EVALUATION OF GRAIN AMARANTH COLLECTIONS FOR PRODUCTIVITY AND QUALITY TRAITS (*Amaranthus* spp.)

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EVALUATION OF GRAIN AMARANTH COLLECTIONS FOR PRODUCTIVITY AND QUALITY TRAITS (*Amaranthus* spp.)

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By

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CERTIFICATE

This is to certify that the thesis entitled **"EVALUATION OF GRAIN AMARANTH COLLECTIONS FOR PRODUCTIVITY AND QUALITY TRAITS (*Amaranthus* spp.)"** submitted by **Miss. KUSUMA V. PATGAR**, for the degree of **MASTER OF SCIENCE (AGRICULTURE)** in **GENETICS AND PLANT BREEDING,** to the University of Agricultural Sciences, Dharwad is a record of research work done by her during the period of her study in this university under my guidance and the thesis has not previously formed the basis for the award of any degree, diploma, associateship, fellowship or other similar titles.

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CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF PLATES

LIST OF APPENDICES

Introduction

I. INTRODUCTION

In relation to major crops in many developing areas of the world the carrying capacity of the land was rapidly being exceeded because of increasing population growth. Not only was the application of technology needed to modernize agriculture, but some what later international attention also became focused on the needs to change cropping cycles and to incorporate other crops, including more minor ones, into the cropping cycles along with the major staples. Apart from this, the genetic erosion and genetic vulnerability as a potential hazard in mono-cropping and continuous cultivation led to concerted action on crop genetic resources. Although it was clear that priority attention had to be given to the major cereals, other cereals and pseudocereals.

In ancient times grain amaranths were basic crops in the America and they have persisted to the present in isolated pockets in traditional agriculture. Amaranths are broad-leaved plants which are striking in appearance due to various coloration of all parts of the plant. They produce small seeds in large quantities.

It belongs to the family Amaranthaceae and genus *Amaranthus*. This genus includes about 60 species of

annual herbs which are native to Central and South America and are distributed in the tropical and subtropical countries of which some occur in India. There are four cultivated grain amaranth species, *viz.*, *A.hypochondriacus* L., (n=16); *A.cruentus* L., (n=17); *A.caudatus* L., (n=16) and *A.edulis* spegazzini (n=16).

The role of the amaranth as an under exploited plant with promising economic value has recently been recognized by the National Academy of Sciences (NAS,1975). Grain amaranth is one of the forgotten food crops, which has all the potential to become a valuable new crop. The crop is highly resistant to drought, diseases and best suited to extreme stress condition. In India, grain amaranths are under cultivation in the North Indian hills and also in plains of Gujarat. In South India, cultivation is scattered in pockets in the tribal regions of Nilgiris, Kolli hills and other tribal areas.

A.caudatus, A.cruentus and *A.hypochondriacus* have been identified (NAS, 1975) as having the potential to increase the world food production. Being versatile in nature, it has diversified uses as a staple food, snack using popped seeds, edible greens, for confectionaries, the flour is used to make chapatis in Himalayas and other minor uses such as dye, medicine and for beer production.

This ancient New World pseudocereal is attractive because of its high leaf and seed protein content, nutritious aminoacid complement and high digestibility of this protein. It has a higher energy density than conventional grains which may be of importance for dietary considerations. The crude protein content of grain amaranth ranges from 8-22% which is higher than in most common grains except soybean. The grain amaranth protein contains lysine (6%) and sulphur containing aminoacids (4.4%) which are limiting aminoacids in other grains. It also contains 3% minerals, 1.5% vitamins, 62% of easily digestible carbohydrate component. Supplementation of cereal flour with amaranth can provide up to 70% of diet energy. Seeds are excellent sources of iron, calcium and zinc. Mature leaves of amaranth contain red-violet pigments - the betacyanins, amaranthin and iso amaranthin which can be used as food colourants. Rice and amaranth in equal proportion approach the FAO/WHO protein specifications (Singhal and Kulkarni, 1988). Amaranth grains when heated pop and taste like a nutty - flavoured popcorn. The popped seeds are light and crisp and can be made into confection (laddoos) with sugar syrup and with these qualities it holds great promise as a subsidiary food crop to combat protein malnutrition in the developing countries.

Information on the nature and magnitude of variability present in the existing material and association among the various characters is a prerequisite for any breeding programme for high yield and quality.

Grain yield being complex character is influenced by its associated characters which are governed by polygenes and also greatly influenced by variations in environmental factors. So to make selection effective it is necessary to separate genetic variability from total variability which enables breeder to adopt suitable breeding programmes. Since yield is associated with its component characters it is essential to know the degree of mutual association prevailing between yield and its component characters which forms basis for selecting the desirable genotypes. Collection and evaluation of germplasm, quantification of magnitude of variability existing for different quantitative characters and classification of germplasm into groups would be useful for the breeder to plan the strategy to develop high yielding genotypes.

However, the correlation between the yield and its component characters is often not real because of inter-relationships existing between the componental characters themselves. Therefore, the analysis of the inter componential correlations is very essential to expose the

direct and indirect contribution of each of the component which is determined by path coefficient analysis (Wright, 1921)

An investigation into the nature and degree of divergence is useful for an understanding of the cause of evolution and for classifying the populations into groups on the basis of diversity particularly when they are overlapping for one or more characters. Hence it necessitates the study of genetic divergence available among the germplasm for identification of diverse parents for their use in hybridization programme.

Because of complexity of yield and its close association with component characters, direct selection for yield is often ineffective in bringing out the expected results. In such situations, the success of selection could be enhanced with the use of selection indices formulated based on discriminant function technique, involving simultaneous selection for important characters. As dietary nutrition is becoming expensive it is important to study the nutritional quality of grain amaranth.

Improvement through breeding was not very effective due to limited knowledge of genetic diversity and also because of its status as an underutilized crop. A comprehensive knowledge of genetic variability,

correlations, path coefficient analysis and selection indices is thus a valuable tool in any crop improvement programme. The amount of work done on the genetics of some of the important quantitative characters is meager. It is in this contest the present study was taken up with the following objectives.

1. To estimate the genetic variability for yield and yield contributing characters.
2. To resolve the yield component traits that contribute and to find pattern of association of these characters with yield and among themselves.
3. To classify the entries on the basis of genetic diversity.
4. To formulate the selection criteria in the form of an index for selection of genotypes.
5. To evaluate the genotypes for nutritional and processing quality.

Review of literature

II. REVIEW OF LITERATURE

Grain amaranth (*Amaranthus* spp.) belongs to the family amaranthaceae. It is one of the forgotten food crops, which has all the potential to become a valuable new crop. There are abundant direct evidences available about the antiquity of the crop which indicates that some amaranths originated even before man took for organized agriculture, graving around the camps and fishing villages of pre-historic people, who conveniently used it for food from as early as 4800 BC (Sauer, 1950, 1967). Grain amaranth reached its peak popularity as a staple crop during Mayan and Aztec civilization in Central America and fell into disuse following Spanish conquest in the sixteenth century. However, cultivation has much declined in the present century and is confined to small pockets, maintained mostly in isolated primitive communities. Though grain amaranth is having high nutritional quality and early cultivation, it has not been given the credit it deserves.

An exhaustive survey of genetic variability and detailed understanding of genetic make up of the crop is an important prerequisite for initiating crop improvement programme. There is a need to identify novel, high quality but cheap source of protein and energy because of the dwindling returns from

existing sources. The breeding work for its genetic improvement is still in infancy after its recent come back. The review of literature relevant to the present study is presented under the following headings.

1. Genetic variability, heritability and genetic advance
2. Correlation and path coefficient analysis
3. Genetic diversity studies
4. Selection indices
5. Nutritional quality studies

2.1 STUDIES ON VARIABILITY, HERITABILITY, AND GENETIC ADVANCE

Success of any crop improvement programme depends on the magnitude of genetic variability and the extent to which the desirable characters are heritable. The estimates of variability in respect of yield and its heritable components in the material with which the breeder is working, are therefore prerequisite for any breeding programme. Hence, it becomes necessary to split the phenotypic variability into heritable and non-heritable components such as genotypic and phenotypic coefficients (GCV and PCV), heritability and genetic advance Genotypic coefficient of variation indicates the relative magnitude of genetic diversity present in the material and helps to compare the genetic variability present for differen characters.

The apparent variability in a crop can be divided into:

1. Variability due to genotype,
2. Variability due to environment and
3. Their interaction

The genotypic variability is the actual heritable component of the apparent variability and is expressed as heritability. Therefore, heritability can be defined as the proportion of the phenotypic (apparent) variability that is due to genotype. The genotypic variability is the result of additive and non-additive effects.

Therefore heritability is defined in two ways (Fisher *et al.*, 1932 ; Panse, 1940; Lush, 1949 and Mather, 1949).

Lush (1949) has proposed heritability as the ratio of additive variance to total variance in a narrow sense. The heritability in broad sense was proposed by Hansen *et al.* (1956) as the ratio of genotypic variance to the total variance.

Heritability influences the selection programme to a larger extent. According to Allard (1956), heritability of yield alone is less and that of yield component is more. However, the gain from a selection for a particular character is the function of its heritability, selection pressure and the variance existing in the basal population. Thus, the genetic gain was expressed by Burton and Devane (1953) as the product of

heritability, phenotypic standard deviation and selection intensity.

The genetic advance is more useful in predicting the actual value of selection than heritability, according to Johnson *et al.* (1955a) although the later value indicates the relative effectiveness of selection based on phenotypic expression of the character.

Charles and Smith (1939), Power (1942) and Power *et al* (1950) separated genotypic variance from the total variance, using estimate of environmental variance in non-segregating populations. Since then the studies on heritability, genetic advance (GA) and their variance component have been estimated for most of the yield contributing characters in several crops.

The literature in respect of genetic variability, heritability and genetic advance in grain amaranth have been reviewed and summarized in Table- 1.

2.2 STUDIES ON CORRELATION AND PATH COEFFICIENT ANALYSIS:

The idea of correlation was first presented by Galton (1889), which was later elaborated by Fisher (1918) and Wright (1921). Correlation coefficient analysis helps to determine the nature and degree of relationship between any two measurable characters. It resolves the complex relations

Table – 1: Review of literature on genetic variability, heritability and genetic advance in grain amaranth (*Amaranthus* spp.)

Sl. No.	Character	Kind of material used and/or method used to study	PCV	GCV	h^2 (b.s)	GA	Reference
1	Plant height	Population of *A. cruentus* derived from a single plant collected in Tanzania	Wide variation was observed		-	-	Hauptli and Jain (1980)
		-	High	-	-	-	Jain *et al.* (1980a,1980b)
		Lines of *A. hypochondriacus*	Wide variation		-	-	Vaidya (1984)
		Populations of *A. cruentus* and *A. hypochondriacus*	-	-	-	High	Ayiecho (1986)
		Twenty genotypes of grain amaranth	Low	Low	High	Very High	Joshi (1986)
		25 genotypes of *Amaranthus* spp.	Moderate	Moderate	Very High	High	Pushpa Rekha (1986)
		Seasonal evaluation of genotypes • During *kharif* • During *summer*	Low Moderate	Low Low	Moderate Moderate	Low Low	Maruthi (1987)
		A. cruentus types	-	-	0.22*	-	Vaidya and Jain (1987)
		A. hypochondriacus types	-	-	0.49	-	Vaidya and Jain (1987)
		35 accessions of *A. hypochondriacus*	Wide variation was observed		-	-	Das *et al.*(1991)
		144 genotypes of grain amaranth	High	High	High	Moderate	Lohithaswa (1992)
		Population of *A. hypochondriacus*	High	High	High	High	Waghmode *et al.* (1998)
		50 genotypes of *Amaranthus hypochondriacus*	High	High	High	Moderate	Ghosh *et al.* (1999)

Contd.

Sl. No.	Character	Kind of material used and/or method used to study	PCV	GCV	h2 (b.s)	GA	Reference
2	Days to 50 per cent flowering	Seasonal evaluation of genotypes • During *kharif* • During *summer*	 Low Low	 Low Low	 High High	 Moderate Moderate	Maruthi (1987)
		144 genotypes of grain amaranth	Low	Low	High	Moderate	Lohithaswa (1992)
		50 genotypes of *A. hypochondriacus*	Low	High	High	Low	Waghmode *et al.* (1998)
3	Days to maturity	Four domesticated species	Wide variation		-	-	Hauptli and Jain (1977)
		Twenty genotypes of grain amaranth	Low	Low	Very high	Very high	Joshi (1986)
		25 genotypes of *Amaranthus* spp.	Low	Low	Very high	Low	Pushpa Rekha (1986)
		Seasonal evaluation • During *kharif* • During *summer*	 Low Low	 Low Low	 High High	 Low Low	Maruthi (1987)
		144 genotypes of grain amaranth	Low	Low	High	Moderate	Lohithaswa (1992)
		50 genotypes of *A.hypochondriacus*	Low	Moderate	High	-	Waghmode *et al.* (1998)
4	Stem girth at collar region	25 genotypes of *Amaranthus* spp.	Moderate	Moderate	Very High	Moderate	Pushpa Rekha (1986)
		Seasonal evaluation • During *kharif* • During *summer*	 Low Moderate	 Low Moderate	 Moderate Very High	 Low Moderate	Maruthi (1987)
		144 genotypes of grain amaranth	Wide variation was observed		Moderate	Moderate	Lohithaswa (1992)

Contd..

Sl. No.	Character	Kind of material used and/or method used to study	PCV	GCV	h2 (b.s)	GA	Reference
5	Number of branches	25 genotypes of *Amaranthus* spp.	Moderate	Moderate	Moderate	Moderate	Pushpa Rekha (1986)
		Seasonal evaluation • During *kharif* • During *summer*	High High	Moderate Moderate	Moderate High	Moderate Low	Maruthi (1987)
		144 genotypes of grain amaranth	Low	Low	Low	Low	Lohithaswa (1992)
		50 genotypes of *A .hypochondriacus*	High	High	High	High	Waghmode *et al.* (1998)
6	Panicle length	--	High	Variability	-	-	Jain *et al.* (1979)
		Genetic resources of grain amaranth collected from different places	High	Variability	-	-	Joshi *et al.* (1983)
		Population of Indian amaranthus	Wide variation		-	-	Vaidya (1984)
		Twenty genotypes of grain amaranth	Low	Low	Moderately high	Very high	Joshi (1986)
		25 genotypes of *Amaranthus* spp.	Moderate	Low	Moderately high	Low	Pushpa Rekha (1986)
		Seasonal evaluation • During *kharif* • During *summer*	Moderate Moderate	Low Low	Low Moderate	Low Low	Maruthi (1987)
		35 accessions of *A. hypochondriacus*	Low	Low	High	-	Das *et al.* (1991)
		144 genotypes of grain amaranth	-	-	High	Low	Lohithaswa (1992)
		50 genotypes of *A. hypochondriacus*	Low	Moderate	Moderate	-	Waghmode *et al.* (1998)
7	Harvest Index	Comparative study • In three weedy species • In four domesticated species	High Low	High Low	- -	- -	Hauptli and Jain (1977) Hauptli and Jain (1977)
		25 genotypes of *Amaranthus* spp.	Low	Low	-	-	Pushpa Rekha (1986)

Contd.

Sl. No.	Character	Kind of material used and/or method used to study	PCV	GCV	h2 (b.s)	GA	Reference
8	Number of spikes per panicle	Twenty genotypes	Low	Moderate	Low	Moderate	Joshi (1986)
		25 genotypes of *Amaranthus* spp.	High	High	Very high	Very high	Puspha Rekha (1986)
		144 genotypes of grain amaranth	High	High	Moderate	Moderate	Lohithaswa (1992)
9	Grain yield per plant	Population of *A. cruentus* derived from a single plant in Tanzania	Wide variation		-	-	Hauptli and Jain (1980)
		--	High	-	-	-	Jain *et al.* (1980a)
		Population of *A. hypochondriacus*	Wide variation		-	-	Mohideen *et al.* (1983)
		Twenty genotypes of grain amaranth	Low	Low	Moderate	Very high	Joshi (1986)
		25 genotypes of *Amaranthus* spp.	High	High	Moderately high	Very high	Puspha Rekha (1986)
		Seasonal evaluation • During *kharif* • During *summer*	High Moderate	Moderate Low	Low Low	Moderate Low	Maruthi (1987)
		Populations of *A cruentus* and *A hypochondriacus*	-	-	0.09*	-	Vaidya and Jain (1987)
		35 accessions of *A hypochondriacus*	Moderate	High	High	High	Das *et al.* (1991)
		144 accessions of grain amaranth species	High	High	Low	Low	Lohithaswa (1992)
		50 genotypes of *A hypochondriacus*	High	High	High	High	Waghmode *et al.* (1998)

* Realised heritability

between the events into simple form of association. Knowledge on phenotypic and genotypic correlations between important characters are of immense help in the selection of suitable plant types. But measure of correlation does not consider dependence of one variable over the other. Direct contribution of each component to the yield and the indirect effect it has, through its association with other components cannot be differentiated from mere correlation studies. A statistical device called path coefficient analysis developed by Wright (1921) fulfills this lacuna. It is a tool in genetic analysis, which partition the association of the components on yield and indirect effect of the characters through other components.

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

Pandey (1979), in *A. hypochondriacus* noticed that harvest index had the highest correlation response, followed by pollen fertility and plant height in F_1 and F_2 populations.

Correlated response in F_1 and F_2 populations revealed that plant height had the highest value with grain yield per plant, followed by harvest index and panicles per plant. Pollen fertility showed negative correlation with yield in F_1 and F_2, while its positive response in parental populations indicated less importance in the selection programme. On the other hand number of days to flowering and length of the panicle showed negative correlation response in F_1, but revealed positive response with grain yield per plant in F_2 generation. Thus improvement in grain yield appears possible through the selection for plant height, harvest index and number of panicles per plant.

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

Mathai and Ramachandra (1981) reported strong positive correlation between crown girth and other yield characters viz, plant weight, stem weight and leaf weight in 67 varieties of *Amaranthus* spp.

Pandey (1981a) studied the genetic association in *A.hypochondriacus*. The data indicated that the genotypic

correlations, in general, were higher than the corresponding phenotypic correlations because of the modifying effect of environment on the association of characters at the genic level. Grain yield had high positive correlation with the number of days to flowering, plant height, number of days to maturity, harvest index and pollen fertility. It had a moderate positive correlation with grain yield, length of the panicle, number of panicles per plant and negative correlation with grains per panicle and 1000 grain weight.

Path analysis in *A.hypochondriacus* by Pandey (1981b) revealed that plant height had the greatest direct effect on the number of panicles per plant followed by number of days to maturity and grain yield per plant. Plant height also had indirect effect via weight of the grains per panicle to grain yield per plant indicating that direct selection for the plant height will result in an increase in number of panicles per plant. Length of the panicles showed negative indirect effect on number of panicles per plant.

Positive correlation was observed by Naidu *et al.* (1982) in all the species of grain amaranth between the mean nitrate reductase activity with grain yield and total dry matter accumulation at harvest; leaf proteinase activity and percentage of protein in grain; leaf nitrate reductase activity

with total reduced nitrogen per plant; root growth with total reduced nitrogen per plant and nitrate reductase activity; level of grain protein with the nitrate reductase activities.

Misra *et al.* (1983) found no relationship between cultivated or wild status of *A. hypochondriacus* in their protein or amino acid content of the seeds. Lysine content of the protein was correlated positively with six other amino acid content and negatively with seven amino acid content. The black seeded wild form AG-16 contained more protein (22.16%) followed by AG-21 (17.85%), AG-21 and AG-24 contained high lysine (both 7.1%).

Mohideen *et al.* (1983) noticed that long duration, lanky growth habit with shy branching grain amaranth types recorded higher yields and suggested that branching had negative relationship with plant height. Hauptli and Jain (1984) by step-wise multiple regression analysis of all traits on yield indicated number of days to flowering to be negatively correlated with yield, while plant height and leaf length were positively correlated.

Analysis of data by Espindola and Gandarillas (1985) revealed close positive phenotypic correlations between yield and stem diameter, however significant correlation was not observed between yield either with 100 seed weight or panicle

diameter. Path coefficient analysis confirmed the importance of panicle length, stem diameter and also 100 seed weight as yield components. Panicle length and diameter were confirmed as the most important components of yield.

Kulkow and Jain (1985) in their study on selection for time of flowering observed that seed yield as measured by total head weight was negatively correlated with days to flowering in *A.cruentus*.

Based on correlation coefficients and multiple step-wise regression, the best yield predictors were found to be plant weight, head weight, threshing percentage and ratio of yield to height in grain amaranth as reported by Ayiecho (1986).

Positive and highly significant phenotypic and genotypic correlations were observed by Pushpa Rekha (1986) for grain yield with all characters except for number of branches per plant, average length of spikelet, terminal spikelet length, harvest index and grain protein per cent. Dry weight of husk with grain showed highest phenotypic direct effect of 0.8820 on yield and low direct effect were obtained for number of spikelets per plant (0.0819). Positive genotypic direct effects were obtained for diameter of stem, length of inflorescence, number of spikelets per plant and dry weight of husk with

grain. Dry weight of inflorescence and number of nodes per plant showed negative direct effect towards yield.

Character association in *Amaranthus* spp. by Maruthi (1987) revealed that number of branches per plant, girth of stem, dry weight of inflorescence showed significant positive phenotypic and genotypic correlation with yield. Grain yield showed negative genotypic correlation with days to 50% flowering, days to maturity and length of inflorescence. Number of nodes per plant and length of the inflorescence showed negative direct effect on yield. Dry weight of the inflorescence exhibited positive and high direct effect (0.7361) on seed yield.

Das *et al.* (1991) in a study on 35 accessions of *A.hypochondriacus* reported that panicle weight, 100 grain weight and panicle length showed significant positive correlation with seed yield per plant. Further, panicle weight showed significant positive correlation with panicle length. Thus selection for these characters would likely to improve the grain yield in amaranth.

Significant positive correlation was observed for grain yield with plant height, inflorescence length, stem girth at collar region and fresh weight of inflorescence. Number of branches had negative significant correlation at genotypic

level and significant positive correlation at phenotypic level. Profound direct effect of number of rachis on grain yield was reported by Lohithaswa (1992).

Agoṇg and Ayiecho (1992) in a study on populations of *A.hypochondriacus* and *A.cruentus* reported that head weight was positively associated with seed yield per plant indicating that selection for heavier heads would result in higher grain yield.

In a study on 50 genotypes of *A.hypochondriacus* Ghosh *et al.* (1999) revealed that days to flowering, number of panicles and main panicle length were significantly correlated with plant height. Seed yield was positively correlated with number of branches per plant, suggesting that seed yield per plant might be improved via selection for number of branches, main panicle length and plant height.

Correlation and path analysis in 66 genotypes of *Amaranthus* spp. revealed that grain yield per plant at genotypic level was positively and significantly associated with plant height, number of inflorescence per plant, number of spikelets per spike and leaf size. This indicated that selection for these traits would lead to an improvement in yield. Plant height exhibited highest direct effect towards grain yield next to leaf size. Leaf size was

indirectly associated via days to flower, days to maturity, plant height and number of inflorescence per plant (Sudhir Shukla and Singh, 2003).

2.3 GENETIC DIVERGENCE BY MAHALANOBIS D^2 ANALYSIS

An insight into the magnitude of variability present in a crop species is of at most importance as it forms the basis for any crop improvement programme. Genetic divergence and genetic variability together have played an important role in evolution of crop plants (Allard, 1961). Last three decades have witnessed major utilization of genetic diversity. A measure of genetic divergence must reflect the differences in gene frequencies and in the absence of experimental technique to measure diversity with respect to genes affecting quantitative characters, phenotype diversity is usually considered to be an indication of underlying genetic differences.

D^2 statistic developed by Mahalanobis (1936) actually provides a measure of magnitude of divergence between the groups under comparison. It considers the variation produced by any character and their consequent effect that it bears on other characters. The technique has been applied in several crops, to select genotypes for further breeding programmes.

In biological populations D^2 statistic was first applied by Nair and Mukherji (1960) to classify the natural and plantation teak tree types, based on four important characters such as specific gravity, nodule structure, nodule elasticity and maximum crushing stress. Its application was extended to plant breeding subsequently. Murthy and Pavate (1962) felt that these techniques can be extended to the situations where overlapping species are to be discriminated and also to the discrimination at sub-species level. They utilized 13 varieties considering four characters together and classified them into four clusters. Since then the technique of Mahalanobis D^2 statistic has been employed widely to resolve genetic divergence at inter-varietal, sub-specific and species levels in several crops. A brief review in this aspect in grain amaranth and other cereal crops viz., rice, sorghum and wheat is given below.

Hauptli (1983) investigated inter specific and intra specific diversity and genetic advance in New World land races of grain amaranth using nine enzyme loci. Approximately equal within and between species components were revealed by partitioning of diversity for three crop species. Low levels of heterozygocity inspite of intra specific diversity, implied a high level of interbreeding. Genetic distance between grain

amaranth crop species was found to be smaller than that between related weedy species. Further in the study of several quantitative traits in six diverse populations, between population mean squares were found to be highly significant for every trait, implying high intrapopulation diversity. However, numerically low differences between family means implied low heterozygocity.

Fotokun (1985) studied forty accessions from 12 countries for 22 characters using cluster analysis and principal component analysis. The latter suggested that leaf length, leaf dry weight per plant and total above ground dry matter yield per plant were the most important characters in forming the six groups revealed by cluster analysis. Where as some accessions from a given country were in different clusters, 115 accessions predominantly from Western Africa were in one cluster (Group 1) with three forms from France, India and the USA respectively. Group-I, IV and V were thought to be of value in breeding vegetable amaranthus and groups II and III and possibly V in breeding grain amaranth.

Lohithaswa (1992) assessed genetic diversity in 144 genotypes of grain amaranth using Mahalanobis D^2 statistic. In D^2 analysis ten clusters were resulted out of which one was biggest having 124 entries and all others were small or

solitary clusters. Cluster IV, IX and X were found to be superior with respect to grain yield and other yield attributes. Fresh weight of plant, fresh weight of inflorescence and plant height were found to be the most important characters contributing towards genetic diversity. There is no perfect relation between genetic diversity and geographic diversity.

Joshi and Rana (1995) studied the genetic divergence in 20 genotypes of *A.hypochondriacus*. On the basis of D^2 analysis, the genotypes were grouped into 9 clusters. The cluster III and IX showed the maximum inter-cluster distance (192.10), followed by V and IX (177.05) and I and IX (170.20), indicating that genotypes belonging to these groups were genetically more diverse from each other. The popping size contributed the maximum divergence (65.48%) followed by protein content (18.62%), grain yield (8.44%), inflorescence length (4.42%), days to maturity (4.42%) and 1000 grain weight (1.52%).

Sudhir Shukla and Singh (2002) assessed the genetic divergence in 66 strains of *A.hypochondriacus* using Mahalanobis D^2 analysis. The 66 strains were grouped in nine clusters depending upon the genetic constitution. The cluster I contained 22 strains followed by cluster VII with 12 strains. The intra-cluster values varied form 0.0 to 2.253. The

maximum was found in VI followed by III and I. The inter-cluster distance was maximum between VIII and IX followed by II and VIII and III and VIII. In this study, the days to flower contributed the maximum towards divergence followed by plant height, nodes/plant and leaf size.

Genetic divergence in sixty-eight genotypes of grain amaranth was studied by Verma *et al.* (2002) and were grouped into 9 clusters. The clustering pattern revealed that the genetic diversity might not be related to the geographical diversity. The average intercluster distance was maximum between cluster VIII and IX followed by VI and VIII, II and VIII, and V and IX, indicating that these groups of genotypes were highly divergent from each other. The genotypes in these clusters revealed substantial differences in the means for the 4 traits studied.

Rice:

D^2 statistic on upland rice varieties was studied by Gomathinayagam *et al.* (1990). The forty entries of rice were grouped into four different clusters by Tocher's method and found that, there was wide genetic diversity in the material from the same geographical location, which could result from non-characteristic selection forces in the region or due to genetic drift in the material chosen. The authors suggested

intercrossing of genotypes from the clusters showing superior cluster means for desired characters might result in the production of better upland rice varieties.

The nature and magnitude of genetic divergence was assessed in 28 genotypes of rainfed rice using Mahalanobis D^2 statistic. The population was grouped into five clusters. The geographical diversity has not been found related to genetic diversity. The varieties belonging to clusters I and V having greater statistical distance may be selected for hybridization programme as they are expected to produce good segregants (Vivekanandan and Sukanya Subramanian, 1993).

Roy and Panwar (1993) studied genetic divergence in ninety nine genotypes of rice for eleven characters related to bacterial blight severity, yield and its contributing characters. The genotypes were grouped into 16 clusters. The genetic diversity was not related to geographical diversity. Genetic diversity among 44 breeding lines and two improved cultivars was studied under rainfed upland condition using Mahalanobis D^2 analysis. Cluster with 12 genotypes was the largest while cluster XI and XII were monogenotypic. Genotypes in cluster IX had the highest intra-cluster distance. The maximum intercluster distance (3920) was observed between genotypes of cluster VII and XII (Chauhan and Chauhan, 1994).

Hegde and Patil (2000) assessed the genetic divergence in 40 genotypes of rainfied rice using Mahalanobis D^2 statistic. These varieties fell in seven clusters. Total spikelets per panicle, photosynthetic rate and 1000 grain weight contributed maximum to the total genetic divergence. The average intercluster D value was maximum (51.88) between the cluster V and VII indicating high genetic divergence between the cultivars of these two cluster. Based on the genetic distance, mean performance and clustering pattern, hybridization of the cultivars were suggested to be appropriate in breeding.

Rather *et al.* (2001) studied genetic divergence in 56 rice cultivars using Mahalanobis D^2 statistic. The genotypes were grouped into 8 clusters. The cluster I comprised 38 of 56 genotype. The clusters IV, V, VII and VIII included 1 genotype each. Maximum inter-cluster D values were observed between the cluster V and VIII, followed by IV and VIII. Geographical origin was not found to be a good parameter of genetic divergence. The 100 grain weight and length: breadth ratio of grain was important components of divergence. Based on mean performance of plant height, maturity, spikelet fertility and grain yield and inter-cluster distance, the genotypes from

clusters II and IV may be used for initiating the hybridization programmee.

Bidhan Roy *et al.* (2002) assessed nature and magnitude of genetic diversity in 50 high yielding varieties and traditional germplasm of rice. The genotypes were grouped into 10 clusters. The pattern of distribution of genotypes within various clusters was random and independent of geographical origin. Cluster IV and X were identified as most diversified groups, followed by IV and IX. Days to 50% flowering, grain length, kernel breadth and grain yield per plant were found to be the major component characters contributing towards genetic diversity. The genotypes with high mean value in any cluster may be directly used for adoption or used in hybridization programme.

Sorghum:

Sabharwal *et al.* (1995) grouped 56 sorghum genotypes into 12 clusters by applying Mahalanobis D^2 analysis. The clustering pattern revealed that there was no association between genetic divergence and geographical diversity. Biradar *et al.* (1996) studied 67 maintainer lines of sorghum using D^2 statistic for genetic diversity. They evaluated the sorghum genotypes for 21 quantitative yield components and grouped them into 20 clusters. Days to 50 per cent flowering

contributed most to divergence, followed by internodal length, plant height and panicle length. There was no association between geographical diversity and genetic diversity.

Biradar *et al.* (1997) extended their D^2 analysis to 61 restorers of diverse cytoplasmic genetic male sterility. Days to 50 per cent flowering contributed most to divergence followed by internodal length, plant height and panicle length. There was no association between geographical diversity and genetic diversity.

In a study involving 177 accessions of sorghum from North Shewa and South Welo region of Ethiopia on 14 phenotypic characters using canonical discriminate analysis and cluster analysis, 177 accessions where grouped into three clusters, linked by few phenotypically intermediate land races (Teshome *et al.*, 1997).

Asthana *et al.* (1998) assessed 52 sorghum genotypes from USA, Mexico, Sudan, Africa and India. Using D^2 statistic, twenty yield related characters were partitioned into 13 clusters. There was absence of any relationship between geographic distance and genetic diversity. The trait panicle size contributed most towards genetic divergence of grain yield

followed by grains per panicle, gross panicle weight and leaf area.

Ayana and Bekele (1999) assessed genetic divergence among 415 sorghum accessions for 15 quantitative characters by cluster analysis. They grouped the accessions into ten clusters. Kadam *et al.* (2001) observed considerable amount of genetic diversity among the 64 genotypes of sweet sorghum. The genotypes were grouped in 13 clusters. The maximum number (12) of genotypes were grouped into cluster I followed by cluster II and VI each containing 8 genotypes. The clustering pattern of these genotypes did not necessarily follow the geographical distribution.

Wheat:

Jatsara (1980) analyzed the genetic divergence in 40 strains of bread wheat including material of Mexican and Indian origin using D^2 statistic. Plant height contributed the most to genetic divergence amongst the five traits studied.

Behl *et al.* (1985) used Mahalanobis D^2 statistic to measure genetic divergence in 72 F_1's and their parents in line x tester analysis of wheat. Parents and hybrids were grouped into 11 clusters. Heterosis was greatest when the cluster distance between the parents was low.

In a study of genetic diversity by D^2 statistic, 40 wheat genotypes were grouped into 8 clusters. The clustering pattern indicated that geographic diversity was not a reliable criterion. There was wide range of variation in the intra cluster mean values in respect of each of the quantitative traits studied. The yield components viz. number of tillers per plant, number of grains per ear and grain yield contributed the most to the genetic divergence (Sethi *et al.*, 1992).

Genetic divergence measured by Mahalanobis D^2 statistic for nine quantitative traits in 121 indigenous and exotic varieties of wheat indicated their grouping into 27 clusters. Grouping of varieties in different cluster was not related to their geographical origin though in many cases genotypes evolved in common habitat tended to group in the same cluster. Cluster means of different characters suggested wide range of variations for plant height, peduncle length, number of grains per ear, 1000 grain weight and gain yield per plant (Redhu *et al.*, 1995).

Shivakumar and Singh (1997) studied genetic divergence among 25 elite lines of Triticale along with Sonalika cultivar of bread wheat using Mahalanobis D^2 analysis. They were grouped in 4 clusters. The maximum genetic divergence was observed between clusters II and IV, followed by III and IV, II

and III and I and IV. The spike length, days to heading and maturity, plant height, spikes per 0.5m^2, tillers per plant and grain yield had sizeable individual contribution towards genetic divergence.

Vishal Suri and Sharma (1999) assessed D^2 statistic in 200 genotypes of wheat and are grouped into sixteen clusters. The genetic divergence was independent of pedigree as well as place of origin. The intercluster distance ranged from 1.48 to 2.61. The members of the cluster IV and VIII exhibited maximum divergence (intercluster distance = 7.80). Grain yield and tiller number were major contributor towards genetic divergence with moderate contribution from 1000 grain weight, grains per ear and harvest index.

Bergale *et al.* (2001) assessed 50 genotypes of wheat for Mahalanobis D^2 analysis and they were grouped into 11 clusters with variable number of genotypes suggesting considerable amount of genetic diversity in the material. Cluster III has been identified for selecting parents for incorporating early maturity, dwarfness, high flag leaf area and good harvest index, cluster IV for more grains per spike, cluster X for number of spikes per plant, cluster XI for spike length and bold seed and cluster VI for grain yield per plant. Contribution of plant height was maximum towards

divergence, followed by days to flowering, grains per spike, 1000 grain weight and days to maturity.

2.4 SELECTION INDICES

The discriminant function technique was developed by Fisher (1936) and its use for plant selection was first proposed by Smith (1936). This technique facilitates discrimination of optimum relative weights to be assigned to any individual or combination of quantitative characters. Hazel (1943) observed that selection of metric character based on combination of different characters would be effective indication of true genotypic worth through discrimination of environmental portion in the total variance. Lerner (1958) showed that continuous direct selection in a character will not only reduce the genetic advance but also result in the loss of other characters. Importance of multiple selection was stressed by Brim *et al.* (1959).

The studies regarding selection indices in grain amaranth are not available. Hence, selection indices on other crops have been reviewed here.

Dhagat *et al.* (1977) formulated selection index for 18 diverse varieties of *Setaria italica* and the highest relative efficiency of selection was found for the combination of 1000

seed weight, grain weight and length of main ear and grain yield (106.03%).

Singh (1977) studied the selection indices in rye and showed that combined selection for leaf width, plant height, tiller number and total green matter would give maximum genetic gain in total dry weight per plant. Other work has shown that it is possible to manipulate the extent of genetic gain in individual traits.

Selection index in soybean comprising pod number per plant, seed number per plant, yield per plant which estimated to be 49.74% gave more efficiency than direct selection for yield (Salehuzzaman and Joardan, 1977).

Godawat and Gupta (1981) constructed the selection indices in rice based on number of ears per plant, 1000 grain weight and ear length, and revealed that these traits only showed a slight improvement (<0.5% at best) over selection for grain yield per plant.

In the evaluation of two groups of indices for yield in 72 lines of ragi, Mishra and Patnaik (1983) observed that the efficiency of indices over direct selection in terms of predicted genetic advance ranged from 93.8 to 118.3% but in terms of rank correlation it ranged from 61.4 to 95%. There was no

significant difference between test-trial yields of index selected and directly selected lines.

Rao *et al.* (1984) observed that selection indices based on phenotypic correlation and path coefficient produced 3 percent and 9 percent superiority respectively in genetic advance over an index based on economic weights in case of rice.

Chauhan *et al.* (1986) concluded from their studies on rice genotypes that anyone of the traits including days to flowering, leaf length, tillers per plant and grains per panicle could be used as a selection criterion. The study conducted by Jangle *et al.* (1987) in rice suggested that selection for panicle weight, flag leaf length, 1000 grain weight and panicle length would be most beneficial in increasing yield. Wu *et al.* (1987) in rice suggested that selecting individuals with a high panicle weight per plant may achieve both high yields and good grain quality.

In a study of eight yield components in 25 lines of rice selection for 1000 grain weight, plant height or days to 50 per cent flowering was predicated to be more efficient than direct selection for yield. Selection indices comprising yield and one or more yield components were most efficient (Rahangdale *et al.*, 1987). Cheng and Huang (1988) concluded from their studies that number of grains per panicle, biological yield,

harvest index and grain weight could be utilized as indices for selection for yield.

Lu (1988) predicted that selection for grain number per panicle would be effective in breeding for high yield. Similar observations were reported by Deosarkar *et al.* (1989). Further they reported that indices based on plant height and 1000 grain weight was also likely to bring about described improvement in yield. Similarly Soares *et al.* (1990) also concluded that percentage grain filling and 1000 grain weight should be used as selection criteria to increase rice yields. In agreement with this, Saimuraliraj (1992) found that selection based on a combination of these two characters and also number of productive tillers per plant and panicle weight would be superior to straight selection for grain yield.

Gravois and McNew (1993) developed the selection indices in rice from the additive genetic and phenotypic variance and covariances. The selection indices indicated that selecting for increased yield via selection for either panicle weight or panicle number alone would be ineffective. A selection index that included selection for both increased panicle weight and panicle number to increase yield, was estimated to be 91% as effective as selecting for yield directly.

Khulbe and Pant (1999) constructed selection indices and their efficiency was expressed in terms of predicted genetic advance using 36 genotypes of Indian mustard. Efficiency of indices over direct selection ranged from 0.21 to 2.31. Selection based on harvest index alone gave an advance of 1.75 over direct selection. Maximum advance was achieved only when the characters viz., siliqua length, seeds per siliqua, 100 seed weight, harvest index and oil content were included suggesting that emphasis should be laid upon these characters while making selection for yield.

Amitava Paul *et al.* (2000) observed that out of various selection indices constructed for yield in determinate pigeon pea using 19 genotypes showed that the selection index including recemes per plant, flowers per plant, pods per plant, days to flowering and plant height was best, giving an expected genetic gain of 124.69% over normal selection.

Sable *et al.* (2001) formulated selection indices using 30 genotypes of chickpea and revealed that none of the single character indices showed relative efficiency over straight selection for seed yield alone.

2.5 NUTRITIONAL QUALITY STUDIES (PROTEIN AND MINERALS)

Grain amaranth is a nutritious pseudocereal yielding high amounts of energy. They are rich source of protein and are excellent source of micronutrients.

Downton (1973) reported that grain amaranth, (*Amaranthus edulis*), has high protein content (14.5%). Amaranth varieties recorded a protein score of 67 against 58 in barely, 35 in corn and 63 in buckwheat. Leucine was limiting amino acid in amaranth while lysine in wheat, barely and corn.

Schmidt (1977) documented 12.6 to 15.6 per cent crude protein and 4.3-5.4 per cent crude fat in grain amaranth. It was higher in calcium, magnesium and iron content when compared to other cereal grains.

According to Barker *et al.* (1979), amaranth has higher protein (15.5-16.5%), sodium, calcium, iron and manganese when compared to most conventional grains. It also has high biological value (73%) and calorie content (390 kcal).

Pant (1983) found that amaranthus seed of different varieties had 14.5-17.9 per cent protein, 2.5-3.9 per cent minerals and 2.06-2.16 per cent fibre. The iron content was 7.5-12.2 mg/100g.

Crude protein content in different species of grain amaranth ranged between 13.2 to 17.6 per cent, zinc content ranged between 3.6 to 3.9 mg/100g and iron 9.1 to 21.7mg/100g (Teutonico and Knorr, 1985).

In a study of the composition of 14 selections of amaranthus species Bressani *et al.* (1987) observed that protein content varied from 12.5 to 16.0 per cent, fat from 8.25 to 12.85 per cent. They have also reported that 27 species of amaranthus contained 12.8 to 17.4 per cent protein.

Pederson *et al.* (1987) studied the nutritive value, protein and minerals of raw and processed grain. The black grains had a much higher content of dietary fibre (16%) than pale grains (8%) and a higher protein content but lower protein digestibility. The black grains had higher content of calcium and phosphorus than pale grains.

Prakash and Pal (1992) studied the seed protein, fat and fatty acid composition of 41 grain amaranth species. The protein content varied from 103 to 183 g/kg and fat from 8 to 69g/kg.

The protein content of amaranth grains ranges between 11.8 to 17.6 percent. The variation amongst the different species may be of a genetic nature, though it may also due to

environmental conditions and cultural practices (Bressani, 1993).

Geetha *et al.* (1994) observed that in eleven grain amaranth cultivars the protein content ranged from 15.2 to 19.6g per cent, ash content from 2.0 to 2.5% on dry weight basis. Iron content ranged from 6.2% to 13.0 per cent.

Munjal *et al.* (1999) in 12 grain amaranth cultivars revealed that the content of crude protein was in the range of 12.34-16.86 per cent on dry weight basis, while the iron content ranged from 8.58-17.00 mg/100g. The cultivar RGAS-92-1 contained the highest amount of iron (17mg/100g) while the cultivar Rasana-2 contained the highest amount of crude protein (16.86%).

No significant difference was observed by Bhuvaneswari *et al.* (2001) in protein content between seeds of IC-42258-1 (14.17g/100g) and R-104-1-1 (12.01 g/100g).

2.5.1 Processing (Popping):

Mohideen *et al.* (1983) reported popping ability of eight distinct and uniform white seeded grain amaranth types, which varied from 1:1.5(V/V) in A-90 to 1:3.3 (v/v) in A-144. In general, a popping volume of 2 to 2.5 times (v/v) was obtained in different types.

Joshi (1985) evaluated the new variety of amaranth viz., Annapurna and observed that popping quality is excellent and the grain pops to 4.5 times of its size.

Malleshi and Desikachar (1985) studied the popping characteristics of some minor millets and observed wide variation in yield as well as volume expansion of popped grains. Among foxtail millet varieties, the yield and volume expansion of popped grains varied form 47 to 84 per cent and 4.8 to 8.3ml/g, respectively.

Thorat *et al.* (1988) studied the effect of various grain parameters on popping quality of sorghum. The results indicated that there was significant genotypic difference in kernel weight, volume of pop, expansion ratio and popping percentage.

Manju Singh and Sarita Srivastava (1993) observed that the genotypes of sorghum exhibited significant differences in popping per cent at different moisture levels of all the genotypes. SPV-881 had the highest popping volume at 12% grain moisture level.

Hadimani *et al.* (1995) studied the physico-chemical composition and processing characteristics of 38 pearl millet cultivars. The yield and expansion ratio of popped grains ranged from 8.3 to 77.1% and 2.3 to 11.3% respectively.

Material and methods

III. MATERIAL AND METHODS

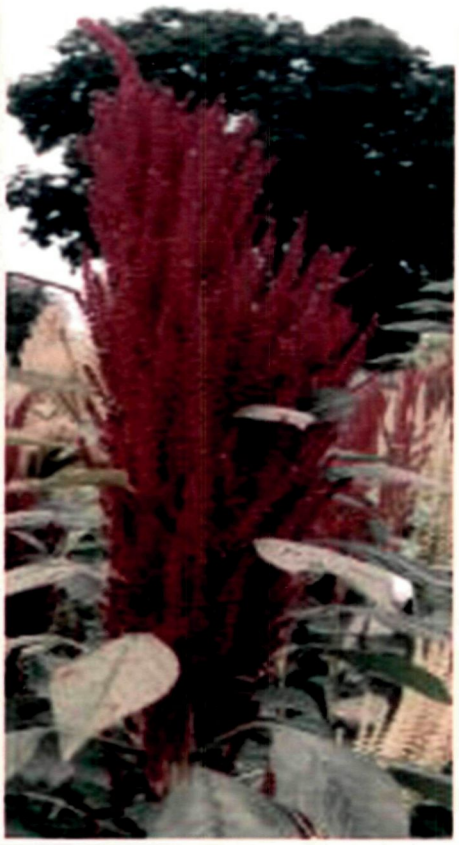
3.1 EXPERIMENTAL MATERIAL

The material used for the current study comprised of sixty four genotypes of grain amaranths obtained from University of Agricultural Sciences, G.K.V.K., Bangalore. The investigations were carried out in the Botany garden of Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad during *kharif* season, 2002.

The study was made to assess the genotypes for the extent and nature of variability present, to determine the contribution of different quantitative characters to yield and also to determine the nutritional quality of grain. Inflorescence of different grain amaranth species selected for the present study are given in the Plate 1.

3.2 EXPERIMENTAL DESIGN AND LAYOUT

The experiment was laid out in 8 x 8 simple lattice design, during *kharif* under irrigated conditions. Each genotype was sown in single row leaving 60 cm between the rows. In each row plant to plant distance was maintained at 20 cm by thinning. All normal recommended agronomic practices, irrigation and plant protection measures were followed during the crop growth period.



A. hypochondriacus (red)

A. hypochondriacus (green)

A. edulis

A. cruentus

Plate 1. Inflorescence of different grain amaranth species

3.3 RECORDING OBSERVATIONS

When the crop was 30 days old, randomly selected five plants in the center were tagged excluding border plants in each line. The observations were recorded on them for the following quantitative characters in each replication. The average values were computed as treatment mean under each replication.

3.3.1 Days to 50 per cent flowering

Number of days taken from the day of sowing to the day on which 50 per cent of the plants flowered in each line was recorded.

3.3.2 Days to maturity

The number of days taken from the day of sowing to the day on which the plants turned light yellow, which coincided with free separation of seeds from the inflorescence.

3.3.3 Stem girth at collar region (cm)

At the collar region stem girth was measured at the time of harvest.

3.3.4 Number of leaves

Number of fully opened leaves borne on the main stem was recorded at the time of harvest.

3.3.5 Number of branches per plant

Total number of the branches borne directly on the main stem including small rudimentary ones was counted and recorded.

3.3.6 Plant height (cm)

Height of the main stem from the ground level to the tip of the plant was recorded at the time of harvest.

3.3.7 Panicle fresh weight (g)

Fresh weight of the panicle was recorded in grams separating it from the stem.

3.3.8 Panicle length (cm)

The length of the panicle from the base of the compound spike to the tip was recorded in centimeters.

3.3.9 Number of spikes per panicle

Number of spikes borne on the main stem as well as on lateral branches were counted and recorded.

3.3.10 Dry weight of panicle (g)

Panicle of each plant was dried under sunlight and the dry weight of panicle was recorded.

3.3.11 Dry weight of stem (g)

Dry weight of each plant was dried in the sunlight and the dry weight of stem was recorded.

3.3.12 Harvest index (HI)

The ratio of the seed yield per plant to the total dry matter of the plant was calculated and expressed in percentage.

$$HI\ (\%) = \frac{\text{Economic yield}}{\text{Total biological yield}} \times 100$$

3.3.13 Seed yield per plant (g)

The total seeds obtained from each selected plant was weighed in grams and then averaged.

3.4 ANALYSIS OF QUALITY CHARACTERS

Grain amaranth is a nutritious pseudocereal yielding high amounts of energy. They are rich source of protein and are excellent source of micronutrients. The present study was undertaken to estimate crude protein, iron and zinc content.

3.4.1 Crude protein

One representative sample from each genotype in each replication was taken for protein analysis. The total nitrogen was estimated by micro kjeldhal distillation method (A.O.A.C., 1970). The crude protein was computed by multiplying total nitrogen by the factor 6.25 to arrive at the protein content and expressed in percentage.

$$\text{Nitrogen (\%)} = \frac{\text{TV} \times \text{N of acid} \times 0.014 \times V_1}{\text{Weight of sample} \times V_2} \times 100$$

TV = Titre value

N = Normality of acid (HCl)

V_1 = Volume of digested sample

V_2 = Volume taken for distillation

3.4.2 Iron and zinc

The selected genotypes, rich in protein content and good in popping quality were analyzed for iron and zinc content.

The samples were digested according to the procedure given by Jackson (1973) using diacid mixture of nitric acid and perchloric acid using (HNO_3 : $HClO_4$) in 9:4 ratio and determined by the Atomic absorption spectrophotometer (SHIMADZO model AA-6650).

One gram of sample was added with 5 ml of HNO_3 and left overnight for predigestion. Then sample was digested with 15-20 ml of diacid mixture till all the $HClO_4$ evaporated and snow-white residue was got. The solution was made filtered through Whatman No.42 and volume made up to 100 ml with glass-distilled water. The amount of iron and zinc were determined by absorption spectrophotometer.

3.4.3 Processing

3.4.3.1 Popping

It is the most common processing technique followed conventionally. Hence genotypes were evaluated for popping quality.

A known quantity of grains were put in boiling water for a minute and then drained. The grains were dried in shade. The conditioned grains were put on a hot iron pan and stirred briskly over steady fire. The pops were removed after the hissing sound stopped. The popped and un-popped grains were separated by sieving. The popping yield was calculated using the formula and expressed in percentage.

$$\text{Popping yield (\%)} = \frac{\text{Popped grain weight}}{\text{Total (Popped + un-popped) weight}} \times 100$$

3.4.3.2 Expansion volume

One representative sample from each accession in each replication was taken to find out volume expansion. 5 grams of the seeds were taken and pops prepared. The ratio of the volume of popped grains to that of native grains was taken as the expansion volume.

$$\text{Expansion volume (ml/g)} = \frac{\text{Volume of popped grain}}{\text{Equivalent weight of un-popped grains}}$$

3.5 STATISTICAL ANALYSIS

The statistical analysis of the data on individual character was carried out on the mean values of five plants over three replications. The data was analyzed using software Statistical Package for Agricultural Research (SPAR) developed by Indian Statistical Research Institute, New Delhi. Statistical methods followed are given below:

3.5.1 Analysis of variance (ANOVA)

The programme for simple lattice design was run in the computer for the data on mean values of thirteen characters. The efficiency of Simple Lattice Design over Randomized Complete Block Design (RCBD) was calculated. The efficiency was found to be on par with RCBD. Therefore, analysis of variance following RCBD was followed.

The data on the mean values of the thirteen characters were analysed for their variance following RCBD as proposed by Sundararaj *et al.* (1972).

Source of variation	Degrees of freedom	Mean sum of square	F- value
Replication	(r-1)	MSS_r	MSS_r/MSS_e
Genotypes	(g-1)	MSS_g	MSS_g/MSS_e
Error	(r-1) (g-1)	MSS_e	
Total	(gr-1)		

Where, r = number of replications

G = number of genotypes (treatments)

MSS_r, MSS_g, MSS_e = mean sum of squares due to replications, genotypes and error respectively

The significance was tested by comparing with the table value given by Hayes *et al.* (1965). Further, standard error of means (SEm) critical difference (CD) and coefficient of variation (CV) were worked out using appropriate formulae for comparing means of genotypes.

3.5.2 Estimation of variance components

Phenotypic and genotypic components of variance were estimated with the help of following formulae:

$$\text{Genotypic variance } (\sigma^2_g) = \frac{MSS_g - MSS_e}{\text{Number of replications}}$$

Phenotypic variance (σ^2_p) = Genotypic variance + MSS_e

3.5.3 Estimation of genetic variability

Both genotypic and phenotypic coefficients of variability for all the characters were computed as per the method given by Burton and Devane (1953).

3.5.4 Genotypic Coefficient of Variability (GCV)

$$GCV = \frac{\sigma_g}{\overline{X}} \times 100$$

Where, σ_g = Genotypic standard deviation

$\overline{X}$ = General mean of the character

3.5.5 Phenotypic Co-efficient of Variability (PCV)

$$PCV = \frac{\sigma_p}{\overline{X}} \times 100$$

Where, σ_p = Phenotypic standard deviation

$\overline{X}$ = General mean of the character

3.5.6 Estimation of heritability

Broad sense heritability for all the thirteen characters were worked out using the formula given by Hanson *et al.* (1956).

$$\text{Percentage} \quad h^2 = \frac{\sigma^2_g}{\sigma^2_P} \times 100$$

Where, σ^2_g = genotypic variance

σ^2_P = phenotypic (total) variance

3.5.7 Genetic advance (GA)

Genetic advance as per cent of mean for each character was worked out by adopting the formula given by Johnson *et al.* (1955).

Genetic advance (GA) = $h^2.\sigma_p.K$

Where, h^2= Heritability in broadsense

K = Selection differential, K=2.06 at 5 per cent intensity of selection (Lush, 1949)

σ_p= Phenotypic standard deviation

Further, genetic advance as per cent mean (GAM) was worked out by using the formula given below:

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

Where,

GA = Genetic advance

$\overline{X}$ = General mean of the character

3.6 ASSOCIATION ANALYSIS

3.6.1 Simple correlation

The correlation co-efficient were calculated to determine the degree of association of characters with yield and also among the yield components. Phenotypic and genotypic correlation co-efficient were compared against table 'r' values given by Fisher and Yates (1963) at 'n-2' d.f at the probability levels of 0.05 and 0.01 to test their significance. Genotypic and phenotypic correlations were computed by using the formula given by Weber and Moorthy (1952).

$$r_g = \frac{COVxy_g}{\sqrt{\sigma^2 x_g \times \sigma^2 y_g}}$$

Where,

$COV\ xy_g$ = genotypic covariance for xy

$\sigma^2 x_g$ and $\sigma^2 y_g$ = genotypic variance of the characters x and y

r_g = genotypic correlation

$$r_p = \frac{COVxy_p}{\sqrt{\sigma^2 x_p \times \sigma^2 y_p}}$$

Where,

$COV\ xy_p$ = phenotypic covariance for xy

σ^2x_p and σ^2y_p = phenotypic variance of the characters x and y

r_p = Phenotypic correlation

3.6.2 Path coefficient analysis

Path coefficient analysis was carried out using the phenotypic correlation coefficients to know the direct and indirect effects of the yield components on yield as suggested by Wright (1921) and illustrated by Dewey and Lu (1957).

Standard path coefficients which are the standardized partial regression coefficients, were obtained by solving the following set of 'P' simultaneous equation through the use of "DOO LITTLE TECHNIQUE" as described by Goulden (1959).

$P_{01}+P_{02}.r_{12}+----------P_{0n}\ r_{1n} = r_{01}$

$P_{01}.r_{12}+P_{12}.r_{02}+----------P_{0n}\ r_{2n} = r_{02}$

-

-

-

-

$P_{01}r_{1n}+P_{02}.r_{2n}+----------P_{0n} = r_{0n}$

Where, P_{01}, P_{02} ----------P_{0n} are the direct path coefficients of variables 1, 2, ----------n on the dependent variable 0, r_{12}, r_{13} ----------r_{1p}----------r_p (p-1) are the possible correlation coefficients between various independent variables and r_{01}, r_{02}, ---------- r_{0p} are the

correlations between dependent variable and independent variable.

$$P^2_{0x} = 1-(P^2_{01}+2P_{01}P_{02}\, r_{12}+2P_{01}P_{03}\, r_{13}+\text{----------}+P^2_{02}+2P_{02}\, P_{03}\, r_{13}+ \text{----------} + P^2_{0P})$$

$$\text{Residual effect} = \sqrt{P^2_{0X}}$$

3.7 GENETIC DIVERSITY

3.7.1 Mahalanobis D^2 analysis

The formula given by Mahalanobis (1936) was used to compute the distances between different populations. The square of the Mahalanobis generalized distance between any two populations is given by the formula,

$$\delta^2 = \sum \delta_i\, \delta_j\, r_{ij}$$

Where,

δ^2= Square of generalized distances

r_{ij}= Reciprocal of the common dispersion matrix

δ_i= $(u_{i1}-u_{i2})$

δ_j= $(u_{i1}-u_{j2})$

Where,

u= Vector of mean values for all the characters. The formula for the estimation of distance D for the samples

$$D^2_p = d^1 s^{-1} d$$

Where,

D^2_p= Square of the distance considering p variables

d = Vector of observed differences of the mean vales of all the characters = $(x_{i1} - x_{i2})$

x_{i1} = Vector of the mean values of all the characters

s^{-1} = Inverse of variance and covariance matrix

Since investigating the matrix is complicated the original correlation variables (x_i) were transformed to non-correlated variables (y_i). So the computation of D^2 values reduces to simple summation of the square of the difference between the values of transformed variables of the two populations. This transformation is done by pivotal condensation method. These newly transformed uncorrelated variables were used to calculate the square of distance using the formula,

$$D^2 = (y_{i1} - y_{i2})^2$$

Where,

y= vector of transformed mean values

The square of these D^2 values gives the general distance between the two populations. The D^2 values were arranged in matrix form.

The significance of D^2 values between any two populations is tested using the following formula,

$$T^2 = \frac{N_1 \times N_2}{N_1 + N_2} \times D^2$$

Using T^2, the F value was calculated using the formula,

$$F = \frac{N_1 + N_2 - P - 1}{(N_1 + N_2 - 2)P} \times T^2$$

This computed F value was compared with the table F value at five per cent and one per cent level of significance at P and (N_1+N_2-P-1) degrees of freedom.

3.7.2 Clustering of D^2 values

All the $[n(n-1)/2]D^2$ values were clustered using Tocher's method as described by Rao (1952).

3.7.3 Intra-cluster distance

The intra-cluster distances were calculated by the formula given by Singh and Chaudhary (1977)

$$\text{Square of intra-cluster distance} = \frac{\sum D_i^2}{n}$$

Where,

$\sum D_i^2$ = Sum of distance between all possible combination of the entries included in a cluster

n = Number of all possible combinations

3.7.4 Inter-cluster distance

The inter-cluster distances were calculated by the formula given by Singh and Chaudhary (1977).

$$\text{Square of intra-cluster distance} = \frac{\sum D_i^2}{n_i n_j}$$

Where,

$\sum D_i^2$ = Sum of distances between all possible combination ($n_i n_j$) of the entries included in the cluster study (i and j)

n_i = Number of entries in cluster i

n_j = Number of entries in cluster j

3.8 SELECTION INDICES

3.8.1 Formulation of selection indices

The discriminant function technique of Fisher (1936) used by Smith (1936) to propose a selection model for selecting several characters simultaneously was adopted. The function aims at discriminating the desirable genotypes from undesirable ones based on their phenotypic performance. The genetic worth of an individual as described by Smith (1936) is,

$H=a_1G_1 + a_2G_2+----------+a_nG_n$

Where,

$G_1,G_2,-------G_n$ are the genotypic values of individual characters.

$a_1,a_2----------a_n$ signify their relative importance

Phenotypic performance of various characters is used in defining another function (I) as

$I= b_1P_1+b_2P_2+----------+b_nP_n$

Where,

$b_1,b_2---------b_n$ are to be estimated such that the correlation between H and I i.e., r (HI) becomes maximum. When one such function is obtained discrimination of desirable genotypes from the undesirable ones will be possible on the basis of phonotypic performance i.e., P_1, $P_2,----------P_n$ directly.

The maximization of r(HI) leads to set of simultaneous equations which upon solving give the direct estimate of bi-values. They are as follows,

$b_1P_{11}+b_2P_{12}+----------+b_nP_n=a_1G_{11}+a_2G_{12}+----------+a_nG_n$

$b_1P_{21}+b_2P_{22}+----------+b_nP_{2n}=a_2G_{22}+a_2G_{22}+----------+a_nG_n$

.
.
.
.

$b_1P_{n1}+b_2P_{n2}+----------+b_nP_{nn}=a_1G_{n1}+a_2G_{n2}+----------+a_nG_n$

This in the matrix form becomes,

$$\begin{pmatrix} P_{11}P_{12}.....P_{1n} \\ P_{21}P_{22}.....P_{2n} \\ . \\ . \\ . \\ P_{n1}P_{n2}.....P_{nn} \end{pmatrix} \begin{pmatrix} b_1 \\ b_2 \\ . \\ . \\ . \\ b_n \end{pmatrix} = \begin{pmatrix} G_{11}G_{12}.....G_{1n} \\ G_{21}G_{22}.....G_{2n} \\ . \\ . \\ . \\ G_{n1}G_{n2}.....G_{nn} \end{pmatrix} \begin{pmatrix} a_1 \\ a_2 \\ . \\ . \\ . \\ a_n \end{pmatrix}$$

The solution of these equations gives the estimates of bi values in the following manner $b = P^{-1} Ga$.

Where, b is column vector

P^{-1} is the inverse of phenotypic variance and covariance matrix.

G is the genotypic variance and co-variance matrix and a is the column vector for the economic weights.

The selection index is given by the mathematical description of the function (I) and the selection criterion or the index value for each individual may be determined and written as,

$I = b_1P_1+b_2P_2+..... + b_nP_n$

3.8.1 Expected genetic gain and relative efficiency from the use of the selection index

a) Genetic advance based on single character

The expected gain through selection for a single character was calculated using the formula suggested by Johnson *et al.* (1955b).

$$GA = \frac{g_{1.2}}{\sigma_{P1}} \times K$$

Where,

$g_{1.2}$ = Genotypic covariance between selected and unselected characters.

σ_{P1} = Phenotypic standard deviation of the selected character

K = Selection differential at 5 per cent.

b) Genetic advance based on a combination of a character

The expected genetic advance through selection based on a combination of characters was predicted by the formula given by Robinson *et al.* (1951).

$$GA\ (SI) = Z/P\sqrt{P_i G_{iy}}$$

Where,

GA (SI) = Genetic advance based on selection index

Z/P = K = Selection differential (2.06 at 5%)

P_i = Coefficients of a selection index

G_{iy} = G_{1y}, G_{2y}, G_{3y} ..... G_{ny}.

i.e., genotypic covariance between the selected (x) and unselected (y) characters.

c) Relative efficiency (RE)

Considering the efficiency of yield alone as 100 per cent, the relative efficiency of a particular selection index was computed as per the formula of Brim *et al.* (1959) as,

$$RE = \frac{\text{GA of the selection index}}{\text{GA by straight selection}} \times 100$$

Experimental results

IV. EXPERIMENTAL RESULTS

The results obtained from the analysis of data for each character separately are presented under the following headings:

1. Analysis of variance
2. Correlation and path coefficient analysis
3. Genetic diversity
4. Selection indices
5. Quality characters

4.1 ANALYSIS OF VARIANCE

The mean values for all the thirteen characters recorded on 64 genotypes are presented in Appendix I. The mean sum of squares due to various sources of variation for different traits are presented in Table 2. The mean sum of squares were found significant for all the characters studied.

4.2 GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE

To understand the extent to which the observed variations were due to genetic factors, the range, mean, phenotypic variance (PV), genotypic variance (GV), phenotypic and genotypic coefficient of variation (PCV and GCV), heritability (broad sense), genetic advance and genetic

Table 2 : Analysis of variance for thirteen characters in grain amaranth

Source of variation	d.f.	Mean sum of squares (MSS)												
		X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}	X_{13}
Genotype	63	37.864**	374.150**	1.467*	264.244**	75.480**	1034.582**	15629.418**	1382.070**	426.249**	2502.100**	1346.193**	54.843**	390.79**
Error	126	0.297	68.331	0.382	10.739	3.731	88.026	197.053	26.745	36.604	28.177	33.441	1.977	4.522
CV (%)		1.040	7.562	10.452	8.781	11.055	5.646	5.733	6.574	9.914	5.112	6.085	10.094	7.802

* = Significant at 5 per cent level
** = Significant at 1 per cent level

X_1 – Days to 50% flowering
X_2 – Days to maturity
X_3 – Stem girth at collar region
X_4 – Number of leaves
X_5 – Number of branches
X_6 – Plant height
X_7 – Panicle fresh weight
X_8 – Panicle length
X_9 – Number of spikes/panicle
X_{10} – Dry weight of panicle
X_{11} – Dry weight of stem
X_{12} – Harvest index (%)
X_{13} – Seed yield/plant

advance over mean for all the thirteen characters are presented in Table 3. The values of phenotypic and genotypic coefficient of variation, heritability and genetic advance are graphically represented in Fig.1 and 2. It is apparent from the Table that large amount of variability available with respect to various characters under study.

Phenotypic coefficient of variation ranged from 6.83 per cent (days to 50 per cent flowering) to 42.35 per cent (seed yield per plant). Genotypic coefficient of variation ranged from 6.75 per cent (days to 50 per cent flowering) to 41.63 per cent (seed yield per plant). The estimates of broad sense heritability ranged from 48.6 per cent (stem girth at collar region) to 97.7 per cent (days to 50 per cent flowering). Genetic advance expressed as per cent of means ranged from 13.74 (days to 50 per cent flowering) to 85.78 (seed yield per plant). Results with regard to variability parameters are presented below characterwise.

4.2.1 Days to 50 per cent flowering

Overall mean for days to 50 per cent flowering in the collection was 52.40 days with a wide range of variation from as early as 41.67 days to as late as 56.67 days.

Table 3 : Genetic parameters for thirteen different characters in grain amaranth (*Amaranthus* spp.)

Sl. No.	Characters	Range		Mean	Variance		Coefficient of variation		Heritability (%)	Genetic advance at 5% (GA)	Genetic advance as per cent mean (GAM)
		Min.	Max.		Phenotypic	Genotypic	Phenotypic (PCV)	Genotypic (GCV)			
1	Days to 50% flowering	41.67	56.67	52.40	12.82	12.52	6.83	6.75	97.7	7.20	13.74
2	Days to maturity	76.31	120.90	109.30	170.27	101.94	11.94	9.24	59.9	16.09	14.72
3	Stem girth at collar region (cm)	4.11	7.55	5.91	0.74	0.36	14.59	10.17	48.6	0.86	14.55
4	Number of leaves	11.13	59.33	37.42	95.24	84.50	26.15	24.63	88.7	17.84	47.68
5	Number of branches	7.40	27.60	17.47	75.48	71.75	30.09	27.99	86.5	9.37	53.63
6	Plant height (cm)	100.33	199.20	166.15	403.54	315.52	12.09	10.69	78.2	32.36	19.48
7	Panicle fresh weight (g)	84.40	433.07	243.13	5341.17	5144.12	29.85	29.29	96.3	145.00	59.64
8	Panicle length (cm)	31.13	126.33	78.66	478.52	451.78	27.81	27.02	94.4	42.54	54.08
9	Number of spikes/ panicle	32.93	87.20	61.02	166.49	129.88	21.14	18.68	78.0	20.74	33.98
10	Dry weight of panicle (g)	42.20	177.47	100.09	852.82	824.64	28.13	27.66	96.7	58.17	58.12
11	Dry weight of stem (g)	24.13	171.00	95.03	471.03	437.58	22.84	22.01	92.9	41.53	43.70
12	Harvest index (%)	5.83	25.03	13.93	19.59	17.62	31.78	30.14	89.9	8.20	58.87
13	Seed yield / plant (g)	10.71	59.82	26.79	133.28	128.76	42.35	41.63	96.6	22.98	85.78

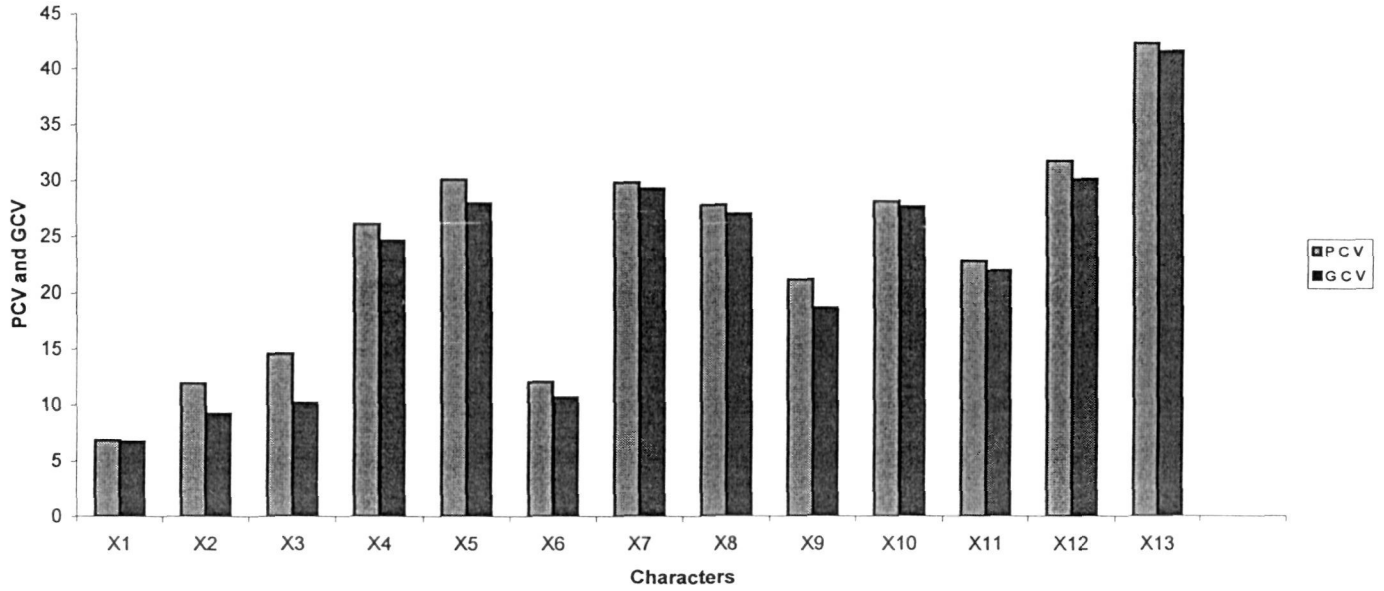


Fig-1: Phenotypic and Genotypic coefficient of variation for thirteen characters

X_1 – Days to 50% flowering
X_2 – Days to maturity
X_3 – Stem girth at collar region
X_4 – Number of leaves
X_5 – Number of branches
X_6 – Plant height
X_7 – Panicle fresh weight
X_8 – Panicle length
X_9 – Number of spikes/panicle
X_{10} – Dry weight of panicle
X_{11} – Dry weight of stem
X_{12} – Harvest index (%)
X_{13} – Seed yield/plant

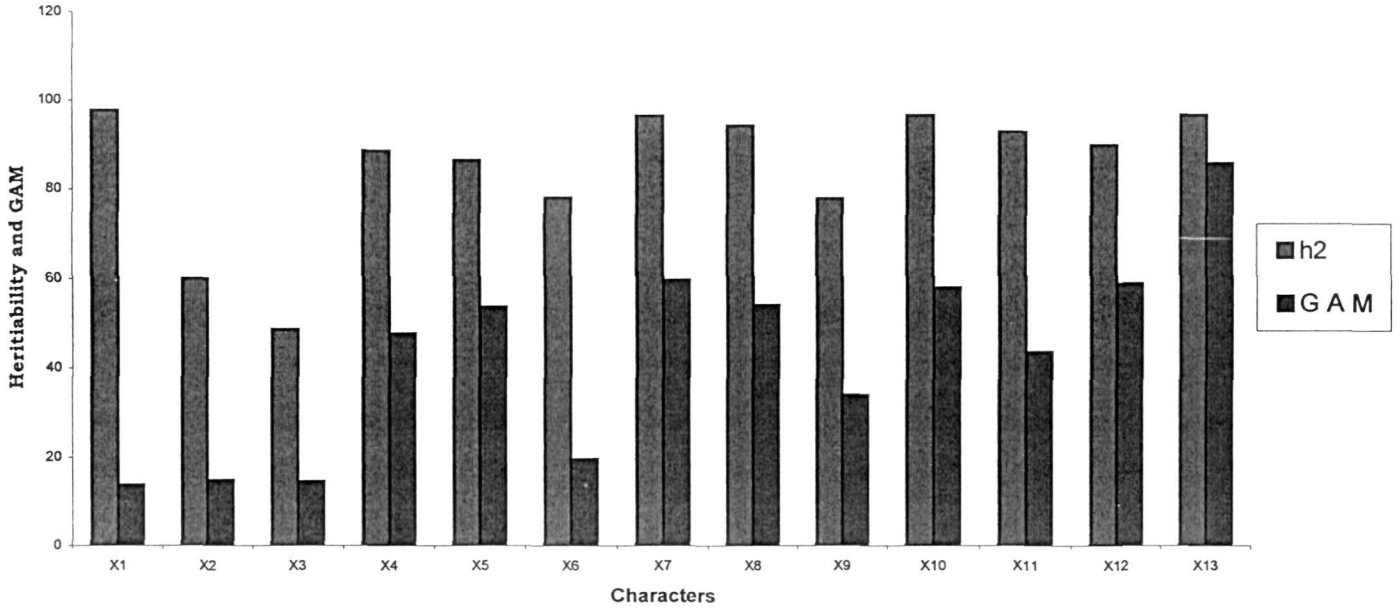


Fig-2: Heritability and Genetic Advance as per cent mean for thirteen characters

X_1 – Days to 50% flowering
X_2 – Days to maturity
X_3 – Stem girth at collar region
X_4 – Number of leaves
X_5 – Number of branches
X_6 – Plant height
X_7 – Panicle fresh weight
X_8 – Panicle length
X_9 – Number of spikes/panicle
X_{10} – Dry weight of panicle
X_{11} – Dry weight of stem
X_{12} – Harvest index (%)
X_{13} – Seed yield/plant

The accessions BGA-2 (41.67 days) and Eidual Tivan (42.00 days) were the earliest to reach 50 per cent flowering, while the genotype IC-74656 (56.67 days) and IC-35479 (56.33 days) were late to reach 50 per cent flowering as compared to check, Annapurna which took 50.67 mean number of days for flowering. The genotypic and phenotypic coefficients of variation were 6.75 per cent and 6.83 per cent, respectively. This trait had high heritability (97.7%) with low expected genetic advance (7.20) and moderate genetic advance as per cent mean (13.74%).

4.2.2 Days to maturity

All genotypes displayed a wide range of variation for this character with a mean of 109.30 days. The range in the collection varied from 76.31 days to 120.90 days.

The genotype IC-95414 completed maturity in 76.31 mean number of days, while IC-120588 and IC-35722 took 120.90 and 120.80 mean number of days to mature, respectively, as compared to the check, Annapurna which took 89.61 days. The estimate of GCV (9.24%) and PCV (11.94%) were low. Moderate heritability (59.9%) was observed for this character. The expected genetic advance was moderate (16.09).

The character exhibited moderate genetic advance as per cent mean (14.72).

4.2.3 Stem girth at collar region

This trait showed significant difference among the genotypes. The overall mean was 5.91 cm with a range of 4.11 cm (IC-95414) to 7.55 cm (IC-81694), over the check, Annapurna (5.55 cm).

Phenotypic (0.74) and genotypic (0.27) variance were low with the influence of environment at a lesser degree. Moderate PCV (14.59%) and GCV (10.17%) were accompanied by moderate heritability estimate of 48.6 per cent. This character showed low expected genetic advance (0.86cm) and moderate genetic advance value of 14.55 per cent over mean.

4.2.4 Number of leaves

This character revealed a wide variation of 11.13 to 59.33 leaves per plant and mean number of leaves recorded was 37.42 per plant. The lowest number of leaves were observed in the accession Eidual Tivan (11.13) followed by BGA-2 (18.67) and highest number of leaves were observed in the genotype GA-Suvarna (59.33) and GA-1 (56.20), Annapurna had 42.27 mean number of leaves.

Phenotypic and genotypic variance values were 95.24 and 84.50 with high PCV and GCV of 26.15 and 24.63 per cent, respectively. This trait exhibited high heritability (88.7%) with moderate genetic advance of 17.84 and the per cent mean genetic advance was high (47.68%).

4.2.5 Number of branches

A wide range of variation was observed for this character. Number of branches varied from 7.40 to 27.60 in the collection with overall mean of 17.47 branches per plant. The accession IC-32195 (7.40) showed less number of branches followed by check, Annapurna (8.47), while the genotype IC-35742 was highly branching (27.60) followed by GA-Suvarna (27.07).

The genotypic and phenotypic coefficients of variation were 30.09 and 27.99 per cent, respectively. This trait had high estimate of heritability (86.5%) coupled with high per cent mean genetic advance (53.63%). But the expected genetic advance was 9.37

4.2.6 Plant height

Plant height varied from 100.33 to 199.20 cm with an overall mean of 166.15 cm. The accession IC-95414 was the shortest genotype (100.33 cm) in the collection while

IC-35635 the tallest (199.20 cm) followed by IC-35663 (196.67 cm) and SKNA-7 (194.47 cm). The height of Annapurna was 165.87 cm.

GCV and PCV were 10.69 and 12.09 per cent, respectively. The genotypic and phenotypic variances recorded were 315.52 and 403.54, respectively. This trait exhibited fairly high heritability of 78.2 per cent coupled with high expected genetic advance (32.36). The per cent mean genetic advance was moderately high (19.48).

4.2.7 Panicle fresh weight

The results revealed that this character showed a wide range of variation. The panicle fresh weight varied from 84.40 to 433.07g with a mean of 243.13g. The accession BGA-2 recorded maximum weight of 433.07 g while IC-95414 recorded lowest weight of 84.40 g as compared to the check, Annapurna (323.73g)

This character exhibited high phenotypic and genotypic coefficient of variability values of 29.85 and 29.29, respectively. The meager difference between them indicates very low influence of extraneous factors. The heritability estimate (96.3%) and genetic advance over per cent mean (59.64%) were high. The phenotypic and genotypic variances

were 5341.17 and 5144.12, respectively which indicates high environmental influence on the expression of this trait.

4.2.8 Panicle length

Panicle length varied from 31.13 to 126.33 cm with an over all mean of 78.66 cm. The genotype IC -95358 (31.13 cm) had shorter panicle followed by accession Eidual Tivan (32.20 cm) and IC-95414 (35.07 cm). The accession IC-35696 had longest panicle (126.33 cm) in the collection followed by accession IC-81694 (119.33 cm). The panicle length of check, Annapurna was 86.27 cm.

GCV and PCV were 27.02 and 27.81 per cent, respectively. High heritability estimate (94.4%) coupled with high per cent mean genetic advance (54.08) was observed. The expected genetic advance was also high (42.54cm).

4.2.9 Number of spikes per panicle

The range observed for number of spikes per panicle was 32.93 to 87.20. The average number of spikes per panicle was 61.02. The genotype RGAS-92-10-1 beared very les number of spikes (32.93) in the collection followed by IC-95358 (40.27), while the accession IC-35696 had highest number of spikes per panicle (87.20) as compared to the check, Annapurna which showed 73.40 mean number of spikes per panicle.

The value of PCV was moderately high (21.14 per cent) and that of GCV moderate (18.68 per cent). A high heritability (78.0 per cent) coupled with high per cent genetic advance over mean (33.98%) was observed. The genetic advance (20.74) was moderate. The components of variance observed were 166.49 for phenotypic variance and 129.88 for genotypic variance.

4.2.10 Dry weight of panicle

The dry weight of panicle ranged from 42.20 to 177.47g with a mean dry weight of 100.09g. The accession BGA-2 (177.47g) recorded the highest value followed by IC-35696 (177.13g) and IC-8170-A (155.13g), while the genotype IC-95414 (42.20g) recorded lowest value followed by IC-2935514 (57.60g). The mean dry weight of panicle of the check, Annapurna was 111.33 g.

The phenotypic (28.13%) and genotypic (27.66%) coefficient of variations were high. A high heritability of 96.7 per cent was observed. The expected genetic advance (58.17g) and the per cent genetic advance over mean (58.12) were also high. The components of variance *viz.*, phenotypic and genotypic variance were 852.82 and 824.64, respectively.

Hence, fairly high environmental influence on the expression of this character is indicated.

4.2.11 Dry weight of stem

The germplasm showed wide variability for this character which ranged from 24.13 to 171.00g. The overall mean was 95.03g. The accessions IC-95414 and IC-81694 recorded the lowest and highest values of 24.13g and 171.00g, respectively, whereas, the check, Annapurna had 95.53g.

The phenotypic and genotypic variance values were 471.03 and 437.58, respectively. The phenotypic and genotypic coefficient of variation was 22.84 and 22.01 per cent, respectively. The heritability estimate was high (92.9%) coupled with high expected genetic advance (41.53g) and high per cent genetic advance over mean (43.70).

4.2.12 Harvest index

A wide range was observed for harvest index with minimum value being 5.83 per cent and maximum value being 25.03 per cent. The average harvest index was noticed to be 13.93 per cent. The lowest harvest index was recorded by accession IC-95567 (5.83%), followed by the genotype IC-45517 (6.93%), while the highest harvest index recorded in the variety Suvarna (22.47%), followed

by IC-42004 (21.58%) and BGA-2 (21.08%). The harvest index recorded by the check, Annapurna was 25.3%.

The PCV (31.78 per cent) was high, so also the GCV (30.14 per cent). However, the heritability (89.9%) was high for the character because of the less difference between the magnitude of PCV and GCV, consequently the per cent genetic advance over mean was high (58.87). But the expected genetic advance was low (8.20%).

4.2.13 Seed yield per plant

Seed yield per plant exhibited a wide amount of variation ranging from 10.71 to 59.82 grams per plant. The over all mean was 26.79g. The genotype IC-95567 was poor yielder (10.71g) on per plant basis, followed by AG-114 (11.15g). The genotype BGA-2 (Plate 2) recorded maximum seed yield per plant (59.82g) followed by BAS-3 (59.75g), the check, Annapurna (52.32 g) and Suvarna (48.61g).

The phenotypic and genotypic variance were 133.28 and 128.76 respectively, which were accompanied by high PCV of 42.35 per cent and GCV of 41.63 per cent. The seed yield per plant exhibited high estimate of heritability (96.60%) and high per cent genetic advance over mean (85.78) but, the expected genetic advance was moderately high (22.98g).

High yielding genotype (BGA-2)

Check (Annapurna)

Plate2: Inflorescence of high yielding genotype with check

4.3 CHARACTER ASSOCIATION

The genotypic and phenotypic correlation coefficients were computed between characters studied and the data is presented in Table 4 and 5, respectively. Graphical representation of genotypic and phenotypic correlations between yield and yield components is shown in Fig.3.

4.3.1 Association between yield and yield components

Highly significant positive correlation of seed yield with panicle fresh weight, panicle length, number of spikes per panicle, dry weight of panicle, dry weight of stem and harvest index was observed both at phenotypic and genotypic level (Table 4 and 5).

At genotypic level, which is more important than phenotypic level, the magnitude of correlation with seed yield was highest in case of harvest index (0.747) followed by panicle fresh weight (0.587), dry weight of panicle (0.578), panicle length (0.357), number of spikes per panicle (0.346) and dry weight of stem (0.268).

Significant negative correlation of seed yield per plant with days to 50 per cent flowering, days to maturity and number of branches were noticed at genotypic and phenotypic levels.

Table 4 : Phenotypic correlation coefficients between different traits in grain amaranth

Character	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}	X_{13}
X_1	1.000	0.472**	0.326**	0.528**	0.283*	0.361**	0.022	0.295*	0.173	-0.037	0.232	-0.318*	-0.331**
X_2		1.000	0.146	0.220	0.363**	0.241	-0.008	0.127	0.050	-0.057	0.101	-0.404**	-0.457**
X_3			1.000	0.276*	0.164	0.366**	0.250*	0.267*	0.219	0.199	0.482**	0.034	0.112
X_4				1.000	0.296*	0.334**	0.095	0.232	0.206	0.046	0.347**	-0.245	-0.160
X_5					1.000	0.264*	0.029	0.167	-0.009	-0.004	0.157	-0.319*	-0.250*
X_6						1.000	0.324**	0.332**	0.222	0.324**	0.428**	0.037	0.210
X_7							1.000	0.791**	0.311*	0.924**	0.554**	0.202	0.572**
X_8								1.000	0.456**	0.752**	0.542**	0.051	0.344**
X_9									1.000	0.312*	0.376**	0.311*	0.301*
X_{10}										1.000	0.514**	0.168	0.555**
X_{11}											1.000	-0.109	0.268*
X_{12}												1.000	0.692**
X_{13}													1.000

* = Significant at 5% level, ** = Significant at 1% level

X_1 – Days to 50% flowering
X_2 – Days to maturity
X_3 – Stem girth at collar region
X_4 – Number of leaves
X_5 – Number of branches
X_6 – Plant height
X_7 – Panicle fresh weight
X_8 – Panicle length
X_9 – Number of spikes/panicle
X_{10} – Dry weight of panicle
X_{11} – Dry weight of stem
X_{12} – Harvest index (%)
X_{13} – Seed yield/plant

Table 5 : Genotypic correlation coefficients between different traits in grain amaranth

Character	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}	X_{13}
X_1	1.000	0.604**	0.451**	0.568**	0.311*	0.412**	0.019	0.309*	0.196	-0.039	0.241	-0.341**	-0.339**
X_2		1.000	0.211	0.264*	0.521**	0.318*	-0.024	0.125	0.101	-0.068	0.128	0.125	-0.589**
X_3			1.000	0.339**	0.299*	0.594**	0.350**	0.366**	0.279*	0.292*	0.622**	0.099	0.162
X_4				1.000	0.345**	0.388**	0.107	0.252*	0.238	0.050	0.375**	-0.259*	-0.167
X_5					1.000	0.317*	0.028	0.188	-0.026	-0.005	0.173	-0.378**	-0.271*
X_6						1.000	0.355**	0.367**	0.278*	0.363**	0.505**	0.046	0.237
X_7							1.000	0.825**	0.380**	0.955**	0.579**	0.218	0.587**
X_8								1.000	0.540**	0.781**	0.560**	0.048	0.357**
X_9									1.000	0.366**	0.434**	0.375**	0.346**
X_{10}										1.000	0.542**	0.177	0.578**
X_{11}											1.000	-0.109	0.268*
X_{12}												1.000	0.747**
X_{13}													1.000

* = Significant at 5% level, ** = Significant at 1% level

X_1 – Days to 50% flowering
X_2 – Days to maturity
X_3 – Stem girth at collar region
X_4 – Number of leaves
X_5 – Number of branches
X_6 – Plant height
X_7 – Panicle fresh weight
X_8 – Panicle length
X_9 – Number of spikes/panicle
X_{10} – Dry weight of panicle
X_{11} – Dry weight of stem
X_{12} – Harvest index (%)
X_{13} – Seed yield/plant

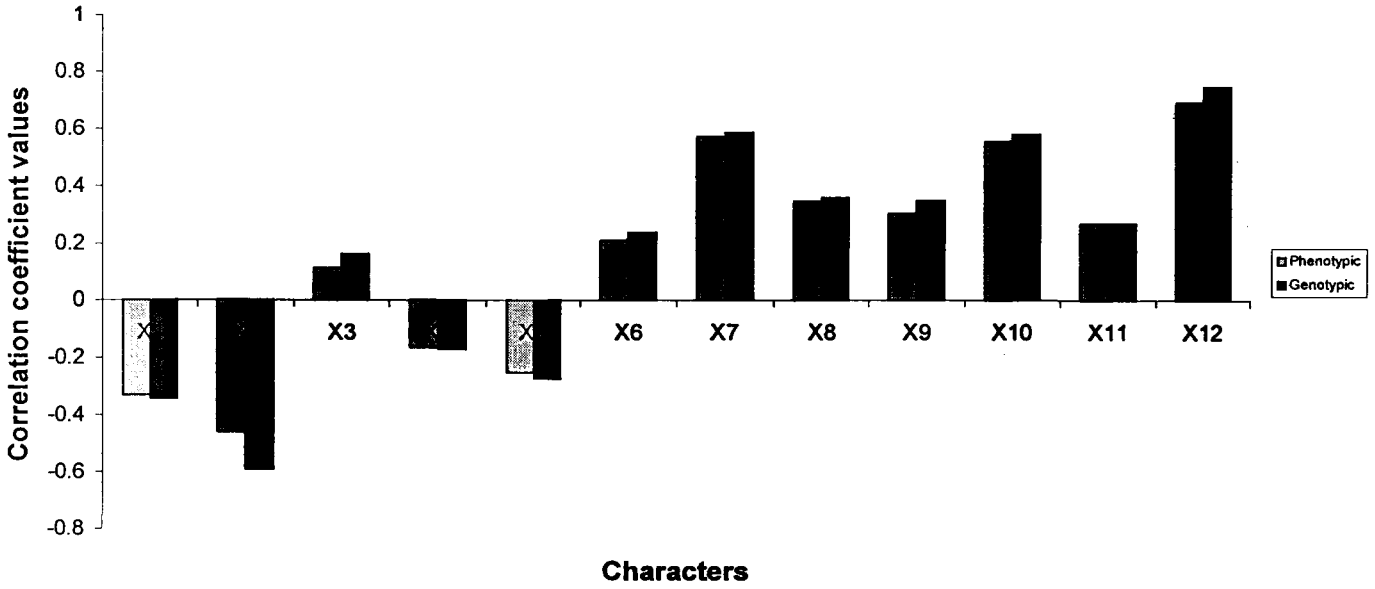


Fig 3: Phenotypic and Genotypic correlations between yield and yield components

X_1 – Days to 50% flowering
X_2 – Days to maturity
X_3 – Stem girth at collar region
X_4 – Number of leaves
X_5 – Number of branches
X_6 – Plant height
X_7 – Panicle fresh weight
X_8 – Panicle length
X_9 – Number of spikes/panicle
X_{10} – Dry weight of panicle
X_{11} – Dry weight of stem
X_{12} – Harvest index (%)

In general, the genotypic correlation coefficients were found to be higher than their respective phenotypic correlation coefficients.

4.3.2 Interrelation between the yield attributing characters

Both genotypically and phenotypically days to 50 per cent flowering showed highly significant positive correlation with days to maturity, stem girth at collar region, number of leaves, number of branches, plant height and panicle length. It showed significant negative correlation with harvest index.

Days to maturity showed significant positive correlation with number of leaves, number of branches and plant height at genotypic level. Highly significant association was observed between days to maturity and number of branches. Days to maturity showed highly significant but negative association with harvest index at phenotypic level.

The association of the stem girth at collar region with days to 50 per cent flowering, number of leaves, plant height, panicle fresh weight, panicle length and dry weight of stem was found to be positive and significant at both phenotypic and genotypic levels. It was positively and significantly associated with number of branches, number of spikes per

panicle and dry weight of panicle at genotypic level, but positive and non-significant at phenotypic level.

Number of leaves per plant was found to be positively and significantly associated with days to 50 per cent flowering, number of branches, plant height and dry weight of stem at both the levels. Significant positive genotypic correlation of this character was observed with panicle length but non-significant at phenotypic level. This trait exhibited significant negative association with harvest index at genotypic level and non-significant at phenotypic level.

Significant positive phenotypic and genotypic correlation of number of branches was observed with days to 50 per cent flowering, days to maturity, number of leaves and plant height. This character showed negative significant correlation with harvest index at both the levels. Negative non-significant correlation was observed for number of branches with number of spikes per panicle and dry weight of panicle at phenotypic and genotypic levels.

Plant height showed highly significant positive phenotypic and genotypic correlation with panicle fresh weight, panicle length, dry weight of panicle, dry weight of stem, days to 50 per cent flowering, stem girth at collar region

and number of leaves. This character also showed positive significant genotypic and phenotypic association with number of branches. Positive significant genotypic correlations were observed between plant height, number of spikes per panicle and days to maturity.

At phenotypic and genotypic level fresh weight of panicle had significant positive association with stem girth at collar region, plant height, panicle length, number of spikes per panicle, dry weight of panicle and dry weight of stem. This trait also exhibited negative non-significant association with days to maturity at both the levels.

Highly significant positive phenotypic and genotypic correlation of panicle length was observed with plant height, panicle fresh weight, number of spikes per panicle, dry weight of panicle and dry weight of stem. In addition, this character also showed significant positive association with days to 50 per cent flowering and stem girth at collar region at both the levels. Association of this trait with number of leaves was significant at genotypic level but not significant at phenotypic level.

Number of spikes per panicle showed a significant positive association with dry weight of panicle, dry weight of

stem, harvest index, panicle length and panicle fresh weight at both phenotypic and genotypic levels. It showed positive significant association with stem girth at collar region and plant height at genotypic level but non-significant at phenotypic level.

Both phenotypically and genotypically dry weight of panicle showed highly significant positive association with plant height, panicle fresh weight, panicle length number of spikes per panicle and dry weight of stem. Further this character showed negative association with days to 50 per cent flowering, days to maturity and number of leaves but the values were found to be non-significant.

Positive and highly significant associations of dry weight of stem with stem girth at collar region, number of leaves, plant height, panicle fresh weight, panicle length, number of spikes per panicle and dry weight of panicle were noticed both at phenotypic and genotypic levels. It also exhibited negative but non-significant association with harvest index.

Non-significant associations were found for harvest index with many of the traits irrespective of the direction at both phenotypic and genotypic levels. However days to 50 per cent flowering, number of branches showed significant correlation

in negative direction both at phenotypic and genotypic level. Further with days to maturity, the phenotypic correlation was found to be negatively significant and genotypic correlation non-significant in the positive direction. Significant positive association of this trait with number of spikes per panicle was found. While with dry weight of stem negative non-significant association was observed at both levels.

In general, the magnitudes of genotypic correlation coefficients were found to be higher than their respective phenotypic correlation coefficients.

4.4 PATH COEFFICIENT ANALYSIS

The correlation values denote only the nature and extent of association existing between the pairs of characters. A dependent character like seed yield is influenced by several component characters which are mutually associated. Each component has two path action *viz.*, direct effect on yield and indirect effects through components which are not revealed by correlation studies. Path coefficient analysis was carried out both at phenotypic and genotypic levels taking grain yield as dependent character and such of the characters found significantly correlated with seed yield *viz.*, panicle fresh weight, panicle length, number of spikes per panicle, dry

weight of panicle, dry weight of stem and harvest index as independent characters. The results obtained are given in the Table 6 and 7 and depicted in Fig.4 and 5. The direct and indirect effects of different characters on seed yield are presented below.

4.4.1 Direct effects of different characters on seed yield

Among the characters studied at phenotypic level, harvest index had highest direct positive effect of 0.481 on seed yield per plant followed by panicle fresh weight (0.310), dry weight of stem (0.141). Low direct effect of 0.0784 for dry weight of panicle and 0.003 for number of spikes per panicle were recorded. The direct contribution to grain yield by panicle length (-0.025) was negative. The residual effect was 0.2362.

At genotypic level, with regard to positive direct effects, the contribution to seed yield per plant by panicle fresh weight (0.623) was highest followed by those of harvest index (0.410) and dry weight of stem (0.160). Low positive direct effect of 0.110 was recorded for number of spikes per panicle towards seed yield per plant. The direct effect of panicle length (-0.276) and dry weight of panicle (-0.046) were negative. The residual effect (0.1099) was relatively low.

Table 6 : Direct (diagonal) and indirect (above and below diagonal) effects of six characters on seed yield in grain amaranth at phenotypic level

Character	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}	Phenotypic correlation co-efficient with yield
X_7	**0.310**	-0.019	0.001	0.072	0.078	0.097	0.572
X_8	0.245	**-0.025**	0.001	0.059	0.076	0.025	0.344
X_9	0.096	-0.011	**0.003**	0.024	0.053	0.150	0.301
X_{10}	0.286	-0.018	0.001	**0.078**	0.072	0.081	0.555
X_{11}	0.171	-0.013	0.001	0.040	**0.141**	-0.053	0.268
X_{12}	0.063	-0.001	0.001	0.013	-0.015	**0.481**	0.692

Residual = 0.2362

X_7 - Panicle fresh weight
X_8 - Panicle length
X_9 - Number of spikes / panicle
X_{10} - Dry weight of panicle
X_{11} - Dry weight of stem
X_{12} - Harvest index

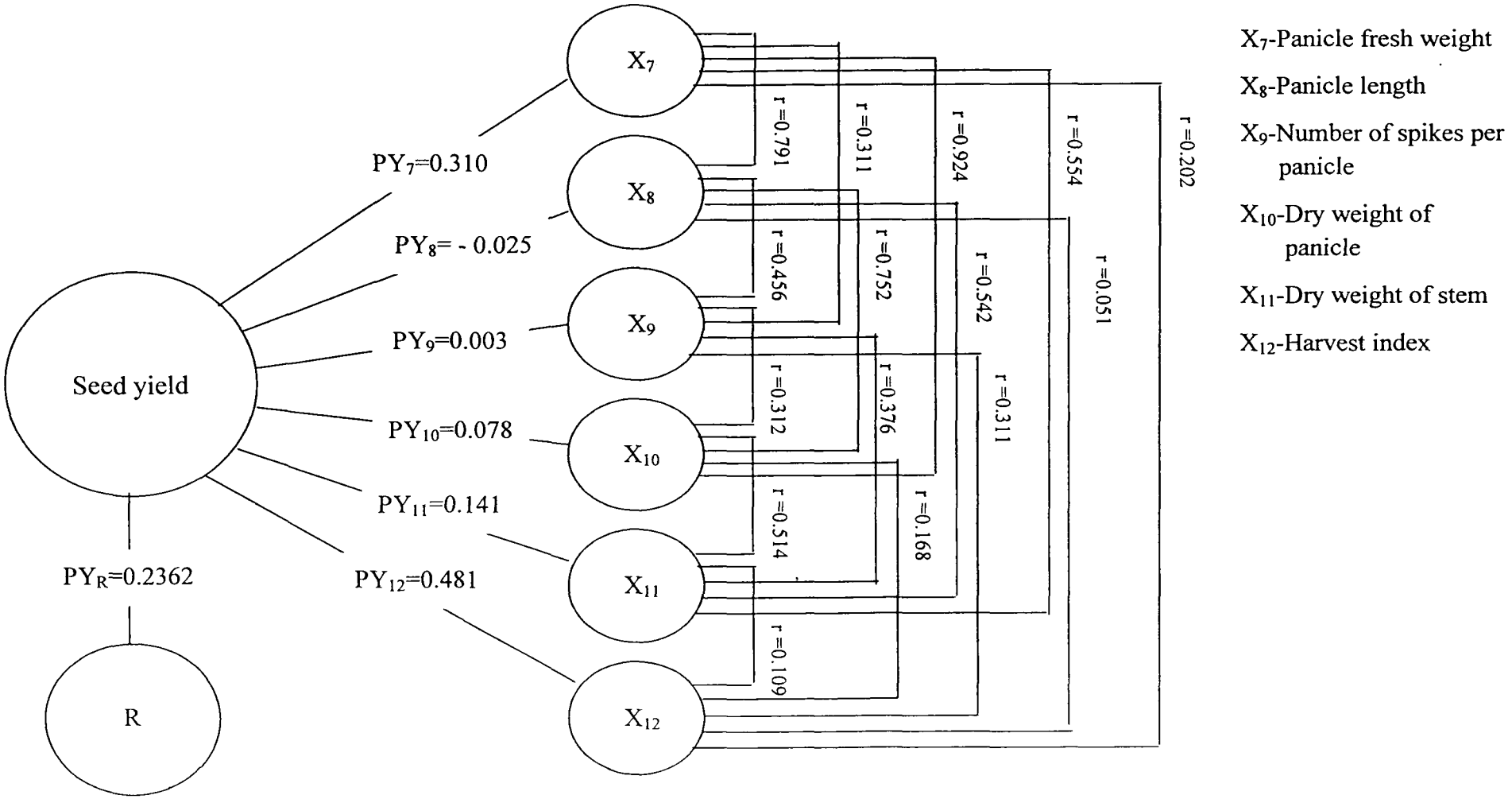


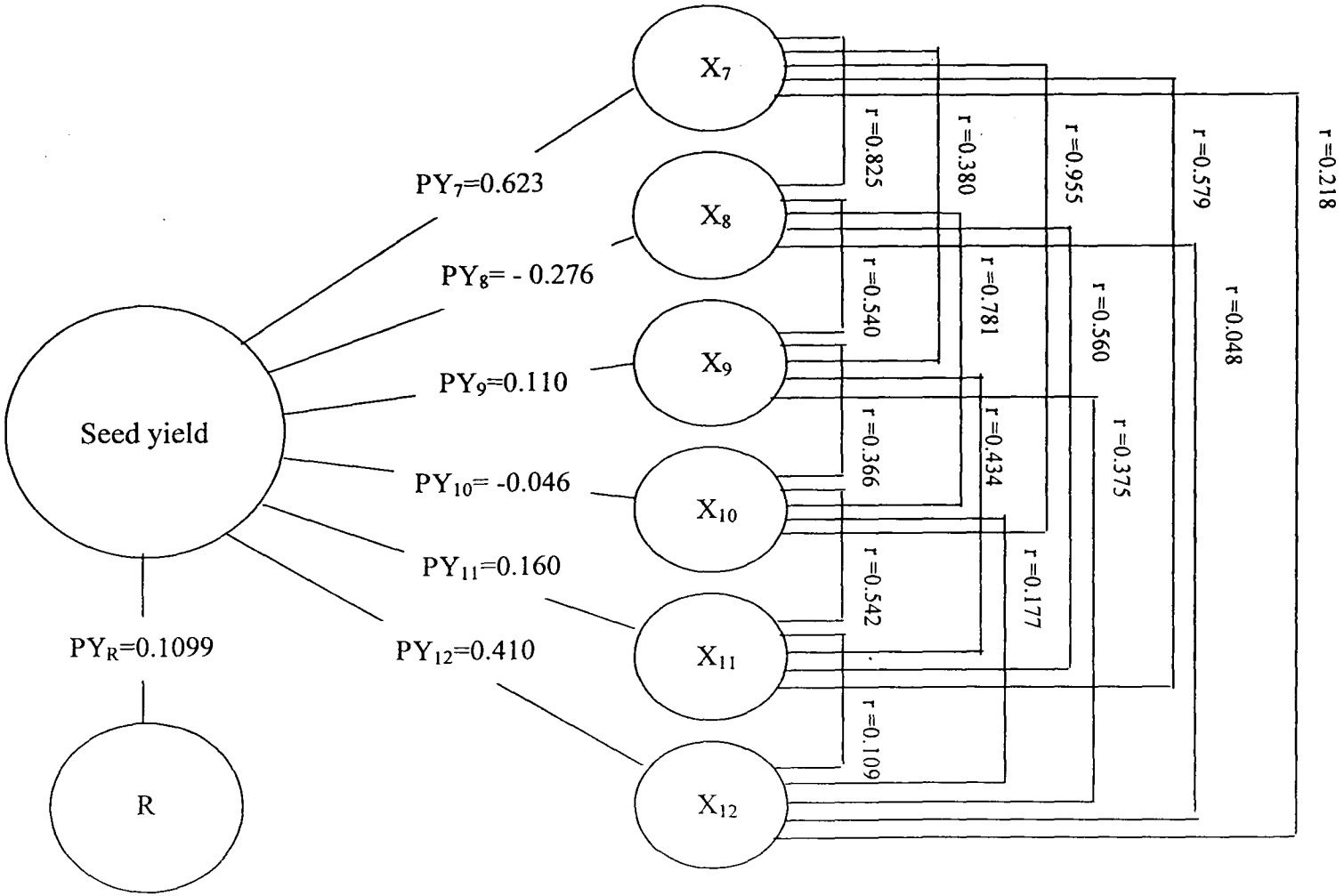
Fig. 4: Phenotypic path diagram of six major components influencing seed yield in grain amaranth

Table 7 : Direct (diagonal) and indirect (above and below diagonal) effects of six characters on seed yield in grain amaranth at genotypic level

Character	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}	Genotypic correlation co-efficient with yield
X_7	**0.623**	-0.228	0.042	-0.044	0.093	0.089	0.587
X_8	0.514	**-0.276**	0.059	-0.036	0.090	0.020	0.357
X_9	0.237	-0.149	**0.110**	-0.017	0.069	0.154	0.346
X_{10}	0.595	-0.216	0.040	**-0.046**	0.087	0.073	0.578
X_{11}	0.361	-0.155	0.048	-0.025	**0.160**	-0.045	0.268
X_{12}	0.136	-0.013	0.041	-0.008	-0.017	**0.410**	0.747

Residual = 0.1099

X_7 - Panicle fresh weight
X_8 - Panicle length
X_9 - Number of spikes / panicle
X_{10} - Dry weight of panicle
X_{11} - Dry weight of stem
X_{12} - Harvest index



X_7-Panicle fresh weight

X_8-Panicle length

X_9-Number of spikes per panicle

X_{10}-Dry weight of panicle

X_{11}-Dry weight of stem

X_{12}-Harvest index

Fig. 5 : Genotypic path diagram of six major components influencing seed yield in grain amaranth

4.4.2 Indirect effects of different characters on seed yield per plant

4.4.2.1 Panicle fresh weight

At phenotypic level, none of the indirect effects of this character were of higher magnitude than its direct effect (0.310). Indirect contribution of this character through harvest index (0.097), dry weight of stem (0.078) and dry weight of panicle (0.072) were positive but of low magnitude. Whereas, the indirect effect of this trait through number of spikes per panicle was negligible (0.001). While it had relatively low negative indirect effect of -0.025 through panicle length.

At genotypic level, this trait exhibited positive and high direct effect on seed yield per plant (0.623). This character influenced seed yield per plant via low positive indirect effect of dry weight of stem (0.093), harvest index (0.089) and number of spikes per panicle (0.042). Its indirect effect via panicle length (-0.228) and dry weight of panicle (-0.044) were negative.

4.4.2.2 Panicle length

At phenotypic level, it had low direct negative effect of -0.025 on seed yield per plant. Its indirect effect through panicle fresh weight (0.245) was in positive direction and

showed low positive indirect influence through dry weight of stem (0.076), dry weight of panicle (0.059), harvest index (0.025) and number of spikes per panicle, which was negligible (0.001).

At genotypic level, this character exerted negative direct contribution of -0.276 on seed yield per plant. It had high positive indirect effect on seed yield via panicle fresh weight (0.514). It also showed positive indirect influence on seed yield through dry weight of stem (0.090), number of spikes per panicle (0.059) and harvest index (0.020) but they were of low magnitude. Its indirect effect through dry weight of panicle (-0.036) was negative and of low magnitude.

4.4.2.3 Number of spikes per panicle

At phenotypic level, this trait had low direct positive effect of 0.003 on seed yield per plant. Its indirect effect through harvest index (0.150), panicle fresh weight (0.096), dry weight of stem (0.053) and dry weight of panicle (0.024) were in positive direction but of lower magnitude.

At genotypic level, this character exerted positive direct contribution of 0.110 on seed yield per plant. It exerted a high magnitude of positive indirect effect through panicle fresh weight (0.237) and harvest index (0.154). Its indirect

influence through dry weight of stem was also positive but of lower magnitude (0.069), while it had relatively low negative indirect effect through panicle length (-0.149) and dry weight of panicle (-0.017).

4.4.2.4 Dry weight of panicle

At phenotypic level, dry weight of panicle exhibited positive but low direct effect (0.078) on seed yield. Its contribution through panicle length (-0.018) was negative and low. This trait exerted a high magnitude of indirect positive effect through panicle fresh weight (0.286). Low amount of positive indirect effect of 0.081, 0.072 and 0.001 were recorded through harvest index, dry weight of stem and number of spikes per panicle, respectively.

At genotypic level, this character had negative direct effect (-0.046) on seed yield. It had a relatively high positive indirect effect on seed yield through panicle fresh weight (0.595). But its indirect effect through panicle length (-0.216) was negative and of low magnitude. It also showed positive but low influence on seed yield through dry weight of stem (0.087), harvest index (0.073) and number of spikes per panicle (0.040).

4.4.2.5 Dry weight of stem

At phenotypic level, it had direct positive effect of 0.141 on seed yield per plant. It had a relatively high positive indirect effect on seed yield through panicle fresh weight (0.171). The indirect influence of this character with panicle length (-0.013) and harvest index (-0.053) were negative and low. Indirect positive effects but of low magnitude was exerted through dry weight of panicle (0.040) and number of spikes per panicle (0.001).

At genotypic level also this character exhibited positive direct effect of 0.160 on seed yield per plant. It had positive indirect influence on seed yield through panicle fresh weight, but of high magnitude (0.361). Its indirect effect through panicle length (-0.155), dry weight of panicle (-0.025) and harvest index (-0.045) was negative and relatively low. It had a low positive indirect influence on seed yield via number of spikes per panicle (0.048).

4.4.2.6 Harvest index

At phenotypic level, this trait exhibited high positive direct effect (0.481) on seed yield per plant. The positive indirect effect of this character on seed yield with panicle fresh weight (0.063), dry weight of panicle (0.013) and number

of spikes per panicle (0.001) was low. But its indirect effect on seed yield through panicle length and dry weight of stem was negative but with negligible magnitude.

Harvest index had a high direct effect on seed yield (0.410). It showed relatively low positive indirect effect on seed yield through panicle fresh weight (0.136) and number of spikes per panicle (0.041). Harvest index had low negative indirect effects on seed yield through dry weight of stem (-0.017), dry weight of panicle (-0.008) and panicle length (-0.013), at genotypic level.

4.5 GENETIC DIVERSITY

4.5.1 Mahalanobis generalized distance (D^2)

The D^2 values between any two varieties were calculated as the sum of squares of the differences between the mean values of all the 13 characters and used for final grouping of the genotypes. Since each genotype produced 63 combinations, 2016 D^2 values were obtained for 64 genotypes.

4.5.2 Group constellations

A method suggested by Tocher (Rao, 1952) was used to group the genotypes into different clusters based on the D^2 values. Sixty four genotypes including one check were grouped into eleven clusters. The distribution pattern of genotypes

into various clusters is given in Table 8. Among 11 cluster, cluster I was the biggest with 35 genotypes followed by cluster IV with 10 genotypes, cluster II with 9 genotypes and 3 genotypes were grouped in cluster III. The remaining clusters (from V to XI) were all solitary, each containing single genotype.

4.5.3 Intra cluster distance

Intra cluster distance was observed only in the cluster I, II, III and IV as remaining seven clusters (V to XI) contained only one constituent genotype. Intra cluster distance was highest in the cluster II with D^2 value of 64.254, followed by cluster IV (64.028), I (55.139) and III (47.878). Intra cluster D^2 and D values are given in Table 9.

4.5.4 Inter cluster distance

Inter cluster D^2 and D values are given in Table 9. Cluster VII and IX were nearest to each other with an inter cluster distance of 49.151 (D=7.011). Cluster III and XI were most diverse clusters as distance between them was 397.178 (D=19.929). Cluster III was most diverse cluster as many clusters showed maximum inter cluster distance with it.

Cluster I which comprised 35 genotypes was closely related with clusters V, VI, X, VIII and IV with respective D

Table 8 : Composition of genotypes in different clusters

Clusters	Number of genotypes	Name of genotypes
I	35	IC-32195, DS-3, RAM-2, IC-35770, IC-66436, IC-95365, IC-35496, RGAS-96-6-2, IC-74656, IC-42015, AG-114, IC-95431, IC-35722, IC-35633, IC-35742, IC-81710, SKWA-6, IC-95567, IC-35378, AG-121, BAS-3, IC-95642, IC-35479, IC-42004, DS-1, IC-120574, IC-32193, IC-41998, Resona-2, SKNA-20, IC-35598, RGAS-92-10-1, IC-95414 (GA-80), IC-120588, SKNA-7
II	9	IC-95358, DS-2, Eidual Tivan, IC-2935514, IC-95365, IC-120573, IC-21803, A-Suvarna.
III	3	BGA-2, BAS-3, BAS-1.
IV	10	RGAS-92-10-1, BAS-4, IC-45517, MGA-2, IC-35635, Annapurna, Suvarna, IC-35665, IC-35696, GA-1
V	1	IC-35663
VI	1	IC-81708
VII	1	IC-8170-A
VIII	1	IC-81696
IX	1	IC-81694
X	1	IC-9615
XI	1	IC-95414

Table 9 : Average inter cluster (above diagonal) and intra cluster (diagonal) D^2 and D values for 11 clusters in grain amaranth

Cluster number		I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	D^2	55.139	124.054	217.798	99.629	75.316	78.217	132.994	86.229	158.980	78.607	207.201
	D	7.426	11.138	14.758	9.981	8.678	8.844	11.532	9.286	12.609	8.866	14.394
II	D^2		64.254	320.899	197.254	77.061	83.679	239.341	86.018	262.273	115.715	118.873
	D		8.016	17.914	14.045	8.778	9.148	15.471	9.275	16.195	10.757	10.903
III	D^2			47.878	143.192	271.409	266.815	108.361	270.583	123.625	239.251	397.178
	D			6.919	11.966	16.474	16.334	10.410	16.449	11.119	15.468	19.929
IV	D^2				64.028	144.631	142.386	72.734	150.568	101.335	130.742	280.321
	D				8.002	12.062	11.933	8.528	12.271	10.068	11.434	16.743
V	D^2					0.000	53.799	185.450	66.419	206.676	102.491	170.479
	D					0.000	7.335	13.618	8.150	14.376	10.124	13.057
VI	D^2						0.000	180.660	49.241	199.771	85.331	163.815
	D						0.000	13.441	7.017	14.134	9.237	12.799
VII	D^2							0.000	188.751	49.151	162.343	324.433
	D							0.000	13.739	7.011	12.74	18.012
VIII	D^2								0.000	209.694	87.110	155.036
	D								0.000	14.481	9.333	12.451
IX	D^2									0.000	193.057	32.607
	D									0.000	13.894	18.778
X	D^2										0.000	171.459
	D										0.000	13.094
XI	D^2											0.000
	D											0.000

values of 8.678, 8.844, 8.866, 9.286 and 9.981 whereas, it was more diverse from clusters III, XI, IX, VII and II with D values of 14.758, 14.394, 12.609, 11.532 and 11.138 respectively.

Cluster II showed minimum diversity with cluster V, VI, VIII, X, XI and I with D values of 8.778, 9.148, 9.275, 10.757, 10.903 and 11.138. The farthest clusters from second cluster were III, IX, VII and IV showing D values of 17.914, 16.195, 15.471 and 14.045, respectively. Cluster III was in close proximity to cluster VII, IX and IV with D values of 10.410, 11.119 and 11.966 respectively. The remaining clusters XI (D=19.929), II (D=17.914), V (D=16.474), VIII (D=16.449), VI (D=16.334), X (D=15.468) and I (D=14.758) showed the maximum D values.

Cluster IV was closely related to VII, I and IX as reflected by the least inter cluster D values of 8.528, 9.981 and 10.068 and so the farthest relationship against cluster XI (D=16.743). Cluster V consisting of only one genotype presented least D value estimates of 7.335, 8.150, 8.678 and 8.778 from clusters VI, VIII, I and II respectively. It showed maximum D value of 16.474 from the cluster III.

Cluster VI showed close proximity to cluster VIII, V, I, II and X where the D values were 7.017, 7.335, 8.844, 9.148 and 9.237 respectively. The cluster III showed maximum D value of 16.334 with this cluster. Cluster VII was closely spaced to clusters IX (D=7.011), IV (D=8.528) and III (D=10.410). Cluster XI (D=18.012) and II (D=15.471) showed considerable divergence from this cluster.

Cluster VIII which also formed a solitary cluster of a single genotype, was in close proximity to clusters VI (D=7.017), V (D=8.150), II (D=9.275), I (D=9.286) and X (D=9.333). It showed maximum inter cluster distance with cluster III, IX, VII, XI and IV, the D values being 16.449, 14.481, 13.739, 12.451 and 12.271 respectively. Cluster IX was placed closer to the cluster VII (D=7.011). It showed maximum inter cluster distance of 18.778 with cluster XI and 16.195 with cluster II.

Cluster X was nearer to clusters I (D=8.866), VI (D=9.237) and VIII (D=9.333) and this showed maximum divergence from clusters III, IX and XI with D values of 15.468, 13.894 and 13.094 respectively. Cluster XI was in close proximity to cluster II (D=10.903). It showed maximum inter cluster distance with cluster III (D=19.929), IX (D=18.778), VII (D=18.012), IV (D=16.743), I (D=14.394), X

(D=13.094), V (13.057), VI (D=12.799) and VII (D=12.451). Table 9 shows average inter cluster D^2 values while, table 10 indicates relative proximity (distance) of each cluster with other clusters.

4.5.5 Contribution of different characters towards divergence

The respective per cent contribution of each character towards divergence is presented in Table 11. The panicle fresh weight was the largest contributor with 74.70 per cent towards divergence followed by plant height (8.63%), dry weight of stem (7.99%), panicle length (2.18%), days to maturity (1.74%), number of spikes per panicle (1.49%), number of leaves (1.24%), dry weight of panicle (1.14%), seed yield per plant (0.79%) and number of branches (0.10%). It appeared that panicle fresh weight was the major contributor to the differences among these genotypes.

4.5.6 Cluster mean analysis

The mean values of thirteen different characters for 11 clusters are presented in Table 12. The genotype in cluster XI required less number of days (42.33 days) to flowering. Whereas, genotype in cluster VI took maximum number of days for 50 per cent flowering (54.670 days).

Table 10 : Nearest and farthest clusters from each cluster based on D^2 values in grain amaranth

Cluster number	Nearest cluster with D^2 value	Farthest cluster with D^2 value
I	V (75.316)	III (217.798)
II	V (77.061)	III (320.899)
III	VII (108.361)	XI (397.178)
IV	VII (72.734)	XI (280.321)
V	VI (53.799)	III (271.409)
VI	VIII (49.241)	III (266.815)
VII	IX (49.151)	XI (324.433)
VIII	VI (49.241)	III (270.583)
IX	VII (49.151)	XI (352.607)
X	I (78.607)	III (239.251)
XI	II (118.873)	III (397.178)

Table 11 : Per cent contribution of the characters towards divergence in grain amaranth

Sl. No.	Characters	Contribution (%)
1	Days to 50% flowering	0.00
2	Days to maturity	1.74
3	Stem girth at collar region (cm)	0.00
4	Number of leaves	1.24
5	Number of branches	0.10
6	Plant height (cm)	8.63
7	Panicle fresh weight (g)	74.70
8	Panicle length (cm)	2.18
9	Number of spikes per panicle	1.49
10	Dry weight of panicle (g)	1.14
11	Dry weight of stem (g)	7.99
12	Harvest index (%)	0.00
13	Seed yield per plant (g)	0.79

Table 12 : Cluster mean values for thirteen characters in grain amaranth

Cluster	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}	X_{13}
I	53.657	113.777	5.975	37.648	18.068	166.435	238.501	82.540	63.337	102.715	95.354	12.819	23.607
II	50.631	109.801	5.548	35.229	17.223	159.223	147.713	42.089	50.297	62.703	77.086	13.472	20.423
III	46.447	98.040	5.777	33.133	13.887	166.267	432.757	103.443	58.153	177.243	105.197	18.907	53.240
IV	52.835	106.094	6.212	40.761	17.307	177.613	313.232	91.793	62.246	124.998	103.245	16.832	36.361
V	53.670	120.71	5.370	39.200	18.470	194.670	189.670	63.530	54.930	81.330	87.600	11.910	20.020
VI	54.670	76.33	5.710	51.730	16.530	173.130	192.000	62.530	61.870	83.270	101.330	14.930	26.590
VII	51.000	109.49	5.490	40.400	15.800	174.130	342.400	107.870	86.130	155.130	131.600	12.940	33.380
VIII	50.330	81.27	5.870	20.130	12.670	162.870	180.400	77.530	42.930	91.730	100.330	8.490	46.710
IX	54.000	104.55	7.550	51.130	26.470	192.400	351.130	119.330	42.270	150.330	171.000	15.770	38.320
X	46.000	101.14	5.760	41.330	17.470	102.930	223.00	72.400	86.330	99.470	86.470	14.190	24.730
XI	42.330	76.31	4.110	21.000	8.730	100.330	84.400	35.070	42.930	42.200	24.130	18.290	21.370

X_1 – Days to 50% flowering
X_2 – Days to maturity
X_3 – Stem girth at collar region
X_4 – Number of leaves
X_5 – Number of branches
X_6 – Plant height
X_7 – Panicle fresh weight
X_8 – Panicle length
X_9 – Number of spikes/panicle
X_{10} – Dry weight of panicle
X_{11} – Dry weight of stem
X_{12} – Harvest index (%)
X_{13} – Seed yield/plant

The short duration (76.31 days) genotype accounted in cluster XI, while the genotype of cluster V was of longest duration (120.71 days). Cluster mean for stem girth at collar region ranged from 4.110 cm to 7.550 cm represented by cluster XI and IX respectively. With regard to number of leaves the genotype of cluster XI recorded the lowest mean value (21.00), while the genotype of cluster VI had higher number of leaves (51.730). Lowest number of branches per plant was observed in cluster XI (8.730) whereas, it was highest for cluster IX (26.470).

The genotype included in cluster XI was dwarf (100.330 cm) while the tall genotype in cluster IX (192.400 cm). The genotype in cluster XI showed minimum mean value for panicle fresh weight (84.400 g), while the genotype included in cluster III recorded higher (432.756 g) mean value for panicle fresh weight. In case of panicle length, cluster XI had the minimum average value (35.070cm) while the maximum (119.330cm) in cluster IX.

The number of spikes per panicle was maximum in cluster X (86.330) and minimum in cluster IX (42.270). Genotype included in cluster XI recorded least dry weight of panicle (42.200 g) while the genotype in cluster III recorded maximum dry weight of panicle (177.243 g). The genotype

with low mean value for dry weight of stem (24.130 g) was observed in cluster XI and genotype with high dry weight of stem found in cluster IX (171.00 g).

Cluster VIII recorded low harvest index (8.490%) whereas, highest harvest index was observed in cluster III (18.907%). Cluster III had the maximum seed yield per plant (53.240 g) while the genotype of cluster V showed low mean seed yield (20.020 g).

4.6 SELECTION INDICES

Selection indices for seed yield were constructed by involving such of the characters which had high GCV, significant correlation with yield and also had high genetic advance. The indices formulated therefore included panicle fresh weight (X_7), panicle length (X_8), number of spikes per panicle (X_9), dry weight of panicle (X_{10}) and harvest index (X_{12}). Seed yield per plant (X_{13}) was considered as the dependent variable in the analysis. Expected genetic advance for each of the selection indices was computed at 5 per cent selection intensity, relative efficiency for each selection index was calculated taking relative efficiency by straight selection for seed yield as 100 per cent. The estimated values of genetic

advance and relative efficiency of selection indices constructed are given in Table 13.

Among individual characters, highest and lowest efficiency in grain yield was brought out when selection was based on panicle weight (644.45%) and harvest index (35.79%). The efficiency of other characters in decreasing order are dry weight of panicle, panicle length and number of spikes per panicle.

Among the two character combinations, highest efficiency of 595.96 per cent was obtained for X_7X_{10} combination followed by X_7X_8 (524.49%), X_8X_{10} (194.92%), X_7X_9 (181.44%) and X_7X_{12} (155.76%). For rest of the two traits combination relative efficiency was below 100 per cent.

Among the three character combinations, highest efficiency of 607.16 per cent was recorded for $X_7X_8X_{10}$ combination followed by $X_7X_9X_{10}$ (596.26%), $X_7X_{10}X_{12}$ (595.96%), $X_7X_8X_{12}$ (536.76%), $X_7X_8X_9$ (527.18%), $X_7X_9X_{12}$ (214.50%), $X_8X_{10}X_{12}$ (199.52%) and $X_8X_9X_{10}$ (195.83%).

The highest relative efficiency of 607.69 per cent was registered for $X_7X_8X_9X_{10}$ combination among four character combination. It was followed by $X_7X_8X_{10}X_{12}$ (607.52%), $X_7X_9X_{10}X_{12}$ (596.28%) and $X_7X_8X_9X_{12}$ (543.08%).

Table 13: Selection indices, their genetic advance and relative efficiency over straight selection for seed yield in grain amaranth

Sl. No.	Index	Genetic advance	Relative efficiency
1	X_{13}	39.0127	100.00
2	X_7	251.4162	644.45
3	X_8	75.1948	192.74
4	X_9	40.2034	103.05
5	X_{10}	101.6661	260.60
6	X_{12}	13.9616	35.79
7	$X_7 + X_8$	204.6171	524.49
8	$X_7 + X_9$	70.7837	181.44
9	$X_7 + X_{10}$	232.5012	595.96
10	$X_7 + X_{12}$	60.7677	155.76
11	$X_8 + X_9$	32.4922	83.29
12	$X_8 + X_{10}$	76.0443	194.92
13	$X_8 + X_{12}$	4.9446	12.67
14	$X_9 + X_{10}$	26.6335	68.27
15	$X_9 + X_{12}$	4.1572	10.66
16	$X_{10} + X_{12}$	22.6581	58.09
17	$X_7 + X_8 + X_9$	205.6675	527.18
18	$X_7 + X_8 + X_{10}$	236.8700	607.16
19	$X_7 + X_8 + X_{12}$	209.4036	536.76
20	$X_7 + X_9 + X_{10}$	232.6168	596.26
21	$X_7 + X_9 + X_{12}$	83.6824	214.50
22	$X_7 + X_{10} + X_{12}$	232.5015	595.96
23	$X_8 + X_9 + X_{10}$	76.3988	195.83
24	$X_8 + X_9 + X_{12}$	32.6491	83.69
25	$X_8 + X_{10} + X_{12}$	77.8391	199.52
26	$X_9 + X_{10} + X_{12}$	31.3736	80.42
27	$X_7 + X_8 + X_9 + X_{10}$	237.0746	607.69
28	$X_7 + X_8 + X_9 + X_{12}$	211.8693	543.08
29	$X_7 + X_8 + X_{10} + X_{12}$	237.0092	607.52
30	$X_7 + X_9 + X_{10} + X_{12}$	232.6237	596.28
31	$X_7 + X_8 + X_9 + X_{10} + X_{12}$	237.3453	608.39

X_7 – Panicle fresh weight
X_8 – Panicle length
X_9 – Number of spikes per panicle
X_{10} – Dry weight of panicle
X_{12} – Harvest Index
X_{13} – Seed yield per plant

An efficiency of 608.39 per cent was recorded when all the five component traits were included in the selection index.

4.7 QUALITY CHARACTERS

Amaranth grains are rich source of protein and are excellent source of micronutrients. The data on protein per cent, popping percentage and popping expansion volume are presented in Table 14.

4.7.1 Grain protein content

The observed range of variation for grain protein was 9.57 to 16.67 per cent with an average protein content of 13.64 per cent. The accession IC-66436 (9.57%) recorded lowest protein and the accession DS-2 (16.67%) recorded the highest grain protein content as compared to the check, Annapurna (12.83%).

4.7.2 Popping percentage

The popping percentage of amaranth grains ranged from 1.01 to 97.49 per cent with an overall mean of 65.04 per cent. Highest popping percentage was recorded by the accession IC-81710 (97.49%) followed by IC-95414 (GA-80) (96.46%) and the lowest popping percentage recorded by the accession IC-120588 (1.01%) as compared to the check, Annapurna (84%).

Table 14 : The mean values of three quality characters for the sixty four genotypes of grain amaranth

Sl. No.	Genotypes	Protein content (%)	Popping percentage	Popping expansion volume (ml/g)
1	IC-95414(GA-80)	14.12	96.46	5.54
2	Resona-2	13.98	60.61	5.04
3	IC-35378	13.99	62.00	3.55
4	IC-42015	13.53	91.95	5.61
5	IC-8170-A	14.31	79.30	5.62
6	IC-95414	13.26	94.00	3.35
7	IC-32195	12.15	20.10	3.63
8	IC-35696	13.65	61.00	4.68
9	IC-35633	13.60	85.93	4.43
10	IC-120709	13.90	70.20	4.25
11	IC-35598	15.43	16.00	2.53
12	IC-95365	14.44	43.37	3.01
13	IC-35742	13.66	14.50	2.78
14	IC-81708	13.26	81.00	2.35
15	IC-41998	13.00	67.34	4.20
16	IC-95615	14.51	95.48	5.57
17	IC-95567	12.45	8.54	2.41
18	IC-74656	13.66	13.50	2.62
19	IC-35665	14.45	77.16	6.14
20	IC-95431	12.80	8.12	2.16
21	IC-81694	14.57	91.96	6.85
22	AG-21	13.00	84.42	4.61
23	IC-120588	13.33	1.01	2.42
24	GA-1	14.18	24.00	2.30
25	AG-114	12.87	82.83	4.91
26	SKWA-6	14.34	89.33	5.13
27	IC-81710	14.51	97.49	5.82
28	IC-120573	15.49	10.00	2.62
29	IC-2935514	12.08	93.00	5.39
30	RGAS-92-10-1	13.13	90.96	5.23
31	IC-35479	13.35	84.85	5.23
32	IC-35722	12.15	70.86	4.71
33	IC-120574	13.14	6.53	2.61
34	IC-21803	13.66	90.96	4.85
35	IC-95642	13.66	85.87	4.92
36	SKNA-20	13.08	77.00	4.87
37	BGA-2	15.96	94.97	6.46
38	Eidual Tivan	11.95	88.94	4.91

Contd..

Sl. No.	Genotypes	Protein content (%)	Popping percentage	Popping expansion volume (ml/g)
39	SKNA-7	13.00	5.50	2.61
40	IC-32193	12.37	91.92	5.42
41	IC-35496	14.25	81.41	3.33
42	RGAS-92-10-1	15.75	74.50	4.71
43	RAM-2	12.43	84.00	4.30
44	IC-81696	11.62	76.90	2.57
45	RGAS-96-6-2	12.75	20.61	2.13
46	IC-66436	9.57	95.48	5.65
47	MGA-2	14.85	75.50	4.08
48	IC-35770	11.82	77.16	4.03
49	IC-45517	14.51	59.30	4.02
50	IC-35663	11.94	9.00	2.76
51	IC-35635	12.46	82.83	3.13
52	IC-95365	14.25	6.53	2.14
53	IC-42004	13.93	91.89	6.14
54	IC-95358	13.07	64.50	3.24
55	A-Suvarna	13.20	74.88	5.84
56	Suvarna	14.18	96.00	4.56
57	DS-1	16.16	92.30	6.14
58	DS-2	16.67	64.56	3.06
59	DS-3	14.13	20.19	4.15
60	BAS-1	16.66	61.08	4.62
61	BAS-2	11.63	91.70	5.27
62	BAS-3	15.69	95.23	6.32
63	BAS-4	14.84	74.37	4.56
64	Annapurna	12.83	84.00	5.14
Mean		**13.64**	**65.04**	**4.26**
SEm±		**0.417**	**1.052**	**0.088**
CD at 5%		**0.825**	**2.082**	**0.175**

4.7.3 Popping expansion volume

The mean expansion volume of the popped grains was 4.27 ml/g, with a wide variation of 2.13 to 6.85 ml/g. The accession RGAS-96-6-2 showed lowest expansion volume of 2.13 ml/g followed by the accession IC-95365 (2.14 ml/g) and the highest popping expansion volume of 6.85 ml/g recorded by the accession IC-81694. The popping expansion volume of the check, Annapurna was 5.14 ml/g

4.7.4 Minerals

The genotypes which possess good protein content and popping quality were analyzed for mineral content *viz.*, iron and zinc. The results are presented in Table 15.

The mean iron content of selected genotypes was 12.57 mg/100 g, with the range of 10.73-13.38 mg/100 g. The accession IC-35665 possessed higher iron content (13.38 mg/100 g) followed by accession BGA-2 (13.28 mg/100 g) and the least iron content was observed in accession IC-81694 (10.73 mg/100 g) as compared to the check, Annapurna (12.28 mg/100g).

The zinc content of grain amaranth genotypes ranged from 2.48 mg/100 g (Suvarna) to 3.86 mg/100 g (BGA-2). The

Table 15: Mean values of iron and zinc content of the genotypes promising for quality characters

Sl. No.	Genotypes	Iron (mg/100 g)	Zinc (mg/100 g)
1	BGA-2	13.28	3.86
2	SKWA-6	13.11	3.32
3	IC-8170-A	13.12	3.23
4	IC-95642	12.89	3.06
5	IC-35665	13.38	3.17
6	IC-42004	11.94	3.49
7	Suvarna	12.39	2.48
8	IC-81694	10.73	2.60
9	Annapurna (check)	12.28	3.24
Mean		**12.57**	**3.16**
SEm±		**0.3281**	**0.1253**
CD at 5%		**0.7565**	**0.2890**

mean zinc content was 3.16 mg/100g and the check, Annapurna recorded a zinc content of 3.24mg/100g.

4.8 Promising genotypes identified based on character combination and their quality characters

Selection indices study indicated that the character combination panicle fresh weight + panicle length + dry weight of panicle was best compared to other combinations. From twenty five genotypes showing high mean performance for these three characters, twelve genotypes have been identified and compared for quality characters (Table 16).

It was observed that the genotypes BAS-1 was promising for the three character combination (432.60, 126.33, 177.13) followed by the genotype BGA-2 (433.07, 96.67, 177.47), BAS-3 (432.60, 87.33, 177.13), IC-81694 (351.13, 119.33, 150.33), IC-8170-A (342.40, 107.87, 155.13), IC-35665 (331.93, 106.53, 152) and GA-1 (332.07, 106.87, 112.27).

The accession BAS-1 had good character combination, high protein content (16.66%) but poor in popping percentage (61.08) and expansion volume (4.62 ml/g) as compared to the genotypes BGA-2 and BAS-3 which showed good character combination and quality characters.

Table 16 : Promising genotypes with respect to the character combination of selection indices and their quality character

Sl. No.	Genotype	Character combination			Quality characters		
		Panicle fresh weight (g) X_7	Panicle length (cm) X_8	Dry weight of panicle (g) X_{10}	Protein (%)	Popping percentage	Expansion volume (ml/g)
1	IC-8170-A	342.40	107.87	155.13	14.31	79.30	5.62
2	IC-35665	331.93	106.53	152.00	14.45	77.16	6.14
3	IC-81694	331.13	119.33	150.33	14.57	91.96	6.85
4	GA-1	332.07	106.87	112.27	14.18	24.00	2.30
5	BGA-2	433.07	96.67	177.47	15.96	94.97	6.46
6	RGAS-92-10-1	299.73	99.83	125.93	15.75	74.50	4.71
7	IC-66436	289.40	98.60	122.73	9.57	95.48	5.65
8	BAS-1	432.60	126.33	177.13	16.66	61.08	4.62
9	IC-95365	253.33	92.33	122.93	14.44	43.37	3.01
10	Suvarna	321.60	93.20	110.60	14.18	96.00	4.56
11	BAS-3	432.60	87.33	111.33	15.69	95.23	6.32
12	Annapurna (Check)	323.73	86.27	111.33	12.83	84.00	5.14

Discussion

V. DISCUSSION

Improvement through breeding programme in any crop depends on the availability of genetic variability in the germplasm. The utility of such germplasm could be judged based on the knowledge of extent of variability, character association, direct and indirect influencing effect of different characters (path analysis), formulation of selection indices and genetic divergence in the material. In the present investigation, evaluation of 64 lines of grain amaranth was done to assess their genetic potential by studying grain yield and other quantitative characters. The information obtained on variability parameters, correlation coefficients, path coefficient analysis, genetic divergence, selection indices and quality characters are discussed in this chapter.

5.1 VARIABILITY, HERITABILITY AND GENETIC ADVANCE

The basic idea of the study was to partition the variation into heritable and non-heritable components which helps to know the breeding value of a character. Thus the components of variation such as phenotypic variance, genotypic variance, phenotypic coefficient of variation, genotypic coefficient of variation, heritability, genetic advance and genetic advance over mean were computed in respect of yield and its

attributing characters. Table 17 indicates the relative magnitude of genetic parameters observed for different characters.

The analysis of variance for all the 13 characters revealed significant differences among the genotypes. This information suggests that sufficiently high variability exists for all the characters studied and considerable improvement can be achieved in these characters by selection. However the analysis of variance by itself is inconclusive in explaining all the inherent genotype variability in the collection. This is evident by partitioning the total genetic variability inherent in the genotypes from the phenotypic variance (Charles and Smith, 1939; Grafius, 1964). Thus it is necessary to work out the phenotypic and genotypic coefficients of variation which indicate the extent of variability existing for various traits.

The characters *viz.*, number of leaves, number of branches, panicle fresh weight, panicle length, dry weight of panicle, dry weight of stem, harvest index and seed yield per plant, showed high phenotypic and genotypic coefficient of variation suggesting that these characters are under the influence of genetic control. Hence, these characters can be relied upon and simple selection can be practiced for further improvement. High variability for days to maturity, harvest

Table 17: Relative magnitude of genetic parameters for thirteen characters in grain amaranth

Sl. No.	Characters	PCV	GCV	Heritability	Genetic advance as per cent mean
1	Days to 50% flowering	Low	Low	High	Moderate
2	Days to maturity	Low	Low	Moderate	Moderate
3	Stem girth at collar region (cm)	Moderate	Moderate	Moderate	Moderate
4	Number of leaves	High	High	High	High
5	Number of branches	High	High	High	High
6	Plant height (cm)	Moderate	Moderate	High	Moderate
7	Panicle fresh weight (g)	High	High	High	High
8	Panicle length (cm)	High	High	High	High
9	Number of spikes per panicle	Moderate	Moderate	High	High
10	Dry weight of panicle (g)	High	High	High	High
11	Dry weight of stem (g)	High	High	High	High
12	Harvest index (%)	High	High	High	High
13	Seed yield per plant (g)	High	High	High	High

index and seed yield per plant was reported by Hauptli and Jain (1977, 1980). High PCV and GCV for panicle length was observed by Vaidya (1984). High variation for number of branches and seed yield per plant was reported by Waghmode *et al.* (1998). Mohideen *et al.* (1983) also reported wide variation for seed yield.

Moderate values of genotypic and phenotypic coefficient of variability were observed for stem girth at collar region, number of spikes per panicle and plant height. Pushpa Rekha (1986) and Maruthi (1987) observed moderate variation for stem girth at collar region and plant height. In contrary to this Ghosh *et al.* (1999), Das *et al.* (1991) reported high phenotypic and genotypic coefficient of variability for plant height. The characters days to 50 per cent flowering and days to maturity showed lower values of phenotypic and genotypic coefficient of variability, which is in conformity with the findings of Lohithaswa (1992). Low variability present in these characters indicates that selection might have been practiced for these characters in the early generations and it hinders the improvement of these traits through selection in the germplasm.

The coefficient values indicated considerable amount of variability existing for all the characters except days to 50 per

cent flowering. Very low difference between phenotypic coefficient of variation values and genotypic coefficient of variation values were observed for days to 50 per cent flowering, panicle fresh weight, panicle length, dry weight of stem indicating a low level of environmental factors operating but the influence of extraneous factors was high for seed yield per plant, number of spikes per panicle, harvest index, days to maturity, stem girth at collar region, number of branches, number of leaves and dry weight of panicle (Lohithaswa, 1992).

The coefficient of variation reveals the extent of variability present for different characters and it does not indicate the heritable portion. To obtain the knowledge of heritable portion of the variability it is essential to know the heritability estimates of the different characters. Practically, heritability estimate is of greater value to the breeder, since it indicates the degree of dependence of genotypic value on phenotypic value. The effectiveness of selection for any character depends not only on the amount of phenotypic and genotypic variability, but also on the magnitude of heritability. In the present study, broad sense heritability was used and it includes both additive and non-additive gene effects (Hanson *et al.*, 1956).

In general, broad sense heritability estimates were high for all the characters studied except days to maturity and stem girth at collar region which showed moderate heritability. This means that these characters were least influenced by the environment. Pushpa Rekha (1986) reported high heritability for plant height, panicle length, number of spikes per panicle and seed yield per plant. While Joshi (1986) revealed high heritability for plant height and days to maturity. Das *et al.* (1991) observed high heritability for panicle length, seed yield per plant. High heritability for plant height, number of days to 50 per cent flowering, number of branches and seed yield per plant was reported by Waghmode *et al.* (1998). High heritability for plant height was also observed by Ghosh *et al.* (1999). Moderate heritability for stem girth at collar region was obtained by Maruthi (1987).

The estimates of heritability however, indicate only the effectiveness with which selection of genotypes can be based on their phenotypic performance but fail to indicate the amount of progress expected from selection (Johnson *et al.*, 1955). Therefore heritability estimates appear to be more meaningful when accompanied by estimates of genetic advance. Genetic advance is the measure of improvement that can be achieved by practicing selection in a population.

Genetic advance under selection depends mainly on the amount of genetic variability in the base population, intensity of the selection and magnitude of the masking effect of the environmental and interaction components of variability on genetic variability.

High heritability coupled with high genetic advance was observed for number of leaves, number of branches, panicle fresh weight, panicle length, number of spikes per panicle, dry weight of panicle, dry weight of stem, harvest index and seed yield per plant. This indicates that substantial improvement for these characters could be achieved through direct selection and these traits are considered to be governed by additive genes. Pushpa Rekha (1986) reported high heritability coupled with high genetic advance for number of spikelets per spike and seed yield per plant. Das *et al.* (1991) reported high heritability coupled with high genetic advance for seed yield per plant. Waghmode *et al.* (1998) obtained high heritability and high genetic advance for number of branches and seed yield per plant.

High heritability coupled with moderate genetic advance was observed for plant height and days to 50 per cent flowering. This indicates that these characters were less influenced by environment but governed by both additive and

non-additive gene action. Hence, simple selection is suggested for further improvement in the later generations. Maruthi (1987) reported high heritability coupled with high genetic advance for days to 50 per cent flowering. Ghosh *et al.* (1999) observed high heritability with moderate genetic advance for plant height.

The characters *viz.*, stem girth at collar region and days to maturity showed moderate estimates of heritability and genetic advance suggesting that additive and non-additive nature of gene actions were equally important in the inheritance of these characters. Response to selection might be moderate for these characters. According to Panse and Khargonkar (1957), if the heritability of a particular character is high in a specific environment coupled with low genetic advance, then it is mainly due to non-additive gene action, whereas the heritability is due to additive gene action, if high heritability is associated with high genetic advance.

5.2 CORRELATION AND PATH COEFFICIENT ANALYSIS

5.2.1 Correlations

The phenotype of a plant is the result of interaction of a large number of factors. Therefore, the final yield is the sum total of the effects of several component characters and is polygenically controlled quantitative character. The influence

of these characters can be known through the correlation studies. Correlation coefficient measures the magnitude and direction of association among the characters. Correlation coefficient between characters assumes its importance due to genetic causes of correlation through the pleiotrophic action of genes, improvement brought about by selection through related characters and natural selection. The inter relationship among the economic characters are of immense help in effective selection programme. Simultaneous improvement in two or more characters is possible when positive correlations were observed, whereas negative associations indicate the need to compromise between desirable characters.

The degree and direction of association among characters is measured by genotypic and phenotypic correlation coefficient. The relationship between genotypic and phenotypic correlation indicates that the characters having high heritability estimates have lower environmental correlations than the genotypic correlations (Falconer, 1981). When all the correlations are in same direction highly heritable characters possess high genetic correlations than phenotypic correlation because phenotypic correlation includes both genotypic and environmental correlations. If heritability of two characters is

low coupled with a higher environmental correlation, then phenotypic correlation exceeds genotypic correlations.

5.2.2 Correlation between yield and its components

In the present study both genotypic and phenotypic correlations were worked out for yield and yield component characters. Table 18 indicates the association pattern of different yield components with seed yield, observed in the present study. In general, genotypic correlations were higher than the corresponding phenotypic values. Low phenotypic correlations can be explained due to masking or modifying effects of environment on genetic association between characters. This observation is in conformity with the findings of Pandey (1981a) who attributed this to the modifying effect of environment on the association of characters at the genic level. Genotypic and phenotypic association of grain yield was positive and significant with panicle fresh weight, panicle length, number of spikes per panicle, dry weight of panicle, dry weight of stem and harvest index. This suggests that selecting for these characters would likely to improve the seed yield in grain amaranth. Strong correlation between seed yield and dry weight of panicle was observed by Kulakow and Jain (1985) as they considered head weight as a measure of seed yield to correlate with other

Table 18 : Phenotypic and genotypic correlation of different characters with yield

Sl. No.	Characters	Genotypic		Phenotypic	
		Direction	Magnitude	Direction	Magnitude
1	Days to 50% flowering	Negative	Moderate	Negative	Moderate
2	Days to maturity	Negative	High	Negative	Moderate
3	Stem girth at collar region (cm)	Positive	Low	Positive	Low
4	Number of leaves	Negative	Low	Negative	Low
5	Number of branches	Negative	Low	Negative	Low
6	Plant height (cm)	Positive	Low	Positive	Low
7	Panicle fresh weight (g)	Positive	High	Positive	High
8	Panicle length (cm)	Positive	Moderate	Positive	Moderate
9	Number of spikes per panicle	Positive	Moderate	Positive	Moderate
10	Dry weight of panicle (g)	Positive	High	Positive	High
11	Dry weight of stem (g)	Positive	Low	Positive	Low
12	Harvest index (%)	Positive	High	Positive	High

characters. Hauptli and Jain (1977) observed that allocation of biomass to seed production is positively correlated with yield. Naidu *et al.* (1982) observed positive correlation between grain yield and total dry matter accumulation at harvest. Mathai and Ramachandra (1981) reported strong positive correlations of grain yield with stem weight and number of spikelets per plant. Ayiecho (1986) suggested plant weight and head weight as best yield predictors. Significant strong correlation of seed yield with panicle length, dry weight of panicle, number of spikelets per plant, diameter of stem and total dry matter was observed by Pushpa Rekha (1986). Pandey (1979, 1981a) noticed that harvest index had highest correlation with seed yield per plant. Das *et al.* (1991) reported positive significant association of seed yield with panicle weight and panicle length. Positive association of plant height and number of spikelets per spike with seed yield per plant was reported by Sudhir Shukla and Singh (2003).

Seed yield is negatively and significantly associated with days to 50 per cent flowering, days to maturity and number of branches. Maruthi (1987) observed negative significant association of seed yield with days to 50 per cent flowering and days to maturity. Mohideen *et al.* (1983) noted shy branching types recording higher yields.

5.2.3 Association among yield components

At this point, it is intended to consider issues concerning the significant inter relationships among the characters other than seed yield which might aid in conceiving an ideal plant type. Plant height exhibited significant positive association with days to 50 per cent flowering, days to maturity, stem girth at collar region, number of leaves, number of branches, panicle fresh weight, panicle length, number of spikes per panicle, dry weight of panicle and dry weight of stem suggesting that taller plants with longer panicle, more number of branches and heavier panicle would result in higher seed yield. Ghosh *et al.* (1999) observed positive significant correlation of this trait with days to flowering, panicle length and number of branches. Positive significant association of plant height with number of primary branches and number of spikes per panicle was reported by Sudhir Shukla and Singh (2003).

Panicle fresh weight showed significant positive correlation with stem girth at collar region, plant height, panicle length, number of spikes per panicle, dry weight of panicle and dry weight of stem. This indicates, selecting for these characters would increase the yield. Positive significant association of this character with plant height, panicle length,

stem girth at collar region, number of spikes per panicle and dry weight of stem was observed by Lohithaswa (1992).

Panicle length showed positive significant association with days to 50 per cent flowering, stem girth at collar region, number of leaves, plant height, panicle fresh weight, number of spikes per panicle, dry weight of panicle and dry weight of stem. Longer panicles provide sites for more number of spikes per panicle and thereby increasing panicle weight. Therefore, the close relationship between panicle length, number of spikes per panicle and panicle fresh weight might be expected. Pushpa Rekha (1986) observed that panicle length showed positive significant association with plant height, stem girth, number of spikes per panicle, total dry matter and dry weight of panicle. Das *et al.* (1991) observed significant positive correlation of this character with panicle weight. Maruthi (1987) observed positive significant association of this trait with days to 50 per cent flowering and plant height. Positive association of panicle length with plant height and days to flowering was reported by Ghosh *et al.* (1999).

Number of spikes per panicle showed significant positive association with stem girth at collar region, plant height, panicle fresh weight, panicle length, dry weight of panicle, dry weight of stem and harvest index. Sudhir Shukla and Singh

(2003) observed positive significant association of number of spikes per panicle with plant height. However, it was negatively associated with panicle length.

Dry weight of panicle had positive significant association with stem girth at collar region, plant height, panicle fresh weight, panicle length, number of spikes per panicle and dry weight of stem. Maruthi (1987) reported significant positive association of this trait with girth of stem and total dry matter. Positive association of dry weight of panicle with plant height, girth of stem, panicle length, number of spikes and total dry matter was observed by Pushpa Rekha (1986).

Dry weight of stem exhibited positive significant association with stem girth at collar region, number of leaves, plant height, panicle fresh weight, panicle length, number of spikes per panicle and dry weight of panicle. Similar observations were also reported by Lohithaswa (1992).

Harvest index had positive significant association with number of spikes per panicle and showed significant negative association with days to 50 per cent flowering, number of leaves and number of branches. Negative association of harvest index with number of leaves and number of branches may be due to the fact that, an increase in number of leaves

and branches leads to an increase in biological yield, thereby decreasing the harvest index. Pushpa Rekha (1986) reported negative significant association of this trait with number of branches.

Studies made by various workers on correlation, in several crop plants revealed that strength and direction of correlation in different character combinations depends on the nature of experimental material and environmental conditions in which they have studied (Falconer, 1960). However, in grain amaranth on the basis of results obtained in the present investigation, it is necessary that greater emphasis has to be laid for improving seed yield by adopting selection on panicle fresh weight, panicle length, number of spikes per panicle, dry weight of panicle, dry weight of stem and harvest index as they showed very high positive and significant association with seed yield per plant.

From the above observations, the improvement in grain yield appears possible through the selection of aforesaid characters.

5.2.4 Path coefficient analysis

The computed correlation coefficient values are useful in explaining the nature and extent of association existing

between pairs of characters. The economic character like seed yield is dependent on several component characters which are mutually related. Correlation explains the true association existing between the component characters with dependent character (seed yield). Slight change in any component will ultimately disturb the complex, hence character has to be analysed for its action which is done through path analysis, where the two types of action namely direct effect of component character on seed yield and the indirect effects through other component characters on seed yield are obtained which cannot be recorded by the correlation studies.

The concept of path analysis was originally developed by Wright (1921), but the technique was first used in plant breeding by Dewey and Lu (1957). The path analysis of Dewey and Lu (1957) permits the separation of correlation coefficients into components of direct and indirect effects and measure the relative importance of each factor. In the present study six characters, *viz.*, panicle fresh weight, panicle length, number of spikes per panicle, dry weight of panicle, dry weight of stem and harvest index were considered for path analysis.

In the genotypic path, panicle fresh weight had high direct positive effect on seed yield per plant. Positive but indirect effects of panicle fresh weight was exerted through

number of spikes per panicle, dry weight of stem and harvest index. Characters such as panicle length and dry weight of panicle showed negative indirect effects. Direct selection for panicle fresh weight alone can bring about considerable improvement in yield due to its high direct effect and positive indirect effects through other characters.

Panicle length showed negative direct effect on seed yield (Maruthi, 1987 and Pandey, 1981). Panicle length showed negative indirect effect via dry weight of panicle, but positive effects were showed through panicle fresh weight, number of spikes per panicle, dry weight of stem and harvest index.

Positive direct effect of number of spikes per panicle was seen on seed yield per plant and this was supplemented by positive indirect effects through panicle fresh weight, dry weight of stem and harvest index, but characters *viz.*, panicle length, dry weight of panicle had negative and indirect effects. Lohithaswa (1992) reported high direct effect of number of spikes on seed yield.

The direct negative effect of dry weight of panicle on seed yield was increased by the indirect negative effect of panicle length (Pushparekha, 1986). However high indirect positive effect of panicle fresh weight and low effects of number of

spikes per panicle, dry weight of stem and harvest index made the correlation positive and significant.

Dry weight of stem showed direct positive effect on seed yield which was supported by positive indirect effect of panicle fresh weight and number of spikes per panicle (Lohithaswa, 1992). But the characters such as panicle length, dry weight of panicle and harvest index had negative indirect effects.

Harvest index had high positive and direct effect on seed yield. Characters like panicle length, dry weight of panicle and dry weight of stem had negative indirect effects. The characters *viz.*, panicle fresh weight and number of spikes per panicle had positive indirect effect through harvest index on seed yield.

Phenotypic path analysis indicated that harvest index and panicle fresh weight had high positive direct effects, while other characters showed negligible direct or indirect positive effects except panicle length which showed negative direct effect on seed yield.

From the study of path analysis, it can be concluded that panicle fresh weight and harvest index were the most important components in selection for high yield through their direct effects and indirect effects.

5.3 GENETIC DIVERSITY ANALYSIS

Genetic relationship among genotypes can be measured by similarity or dissimilarity of any number of quantitative characters assuming that the difference between characters of genotypes reflect the divergence of genotypes. In heterosis breeding programme the diversity of parents is always emphasized. More diverse the parent within a reasonable range, better the chances of improving economic characters under consideration in the resulting offspring.

Generalized distance which had been employed in the present study, is a statistic related to the coefficient of racial likeness developed by Mahalanobis (1936) and Rao (1952). It is a weighted coefficient, similar to squared distance, in which both the variance of separate characters and the correlations among the characters are taken into account. The pattern obtained by D^2 does not substantially change with the addition of more characters. It is based on second degree statistics and is self weighing on the basis of genetic variability of the characters. D^2 values between pair of populations amounts to a measure of genetic divergence when the effect of environment has been same for populations under study.

Based on D^2 values 64 genotypes were grouped into eleven clusters indicating presence of appreciable amount of diversity among the genotypes under study. The maximum number of genotypes (35)were grouped into cluster I, followed by cluster IV and II which contain 10 and 9 genotypes respectively. Cluster III had three genotypes, while the remaining clusters (V to XI) were solitary clusters. The intra cluster D^2 values ranged from 47.878 to 64.254. The average intra- cluster distance between the members of cluster II was maximum followed in descending order by cluster IV, I and III, suggesting that genotypes in cluster II were relatively more diverse than the genotypes in the above selected clusters.

Theoretically speaking, the maximum amount of heterosis is expected in cross combination involving the parents belonging to most divergent cluster. In the present study, the inter cluster D^2 values also ranged widely with minimum value of 49.51 and maximum value of 397.178. Cluster III and XI were strikingly diverse from rest of the clusters. The divergence between these two clusters was high as evident from their high inter cluster D^2 value (397.178). Therefore, the genotypes falling in these clusters were genetically more divergent. Intercrossing the genotypes from these two clusters may generate wider variability and is

expected to throw high yielding transgressive segregants in a population improvement programme. The minimum inter cluster D^2 value (49.151) was observed between cluster VII and IX, indicating close genetic relationship between genotypes of these two clusters.

5.3.1 Contribution of characters towards divergence

Among the thirteen characters studied, the most important character contributing to the divergence was fresh weight of panicle followed by plant height, dry weight of stem, panicle length, days to maturity, number of spikes per panicle, number of leaves and dry weight of panicle, while negligible contribution was from seed yield per plant and number of branches. These observations are also in accordance with earlier workers for panicle fresh weight (Lohithaswa, 1992; Asthana *et al.*, 1998), for number of spikes per panicle (Hegde and Patil, 2000), for panicle length (Joshi and Rana, 1995; Biradar *et al.*, 1997; Asthana *et al.*, 1998), for seed yield (Fatokun, 1985; Sethi *et al.*, 1992; Joshi and Rana, 1995; Shivakumar and Singh, 1997; Vishal Suri and Sharma, 1999), for plant height (Shivakumar and Singh, 1997; Bergale *et al.*, 2001; Sudhir Shukla and Singh, 2002) and for days to maturity (Joshi and Rana, 1995; Bergale *et al.*, 2001).

The above results imply that in order to select genetically diverse genotypes for hybridization the material should be screened for the important traits like, panicle fresh weight, plant height, dry weight of stem, panicle length, days to maturity, number of spikes per panicle, number of leaves, dry weight of panicle, seed yield per plant and number of branches.

5.3.2 Analysis of cluster means

Analysis of cluster means indicated substantial variation among the eleven clusters grouped according to D^2 analysis. Based on the range of means it is possible to know the characters influencing divergence. In the present study the clusters III, X and XI had early flowering genotypes whereas, clusters I, II, IV, V, VI, VII, VIII and IX were comprised of late flowering genotypes. The genotypes present in clusters III, VI, VIII, X and XI could be regarded as the source for earliness and clusters I, II, IV, V, VII and IX had late maturing types. The results indicate the amount of diversity available in the germplasm.

Cluster XI included the genotypes with less stem girth at collar region and the remaining cluster had more stem girth at collar region. More number of leaves were observed in cluster

VI and IX. The clusters VIII and XI had less number of leaves, while remaining clusters were medium. Branches per plant were more in cluster IX and low in cluster XI and medium in remaining clusters.

Dwarf plants were found in cluster X and XI, while tall plants in clusters I, II, III, IV, V, VI, VII, VIII and IX. Panicle fresh weight was high in clusters III, IV, VII and IX and low in cluster XI. The clusters I, II, V, VI, VIII and X were having moderate panicle fresh weight. Clusters II and XI can be categorized in short panicle length group. Long panicle was observed in clusters III, VII and IX, while remaining clusters had intermediate panicle length.

Less number of spikes per panicle was observed in clusters VIII, IX and XI and maximum spikes in clusters VII and X, while in others it was intermediate. The cluster XI had low dry weight of panicle and moderate in clusters II, V, VI, VIII and X. Maximum dry weight of panicle was observed in clusters I, III, IV, VII and IX. Dry weight of stem was maximum in clusters III, IV, VI, VII, VIII and IX and low in cluster XI and moderate in remaining clusters. It can be observed that cluster VIII had low harvest index and in other clusters the harvest index was high. Seed yield per plant found to be high in clusters III, IV, VII, VIII and IX and low in

clusters I, II, V, VI, X and XI. So hybridization between genotypes of divergent clusters will lead to accumulation of favourable genes in a single variety and also it is suggested to create variability for developing the varieties involving a large number of divergent lines instead of closely related ones (Bergale *et al.*, 2001).

In the present investigation it was observed that the genotypes in cluster III can be chosen for hybridization programme, as it recorded highest cluster mean values for panicle fresh weight, dry weight of panicle, harvest index and seed yield per plant. However for earliness genotype from cluster XI and for high panicle length and dry weight of stem genotype from cluster IX may be included in hybridization programme. The genotype from the solitary cluster X, which had highest number of spikes per panicle can also be considered as parent in breeding programme. It is suggested that crosses should be effected among the genotypes of said clusters, for improving more than one economic characters to develop potential segregants and future selection needs to be made in above, to develop high yielding cultivars in grain amaranth.

5.4 SELECTION INDICES

Yield is a complex character which depends on many other characters. Therefore, selection for yield based on yield alone may not prove to be highly efficient. Selection of superior genotypes based on discriminant function renders selection easy and a selection index worked out with the help of this function would provide a total score obtained from consideration of two or more component characters of yield simultaneously. In the present study selection indices were formulated with those characters possessing positive and significant correlations, high heritability and high genetic advance with yield.

Taking into consideration, selection indices based on individual characters it was noticed that all the traits showed higher relative efficiency than direct selection for yield, except harvest index. It is probable that, higher relative efficiency of these is due to their higher correlation high genetic advance and high heritability. In majority of the cases, wherever panicle fresh weight was included, selection indices showed higher relative efficiency than those lacking it. It is a point to note that wherever harvest index and number of spikes per panicle were included in the selection index either individually or in combination, efficiency of that index is not much improved.

Though the selection index comprising of all the five characters had a greater relative efficiency (608.39%) over direct selection, relatively

better efficiency was also observed for four character combination of $X_7X_8X_9X_{10}$ (607.69%), $X_7X_8X_{10}X_{12}$ (607.52%) and for three character combination of $X_7X_8X_{10}$ (607.16%). However, a practical breeder would prefer to use an index which would lead to maximum possible genetic gain by using a minimum number of characters. Therefore, it is suggested that combination of panicle fresh weight, panicle length and panicle dry weight could be advantageously exploited in the grain amaranth breeding programme.

5.5 QUALITY CHARACTERS

In view of the growing demand for staple food grain in a country like India, where rice and wheat production may reach a plateau, exploitation of pseudocereal becomes inevitable in combating the malnutrition. Grain amaranth, being a pseudocereal is rich in good quality protein and minerals and is used to supplement cereal in bakery products. From this point of view, the present investigation was undertaken to study the quality characters like protein content, popping per cent, popping expansion volume and minerals (iron and zinc).

5.5.1 Protein content

The high protein content of grain amaranth is itself a matter of great significance. However, the contribution which any source of protein makes to the fulfillment of requirements

depends not only on the quantity present in that source, but also on its quality as determined by its amino acid composition. It has been reported that grain amaranth is a typical pseudocereal with high protein content (Becker *et al.*, 1981). In the present investigation the protein content ranged from 9.57 to 16.67 per cent. Similarly, the wide range of protein content was observed by Pant (1983), Bressani *et al.* (1987), Bressani (1993) and Munjal *et al.* (1999). The wide variation in the protein content among genotypes may be attributed to differences in their genetic makeup, nitrogen fertilization, age and season (Bressani, 1987).

5.5.2 Popping

The results indicated that there was wide variation among the genotypes for popping percentage. The expansion volume of pops also showed wide variation among the genotypes. However the expansion ratio of the pops observed in the present study was higher as compared to the results reported by Mohideen *et al.* (1983). Similarly wide range of popping per cent and expansion volume were observed by Malleshi and Desikachar (1985), Hadimani *et al.* (1995).

Higher expansion ratio and popping percentage of the genotypes indicate good popping quality. The consumer

preference mainly depends on the genotypes which have greater increase in volume and good popping qualities, because these qualities of the grain provide bulk to the diet.

5.5.3 Minerals

Grain amaranth being rich in protein, is also a good source of minerals. The genotypes which were good in protein and popping quality were analysed for minerals like iron and zinc. The iron content observed in the present study ranged from 10.73–13.38 mg/100 g and the zinc from 2.48 - 3.86 mg/100 g among the selected genotypes. Pant (1985) observed a range of 7.5-12.2 mg/100g, Teutonico and Knorr (1985) recorded 9.1 to 21.7 mg/100g and Munjal *et al.* (1999) observed 8.58 - 17.0 mg/100g of range for iron content. Teutonico and Knorr (1985) observed that zinc content ranged between 3.6 to 3.9 mg/100g. The mineral content varies widely between the genotypes in relation to climate, cultural method and mineral content of soil.

5.6 PROMISING GENOTYPES IDENTIFIED BASED ON CHARACTER COMBINATION AND THEIR QUALITY CHARACTERS

Based on the selection indices it was observed that the character combination of panicle fresh weight, panicle length, dry weight of panicle (X_7 X_8 X_{10}) showed higher relative

efficiency. The genotypes promising for this character combination were compared for their quality characters. The Fig 6 depicts information on promising genotypes for the character combination.

The genotypes BGA-2 and BAS-3 showed high mean performance for the character combination and quality parameters along with yield compared to the check Annapurna. These genotypes should be further evaluated at large scale and at different locations before releasing it for commercial cultivation.

Future line of work

The major attention has to be focused on commercialization of the crop and modernization of traditional cultivation as well as expansion to new areas of the developing world because of its nutritional attributes.

1. Variability studies indicated that characters *viz.,* number of branches, panicle fresh weight, panicle length, plant height, number of spikes per panicle, dry weight of panicle, dry weight of stem and seed yield per plant had high genetic variability. This indicates that there is variation available for these traits, which can be exploited either by direct selection for improving these characters or by involving

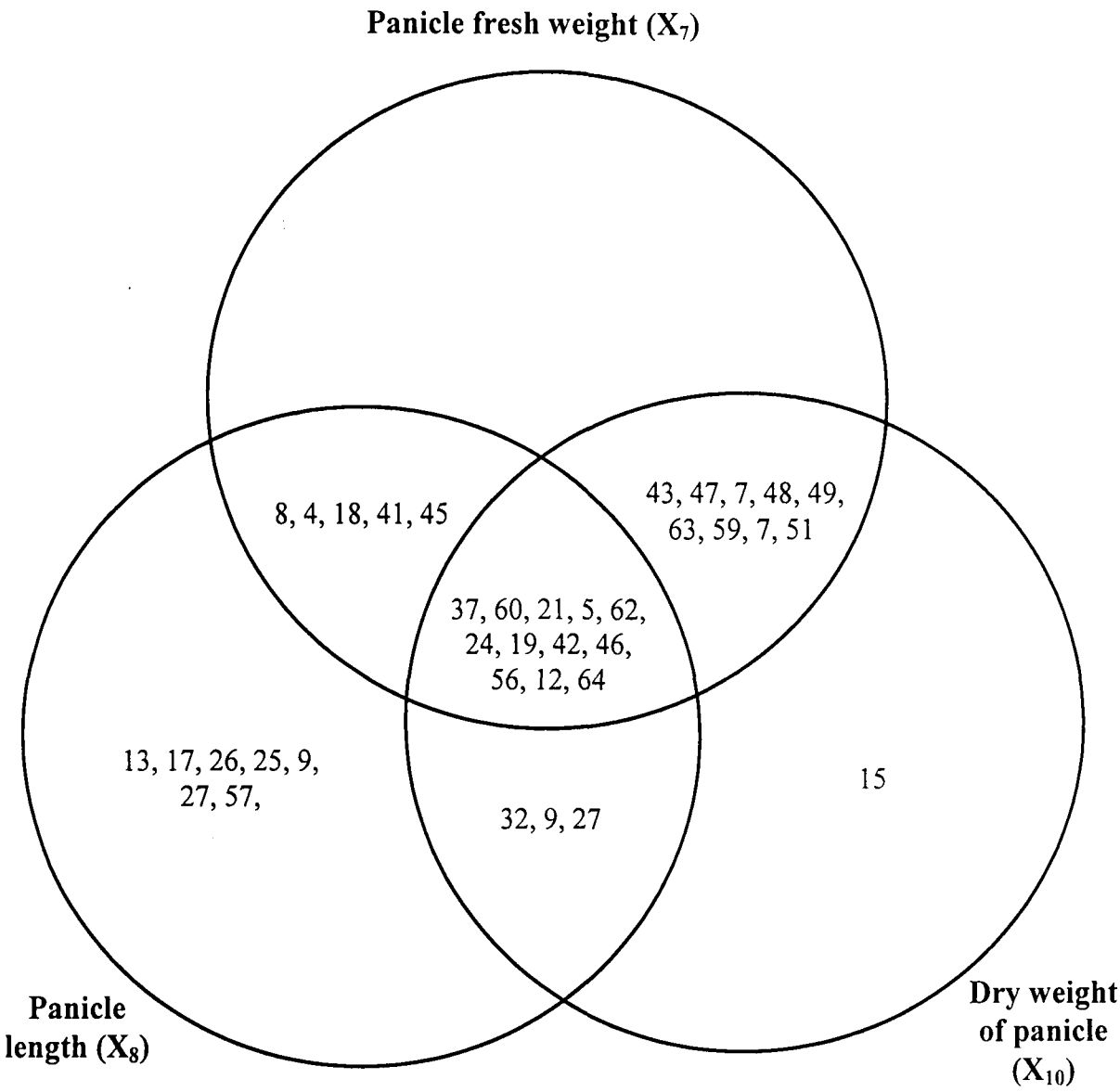


Fig 6: Ven diagram depicting promising genotypes with respect to character combination based on selection indices.

Note: Numbers in the figure corresponds to respective genotypes in the appendix-I

2. them in hybridization work giving due consideration to diversity and possible complementation of yield components in such planned hybridization work.

3. Crosses can be planned between genotypes of cluster III with genotypes of cluster II and cluster XI to get wide spectrum of variability for different yield contributing characters which will facilitate to identify superior genotypes with respect to more than one character and also possible to improve more than one character, simultaneously.

4. The higher nutritional content of the grains provides a good opportunity for the development of varieties with higher nutritional quality and the challenge is to incorporate amaranth into existing food formulations to modify their functional and nutritional quality as well as to create entirely new products from grain amaranth.

5. Based on the mean performance of the genotypes the accession BGA-2 and BAS-3 were identified as significantly better yielder than the check. These genotypes are also promising for the character combination and quality character. These genotypes may be further evaluated preferably over locations and years to confirm their superiority before considering for possible identification release as commercial cultivar.

Summary

VI. SUMMARY

The investigation was undertaken at the botany garden, University of Agricultural Sciences, Dharwad for studying the nature of genetic variability, the pattern of association between different characters, direct and indirect contribution of yield components on seed yield, nature and extent of genetic divergence, formulation of selection indices and nutritional quality characters. Sixty four genotypes including one check formed the experimental material for the present investigation. The data was subjected to statistical analysis for elucidating the information on variability, correlation, path analysis, diversity and selection indices.

Wide range of variation was observed for all the character. Genotypes differed significantly for all the characters as evidenced by 'F' test of ANOVA. Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were found to be separated very narrowly, higher GCV and PCV were obtained for number of leaves, number of branches, panicle fresh weight, panicle length, dry weight of panicle, dry weight of stem, harvest index and seed yield per plant. Moderate values of PCV and GCV were observed for stem girth at collar region, plant height and

number of spikes per panicle and low GCV and PCV were reported for days to 50 per cent flowering and days to maturity.

Heritability in broad sense, was high for all the characters studied except for days to maturity and stem girth at collar region which exhibited moderate heritability. The per cent mean genetic advance was highest for number of leaves, number of branches, panicle fresh weight, panicle length, number of spikes per panicle, dry weight of panicle, dry weight of stem, harvest index and seed yield per plant.

Higher expected genetic advance with high heritability was observed for plant height, panicle fresh weight, panicle length, dry weight of panicle, dry weight of stem and seed yield per plant.

Seed yield per plant was found correlated significantly and positively at both phenotypic and genotypic level with panicle fresh weight, panicle length, number of spikes per panicle, dry weight of panicle, dry weight of stem and harvest index.

Positive and highly significant correlation was observed for days to 50 per cent flowering with days to maturity, stem girth at collar region, number of leaves and plant height; days

to maturity with number of branches; plant height with panicle fresh weight, panicle length, dry weight of panicle and dry weight of stem; panicle fresh weight with panicle length, dry weight of panicle and dry weight of stem; panicle length with plant height, number of spikes per panicle both at genotypic and phenotypic level.

Path analysis revealed that panicle fresh weight was the major character which exhibited highest positive direct effect on seed yield followed by harvest index. Therefore emphasis may be laid on these characters for improving seed yield. However panicle length although exhibited significant positive correlation, its direct contribution was negative, but their maximum indirect contribution was through panicle fresh weight. The indirect contribution of all the characters through panicle length was negative. Number of spikes per panicle and dry weight of stem exhibited low and positive direct effect on seed yield.

Considerable amount of genetic diversity was noticed in the material. The per cent contribution of characters indicated that panicle fresh weight was the major contributor towards divergence followed by plant height, dry weight of stem. The genotypes were grouped into 11 clusters. Cluster I

was the largest with 35 genotypes while clusters from V to XI were solitary clusters.

The inter cluster D^2 values also ranged widely from 49.151 between cluster III and IX to 397.178 between cluster III and XI indicating the presence of considerable diversity among the genotypes. It was observed that cluster III was distantly placed from clusters II and XI. And these clusters also recorded highest mean values for one or more characters. Therefore crosses can be effected between genotypes of cluster III with genotypes of cluster II and XI to yield wide spectrum of variability for different characters which help to identify superior genotypes and also to improve more than one character simultaneously.

Selection index consisting of panicle fresh weight, panicle length and panicle dry weight had relatively higher efficiency compare to other indices. An interesting point was that increase in efficiency of most of the indices was mainly attributable to panicle fresh weight and it is observed that harvest index had not contributed much to increase the efficiency.

The quality characters showed that, the protein content ranged between 9.57 to 16.67 per cent. The popping percentage varied from 1.01 to 97.49 per cent and popping expansion volume recorded a range of 2.13 to 6.85 ml/g. The

iron content ranged between 10.73 to 13.38 mg/100 g and that of zinc was 2.48 - 3.86 mg/100g.

The genotype BGA-2 and BAS-3 were promising for yield and also with respect to the character combination selected based on selection indices. They also had good quality characters.

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Appendix

Appendix -1 : Means of different quantitative characters of grain amaranth genotypes

Sl. No.	Genotype	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}	X_{13}
1	IC-95414(GA-80)	54.00	104.99	6.35	50.66	18.53	164.07	194.87	64.27	61.33	84.93	112.53	12.70	23.00
2	Resona-2	54.00	109.75	6.13	44.60	18.80	162.13	207.73	72.40	63.73	94.47	102.53	12.03	24.15
3	IC-35378	51.33	109.47	5.16	40.47	13.40	155.00	234.80	84.60	64.80	101.53	76.00	14.58	26.47
4	IC-42015	55.33	109.88	7.19	44.00	21.33	173.47	253.87	92.07	62.67	91.60	112.40	11.25	23.28
5	IC-8170-A	51.00	109.49	5.49	40.40	15.80	174.13	342.40	107.87	86.13	155.13	131.60	12.94	33.38
6	IC-95414	42.33	76.31	4.11	21.00	8.73	100.33	84.80	35.07	42.93	42.20	24.13	18.29	21.37
7	IC-32195	54.00	112.26	6.11	31.93	7.53	169.20	283.00	82.47	65.00	117.33	108.93	13.20	26.65
8	IC-35696	55.67	113.16	5.82	44.73	17.60	177.27	322.80	124.60	87.20	110.33	98.33	20.69	39.71
9	IC-35633	56.00	109.39	5.32	40.47	16.67	153.93	244.80	91.87	59.20	110.47	82.67	12.36	20.33
10	IC-120709	51.00	118.47	4.47	39.73	20.00	163.07	173.40	42.67	56.13	69.00	92.17	7.81	31.00
11	IC-35598	53.67	118.54	4.63	37.33	26.40	141.47	233.33	84.40	57.40	92.60	52.67	8.53	12.98
12	IC-95365	54.67	105.72	5.84	34.93	12.73	173.53	253.33	92.33	67.73	122.93	94.93	11.46	23.56
13	IC-35742	51.33	118.27	5.48	35.07	27.60	156.93	243.67	87.00	55.87	108.00	81.47	7.31	13.36
14	IC-81708	54.67	76.33	5.71	51.73	16.53	173.13	192.00	62.53	61.87	83.27	101.33	14.93	26.59
15	IC-41998	53.67	118.65	5.32	39.07	16.33	181.33	231.33	85.67	41.40	112.07	71.53	9.71	17.58
16	IC-95615	46.00	101.14	5.76	41.33	17.47	102.93	223.00	72.40	64.67	99.47	86.47	14.19	24.73
17	IC-95567	53.67	120.11	6.35	43.60	18.73	165.87	231.53	86.47	55.67	97.40	92.07	5.83	10.71
18	IC-74656	56.67	120.73	6.25	36.27	17.33	191.67	256.87	92.67	67.53	101.73	101.67	14.29	26.05
19	IC-35665	54.00	106.17	6.31	46.67	14.60	186.13	331.93	106.53	86.73	152.00	100.33	18.75	40.52
20	IC-95431	55.67	120.47	5.29	34.20	14.13	144.93	251.80	86.07	61.13	98.53	104.53	12.21	22.10
21	IC-81694	54.00	104.55	7.55	51.13	26.47	182.40	351.13	119.33	86.33	150.33	171.00	15.77	38.32
22	AG-21	54.00	120.33	5.67	36.40	25.47	169.87	221.87	77.13	63.07	97.87	91.60	11.74	21.61
23	IC-120588	54.00	120.90	6.58	24.67	14.27	154.00	192.20	67.67	65.00	82.33	103.33	13.78	12.89
24	GA-1	54.33	112.21	6.81	56.20	22.20	186.53	332.07	106.87	63.93	112.27	132.60	8.74	21.07
25	AG-114	51.00	120.46	5.60	31.27	22.07	163.20	251.20	92.67	63.80	92.60	104.53	11.18	11.15
26	SKWA-6	54.33	112.35	5.54	40.60	12.67	153.33	231.47	87.60	67.07	100.53	102.53	14.16	30.15
27	IC-81710	54.00	101.23	6.22	36.47	19.33	173.13	231.07	91.07	63.07	108.67	100.80	11.15	22.81
28	IC-120573	51.67	120.36	5.36	33.80	23.07	174.87	170.33	40.40	41.93	66.53	74.73	11.33	15.92
29	IC-2935514	46.00	106.17	5.85	40.87	9.87	161.27	131.07	41.93	63.40	57.60	91.20	18.06	26.62
30	RGAS-92-10-1	51.00	107.40	5.79	34.87	17.53	184.67	199.13	61.87	67.00	88.53	102.33	15.75	30.39
31	IC-35479	56.33	120.37	5.78	36.93	22.53	143.60	223.20	82.67	53.07	103.13	96.07	6.93	13.26
32	IC-35722	54.00	120.80	5.75	22.87	14.13	165.53	240.53	86.73	73.40	108.80	102.47	14.89	21.38

Contd..

33	IC-120574	50.33	120.39	6.37	22.20	21.13	155.33	222.73	73.27	73.13	98.53	81.73	17.48	31.27
34	IC-21803	51.00	101.64	6.28	31.67	21.73	165.20	182.47	61.87	60.13	77.13	93.80	11.60	20.44
35	IC-95642	54.00	112.25	6.35	43.53	21.73	182.27	233.60	83.73	66.40	104.53	123.40	14.97	34.16
36	SKNA-20	51.00	120.43	5.43	51.87	21.20	182.53	222.27	85.53	59.27	100.40	132.53	8.70	19.80
37	BGA-2	41.67	90.08	5.77	19.13	12.00	161.20	433.07	96.67	53.73	177.47	109.33	21.08	59.82
38	Eidual Tivan	42.00	90.27	5.27	11.13	10.87	154.33	113.07	32.20	49.87	68.47	48.53	20.19	26.10
39	SKNA-7	55.33	120.53	7.29	32.07	21.47	186.47	202.00	57.67	75.87	87.60	87.27	19.53	34.13
40	IC-32193	54.00	107.20	5.63	42.40	14.53	153.07	222.07	58.93	59.40	102.87	92.53	11.92	20.63
41	IC-35496	50.33	113.15	5.63	31.80	22.87	163.67	267.13	97.00	56.00	102.73	81.60	12.06	21.69
42	RGAS-92-10-1	53.33	113.19	6.45	39.00	22.33	192.93	299.73	99.83	32.93	125.93	97.60	14.35	29.53
43	RAM-2	54.00	113.58	7.33	44.47	14.80	173.00	278.00	83.20	56.00	114.93	113.33	10.02	20.00
44	IC-81696	50.33	81.27	5.87	20.13	12.67	162.87	180.40	77.53	42.27	91.73	100.33	8.49	46.71
45	RGAS-96-6-2	53.33	120.40	6.53	36.13	24.73	173.93	256.93	88.27	66.40	95.60	98.33	13.33	26.60
46	IC-66436	54.00	106.10	5.11	44.20	21.87	172.07	289.40	98.60	72.07	122.73	91.33	15.36	33.96
47	MGA-2	44.67	92.68	4.83	26.07	15.80	163.93	311.73	73.73	65.00	147.13	102.93	16.98	42.86
48	IC-35770	54.00	113.24	6.19	44.47	10.27	153.07	279.33	84.93	65.93	115.93	92.20	12.90	26.64
49	IC-45517	54.00	120.20	6.24	35.67	16.73	167.60	308.67	72.27	53.87	131.53	102.13	6.50	12.42
50	IC-35663	53.67	120.71	5.37	39.20	18.47	194.67	189.67	63.53	54.93	81.33	87.60	11.91	20.02
51	IC-35635	54.00	105.13	6.67	50.40	13.87	199.20	279.73	82.80	72.80	116.93	92.13	20.40	46.85
52	IC-95365	52.67	120.76	5.25	30.00	17.60	154.00	151.47	46.93	56.00	60.67	77.87	13.44	17.12
53	IC-42004	54.00	106.22	6.13	37.60	18.73	177.53	228.93	83.07	74.20	105.13	73.00	21.43	37.74
54	IC-95358	53.67	105.22	5.15	35.60	12.27	142.80	111.87	31.13	40.47	43.80	62.07	14.67	15.05
55	A-Suvarna	54.00	120.05	7.17	59.33	27.07	174.67	182.87	45.27	44.47	77.73	91.07	9.96	16.70
56	Suvarna	53.67	95.29	7.09	26.07	18.20	144.27	321.60	93.20	52.80	110.60	113.07	22.47	48.61
57	DS-1	53.67	106.50	6.42	38.07	19.53	177.87	227.33	88.00	74.40	105.33	72.67	21.58	37.98
58	DS-2	54.00	105.27	5.13	34.93	12.53	142.80	112.87	36.40	40.27	43.40	62.33	14.19	14.86
59	DS-3	53.67	112.50	6.59	30.80	7.40	169.67	283.53	81.80	65.20	116.27	107.67	12.66	26.99
60	BAS-1	56.00	113.15	6.01	43.33	17.33	175.60	432.60	126.33	65.20	177.13	97.93	14.99	40.15
61	BAS-2	53.67	107.72	5.79	41.40	14.60	153.87	222.67	75.20	58.60	103.40	92.20	11.70	20.80
62	BAS-3	41.67	90.89	5.55	18.67	12.33	162.00	432.60	87.33	55.53	177.13	108.33	20.65	59.75
63	BAS-4	53.67	113.30	6.35	40.53	23.27	182.40	300.33	71.73	33.80	131.93	97.80	14.41	29.72
64	Annapurna	50.67	89.61	5.55	42.27	8.47	165.87	323.73	86.27	73.40	111.33	95.53	25.03	52.32
	Mean	**52.40**	**109.30**	**5.91**	**37.32**	**17.47**	**166.15**	**244.85**	**78.65**	**61.02**	**103.82**	**95.03**	**13.93**	**27.26**

EVALUATION OF GRAIN AMARANTH COLLECTIONS FOR PRODUCTIVITY AND QUALITY TRAITS (*Amaranthus* spp.)

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ABSTRACT

A field experiment was conducted during *kharif* 2002 to study the genetic variability, correlation, path coefficient analysis, genetic diversity and selection indices for productivity traits and variability for quality traits like protein content, minerals and popping quality in grain amaranth (*Amaranthus* spp.). The experiment was laid out in 8 × 8 simple lattice design with four replications .The study included 64 genotypes and observations were recorded on thirteen productivity traits.

The study revealed wide range of variability, high heritability and high genetic advance as per cent mean for number of leaves, number of branches, panicle fresh weight, panicle length, dry weight of panicle, dry weight of stem, harvest index and seed yield per plant. Correlation studies revealed significant association of seed yield with panicle fresh weight, panicle length, number of spikes per panicle, dry weight of panicle, dry weight of stem and harvest index. The maximum positive direct effect on seed yield per plant was exhibited by panicle fresh weight followed by harvest index at genotypic level.

Sixty four genotypes were grouped into eleven clusters based on D^2 analysis. Higher inter-cluster distance was noticed between cluster-III and XI, while higher intra-cluster value was noticed in cluster-II. The genotypes in the cluster-III showed highest cluster mean values for panicle fresh weight, harvest index and seed yield per plant. Selection index involving panicle fresh weight, panicle length and panicle dry weight was the best which exhibited the highest relative efficiency and suggested to consider these characters while making selection. The genotypes were also evaluated for protein, mineral and popping quality. The iron content was high in IC-35665 and zinc in BGA-2. BGA-2 and BAS-3 were found to be promising for yield, protein and popping quality as compared to the check. These may be utilized for future grain amaranth improvement programme.