light irrigation was given after sowing. The seed was hand sown at shallow depth to get good stand. The plot was fertilized @ 40 kg N, 40 kg P_2O_5 and 20 kg K_2O/ha, irrigated and weeded twice. One month after sowing, 40 kg N/ha was given as top dressing.

3.3 Observations recorded

Data was recorded on five randomly selected plants in each treatment, in each replication on ten characters as described below and averages were worked out.

1. Days to 50 per cent flowering

Number of days from sowing to the date when 50 per cent plants in each plot flowered was recorded.

2. **Days to maturity**

Number of days from sowing to maturity of the crop was recorded.

3. \ **Plant height at flowering (cm)**

The height of the plant was measured in cm from base of stem at soil surface upto the tip of the inflorescence.

4. **Number of spikelets per inflorescence**

The spikes are present on inflorescence in alternate manner. All the spikelets comprising the inflorescence were counted.

5. Length of inflorescence (cm)

Length of inflorescence was measured from the first spikelet on inflorescence upto the top of the inflorescence.

6. **Girth of inflorescence (cm)**

The thread was wrapped around the inflorescence at middle and its length in cm was recorded as girth of the inflorescence.

7. **Grain yield per plant (g)**

The grain yield of each of the five individual plants was recorded and the average calculated represented yield per plant (g).

8. **Leaf area per plant (cm^2)**

It was measured on randomly selected three plants in each plot at initiation of flowering stage on automatic leaf area meter, and averages were worked out.

9. **50 ml volume seed weight (g)**

The seeds were taken in 50 ml measuring cylinder and seed quantity was weighed.

10. **Grain oil content** (%)

The oil content from the grains was worked out with the NMR (Nuclear Magnetic Resonance) machine.

3.4 Statistical methodology

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).

The genotypic mean squares (GMS) were tested for their significance against error mean squares (EMS) by "F test for m = (g-1) and *m* = (r - 1) (g -1) degrees of freedom.

Where,

g = Number of genotypes and

r = Number of replications

The characters showing significant differences were only subjected to further analysis

b. **Estimation of mean and range**

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

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

Where,

X = Mean of character

XXi = Total of all the observations for character and

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 by using the respective mean squares from variance table (Johnson *et al.,* 1955) as below.

Environmental variance 6^2e = EMS

$$\text{Genotypic variance } 6^2g = \frac{\text{GMS - EMS}}{r}$$

Phenotypic variance $6^2p = 6^2g + 6^2e$

Where,

GMS = Genotypic mean sum of squares

EMS = Error mean sum of squares and

r = Number of replications

d. **Estimation of coefficient of variation**

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

i. Genotypic coefficient of variation (GCV)

$$\text{GCV} = \frac{}{X} \text{xlOO}$$

Where,

6^2g = Genotypic variance and X = Mean of character

ii. Phenotypic coefficient of variation (PCV)

$$PCV = \frac{\sim}{X} x1OO$$

Where,

6^2p = Phenotypic variance and

X = Mean of character

e. **Estimation of heritability**

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

$$h2 = \frac{}{6^2p} x\ 100$$

Where,

6^2g = Genotypic variance

6^2p = Phenotypic variance

The high, medium and low heritability estimates were classified as per Robinson (1966) as

Low = Below 10 %

Moderate = 10-30 %

High = Above 30 %

f. **Genetic advance (GA)**

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

i. $$GA = K\ x \frac{6^2g}{6^2p} x\ \wedge \overline{6^2p}$$

Where,

6^2g = Genotypic variance

6^2p = Phenotypic variance

K = Selection differential (At 5 % selection **intensity,** the value of K = 2.06)

ii. GA as percentage of mean

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

Where,

GA = Genetic advance

X = Character mean

3.4.2 Corrlelation

Analysis of covariance was carried out by taking two characters at a time. The genotypic covariances were then calculated as per the formulae discribed by Singh and Chaudhari (1977) as below.

Environmental covariance (Cov.e-1.2) = EMP

$$\text{Genotypic covariance (Cov.gi.2)} = \frac{\text{GMP - EMP}}{r}$$

Phenotypic covariance (Cov.pi.2) = [Cov.gi.2] + [Cov.ei.2]

The appropriate variances and covariances were used for calculating phenotypic and genotypic correlation coefficients (Johnson *et ah,* 1955).

The phenotypic correlation coefhceint (rp) was calculated as.

$$_{r}p_{12} = \frac{Gov.\ pi.2}{\wedge / (6 » \ .\ (6^2p_2)}$$

Where,

rpi.2 = Phenotypic correlation coefficient between character land 2

Cov.Pi 2 = Phenotypic covariance between character 1 and 2.

6^2pi & 6^2p2 = Phenotypic variance of character 1 and 2 respectively.

The significance of the phenotypic correlation coefficient was tested by refering to Fisher and Yates (1943) table.

The genotypic correlation coefficient (rg) was calcualted as

$$\frac{Cov.\ gi\ 2}{J(62gi) \bullet (6^2g_2)}$$

Where,

rgi ? = Genotypic correlation coefficient between character 1 and 2

Cov.gi.2 = Genotypic covariance between character 1 and 2.

6^2gi & 6^2g? = Genotypic variance of character 1 and 2 respectively.

The significance of correlation was tested by ^{s}t' test

3.4.3 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 Scwall Wright (1921).

The second step in the 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 Xi, X2, X3 and these component showed following type of association with each other.

Y C ^———-X2

t ^ ^ ^ ^ - X 3)

R

In path diagram the yield is the result of Xi, X2, X3 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 Pij.

Path coefficients were obtained by solving a set of simultaneous equation of the form.

Tny ~ I ny + r_n2P2y + r_n3P3y + ...

Where,

r_{ny} = represents the correlation between one component and yield, P_{ny} represents path coefficient between that character and yield and r_n2 represents correlation between that character and each of the other components in turn.

r_{1y}	rn	ri2	rw	••••	ri_n
r_{2y}	*T21*	T22	T23	....	' r2n
	r_ni	**r_n2**	**r_n3**	**....**	**1**

Matrix-A Matrix-B

Where,

ri2 - r2i and so on and $n_{y/}$ correlation between one component character and yield. The B matrix was inverted (B^{-1}) and path coefficient (Pij) were obtained as

(Pij) = A x (B-i)

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

Indirect effects = rij x Pij

Where,

i = 1 to 9

j = 1 to 9

Pij = Ply *Ply*........Pny

Path coefficient (Pij) correlation coefficient (rij) and residual factors (R) were diagramatically presented. The residual factor i.e. variation in yield unaccounted for by these associations was calculated with the following formula.

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

Where,

R^2 = Ply riy + P2y T2y + ...+ Pny r_{ny}

Where,

Pi $_y$, P2y........Pny = Path values

n $_y$, *riy*........r_{ny} = Correlation coefficients

3.4.4 Genetic divergence

D^2 analysis

The analysis of divergence was carried out by D^2 statistic of Mahalnobis' (1936) as described by Rao (1952). Analysis of variance for the individual characters studied was worked out as per RBD to test the significance of differences among the genotypes as described under section 3.4.1. The characters exhibiting significant differences were only used for further analysis of D^2 statisitc. The analysis of co-variance for character pairs, based on plot averages was carried out (Chocharan and Cox, 1957).

a. Wilk's criterion

After testing the difference between the populations for the ten characters, a simultaneous test of significance of differences in the mean values of a number of correlated variables with regard to the pooled effect of the eight characters considered together was carried out using Wilk's criterion (Wilks, 1932) which was estimated using the relationship that

$$A = \frac{| E |}{I\ E + V\ |}$$

Where,

| E | was the determinant of the experimental error sum of squares and sum of products matrix and J E + V |, the determinant of experimental error sum of squares and product matrix. Significance of Wilks A criteria was estimated by X^2 as .

$$X^2pq = V = -m \log e A$$

Where,

$$m = n - \frac{P + q + 1}{2}$$

n = Ni + ...NK-1

= Total number of obs. - 1

P = Number of characters

q = K-l

K = Number of genotypes

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

The generalized distance between any two populations is defined as

$$A^2 = 11\ Aij\ 5iSj$$

Where,

Aij = Reciprocal matrix to the common disperison matrix

5i = Difference between the mean values of the two populations for the i^{th} character

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

D^2 = I Z S^{ij}) di dj

Where,

$S^{1'}$ is the sample estimate of *Xij* and di of 5i.

Since this formula for computation requires inversion of eighth order determinant and then evaluation of 8(8+l)/2 terms whose sum is D^2.

c. **Computation of D^2 values**

For each combination D^2 was calculated.Thus, total 50(49)/2 number of D^2 values were worked out.

d. **Determination of population constellations**

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

A simple device or method suggested by Tocher (Rao, 1952) for cluster formation is to start with two closely related groups and find third group which had the smaller average D^2 from the first two. Simillarly, the fourth group is chosen to have the smaller average D^2 value from the first three and so on. While proceeding further for the cluster formation, if at any stage, the average D^2 value of a group appears to be high than those already listed, then this group does not fit in that former group and is to be taken out side of that cluster.

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

e. **Average intra-cluster distances**

The intra-cluster distances were calculated as

IDi^2/n

Where,

X Di^2 = Sum of distances between all possible combinations of genotypes included in a cluster.

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 II between I and III, between I and IV and so on. Likewise the clusters were taken one by one and the distances between other clusters were calculated as :

$lDi^2/(ninj)$

Where,

ni = Number of genotypes in cluster i and

nj = Number of genotypes in cluster j

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

g. **Cluster diagram**

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

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EXPERIMENTAL RESULTS

4. EXPERIMENTAL RESULTS

The results obtained in the present investigation are presented below.

4.1 Genetic variability and heritability

4.1.1 Analysis of variance

The analysis of variance presented in Table 2, revealed that mean squares due to genotypes were significant indicating that the genotypes under evaluation different significantly for all the characters studied.

Table 2. Analysis of variance for different characters studied

Sr. No.	Characters	M.S.S. Genotype	M.S.S. Error
	D.F.	49	98
1.	Days to 50 % flowering	34.139**	3.982
2.	Days to maturity	174.461**	72.508
3.	Plant height	903.03**	426.255
4.	Inflorescence length	152.333**	56.296
5.	Inflorescence girth	34.861**	18.551
6.	Number of spikelets/ infloresence	152.635**	8.612
7.	Leaf area/ plant	91941.56**	22202.94
8.	50 ml volume seed weight	23.043**	0.2335
9.	Grain oil content (%)	0.2180*	0.00014
10.	Grain yield/plant	46.454**	2.756

*, ** = Significant at 5 % and 1 % level, respectively.

4.1.2 Mean performance and the range of variability

The mean values of genotypes for different characters studied are presented in Table 3, while the estimates of range are given in Table 4.

4.1.2.1 Days to 50 per cent flowering

The variation in days to 50 per cent flowering ranged between 51.67 (IC-120661) to 68 days (IC-35436 and IC-35450). IC-120626 (52.33) was also promising for earliness in flowering.

4.1.2.2 Days to maturity

The variation in days to maturity ranged between 83.67 days (Suvarna) to 112.33 days (IC-32195).

4.1.2.3 Plant height of flowering (cm)

The plant height was maximum (164.60 cm) in case of IC-32190, while it was minimum (68.73 cm) in case of IC-120661.

4.1.2.4 Length of inflorescence (cm)

The mean length of inflorescence among the genotypes studied ranged from 24.06 (Annapurna) to 52.93 cm (IC-21966).

4.1.2.5 Girth of inflorescence (cm)

The mean girth of the inflorescence ranged from 13.80 cm (IC-95266) to 29.00 cm (IC-21966).

4.1.2.6 Number of spikelets/inflorescence

The mean number of spiklets per inflorescence ranged from 26.13 (IC-21925) to 55.40 (IC-21966).

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4.1.2.7 Leaf area/plant *(cm²)*

The mean leaf area per plant ranged from 675.87 (IC-95266) to 1559.60 cm^2 (IC-32190).

4.1.2.8 50 ml volume seed weight (g)

The variation in 50 ml volume seed weight was observed between 32.08 (Suvarna) to 44.76 gram (IC-35524).

4.1.2.9 Grain oil content (%)

The variation in the crude fat content was observed between minimum of 3.05 per cent in case of IC-93945 and maximum of 9.28 per cent in case of IC-35475.

4.1.2.10 Grain yield per plant (g)

The range for grain yield per plant was between 10.93 g (IC-32195) to 26.64 g (IC-32190). The genotype IC-21966 (25.38), IC-35475 (24.52) and IC-35500 (24.40) were at par at 5 per cent level with the highest yielding genotype IC-32190 (26.64).

4.1.3 Estimates of components of variation

The estimates of genotypic (6^2g), phenotypic (6^2p) and environmental (6^2e) variances for different characters studied are presented in Table 4. The magnitude of genotypic variance was the highest for leaf area per plant (23246.210), followed by plant height at flowering (158.925) and number of spikelets per plant (48.008). The phenotypic variances, however ranged between 0.073 to 45449.15. The highest estimate was for leaf area per plant foUwed by plant height (585.180), days to maturity (106.493). The environmental

Table 4. Estimation of range, genotypic (6^2g), phenotypic (6^2p), environmental (6^2e) variances, genotypic (GCV), phenotypic (PCV) coefficients of variation,, heritability and genetic advance (GA) for various characters studied

Sr. No.	Character	Range	62g	6^2p	6^2e	GCV	PCV	Heritability (B.S.) (%)	GA	GA as per cent of mean
1.	Days to 50 % flowering	51.67-68.00	10.052	"14.034	3.982	4.96	5.86	71.60	5.52	8.64
2.	Days to maturity	83.67-112.33	33.984	106.493	72.509	5.95	10.53	31.90	6.78	6.92.
3.	Plant height *(cm)*	68.73 -164.60	158.925	585.180	426.255	10.15	19.48	27.20	13.53	10.89
4.	Length of inflorescence (cm)	24.06 - 52.93	32.012	88.309	56.296	14.86	24.68	36.30	7.01	18.41
5.	Girth of inflorescence (cm)	13,80 - 29.00	5.437	23.988	18.552	10.45	21.95	22.70	2.28	10.21
6.	Number of spikelets/ inflorescence	26.13 - 55.40	48.008	56.620	8.612	16.59	18.01	84.80	13.14	31.46
7.	Leaf area/plant (cm^2)	675.87-1559.60	23246.210	45449.150	22202.940	15.88	22.21	51.10	224.62	23.40
8.	50 ml. volume seed weight (8)	32.08 - 44.76	7.603	7.837	0.234	7.02	7.12	97.00	5.59	14.23
9.	Grain oil content (%)	3.05 - 9.28	0.073	0.073	0.000	10.47	10.47	99.80	0.55	21.26
10.	Grain yield/plant (g)	10.93-26.64	14.566	17.322	2.756	22.66	24.71	84.10	7.20	42.75

a b c d e f g h i j

Characters

HGCV *WFCV*

a. Days to 50 per cent flowering

b. Days to maturity

c. Plant height (cm)

d. Inflorescence length (cm)

e. Inflorescence girth (cm)

f. No.of spikelets/ Inflorescence

g. Leaf area/plant (cm)

h. 50 ml volume seed weight (g)

i. Grain oil content (%)

j. Grain yield/plant (g)

Fig. 1. GCV and PCV

variances ranged between 0.000 to 22202.940, maximum again being for leaf area per plant followed by plant height. The characters, days to 50 per cent flowering, number of spikelets per inflorescence, 50 ml volume seed weight, grain oil content and grain yield per plant exhibited lower values of environmental variance (0.00 to 8.612).

4.1.4 Genotypic and phenotypic coefficients of variation

The estimates of genotypic and phenotypic coefficients of variation are presented in Table 4 and depicted in Fig. 1.

The least genotypic coefficient of variation (4.96) was exhibited by the character, days to 50 per cent flowering, while it was the highest (22.66) in the case of grain yield per plant followed by number of spikelets per inflorescence (16.59), leaf area per plant (15.88), inflorescence length (14.86), oil content (10.47), inflorescence girth (10.45), plant height (10.15).

In general, the phenotypic co-efficients of variation were greater than the genotypic coefficients of variation. The least phenotypic co-efficient of variation (5.86) was observed in case of days to 50 per cent flowering and it was the highest (24.71) in case of grain yield per plant, followed by inflorescence length (24.68), leaf area per plant (22.21), inflorescence girth (21.95), plant height (19.48), numberof spikelets per inflorescence (18.01).

4.1.5 Heritability and genetic advance

The estimates of heritability in broad sense are presented in Table 4 and depicted in Fig. 2. The range for heritability is from 22.70 (girth of infloresence) to 99.8 per cent (oil content).

It is evident that almost all the characters showed high heritability (greater than 30 per cent) except infloresence girth (22.70) and plant height (27.20) which show moderate heritability estimate.

The range of genetic advance was between 0.55 (oil content) to 224.62 (leaf area) with the highest estimate in case of leaf area per plant followed by plant height at flowering (13.53) number of spikelets per inflorescence (13.14) grain yield per plant (7.20). The highest genetic advance as per cent of mean was observed for grain yield per plant (42.75), which was followed by number of spikelets per inflorescence (31.46), leaf area per plant (23.40), grain oil content (21.26). However, its estimate was the lowest (6.92) for days to maturity.

It is evident from the Fig. 2 that heritability and genetic advance as per cent of mean were higher for grain yield per plant, number of spikelets per inflorescence, leaf area per plant. However, days to 50 % flowering, 50 ml volume seed weight and grain oil content had high heritability but comparitively lower estimates of genetic advance.

Girth of inflorescence had lower estimates of both heritability and genetic advance.

d e f g i J

Characters

M Heritability H Expected GA over mean

a.	Days to 50 per cent flowering	b.	Days to maturity
c.	Plant height (cm)	d.	Inflorescence length (cm)
e.	Inflorescence girth (cm)	f.	No.of spikelets/ Inflorescence
g.	Leaf area/plant (cm^2)	h.	50 ml volume seed weight (g)
i.	Grain oil content (%)	j.	Grain yield/plant (g)

Fig. 2. Heritability estimates and expected genetic advance over mean

4.2 **Correlation** studies

Correlation coefficients at both, genotypic and phenotypic levels estimated for all possible combinations among the variables under study are presented in Table 5.

4.2.1 Association of grain yield with its components

The perusal of Table 5 revealed strong positive correlation between grain yield per plant with plant height at flowering (0.729), length of inflorescence (0.717), number of spikelets per inflorescence (0.731), leaf area per plant (0.977), grain oil content (0.436) at genotypic level it had positively significant correlation with girth of inflorescence at genotypic level only but non-significant correlation at phenotypic level. Days to maturity is negatively correlated with grain yield, both at genotypic and phenotypic level. Days to 50 % flowering, 50 ml volume seed weight had non-significant positive correlation, both at genotypic as well as phenotypic level.

4.2.2 Inter relationship of yield components

Days to 50 per cent flowering was strongly and positively correlated with grain oil content, both at genotypic and phenotypic level. Whereas it had positively significant correlation with days to maturity, number of spikelets per inflorescence at genotypic level only. It had also positive but not significant correlation with plant height at flowering, length of inflorescence, girth of inflorescence, leaf area per plant, 50 ml volume seed weight at both the levels.

Table 5. Genotypic and phenotypic correlation coefficients

Sr. No.	Characters	Days to maturity	Plant height at flowering (cm)	Inflorescence length (cm)	Inflorescence girth (cm)	No.of spikelets/ inflorescence	Leaf area (cm^2)	50 ml volume seed weight (g)	Grain oil content (%)	Grain yield/ plant (g)
1.	Days to 50 % flowering	0.352* (0.122)	0.128 (0.071)	0.180 (0.071)	0.145 (0.018)	0.295* (0.246)	0.193 (0.073)	0.025 (0.030)	0.520** (0.442)**	0.201 (0.172)
2.	Days to maturity		-0.566** (-0.273)	-0.578** (-0.295)*	-0.477** (-0.185)	-0.604** (-0.326)*	-0.536** (-0.305)*	-0.315* (-0.170)	-0.267 (-0.147)	-0.538** (-0.263)
3.	Plant height at flowering (cm)			1.000** (0.469)**	0.791** (0.234)	0.956** (0.500)**	0.805** (0.488)**	0.034 (-0.001)	0.494** (0.259)	0.729** (0.353)*
4.	Length of inflorescence (cm)				0.889** (0.286)*	0.843** (0.491)**	0.746** (0.453)**	0.164 (0.108)	0.471** (0.271)	0.717** (0.415)**
5.	Girth of inflorescence (cm)					0.736** (0.293)*	0.361** (0.218)	0.171 (0.093)	0.584** (0.281)*	0.447** (0.179)
6.	No.of spikelets/ inflorescence						0.849** (0.584)**	0.272 (0.248)	0.569** (0.525)**	0.731** (0.642)**
7.	Leaf area (cm^2)							0.167 (0.126)	0.301* (0.212)	0.977** (0.655)**
8.	50 ml. volume seed weight (gm)								0.294* (0.289)*	0.216 (0.199)
9.	Grain oil content (%)									0.436** (0.400)**

*, ** = Significant at 5 % and 1 % respectively.
(Figures in parenthesis are phenotypic correlation coefficients)

Days to maturity showed strong negative association with length of inflorescence, number of spiklelets per inflorescence, leaf area per plant,. While it had shown negative but non-significant association with plant height at flowering, girth of inflorescence, 50 ml volume seed weight and grain oil content, at phenotypic level only.

Plant height at flowering had significant positive correlation with length of inflorescence, number of spikelets per inflorescence, leaf area per plant, both at phenotypic as well as genotypic level. Whereas it had significant positive correlation with girth of inflorescence and grain oil content at genotypic level only. It had also positive nonsignificant correlation at genotypic level but negative correlation at phenotypic level with 50 ml volume seed weight.

It had been observed that the length of inflorescence had shown significant positive correlation with girth of inflorescence, number of spikelets per inflorescence, leaf area per plant, both at genotypic and phenotypic level and with grain oil content at genotypic level only. It had positive but non-significant correlation with 50 ml volume seed weight both at phenotypic as well as genotypic level.

The girth of inflorescence had shown significantly positive correlation with number of spikelets per inflorescence, grain oil content, both at genotypic as well as phenotypic level and with leaf area per plant at genotypic level only. It had also shown the positive but non-significant correlation with 50 ml volume seed weight, both at phenotypic as well as genotypic level.

The number of spikelets per inflorescence had shown strong association with leaf area per plant, grain oil content, both at genotypic as well as phenotypic level. Whereas it had shown positive but non-significant correlation with 50 ml volume seed weight, both at genotypic and phenotypic level.

There was a positive but non-significant correlation between leaf area per plant with 50 ml volume seed weight, both at phenotypic as well as genotypic level. It had significant correlation with grain oil content only at genotypic level. The 50 ml volume seed weight had also positive significant correlation with oil content, both at phenotypic as well as genotypic level. Also the grain oil content had shown strong correlation with most of these characters, both at genotypic and phenotypic level.

4.3 Genotypic path coefficient analysis

The genotypic correlation coefficients being important, were only further partitioned into direct and indirect effects which are presented in Table 6 and depicted in Fig. 4.

a. Days **to** 50 % **flowering**

The days to 50 per cent flowering had negative direct effect (-0.520) on grain yield. Its indirect effects *via* days to maturity, girth of inflorescence, leaf area per plant and grain oil content were

Table 6. Direct and indirect effects of nine causal variables ongrain yield in Amaranth

Sr. No.	Characters	Days to 50% flowering	Days to maturity	Plant height at flowering (cm)	Infloresc ence length (cm)	infloresc ence girth (cm)	No.of spikelets /inflores cence	Leaf area (cm 2)	50 ml volume seed weight	Grain oil content (%)	Genotypic correlation with yield/ plant
1.	Days to 50 % flowering	-0.520	0.137	-0.319	-0.047	0.316	-0.321	0.676	-0.008	0.287	0.201
2.	Days to maturity	-0.183	0.389	1.403	0.152	-1.038	0.658	-1.881	0.109	-0.147	-0.538
3.	Plant height at flowering	-0.067	-0.220	-2.481	-0.270	1.724	-1.041	2.824	-0.012	0.272	0.729
4.	Infloresence length	-0.093	-0.225	-2.542	-0.264	1.938	-0.918	2.618	-0.057	0.260	0.717
5.	Infloresence girth	-0.075	-0.185	-1.964	-0.234	2.179	-0.801	1.266	-0.059	0.322	0.447
6.	No.of spikelets/ infloresence	-0.153	-0.235	-2.373	-0.222	1.603	-1.089	2.980	-0.094	0.314	0.731
7.	Leaf area/plant (cm*)	-0.100	-0.208	-1.996	-0.197	0.786	-0.924	3.510	-0.058	0.166	0.977
8.	*50* ml volume seed weight (g)	-0.013	-0.123	*-0.085*	-0.043	0.373	-0.296	*0.587*	^347	0.162	0.216
9.	Grain oil content (%)	-0.271	-0.104	-1.225	-0.124	1.272	-0.620	1.057	-0.102	0.552	0.436

Resiclual effect = -0.4633427, Underlined figiares denolte direct e fects

X} = Days to 50 V» flowering

X2 = Days to maturity

X3 s Plant height (cm)

X4 ' Inflorescence length (cm)

X5 -Inflorescence girth (cm)

Xg = No. of spikelets / inflo.

X7 =Leaf area C cm^2)

X_s s 50 ml. volume seed weight

Xg soil content (°/o 3

X^o* Grain yield /plant (g)

Fig.3 Path diagram (Genotype)

positive whereas it had negative contribution through plant height at flowering, number of spikelets per infloresence and 50 ml volume seed weight.

b. Days to maturity

The days to maturity had positive direct effect (0.389) on grain yield. Its indirect effects *via* plant height at flowering, length of inflorescence, number of spikelets per inflorescence, 50 ml volume seed weight were positive and higher in case of first character. It had negative indirect effects through days to 50 per cent flowering, girth of inflorescence, leaf area per plant and grain oil content.

c. **Plant height at flowering**

The plant height at flowering had negative direct effect (-2.481) on grain yield. Its indirect effects *via* girth of inflorescence, leaf area per plant and grain oil content were positive and was higher for second character. Its indirect effects *via* remaining all the characters were negative.

d. Length of inflorescence

The length of inflorescence had negative direct effect (-0.264) on grain yield. Its indirect effect *via* girth of inflorescence, leaf area per plant and grain oil content were positive and higher for the first one. It had negative indirect effect through remaining all the characters.

e. Girth of inflorescence

The girth of inflorescence had positive direct effect (2.179) on grain yield. Its indirect effects through leaf area per plant and grain oil content were positive while remaining all the characters had negative indirect effects.

f. Number of spikelets per inflorescence

The direct effect of number of spikelets per plant was negative (-1.089), whereas its indirect effects through girth of inflorescence, leaf area per plant and grain oil content were positive. Its indirect effects through remaining characters were however, negative.

g. **Leaf** area **per plant**

There was positive direct effect (3.510) of leaf area per plant on grain yield and was the highest among all the characters. Its indirect effects through girth of inflorescence and grain oil content were also positive. However, its indirect effects through rest of the characters were negative.

h. 50 ml volume seed weight

The 50 ml volume seed weight had negative direct effect (-0.347) on grain yield. Its indirect effects through the girth of infloresence, leaf area per plant, and the grain oil content were positive. Whereas its indirect effects through rest of the characters were negative.

i. Grain oil content

The direct effect of grain oil content (0.552) on grain yield was positive. It had also positive indirect effects *via* girth of inflorescence, leaf area per plant. Whereas its indirect effects through days to 50 per cent flowering, days to maturity, plant height at flowering, length of inflorescence, the number of spikelets per inflorescence, and 50 ml volume seed weight were negative.

The residual path effect was -0.463, indicating that characters studied were sufficient to express the relationship with grain yield per plant.

4.4 Genetic divergence

4.4.1 Mahalanobis's generalised distance (D^2)

Wilk's criterion showed significant differences between the genotypes for pooled effect of ten characters studied (Wilk's criteria, X^2 = 2713.3 for 490 d.f.). Hence the analysis was further extended to calculate D^2 values. The D^2 values for all the possible pairs of comparison between 50 genotypes are presented in Table 7. The calculated D^2 values ranged from 7.13 to 14758.63, the lowest value being the pair of strains, IC-35416 and IC-35431 and the highest between IC-35475 and IC-93945.

4.4.2 Clustering pattern of the strains

The clustering pattern obtained on the basis of magnitude of D^2 values studied is presented in Table 8. The 50 strains were grouped into eleven clusters. The cluster I consisted the highest

458.22/34	458.64/41
608.39/11	485.99/6
827.71/44	599.98/44
827.71/44	599.98/44
892.20/30	605.93/30
946.00/28	631.58/28
997.88.16	667.50/16
1055.53/32	718.08/32
1109.98/10	784.74/9
1144.82/9	818.19/10
1283.64/49	961.88/22
1464.46/22	1111.05/5
1520.10/5	1169.25/49
1637.28/7	1240.87/26
1707.47/26	1245.39/42
1804.23/42	1330.20/7
2223.84/29	1829.04/29
2432.54/2	1983.82/2
99/45	2502.92
/23	2734.72
/39	2950.86

Genotypes D^2 values	U	y 35367	y 353[illegible]	IC-35397	y [illegible]	y 35409	U 35416	IC-35431	IC-3,5436	U 35470
n	[illegible]	0.00/12	0.00/'	JO/14	0.00/	0.00/16	0.00/17	0018	0.00	0020
CS	[illegible]	9.99/25	[illegible]	.43/4	[illegible]	76/30	7.13/18	7.13/17	19.46/8	28/25
CO	[illegible]	33.30/34	[illegible]	71/37	[illegible]	04/32	7.21/35	7.67/35	38.06/31	20/19
*f	[illegible]	31/18	66/	.37/8	[illegible]	44/28	23/13	01/33	51.3 7/3	73/18 1
in	[illegible]	63/13	20/	.76/3	45/	95/10	92/33	66/13	52.3	3/1
NO	[illegible]	03/17	63/	07/31	06/	65/41	65/37	19/37	84.88/37	.38/8
IN	[illegible]	30/33	42/	40/43	[illegible]	.24/9	62/47	31/12	88.20/20	2/3
00	[illegible]	01/35	[illegible]	10/15	20/	80/44	19/36	42/25	94.41/14	7/3
ON	[illegible]	85/41	34/	95/27	69/	43/5	03/12	22/34	122.5 7/43	2/3
O ri	[illegible]	55/37	34/	41/19	120	108 .13/26	15/25	44/47	129.69/4	7/3
n ri	[illegible]	100 83/20	36/	49/35	140	.01/22	47/34	62/36	147.0 2/18	1/0
CS ri	[illegible]	119 .14/44	108	101 .25/17	158	119 .09/34	06/15	.67/8	156.2 7/48	1/0
CO	[illegible]	148 .04/30	140	105 .59/18	166	L98/7	.00/4	73/20	165.1 2/35	2/3
if n	[illegible]	92/47	[illegible]	.42/47	173.31	.21/42	.25/14	100.95/4	192.3 2/17	24/14
m ri	[illegible]	.18/36	[illegible]	.30/48	182.21,	.87/12	.05/24	105.59*14	219.16/25	1.26/3
NO r-i	[illegible]	188 .35/28	163.86	149 .69/24	238	204 .15/33	124.73/8	120 .07/15	229.22/33	3/2
tN ri	[illegible]	87/16	164.04	175 .10/13	245.80	208 .54/25	139.67/11	147 .02/19	239.92/12	.49/4
00 ri	[illegible]	/96/8	[illegible]	.16/25	[illegible]	.33/13	.30/41	.11/41	259.60/13	[illegible]
ON ri	[illegible]	.91/14	[illegible]	.24/20	[illegible]	.52.11	.10/20	.71/24	266.50/47	[illegible]
O CS	299.46.	50/11	180.93/	.95/36	[illegible]	.19/17	.32/19	.49/11	279.88/15	[illegible]
n CS	03.04/	31/32	185.12	.91/12	[illegible]	.65/18	.94/44	.91/31	320.00/1	[illegible]
rs CS	[illegible]	229 68/10	187	208 .03/33	285	287 .00/49	238 .08/30	218 .40/44	323.48/34	2/4
co CN	[illegible]	230.76/4	[illegible]	278.80/1	[illegible]	[illegible]	247.13/31	3.21.3	357.33/36	[illegible]
rf CN	[illegible]	238.40/15	[illegible]	283.85/34	[illegible]	[illegible]	252.13/43	.53/30	357.61/24	[illegible]
in CN	[illegible]	239.92/19	[illegible]	349.50/11	[illegible]	[illegible]	256.02/3	.98/43	412.78/6	[illegible]

997.88/3
1017.40/43
1064.46/27
1343.05/48
1473.95/38
1791.36/1
2011.08/46
2063.58/6
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Genotypes D² values	U 358	U 35588	y 355	y 35625	U 35633	y 35634	y [illegible]	y [illegible]	y 33942	U 945
[illegible]	10/31	0.00/	0.00/	0.00/34	0.00/35	0.00/36	0.00/	[illegible]	0.00/39	0.00/40
[illegible]	37/3	21.76,	23.01/	30.24/33	7.21/17	30.97/47	26.71,	[illegible]	67.65/23	465.05/50
[illegible]	[illegible]	[illegible]	72/	21/25	7.67/18	02/24	[illegible]	270.54/	125.95/2	824.80/46
[illegible]	[illegible]	[illegible]	[illegible]	30/12	28/33	19/17	31.002	319.69/	134.44/45	3/3
[illegible]	[illegible]	[illegible]	[illegible]	38/41	02/37	49/35	[illegible]	334.60/	196.64/29	8/3
[illegible]	[illegible]	[illegible]	92/	22/18	20/13	65/11	[illegible]	416	202.85/38	9/2
[illegible]	[illegible]	[illegible]	[illegible]	42/13	06/47	45/15	[illegible]	449.55/	341.53/46	7/4
[illegible]	[illegible]	[illegible]	34/	31/35	49/36	62/18	[illegible]	477.96/	384.53/26	2917.55/2
[illegible]	[illegible]	[illegible]	44/	47/17	01/12	44/33	[illegible]	898	474.68/5	5/2
[illegible]	[illegible]	[illegible]	52/	19/44	31/34	36/13	[illegible]	922.35/	519.88/42	7/2
[illegible]	[illegible]	[illegible]	39/	85/30	60/25	.37/34	[illegible]	1063.41	539.42/7	4123.43/7
[illegible]	[illegible]	[illegible]	27*	01/28	.51/4	127.65/37	[illegible]	1091	617.06/50	5/4
[illegible]	[illegible]	33/	122	117.37/36	69/15	33.25/4	[illegible]	1235	704.81/10	4304.10/5
[illegible]	[illegible]	[illegible]	143	119.09/16	49/14	.18/12	[illegible]	1251	.67/9	5/2
[illegible]	[illegible]	31/	148	144.88/32	101.64/8	.27/25	101	1351.96	770.88/22	7/1
[illegible]	[illegible]	233.24/13	171.73,	[illegible]	[illegible]	189.54/41	107.96/3	[illegible]	[illegible]	4911 36/49
[illegible]	[illegible]	253.05/7	175.51	[illegible]	[illegible]	197.95/14	112.42/20	[illegible]	[illegible]	4981.67/9
[illegible]	[illegible]	256.37/25	182.21,	[illegible]	[illegible]	255.90/8	126.33/27	[illegible]	[illegible]	5122 78/32
[illegible]	[illegible]	[illegible]	185	159.59/47	165.12/19	267.77/30	127	1528	871.19/28	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	168.13/9	.07/41	.01/28	[illegible]	1535	.05/30	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	168.71/11	.76/43	.08/16	[illegible]	1551	61/44	[illegible]
[illegible]	[illegible]	[illegible]	.15,	259.81/15	224.32/31	302.28/43	149	1557	1109.97/41	4/4
[illegible]	[illegible]	63/	208	268.88/8	1.17/3	319.67/44	228	1784.63/	1480.55/34	3/4
[illegible]	[illegible]	[illegible]	[illegible]	271.08/24	.52/44	.91/20	[illegible]	2227	1715.68/12	25/3
[illegible]	[illegible]	[illegible]	[illegible]	281.99/4	.87/27	.11/32	[illegible]	2418	1727.59/33	19/1

Table 7. Contd ...

Genotypes D² values	IC-95254	IC-95266	IC-95381	IC-120618	IC-120626	IC-120661	RGAS-92-10-1	GA-1	Suvania	Annapurna
[illegible]	0.00/41	0.00/42	0.00/43	0.00/44	0.00/45	0.00/46	0.00/47	0.00/48	0.00/49	0.00/50
[illegible]	14.81/30	71.73/5	41.70/48	27.18/30	95.77/23	236.96/50	28.43/24	41.70/43	160.54/44	236.96/46
[illegible]	[illegible]	71.73/5	41.70/48	27.18/30	95.77/23	236.96/50	[illegible]	41.70/43	[illegible]	236.96/46
[illegible]	[illegible]	115.93/22	61.27/3	27.88/10	156.64/2	341.53/39	[illegible]	55.35/3	[illegible]	465.05/40
[illegible]	[illegible]	134.39/9	74.40/27	32.13/28	266.49/29	402.52/23	[illegible]	60.38/1	[illegible]	617.06/39
[illegible]	[illegible]	170.52/32	79.40/14	45.80/16	270.51/26	428.77/45	[illegible]	91.93/31	[illegible]	739.29/23
[illegible]	[illegible]	187.63/28	90.04/8	57.62/32	318.42/42	766.99/2	[illegible]	138.83/8	[illegible]	1001.06/45
[illegible]	[illegible]	189.21/16	104.61/31	61.18/9	377.85/5	824.80/40	[illegible]	140.30/14	[illegible]	1159.92/2
[illegible]	[illegible]	240.98/10	122.57/19	75.19/34	428.77/46	960.30/29	[illegible]	143.03/4	[illegible]	1265.73/29
[illegible]	[illegible]	255.86/30	127.74/37	119.14/12	477.96/38	1268.04/26	[illegible]	151.15/6	[illegible]	1884.33/26
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	503.49/22	[illegible]	[illegible]	[illegible]	305.22/9	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	513.58/7	[illegible]	[illegible]	[illegible]	365.25/26	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	572.18/9	[illegible]	[illegible]	[illegible]	370.12/2	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	589.74/32	[illegible]	[illegible]	[illegible]	375.04/12	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	600.52/10	[illegible]	[illegible]	[illegible]	376.27/25	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	638.66/16	[illegible]	[illegible]	[illegible]	385.11/34	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	704.53/28	[illegible]	[illegible]	[illegible]	416.04/2	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	734.99/30	[illegible]	[illegible]	[illegible]	499.89/20	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	839.59/44	[illegible]	[illegible]	[illegible]	519.52/33	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	895.83/41	[illegible]	[illegible]	[illegible]	541.58/13	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	910.84/49	[illegible]	[illegible]	[illegible]	604.10/18	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1001.06/50	[illegible]	[illegible]	[illegible]	663.85/17	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1248.23/34	[illegible]	[illegible]	[illegible]	671.84/22	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1326.86/11	[illegible]	[illegible]	[illegible]	687.59/35	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1464.44/12	[illegible]	[illegible]	[illegible]	706.03/42	[illegible]

Table 7 c< X3

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Genotypes D² values	IC-95254	IC-95266	IC-95381	IC-120618	IC-120626	IC-120661	RGAS-92-10-1	GA-1	Suvarna	Annapurna
[illegible]	292.02/37	722.64/25	480.73/34	349.49/29	1474.70/33	3329.06/12	367.41/48	704.79/34	[illegible]	4155.75/25
[illegible]	315.94/42	727.19/17	517.01/11	381.50/37	1490.91/13	3382.15/33	378.01/28	780.86/11	848.94/23	4270.46/33
[illegible]	387.67/24	755.82/35	739.95/41	387.49/47	1529.88/25	3405.94/25	387.49/44	1077.62/41	870.41/39	4317.85/13
[illegible]	390.76/15	763.65/18	898.00/44	448.39/2	1594.27/36	3422.60/13	401.82/16	1169.00/44	872.96/11	4356.15/11
[illegible]	458.64/4	817.64/47	921.49*30	548.24/8	1690.01/17	3632.81/36	443.77/32	1230.34/30	889.64/36	4690.54/18
[illegible]	464.16/14	896.29/24	942.44/28	550,48/15	1723.40/18	3741.23/17	482.62/9	1259.14/28	910.84/445	4704.72/17
[illegible]	464.42/8	1008.02/15	1017.40/16	553.64/24	1757.42/35	3768.88/18	538.34/10	1343.05/16	946.64/47	4748.28/36
[illegible]	469.15/19	1067.27/37	1066.95/32	583.32/14	1878.91/47	3836.72/35	594.45/22	1388.63/32	972.55/19	4811.58/35
[illegible]	534.33/19	1096.44/20	1127.85/9	599.98/4	2069.80/20	4061.44/47	621.84/1	1478.63/9	973.79/8	4829.82/20
[illegible]	541.00/2	1245.39/4	176.45/10	604.18/19	2078.79/24	4122.43/20	744.60/5	1502.82/10	1073.73/14	5180.85/47
[illegible]	663.67/31	1251.92/38	1397.11/22	751.14/31	2162.31/37	4355.90/24	817.67/42	1771.43/49	1091.92/38	5386.81/37
[illegible]	713.36/3	1356.58/14	1493.20/5	827.71/3	2191.75/15	4412.81/37	835.35/26	1813.83/22	1138.42/31	5583.92/24
[illegible]	739.95/43	1366.62/8	1515.10/19	839.59/45	2407.77/40	4502.66/15	858.70/6	1914.75/5	1169.25/4	5689.34/15
[illegible]	765.65/27	1382.31/46	1684.08/42	860.53/27	2502.92/4	4937.89/4	925.73/21	2133.11/26	1174.42/15	5965.05/8
[illegible]	895.83/45	1510.91/19	1712.42/26	892.11/23	2588.14/14	5005.80/8	946.64/49	2154.10/7	1235.26/24	6050.32/14
[illegible]	995.44/23	1684.08/43	1793.46/7	898.00/43	2607.04/8	5019.28/14	984.92/7	2155.02/42	1283.64/3	6079.98/4
[illegible]	1017.62/48	1771.68/31	2346.73/29	966.61/39	2768.44/19	5180.84/19	1381.54/29	2788.15/29	1305.45/27	6083.06/19
[illegible]	1109.97/39	1804.23/3	2509.82/2	1169.00/48	3060.67/31	5609.57/31	1499.10/2	3004.55/2	1515,10/43	6561.83/31
[illegible]	1405.66/1	1874.89/27	3144.98/45	1535.95/38	3144.98/43	5781.30/3	1878.91/45	3726.28/45	1771.43/48	6809.95/3
[illegible]	1648.69/6	2155.02/48	[illegible]	1602.54/1	3169.99/3	5809.93/43	[illegible]	3996.76/23	2089.92/46	6915.86/27
[illegible]	1784.63/38	2221.76/50	[illegible]	1817.29/6	3256.28/27	5898.70/27	[illegible]	4200.41/39	2252.80/1	7015.04/43
[illegible]	2020.11/21	2740.11/1	[illegible]	2295.22/46	3726.28/48	6579.01/48	[illegible]	5343.56/38	2355.80/6	7784.93/48
[illegible]	2460.70/46	3191.72/6	[illegible]	2304.92/21	4467.18/1	7550.37/1	[illegible]	6579.01/46	2386.60/50	8801.97/1
[illegible]	3219.29/50	3378.29/21	[illegible]	2925.89/50	4907.36/6	8060.49/6	[illegible]	7784.93/50	3204.14/21	9211.29/6
[illegible]	5902.63/40	4240.45/40	[illegible]	5559.34/40	5371.12/21	8771.27/28	[illegible]	11776.37/40	4911.36/40	10321.37/21

Table 8. Composition of the strains in different clusters

Cluster	Number of strains included	Name of the genotypes included
I	20	IC-35416, IC-35431, IC-35633, IC-35385, IC-35589, IC-41991, RGAS-92-10-1, IC-35634, IC-35367, IC-35525, IC-35625, IC-35402, IC-21810, IC-35397, IC-35524, IC-32193, IC-35366, IC-95254, IC-35470, IC-35436
II	7	IC-6646, IC-35580, IC-35527, GA-I, IC-95381, IC-1491, IC-21966
III	10	IC-32195, IC-35532, IC-35588, IC-35409, IC-120618, IC-35556, IC-35196, IC-21925, IC-35526, IC-95266
IV	5	IC-1493, IC-35544, IC-32190, IC-35503, IC-93942
V	2	IC-120661, Annapurna
VI	1	IC-35475
VII	1	IC-35500
VIII	1	IC-81710
IX	1	IC-93945
X	1	IC-120626
XI	1	Suvarna

number of strains i.e. twenty, followed by cluster III with 10 strains. Cluster II had 7 strains while cluster IV had 5 strains. The cluster V had 2 strains while clusters VI, VII, VIII, IX, X and XI were single clusters. Thus, these clusters were solitary in regard to the multivariate compositions.

4.4.3 Intra and inter cluster divergence

The average intra and inter clusters D^2 and D values are prersented in Table 9 and 10, respectively. The maximum statistical distance (D) was found between the clusters VI and IX (121.48), followed by clusters II and IX (107.53), V and VI (97.70), I and IX (90.04), VI and VIII (86.96), II and V (83.83). An examination of intra cluster divergence among the eleven clusters revealed that cluster V had maximum intra cluster distance (D = 15.39) followed by the cluster IV (14.15) and II (13.16), while the intra cluster distance among the strains of cluster III was the lowest (9.67). As the clusters VI, VII, VIII, IX, X andXI were solitary, there was no intra cluster divergence. The mutal relationship among the clusters has been diagramatically shown in Fig. 4.

4.4.4 Cluster means for different characters

The cluster means for the ten characters studied are presented in Table 11. A considerable inter cluster variation is seen among the cluster means for the characters, plant height, days to maturity, girth of inflorescence, number of spikelets per inflorescence, leaf area per plant, and grain yield per plant. The

Table 9. Inter and intra cluster D^2 values

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	161.01	456.82	512.79	1501.57	4422.80	1113.90	652.96	3081.25	8108.80	1851.20	752.84
II		173.27	1536.62	3132.28	7027.87	348.22	1802.05	5176.81	11563.08	3676.10	1660.37
III			93.67	441.20	2191.59	2739.76	270.28	1332.70	4911.00	564.69	318.90
IV				200.24	966.57	4864.65	491.1	457.42	2858.3	333.38	518.92
V					236.96	9546.32	2178.5	302.57	644.92	714.91	2238.26
VI						0	2839.09	7562.63	14758.63	5371.12	3204.14
VII							0	1551.08	4835.35	503.49	671.84
VIII								0	1396.33	477.96	1091.92
IX									0	2407.77	4911.36
X										0	910.84
XI											0

Table 10. Average inter and intra cluster D values

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	12.68	21.37	22.64	38.75	66.50	33.37	25.55	55.50	90.04	43.02	27.43
II		13.16	39.19	55.96	83.83	18.66	42.45	71.95	107.53	60.63	40.74
III			9.67	21.00	46.81	52.34	16.44	36.50	70.07	23.76	17.85
IV				14.15	31.08	69.74	22.16	21.38	53.46	18.25	22.77
V					15.39	97.70	46.67	17.39	25.39	26.73	47.31
VI						0	53.28	86.96	121.48	73.28	56.60
VII							0	39.38	69.53	22.43	25.91
VIII								0	37.36	21.86	33.04
IX									0	49.06	70.08
X										0	30.18
XI											0

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Table 11. Cluster means for characters studied

Cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	Infloresence length (cm)	Inflorescence girth (cm)	No.of spikelets /inflo.	Leaf area (cm^2)	50 ml volume seed weight (g)	Grain oil content	Grain yield/ plant
I	64.88	96.91	129.09	39.57	23.64	44.11	959.80	40.13	7.35	17.05
II	64.43	94.90	134.32	38.33	23.44	45.31	1023.96	38.53	8.44	19.29
III	64.09	99.98	118.52	37.35	20.69	37.17	889.85	39.83	6.24	14.47
IV	65.39	102.13	121.89	37.13	19.84	41.23	1040.01	37.80	5.35	18.39
V	57.33	99.83	90.46	32.99	19.69	34.16	782.74	36.95	4.01	13.72
VI	64.00	97.33	142.33	47.00	25.86	51.40	133 5.40	43.59	9.28	24.52
VII	66.33	95.67	138.60	39.46	26.86	49.13	1320.00	44.15	6.09	24.40
VIII	58.67	105.33	95.33	30.20	15.53	31.00	721.95	32.79	4.60	11.91
IX	57.00	110.67	93.46	35.86	21.46	30.73	747.63	36.16	3.05	12.15
X	52.33	91.00	113.20	35.60	21.13	37.33	828.83	41.10	5.11	13.89
XI	62.67	83.67	127.13	30.13	22.06	42.86	1001.88	32.08	6.25	14.79

cluster meas for plant height ranged from 90.46 to 142.33 cm, the highest and lowest values being for the clusters V and VI respectively. The cluster mean for days to maturity was maximum (110.67), in the case of cluster IX and minimum in the cluster XI (83.67). The maximum cluster mean for girth of inflorescence was observed in case of cluster VII (26.86) which is a single variety cluster and minimum in case of cluster VIII (15.53). The single variety cluster VI exhibited the highest number of spikelets per inflorescence (51.40), while the lowest in case of cluster IX (30.73). The maximum cluster mean for leaf area per plant was observed in case of cluster VI (1335.40), while the minimum in case of cluster VIII (721.95). Also the cluster mean for grain yield per plant was maximum for the cluster VI (24.52) followed by cluster VII (24.40) and was minimum for the cluster VIII (11.91).

The cluster means for days to 50 per cent flowering ranged from 52.33 to 66.33, with the highest and lowest values forthe clusters VII and X, respectively. The cluster means for length of inflorescence varied from 30.13 to 47 with the highest and lowest values for the clusters VI and XI, respectively. Also, there is a variation in the cluster means for 50 ml volume seed weight from 32.08 to 44.15, with highest and lowest values for the clusters VII and XI, respectively. The cluster means for oil content ranged from 3.05 to 9.28, maximum in case of cluster VI and minimum in case of cluster IX.

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DISCUSSION

5. DISCUSSION

Plant breeding deals with the management of genetic variability. Hence its assessment in the available germplasm is of immense value to design a suitable selection procedure, its scope and to identify the superior genotypes. It is therefore necessary to study the nature and magnitude of the genetic diversity systematically for its exploitation in genetic upgradation of biological population. Similarly the assessment of the magnitude and direction of associations between different yield contributing characters especially with yield is also useful in selecting desirable genotypes on the basis of their phenotypic values. Simple correlation coefficients, in this direction are of limited value. Hence, it is important to study the cause and effect relationship between yield and its component characters.

In the present investigation, fifty diverse genotypes of Amaranth from various parts of the country were therefore, assessed to know the nature and magnitude of genetic diversity among them and to study correlations between ten metrical characters and direct and indirect effects of component characters on grain yield. The results obtained on these aspects are presented in chapter four and discussed here under appropriate sub-heads.

5.1 Variability and genetic parameters

5.1.1 Range of variability

A wide range of variability was observed in respect of days to maturity (83.67 to 112.33 days), plant height (68.73 to 164.60 cm), inflorescence length (24.06 to 52.93 cm) inflorescence girth (13.80 to 29 cm), number of spikelets per inflorescence (26.13 to 55.40), leaf area per plant (675.87 to 1559.60 cm^2), grain oil content (3.05 - 9.28 %) and grain yield per plant (10.93 to 26.64 g). This indicated an ample scope for exploitation of the above traits. Hauptli (1984) and Hauptli and Jain (1984) and Rangaswamy *et al.*, (1980) also reported ample variability for various components in Amaranth. The characters like days to 50 per cent flowering, days to maturity and 50 ml volume seed weight however, exhibited comparatively less variability.

5.1.2 Genotypic and phenotypic coefficient of variation

Genetic variability in the material with which the breeder is working is the basis for any successful breeding programme. It is therefore, essential to know the genetic component of variation before variability can be utilized for further genetic improvement in crop plants. Additive genetic variation is the heritable portion of total variation. Genotypic and phenotypic coefficients of variation are important in this respect.

In the present study, higher estimates of genotypic and phenotypic coefficients of variation were observed for grain yield per plant (22.66 and 24.71, respectively) (Table 4) followed by leaf area 4 per plant (15.88 and 22.21 respectively), length of inflorescence (14.86 and 24.68, respectively) and number of spikelets per inflorescence (16.59 and 18.01, respectively), indicating more variability and scope ^ for selection in improving these traits.

Joshi (1986) showed a wide range of variability for plant height, number of leaves per plant, leaf length, leaf width, inflorescence length, number of spikelets per plant, days to maturity, 1000-seed weight, popping size, protein content and seed yield per plant in grains amaranths.

Pawar (1995) observed higher estimates of genotypic and phenotypic coefficients of variation for number of branches per plant followed by grain yield per plant and leaf area per plant in Amaranth.

Lohithaswa *et al.* (1996) reported considerable amount of phenotypic and genotypic variability for fresh weight of the plant, fresh weight of the inflorescence, number of rachis per inflorescence, grain yield followed by dry weight of the stem, stem girth at collar region and plant height in grain amaranthus.

Other characters *viz* days to 50 % flowering (4.96, 5.86), 4, days to maturity (5.95, 10.53), plant height (10.15, 19.48), girth of inflorescence (10.45, 21.95), 50 ml volume seed weight (7.02, 7.12), and grain oil content (10.47, 10.47) indicated low to medium genotypic and phenotypic coefficients of variation, respectively showing limited scope for selection in these traits.

The estimates of genotypic and phenotypic coefficients of variation were nearly equal in case of days to 50 per cent flowering, 50 ml volume seed weight, grain oil content, number of spikelets per inflorescence and grain yield per plant indicating that the variability existing in these characters was due to genetic factors and there is less influence of environmental factors in the expression of these characters.

5.1.3 Heritability (B.S.) and genetic advance

The genotypic co-efficient of variation alone does not indicate the proportion of total heritable variation. The heritability estimates are better indicator in this respect. High heritability indicates the effectiveness of selection based on phenotypic performance but does not necessarily mean a high genetic gain for a particular character (Swarup and Chaugule, 1962). Consideration of both, heritability and genetic advance, is more important for predicting effectiveness of the selection than heritability alone.

The variation in the characters with high heritability estimates associated with high genetic gain may be attributed to additive gene effects and can easily be improved by selection (Panse, 1957). On the other hand, the traits exhibiting high heritability and low genetic gain may be governed by the non-additive gene effects (dominance and epistasis). The characters showing such inheritance can be improved through hybridization. The low heritability estimates suggest that selection for such characters will not be much effective.

According to heritability classification of Robinson (1966), the characters grain oil content (99.80), 50 ml volume seed weight (97.00), number of spikelets per inflorescence (84.80), grain yield per plant (84.10), days to 50 per cent flowering (71.60) and leaf area per plant (51.10) expressed high heritability while days to maturity, plant height, length of inflorescence, girth of inflorescence expressed moderate heritability estimates. Joshi (1986) reported the high heritability estimates and expected genetic advances for 1000-seed ^ weight, inflorescence length and plant height.

The characters *viz* grain yield per plant, grain oil content, number of spikelets per inflorescence, leaf area per plant and length of inflorescence expressed high estimates of heritability in broad sense accompanied with high genetic advance (as percentage of mean) (Table 4, Fig. 2) indicating that these traits are governed by additive gene action and selection for these traits in the genetically diverse material would be more effective for desired genetic improvement. Rangaswamy *et ah* (1980) reported high heritability and genetic advance for plant height. Verma (1989) also reported high heritability and genetic advance for grain yield and number of ears per plant. Pawar (1995) reported higher heritability and genetic advance as per cent of mean for plant height at flowering, number of branches per plant, number of spikelets per plant, leaf area per plant and grain yield per plant in grain amaranthus. Also Lohithaswa *et al.* (1996) observed high heritability coupled with moderate genetic advance for plant height and days to 50 per cent flowering in grain amaranthus.

The characters days to 50 per cent flowering, days to maturity, and 50 ml volume seed weight exhibited high heritability accompanied with lower genetic gain suggesting that variability for these characters are governed by non-additive gene action indicating the limited scope for improving these characters through phenotypic selection.

Thus, considering the estimates of genetic parameters like genotypic coefficient of variation, heritability and genetic advance together, it is evident that length of inflorescence, number of spikelets per inflorescence, leaf area per plant, grain oil content and grain yield per plant are the most important characters. Selection for these traits in could be more effective for improving grain yield in Amaranth.

5.2 Correlation

In the improvement of any crop, yield is the most important character that has to be taken into account. Grain yield is a multiplicative product function of yield attributing plant components. The grain yield production in a plant is an integrated contributory effect of different growth and yield components which are differentially influenced by an array of factors. The knowledge of inter relationship among the characters especially with yield is therefore, useful to the plant breeder for improving the efficiency of selection programme. The phenotypic correlation indicates the extent of observed relationship between two characters. This does not give a true genetic picture of the relationship, because it indicates the effect of both genetic as well as the environmental influences. Genotypic correlation provides an estimate of an inherent association between genes controlling any two characters. Hence it is of greater significance and can be utilized in formulating an effective selection scheme. The estimates of correlation coefficients may also help to identify the characters that prove to be of little or no importance in selection programme.

In the present investigation, the genotypic correlation coefficients were higher than phenotypic correlation co-efficients between most of the characters studied (Table 5). This indicated that there was a strong inherent association between the various characters studied and the genotypic expression of the correlation was comparatively less influenced by environmental variations.

A significant, positive association was observed between grain yield per plant and plant height at flowering, length of inflorescence, number of spikelets per inflorescence, leaf area per plant and grain oil content, both at genotypic and phenotypic levels. However, grain yield per plant was positively correlated with girth of inflorescence at genotypic level only. Aoong *et al.,* (1992) reported strong correlations between head weight, head length and seed yield per plant. Pawar (1995) reported strong positive correlation between grain yield per plant with number of branches per plant, length of inflorescence and girth of inflorescence, in amaranthus. Days to 50 per cent flowering and 50 ml. Volume seed weight had positive but non-significant correlation with grain yield, indicating that it had no inherent relationship with grain yield. Pandey (1981a) and Hauptli and Jain (1984) and Tilekar (1986) reported positive but nonsignificant correlation between number of panicles per plant, length of panicle and plant height with grain yield. However, there was negative but significant correlation between days to maturity and grain yield. Hauptli and Jain (1984) and Pawar (1995) reported negative correlation between the grain yield and days to 50 per cent flowering which is in contradiction with the present findings.

Days to 50 per cent flowering had highly significant positive correlation with grain oil content both at phenotypic and genotypic level, indicating that there is certain inherent relationship between these characters.

The days to maturity had shown significant, negative correlation with all the characters studied excluding oil content indicating that there was reverse relationship among these characters. Pawar (1995) reported the similar results.

The plant height at flowering showed significant, positive genotypic correlation with the length of inflorescence girth of inflorescence, number of spikelets per inflorescence, leaf area per plant, oil content and grain yield. Hauptli and Jain (1984) and Tilekar (1986) also observed the positively significant correlation of plant height with grain yield.

Positive, significant correlations of length of inflorescence with girth of inflorescence, number of spikelets per inflorescence, leaf area per plant, oil content and grain yield per plant, at genotypic level. The girth of inflorescence had significant positive correlation with number of spikelets per inflorescence leaf area, per cent oil content and grain yield. Number of spikelets had significant positive correlation with leaf area, grain oil content and grain yield per plant. The leaf area had significant positive correlation with per cent oil content and grain yield per plant. The 50 ml volume seed weight had positive significant correlation with per cent oil content and had significant positive correlation with grain yield.

Thus, from the critical perusal of the data in Table 5, the characters *viz* plant height at flowering, length of inflorescence, girth of inflorescence, number of spikelets per inflorescence and leaf area were significantly positively correlated with grain yield per plant and each other. Therefore, the desirable plant type in grain amaranth with high grain yield potential should have more plant height, more length of inflorescence, more girth of inflorescence and more number of spikelets per inflorescence and more leaf area per plant. Pandy (1981b) and Tilekar (1986) proposed that selection on the basis of number of panicles per plant, length of panicle and plant height would be more effective in this crop. Pawar (1995) suggested that the desirable plant type in grain amaranth with high grain yield potential should have more number of spikelets per plant, more length and more girth of inflorescence. >

5.3 Path coefficient analysis

Plant breeders have to deal with correlated characters durng the improvement programmes. Grafius (1959) expressed his opinion that there may not be genes for yield *per se,* rather there could be genes which govern the inheritance of component characters. Therefore, rapid improvement in yield is expected to result if selection is practised for component characters. Rate of improvement is expected to be rapid if differential emphasis is laid on the component characters during selection. The basis of differential emphasis could be the degree of influence of component characters on the economic character of interest. Thus, it provides a base to the breeder for designing the most effective selection criterion based on a few reliable component characters.

In the present study leaf area per plant had the highest positive direct effect (3.510) on grain yield per plant followed by girth of inflorescence (2.179), grain oil content (0.552) and days to maturity (0.389). Leaf area per plant had higher indirect effect through girth of inflorescence which has resulted in moderately high positive correlation between leaf area per plant and grain yield per plant.

Hence, increase in leaf area per plant and girth of inflorescence will improve the grain yield in this crop.

Girth of inflorescence had higher positive direct effect (2.179) on grain yield per plant. Also, it had high indirect effect *via* leaf area per plant. Thus, increase in girth of inflorescence and leaf area per plant will improve the grain yield in this crop. Plant height aE flowering had a negative direct effect on grain yield though its association with yield was positive. This might be because of large negative indirect effects *via* days to 50 per cent flowering, days to maturity, length of inflorescence, number of spikelets per inflorescence, 50 ml volume seed weight. Pawar (1995) reported positive direct effect of plant height at flowering, length of inflorescence, girth of inflorescence on grain yield in grain amaranthus.

In the present study the estimate of residual effect was of lower magnitude (-0.463) suggesting that characters included in study are sufficient to explain the variability in the dependent variable.

Based on present investigation, the most desirable idiotypes in grain amaranth thus should possess more leaf area per plant, more number of spikelets per inflorescence, more plant height, more length of inflorescence and more girth of inflorescence.

5.4 Genetic divergence

Genetic divergence which is due to genetic factors is the basis for heritable improvement. Plant breeders have always, therefore, been fascinated by great amount of diversily in crop plants. The precise information about genetic divergence therefore, is crucial for productive breeding programme. The genetically diverse parents are known to produce high heterotic effects and consequently give desirable segregant s in the breeding material. Multivariate analysis (D^2 statistic) is a measure that appraises the genetic variability quantitatively among a set of genotypes (Mahalanobis, 1928). The fifty genotypes of Amaranthus collected from various regions of India under the present study were therefore, assessed for genetic divergence in a set of ten metrical traits.

5.4.1 Diversify based on a set of ten characters

The significance of genotypic differences for all the characters at 1 and 5 per cent level of significance indicated considerable amount of variability in the genotypes (Table 2). Hence, the D^2 values as per Mahalanobis (1936) were estimated based on these ten characters.

The range between the D^2 estimates was from 7.13 to 14758.63. The wide range revealed adequate diversity among the genotypes studied. Fatocun (1985) in Amaranth and Manoharan and Shivsubramanian (1988) in proso millet also revealed wide genetic diversity for grain yield components.

The maximum D^2 value of 14758.63 was observed between a pair of genotypes *viz* IC-35475 and IC-93945, while the lowest D^2 value of 7.13 was observed between IC-35416 and IC-35431.

5.4.2 Cluster formation

Formation of clusters and intra and inter cluster divergence provides the base for the selection of parents for hybridization.

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 different clusters (Rao, 1952). Therefore, crossing between the genotypes belonging to the same cluster is not expected to give desired heterotic response and or desired segregants in further generations. Thus parents belonging to different clusters should be selected for crossing. Wider the distance between the clusters, higher the chances for heterotic effects and desirable segregants. The crosses involving the parents with extreme divergence have also been reported to exhibit decreased heterosis (Moll *et al,* 1965). Therefore while selecting the parents on the basis of the genetic diversity, their *per se* performance and cluster means for the characters for which those are to be included in the breeding programme, also need due consideration.

In the present study, fifty genotypes were grouped in to eleven clusters (Table 8). Cluster I is the largest consisting of 20 genotypes followed by cluster III with 10 genotypes, cluster II with 7 genotypes, cluster IV with 5 genotypes, cluster V with 2 genotypes. The remaining six clusters viz., (VI to XI) are solitary.

The clustering pattern obtained in the present study revealed that the genetic diversity is not necessarily parallel to the geographic diversity. The perusal of Table 1 and 8 indicated that the genotypes originating from different geographical areas could form one cluster, while different genotypes collected from the same area were grouped into different clusters. Faltocun (1985) also observed no clear association between genetic divergence among the genotypes and their geographical origin.

It is apparent from Table 10 and Fig. 4 that the maximum intercluster distance was observed between cluster VI and IX (D = 121.48, followed by cluster II and IX (D = 107.53), cluster V and VI (D = 97.70). Perusal of Table 11 showed that the intra cluster means of cluster VI for most of the characters were high from those of other clusters. This indicated that the genotype in cluster VI might have entirely different genetic architecture from the genotypes included in remaining clusters. The statistical distance between clusters III and VII was the lowest (16.44) followed by V and VIII (17.39) and III and XI (17.85).

This suggested that the genotypes included in these groups may not have wide genetic divergence between them. On the basis of cluster means plant height at flowering, length of infloresence, girth of inflorescence, number of spikelets per inflorescence, leaf area per plant, oil content and grain yield appeared as the major forces of differentiation.

Now considering the cluster means for important grain yield components, the various clusters which can provide the desired parents for hybridization programme aiming at improvement in these characters are listed below.

Characters	Source cluster (s)
Grain yield/plant	VI, VII, II, IV
Plant height at flowering	VI, VII, II, I, IV
Length *o(* inflorescence	VI, I, VII, II
Girth of inflorescence	VII, VI
Number of spikelets/inflorescence	VI, VII, II, I, IV
Leaf area/plant	VI, VII, IV, II
Grain oil content	VI, II

On the basis of inter cluter distance, cluster means and the *per se* performance observed in the present study, the tentative crossing programme involving the genotypes viz., IC-35475, IC-32190, IC-21966, IC-35500, IC-35397, IC-35402, IC-35385, IC-35366 and IC-1491 will be as below, Tentative crossing programme

Sr. No.	Cluster combinations	Possible crosses
1.	IxIV	*IC-35385* x IC-32190 IC-35402 x IC-32190 IC-35397 x IC-32190 IC-35366 x IC-32190
2.	IIxIV	IC-1491 x IC-32190 IC-21966 x IC-32190
3.	IIxVII	IC-1491 xIC-35500 IC-21966 x IC-35500
4.	IVxVI	IC-32190 x IC-35475
5.	VIxVII	IC-35475xIC35500

The D^2 analysis thus proved to be a very useful technique in identifying diverse groups from a larger germplasm.

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SUMMARY AND CONCLUSIONS

6. SUMMARY AND CONCLUSIONS

The present investigation "Genetic divergence and path analysis in grain amaranthus *(Amaranthus hypochondriacus* L.)" was undertaken with fifty genotypes selected from the germplasm collected from different geographical origins, to study the nature and extent of genetic variation, heritability percentage and genetic advance in percentage of mean of ten different characters, their correlations, path coefficient analysis and genetic divergence in amaranth during kharif season of 1997-98.

Observations were recorded on five randomly selected competitive plants from each genotype for the characters days to 50 per cent flowering, days to maturity, plant height at flowering, length of inflorescence, girth of inflorescence, number of spikelets per inflorescence, leaf area per plant, 50 ml volume seed weight, grain cent oil content and grain yield per plant.

6.1 Summary

6.1.1 Variability and genetic parameters

Significant treatment differences and genotypic and phenotypic coefficients of variation revealed existence of substantial amount of variability for all the characters. Heritability (B.S.) of most of the characters in the present study was categorized as high to very high. It was the lowest for girth of inflorescence (22.70 %) and highest for grain oil content (99.80 %), followed by 50 ml volume seed weight

(97 %) and numberof spikelets per inflorescence (84.80 %). Very high heritability coupled with high genetic advance in percentage of mean for length of inflorescence, number of spikelets per inflorescence, leaf area per plant, grain oil content and grain yield per plant advocated high genetic progress under phenotypic selection.

6.1.2 Correlations

In the present study genotypic correlations in general were higher than the corresponding phenotypic correlations. Grain yield per plant was significantly and positively correlated with leaf area per plant (0.977), number of spikelets per inflorescence (0.731), plant height at flowering (0.729), length of inflorescence (0.717), girth of inflorescence (0.447), grain oil content (0.436). However, it had significantly negative correlation with days to maturity (-0.538).

6.1.3 Path co-efficient analysis

The path coefficient analysis revealed that leaf area per plant and girth of inflorescence had the highest positive direct effects on grain yield. Days to maturity, grain oil content also had positive direct effects on grain yield. In addition to these characters, daysto 50 per cent flowering, plant height at flowering, length of inflorescence, number of spikelets per inflorescence and 50 ml. Volume seed weight also had negative direct effects but showed positive correlation with grain yield because of positive indirect effects through other characters.

6.1.4 Genetic divergence

The D^2 values in the present investigation between all possible pairs of 50 genotypes showed adequate diversity and ranged between 7.13 to 14758.63. The genotypes could be clustered into 11 clusters following Tochers method as described by Rao (1952). Out of these 6 clusters VI, VII, VIII, IX, X, XI, were monogenotypic. Cluster I contained maximum number of genotypes (20), followed by cluster III, II, IV, V containing 10, 7, 5 and 2 genotypes, respectively. The intra cluster D values ranged between 9.67 (cluster III) and 15.39 (cluster V). The maximum inter cluster distance was observed between cluster VI and IX (121.48), followed by clusters II and IX (107.53), V and VI (97.70). The clustering pattern of these strains did not necessarily follow the geographical distribution.

6.2 Conclusions

6.2.1 Variability

1. High estimates of genotypic coefficients of variability among genotypes suggest more variability for grain yield per plant, number of spikelets per inflorescence, leaf area per plant and length of inflorescence.
2. High heritability accompained with high genetic gain indicated additive gene control in the inheritance of grain oil content, 50 ml volume seed weight, number of spikelets per inflorescence, grain yield per plant, days to 50 per cent flowering and leaf

area per plant. Phenotypic selection for these traits will therefore bring about high genetic progress.

6.2.2 Correlation and path coefficient analysis

Plant height at flowering, length of inflorescence, girth of inflorescence, number of spikelets per inflorescence, leaf area per plant and grain oil content have strong positive genotypic correlations with grain yield. Leaf area per plant, girth of inflorescence, days to maturity, grain oil content had positive direct effects on grain yield. However, days to 50 per cent flowering, plant height at flowering, length of inflorescence number of spikelets per inflorescence and 50 ml volume seed weight had negative direct effects but showed positive correlation with grain yield are the most yield contributing characters as revealed from the path analysis.

6.2.3 Genetic divergence

1. There is substantial genetic diversity (inter cluster distance (D) from 16.44 to 121.48) among the genotypes studied.

2. The fifty genotypes were grouped into eleven clusters.

3. There was no parallelism between genetic diversity and geographical distribution.
4. The pair of strains viz., IC-35475 and IC-93945 had maximum genetic distance (D^2 = 14758.63) between them. Moreover these strains were mostly divergent from other strains.
5. On the basis of inter cluster distances, cluster means and *per se* performance, the tentative crossing programme involving the genotypes viz., IC-35475, IC-32190, IC-21966, IC-35500, IC-35397, IC-35402, IC-35385, IC-35366 and IC-1491 will be as given in 5.4.2.

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ANIL KRISHNA KAMBL£

A candidate for the degree

of

MASTER OF SCIENCE (AGRICULTURE)

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