

STABILITY ANALYSIS IN GRAIN AMARANTH
[*Amaranthus hypochondriacus* L.]

BY

SAVALIYA PARTH MANISHBHAI

B.Sc. (Hons.) Agriculture



DEPARTMENT OF GENETICS AND PLANT BREEDING
CHIMANBHAI PATEL COLLEGE OF AGRICULTURE
SARDARKRUSHINAGAR DANTIWADA AGRICULTURAL UNIVERSITY
SARDARKRUSHINAGAR - 385 506

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[*Amaranthus hypochondriacus* L.]

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GENETICS AND PLANT BREEDING

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ABSTRACT

A study entitled **Stability analysis in grain amaranth (*Amaranthus hypochondriacus* L.)** was conducted at Centre for Crop Improvement, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar. The experimental material consists of twenty five genotypes were raised in a Randomized Block Design (RBD) with three replications in three different environmental conditions during *rabi* 2019-20. Observations for days to 50 per cent flowering, days to maturity, plant height, length of inflorescence, girth of inflorescence, stem diameter, number of branches per plant, leaf area, biological yield per plant, grain yield per plant, harvest index, test weight and protein content were recorded.

The analysis of variance showed that the presence of highly significant variability for all the traits under study for individual as well as pooled environments. Across all three environments, none of the genotypes performed consistently for any of the characters. In the individual environments (E_1 , E_2 and E_3) and pooled environment genotypic (σ^2_g), phenotypic (σ^2_p) and environmental component (σ^2_e) were found high for leaf area, plant height, biological yield per plant, days to maturity, days to 50 per cent flowering, length of inflorescence and harvest index.

The high GCV (%) and PCV (%) were observed for number of branches per plant, leaf area, grain yield per plant, biological yield per plant, harvest index, plant height and stem diameter for all the individual environments. The GCV (%) was close to the PCV (%) for the majority of traits, indicating a lesser influence of environment and a greater role of genetic factors in trait expression.

Heritability and expected genetic advance as a percentage of mean was found to be high in all individual as well as pooled over environment for number of branches

per plant, leaf area, grain yield per plant, biological yield per plant, harvest index, stem diameter, plant height, days to 50 per cent flowering, length of inflorescence, girth of inflorescence, and days to maturity.

Correlation studies provide reliable information on the type and extent of character correlations. The character grain yield per plant was positively and highly significantly correlated with days to 50 per cent flowering, days to maturity, plant height, stem diameter, leaf area and biological yield per plant at genotypic, phenotypic and environmental levels, respectively. Whereas, girth of inflorescence significantly and positively correlated at genotypic and phenotypic levels, respectively.

Result of path co-efficient analysis suggested that correlation between grain yield with days to 50 per cent flowering, plant height, length of inflorescence, girth of inflorescence, number of branches per plant and biological yield per plant is due to direct and positive effect of a character whereas, direct and negative effect with the days to maturity, stem diameter, leaf area and protein content.

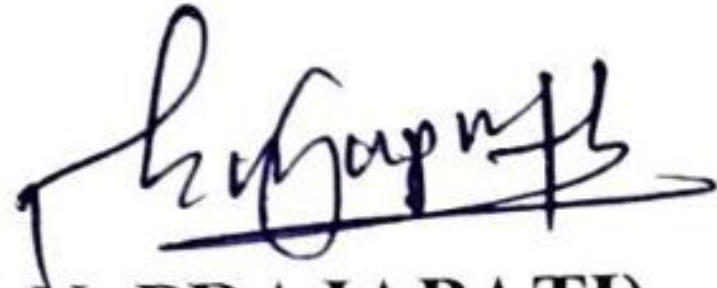
Genotype $\times$ environment interaction showed significant differences for stem diameter, number of branches per plant, leaf area, grain yield and protein content when tested against pooled error. The estimations of the environmental index (I_j) showed that E_1 (day of sowing 11th November, 2019) was the most favourable environment for the grain amaranth. Genotypes SKGPA-150, SKNA-401 and SKNA 808 are showing average stability for grain yield per plant as well as stem diameter, leaf area and protein content whereas, SKGPA-61 showing average stability for grain yield per plant along with stem diameter and protein content. SKNA-903 showing stability for leaf area, and protein content along with grain yield per plant. Whereas, BGA-7-1 showing stability for stem diameter and leaf area along with grain yield per plant. In poor environmental conditions SKGPA-74, SKNA-1313, SKNA-1406, SKNA-1407, SKNA-1503, SUVARNA, ANNPURNA and IC-506575 showing stability for grain yield per plant.

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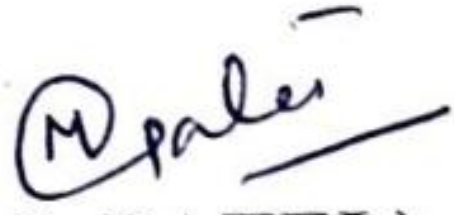
CERTIFICATE – I

Date : 13 / 09 / 2021.

This is to certify that the thesis entitled, “**STABILITY ANALYSIS IN GRAIN AMARANTH** [*Amaranthus hypochondriacus* L.]” submitted for the degree of **MASTER OF SCIENCE** in the subject of **GENETICS AND PLANT BREEDING** is a record of bonafide research work carried out by **SAVALIYA PARTH MANISHBHAI** under my guidance and supervision and that no part of this thesis has been submitted for any other degree, diploma, associateship, fellowship or other similar titles. The assistance and help received during the course of investigation have been fully acknowledged.


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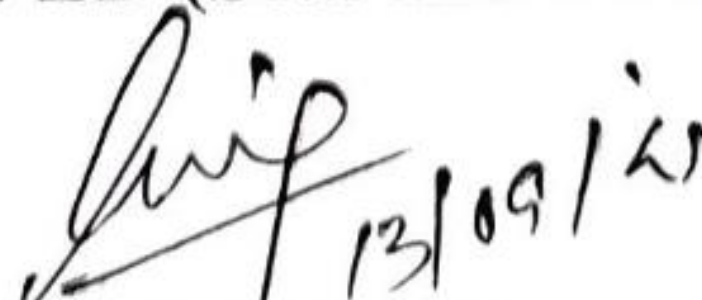


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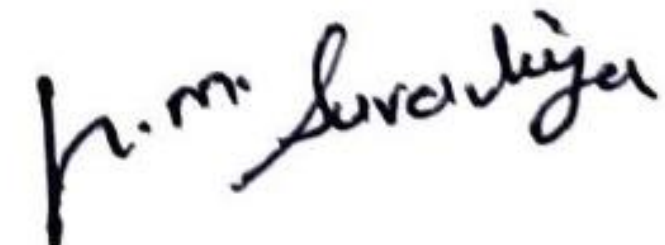
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LIST OF ABBREVIATIONS AND SYMBOLS

@	:	At the rate of
()	:	Bracket
,	:	Comma
C.D.	:	Critical difference
°C	:	Degree Celsius
d.f.	:	Degrees of freedom
S^2d_i	:	Deviation from regression
<i>et al.</i>	:	et alii and others
<i>etc.</i>	:	Etcetera
Fig.	:	Figur
μ	:	General mean
g	:	Gram (s)
>	:	Greater than
Ha	:	Hectare (s)
=	:	is equal to
<	:	Less than
$\bar{X}$	:	Population mean
ml	:	Milliliter
×	:	Multiply
<i>viz.,</i>	:	Namely
Σ	:	N-ray Summation
/	:	Per
%	:	Per cent
b_i	:	Regression co-efficient
;	:	Semi colon
σ	:	Sigma
[]	:	Square bracket
$\sqrt{\quad}$	:	Square root
S.Em.±	:	Standard error of mean
i.e.	:	That is
Via	:	Through

I. INTRODUCTION

Amaranth originating in America and Europe, has being grown for 8000 years as a grain (O'Brien and Price, 1983). Thousands of hectares of this pseudo-cereal were grown by Pre-Columbian civilizations. In India, grain amaranth is grown from tropical lowlands to 3500 m height in the Himalayas (Sauer, 1967). The word 'amaranth' comes from the Greek word 'amarantos', which means never - fading flower'. In Mahesana, Banaskantha, Gandhinagar, Sabarkantha and Kheda districts of Gujarat, Amaranth locally known as Rajagira is grown as a profitable crop. The area under amaranth is increasing day by day where irrigation facilities exist, particularly in North Gujarat and to a significant extent in Middle Gujarat (Gelotar, 2018). Grain amaranth is dicotyledonous crop and grows rapidly. Amaranthus is the vegetable of the poor man. Amaranth is an anemophilous (wind pollination) vegetable crops and it is often pollinated by bees because of their colorful inflorescence.

Ancient amaranth grains of three species, *Amaranthus caudatus* L., *Amaranthus cruentus* L., and *Amaranthus hypochondriacus* L. are used to grow grain from amaranth. India was known to be one of the two major centers of distribution of genus *Amaranthus* and the other was considered to be tropical America.

There are 70 species of amaranth, 40 of which are considered native to America. In both temperate and tropical climates, over 400 varieties of these species are found throughout the world and fall generally into one of four categories: grain, vegetable, ornamental or weed. There is no direct line of division between a "grain" type and a "vegetable" type. If the leaves are consumed when the plants are young, the leaves of amaranth plants that are grown specifically for grain may serve as a food source. Some species that are mainly cultivated in the hot, humid tropics have high quality leaves. The genus *Amaranthus* belongs to the amaranthaceae family, which consists of hardy, weedy, herbaceous and fast-growing cereals such as plant (Opote, 1979).

The amaranth genus is dibasic with $X = 16$ and $X = 17$ chromosomes, almost equally distributed in the Amaranth section. Grant (1959) has reported the information regarding the chromosome number of 30 species of *Amaranthus*. Among these, four have $2n = 32$, while all others have $2n = 34$. Among the 30 species, *Amaranthus caudatus* L. ($2n = 32$), *Amaranthus cruentus* L. ($2n = 34$) and *Amaranthus hypochondriacus* L. ($2n = 32$) are domesticated species and among these three species *Amaranthus caudatus* L. is drooping type and rest two are erect type species.

Amaranth germplasm is catalogued and stored in germplasm banks in 11 countries (Toll and van Sloten, 1982). Feine-Dudley has developed a descriptive taxonomic key for all the cultivated species of the genus *Amaranthus* (Grubben and van Sloten, 1981).

Grain amaranth plant has a main stem axis that ends in a large branched inflorescence. The height of the plant varies from 0.4 m to 1.5 m between different species. The flowers are unisexual, varying in colour as purple, orange, red or gold and are develop on branched flower clusters (glomerules). The floral buds originate directly from the leaf axils. The seeds are quite small (0.9 to 1.7 mm diameter) with varying weight from 1,000 to 3,000 seeds per gram and the colour of seeds can vary from cream to gold and pink to black. Seeds of the vegetable, ornamental and weedy types are shiny black.

In India amaranth is cultivated in Jammu and Kashmir, Himachal Pradesh, Uttarakhand, Sikkim, Assam, Meghalaya, Arunachal Pradesh, Nagaland, Tripura, Jharkhand, Chhattisgarh, Maharashtra, Gujarat, Orissa, Karnataka and Tamil Nadu both hills and plains (Dua *et al.*, 2009).

Amaranth has a "C₄" photosynthetic pathway (along with such plants as corn and sorghum) that makes it uniquely efficient to use sunlight and nutrients at high temperatures. The grain amaranth grows very quickly and its large seed heads can weight up to 1 kilogram and can contain a half-million seeds.

In Mexico, grain amaranth is popped and mixed with a sugar solution to make a confection called "alegria" (happiness). A traditional Mexican drink called "atole" is made of milled and roasted amaranth seed. In Nepal, amaranth seeds are eaten as a gruel called "sattoo" or milled into a flour to make chappatis (Singhal and Kulkarni, 1988).

Amaranth is more correctly termed as "pseudo grain". Among all three of the pseudo-cereal (Chenopods – *Chenopodium* spp., Buck wheat – *Fagofyrum* spp. and Amaranth – *Amaranth* spp.), grain amaranth is the most important. The amaranth is highly edible by gluten intolerant individuals as it does not contain gluten. Grain and leaf types require little fuel to be cooked and are used as food by humans and animals (Kauffman and Hass, 1983; Oke, 1983; Saunders and Becker, 1984; Tucker, 1986). The amaranth grain is one of the most valuable foods because it has high protein content and well-balanced amino acid profile (Gamel *et al.*, 2004). Amaranth species are receiving a great deal of attention in developing countries as a means to fight protein malnutrition due to the presence of high seed protein (about 16 per cent) which is much higher than

most of the common grains except soybeans (Singhal and Kulkarni, 1988; Oleszek *et al.*, 1999).

Amaranth grain contains 6 to 10 per cent oil, most of which is found in the embryo (Betschart *et al.*, 1981, Lorenz and Hawang, 1985; Garcia *et al.*, 1987). Amaranthus seed oil is beneficial for those suffering from hypertension and cardiovascular disease. The average content of three major fatty acids *i.e.*, palmitic, oleic, and linoleic acid (Ping *et al.*, 2002). They also have anti-tumor and anti-oxidant activity (Kim *et al.*, 2006a). Grain amaranth consumption has been shown to be beneficial to diabetic patients based on the studies that improve glucose and lipid metabolism (Kim *et al.*, 2006b). Both the fasting serum glucose levels and the glucose tolerance of the diabetic rats have been improved.

Grain amaranth also contains high levels of calcium, iron, magnesium, phosphorus, copper, manganese cobalt, chromium, iodine, selenium, zinc, molybdenum, and sodium, like other cereals, in addition to proteins, carbohydrates, dietary fiber and lipids, which are also needed by the human body in very limited amounts (Becker *et al.*, 1981) (generally less than 100 micrograms per day).

Potential crops such as amaranth have recently earned worldwide attention in this regard, as this crop contain abundant amount of all the common nutrients needed for normal human development.

The presence of variability within population for different economic characters is important for an effective breeding programme which generally depends on selection of appropriate parents. The most critical and primary steps in any crop improvement programme are the collection, maintenance and evaluation of germplasm. Yield is a dynamic character regulated by several yield attributing characters. Although, most of the yield attributing character are quantitatively inherited and affected by environment, it is difficult to judge whether the observed variability is heritable or not. The parameters such as genotypic and phenotypic coefficients of variation, heritability and genetic advance are helpful in understanding the nature of inheritance of various traits.

Knowledge of the relation between grain yield and its contributing character is important for the selection of plants for potential breeding programme. Correlation coefficient analysis is a helpful methodology that elaborates the degree and extent of relationship between essential plant characters and sets out simple selection parameters that lead to directional model based on yield and its components in the field experiments. Path coefficient analysis, on the other hand, is an effective statistical technique specially

developed to measure the interrelationship of various components and their direct and indirect effects on yield. This methodology can be used to categorize the yield of contributing characters and specific characteristics that generate a given correlation. (Islam *et al.*, 2010).

Stability refers to the constancy in performance of a variety for general cultivation over a wide range of environments. Stability analysis may be carried out both parental and segregating populations in order to the identification of location specific and widely adaptable genotype (Admassu *et al.*, 2008). Gene - environment interaction (or genotype - environment interaction or $G \times E$) is the phenotypic effect of genes and the environment interactions. Study of genotype - environmental interactions is important for enhancing accuracy and precision in the estimation of both genetic and environmental impacts. Amaranth is an environmental sensitive crop. Stable genotypes are required to ensure sustainable crop production.

Genetically stable varieties ensure the stable production and stable production ensures the farmer's benefit. In the present context, measures of the stability of the amaranth varieties useful for the field performances of various parameters at different sowing dates. Stable varieties have exactly the same performance as those that provide the additive performance when genetically boosted. Identification of these stable varieties provide benefits to the farmers and researchers in further development of crop and in research field. The selection of the best genotypes suited to the wide range of environment specifically suitable for each of the growing seasons will help to increase both the selection efficiency and the productivity of amaranth in that region. Therefore, to identify stable varieties or genotypes over different environments, study of genotype $\times$ environment ($G \times E$) interactions is very important from a breeding point of view (Eberhart and Russell, 1966).

It has been emphasized that the analysis of individual yield components will lead to simplification in genetic interpretation of yield stability and thus, it is important to breeders in predicting and evaluating of environmental effects. It is important to identify the stable genotypes in various growing seasons and environment which have great significance to the plant breeders for improvement of this crop.

Considering the growing demand of high-yielding genotypes with good stability under different environmental conditions the present study on “**Stability analysis in grain amaranth (*Amaranthus hypochondriacus* L.)**” has been under taken with the following objectives:

1. To measure the nature and extent of variability in respect of yield and its component traits
2. To determine the magnitude of correlation coefficient and path coefficient between yield and component traits
3. To study the nature and magnitude of genotype $\times$ environment interactions and stability parameters of different genotypes for seed yield and other yield attributes

II. REVIEW OF LITERATURE

The present investigation was aimed to studying genotypic and phenotypic variability, heritability, genetic advance, correlation co-efficient, path co-efficient analysis and stability for various quantitative characters of grain amaranth is reviewed and presented below under following heading.

2.1 Genotypic and phenotypic variability, heritability and genetic advance

2.2 Correlation co-efficient and path co-efficient analysis

2.3 Genotype $\times$ Environment interaction and stability parameters

2.1 Genotypic and phenotypic variability, heritability and genetic advance

Vyas (2000) studied genetic variability in 60 genotypes of grain amaranth. A wide range of variation was observed for seed yield per plant, plant height, panicle length, straw yield per plant, number of branches per plant and harvest index. GCV (%) was high for seed yield per plant, numbers of branches per plant, straw yield per plant and harvest index. The broad sense heritability (h^2_{bs}) estimates were also found to be high for all the characters except panicle length. Expected genetic advance as percent of mean (GA %) was high for seed yield per plant, number of branches per plant and straw yield per plant.

Verma *et al.* (2001) noticed wide range of variability for seed yield per plant, plant height and protein content in grain amaranth (*A. hypochondriacus* L.). Highest heritability and genetic advance were reported for seed yield per plant and plant height.

Dutta *et al.* (2002) studied on grain amaranth (*A. hypochondriacus* L.) revealed presence of genetic variability in seed yield and harvest index. Genetic index flowering time showed high heritability while genetic advance was high for plant height.

Patel (2004) studied genetic variability in fifty genotypes of grain amaranth. A wide range of variation was observed for number of branches per plant, seed yield per plant and plant height. The high heritability estimates were found for 1000-seed weight, days to maturity, protein content and number of branches per plant. Expected genetic advance as percent of mean was high for seed yield per plant, number of branches per plant and protein content.

Patel (2011) studied genetic variability in twenty-eight genotypes of grain amaranth. The GCV, PCV, h^2 and GA as percentage of mean were high for various characters like seed yield per plant, plant height, panicle length and days to maturity. Therefore, more

emphasis should be laid on component traits during selection for the improvement of grain yield.

Ahmmmed *et al.* (2012) genetic variability, heritability analyses were done for yield and its component characters in twenty-two diverse genotypes of stem amaranth. The highest PCV and GCV were observed for primary branches per plant while the lowest PCV was found in plant height and the lowest GCV was found in leaf width. Heritability estimates in broad sense were higher for primary branches per plant, stem weight per plant and yield per hectare. yield per hectare exhibited high value of heritability along with high genetic advance.

Hasan *et al.* (2012) studied variability, heritability for seventeen genotypes of stem amaranth (*Amaranthus tricolor* L.) were evaluated to determine the genetic variability, degree of association between yield and its component characters. The direct and indirect effects of marketable yield were also evaluated. High heritability with high genetic advance as per cent of mean was registered for number of leaves, leaf weight and marketable yield which in fact demonstrated the presence of additive gene effects.

Akaneme *et al.* (2013) studied on variance of five accessions of the amaranth (*A hypochondriacus* L). species obtained from National Centre for Genetic Resources and Biotechnology Ibadan, Nigeria revealed highly significant differences for days to 50 per cent flowering and 500 seed weight. The range, coefficient of variability, phenotypic and genotypic coefficients of variability also revealed high variability for each of the quantitative traits. The highest broad sense heritability (h^2b), GCV, PCV and GA were obtained for days to 50 per cent flowering which was also positively correlated with stem diameter.

Yadav *et al.* (2014) evaluated genotypic variability and character association in grain amaranth genotypes for agronomically useful and yield contributing traits. The characters like lateral spikelet length and grain yield per plant showed high GCV and PCV values. The highest GCV was recorded with grain yield per plant. High heritability exhibited for all the characters like viz., observed to be high in magnitude for days to 80 per cent maturity, days to 50 per cent flowering, inflorescence length and plant height. At genotypic level, seed yield per plant showed highly significant positive correlation with days to 80 per cent maturity and plant height and significant positive correlation with days to 50 per cent flowering. Inflorescence length had significant positive correlation with lateral spikelet length.

Venkatesh *et al.* (2014) studied genetic variability, heritability and genetic advance in grain amaranthus. One hundred germplasm accessions of grain amaranth were evaluated assessing the genetic variability for grain yield and yield related traits. Analysis of variance revealed significant differences among the genotypes for all the characters studied. High PCV and GCV was observed for stem girth, plant height, panicle length and grain yield per plant. On low were observed for days to maturity and grain protein content. All the traits studied exhibited high heritability. High genetic advance as per cent of mean was observed and grain yield per plant indicating scope for improvement of the traits of interest through hybridization and selection.

Sheelamary *et al.* (2016) studied genetic variability, heritability and genetic advance in one hundred genotypes of grain amaranth. On the basis of mean performance highest was recorded by days to 80 per cent flowering followed by plant height and days to 50 per cent flowering. The genotypic coefficient of variation (GCV) was observed for seed yield per plant followed by lateral spikelet length, plant height and inflorescence length. The phenotypic coefficient of variation (PCV) was observed for seed yield per plant followed by lateral spikelet length, plant height, inflorescence length, stem thickness and days to 50 per cent flowering. The phenotypic coefficient of variation (PCV) is higher than the genotypic coefficient of variation for all the characters. High heritability coupled with high genetic advance was observed for hundred seed weight and days to 80 per cent maturity which indicates the predominance of additive gene action making the selection more effective. The results obtained from this study might be helpful for the breeders trying to develop new varieties with better grain features to improve grain amaranth.

Lokeshumar and Murthy (2017) genetic variability studied for yield component traits in grain amaranth (*Amaranthus* spp.). The investigation on genetic variability and genetic divergence with respect to yield component traits estimated using one hundred five germplasm during *kharif*, 2013 at University of Agricultural Sciences, Bangalore. A high phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was observed for all the traits except for 1000-seed weight. Heritability estimates were high for all the characters studied. High genetic advance as per cent mean (GAM) was registered for most of the traits except for 50 per cent flowering, 1000-seed weight and days to maturity.

Shrivastav *et al.* (2017) studied genotypic variability of Amaranth (*Amaranthus paniculatus* L.) including three checks (GA 2, BGA 2 and RMA 7). The analysis of

variance revealed that mean squares due to treatments were highly significant for all characters except seed volume weight (g/10 ml). The magnitude of phenotypic coefficient of variation was higher than corresponding genotypic coefficient of variation for all the characters. The high estimates of phenotypic (PCV) and genotypic (GCV) coefficients of variations were found in case of harvest index, biological yield/plant and low estimates of phenotypic and genotypic coefficients of variations were observed for protein content and seed volume weight. High heritability in broad sense was recorded for plant height biological yield per plant, harvest index, days to maturity and inflorescence length. The high estimates of genetic advance in per cent of mean were recorded for harvest index, biological yield per plant, plant height, number of branches per plant and inflorescence length. All the genotypes were grouped into five different non overlapping clusters. The contribution of ten characters towards divergence showed the highest contribution by plant height followed by biological yield per plant.

Gelotar (2018) studied genotypic coefficient of variation, heritability and genetic advance in nineteen germplasm of grain amaranth and observed highest for the characters viz., number of branches per plant, leaf area, seed yield per plant and plant height. High heritability was observed for plant height, leaf area, days to maturity, seed yield per plant, length of inflorescence, days to flowering and number of branches per plant, while genetic advance was observed for plant height, length of inflorescence, seed yield per plant and days to flowering.

Shah *et al.* (2018) studied twenty-seven diverse genotypes of vegetable amaranth were evaluated for various yield and yield attributing traits. Analysis of variance revealed highly significant differences among all the genotypes under study for all the traits. Range values indicated presence of sufficient genetic variability for all the characters. Phenotypic coefficients of variation were found to be higher than corresponding genotypic coefficients of variation. Most of the traits recorded high phenotypic and genotypic coefficients of variation. All the characters showed the high estimates of heritability coupled with high genetic advance as per cent of mean.

Tiwari (2018) studied twenty-seven genotypes of grain amaranth were used to study genetic variability and heritability which resulted phenotypic variance was higher than the genotypic variance for all the traits. The heritability estimates for all the characters were high and none of the characters showed moderate or low estimates.

Kumar *et al.* (2018) studied on collection and valuation of genetic variability available in twenty-five genotypes of amaranthus (*Amaranthus* spp.) were evaluated.

High magnitude of phenotypic GCV and PCV was observed for test weight, number of leaves plant, stem girth and number of branches plant. The heritability estimates recorded to be high for the characters viz., dry matter per cent, seed yield plot, stem girth, test weight, number of branches plant and plant height. Highest estimates of genetic advance as percentage of mean were obtained for characters namely test weight and stem girth.

Bhalekar *et al.* (2019) studied on sixteen genotypes of grain amaranth for the testing of qualitative and quantitative characters during *rabi* 2017-18 at Rahuri. The results on quantitative characters revealed that genotype RHGA 13-4 gave better performance for yield and yield contributing characters followed by RGAG 12-8 and RGAG 16-11. Among the genotypes, RHGA 13-4 recorded significantly for stem thickness, inflorescence length, plant height and seed yield per hectare while the genotype RGAG 12-27 showed early flowering days and days to maturity.

Rashad and Umakanta (2020) twenty promising genotypes of green amaranth during 2015 at Gazipur. The significant analysis of variance revealed wide range of variability among the twenty genotypes of green amaranth. Except for stem diameter, foliage yield and all the yield contributing morphological traits had high heritability including high genetic advance in percent of mean, high to moderate genotypic and phenotypic variances and coefficient of variations with minimum differences of PCV and GCA indicated that the traits were governed by additive gene actions and had a great scope of selection for the improvement of green amaranth.

2.2 Correlation co-efficient and path co-efficient analysis

Dutta *et al.* (2002) studied genetic variability, correlation, path analysis on grain amaranth (*A. hypochondriacus* L.). Included characters viz., harvest index, plant height, inflorescence length, maturity period, flowering time and test weight had significant positive correlation with seed yield. Path analysis revealed highest positive direct effect of harvest index followed by maturity period, basal girth and plant height, inflorescence length and flowering time had substantial indirect contribution through harvest index.

Shukla and Singh (2003) studied correlation coefficient at both genotypic and phenotypic levels in sixty-six genotypes of amaranthus species. They reported that genotypic correlations were higher than their corresponding phenotypic correlations in all the traits, there by suggesting strong inherent association between various characters at genetic level. They further observed that at genotypic level grain yield per plant showed significant positive associations with plant height and number of inflorescences

per plant. It indicated that selection for these traits would lead to improvement in grain yield. They further reported that significant association of leaf size at genotypic levels with grain yield indicating larger leaves were responsible for increasing higher yield, it may be due to high photosynthetic activity.

Prajapati *et al.* (2005) studied the inter relationship between grain yield and eight yield contributing characters days to 50 per cent flowering, plant height, number of branches per plant, panicle length, days to maturity, 1000- seed weight and harvest index in sixty diverse genotypes of amaranth. The grain yield exhibited significant and positive correlation with harvest index, 1000-seed weight and number of branches per plant.

Rana *et al.* (2005) studied correlation analysis using hundred accessions (Fifty from India and fifty from exotic sources) of grain amaranth (*A. hypochondriacus* L.) germplasm were grown in complete Randomised Block Design (RBD). Correlation and path analysis revealed the significance of inflorescence length and plant height for selecting better yielding genotypes.

Ahmed *et al.* (2012) studied correlation on stem diameter and plant height exhibited highly significant positive correlation with yield per hectare both at genotypic and phenotypic level. Selection based on these traits would give better response for the improvement in marketable yield in stem amaranth.

Hasan *et al.* (2012) correlation studied using seventeen genotypes of stem amaranthus reported strong positive association of yield with stem diameter, dry weight with rind and dry weight without rind. The relationship was non-significant and negative at 1st flowering.

Patil *et al.* (2014) studied on path coefficient analysis in twenty-two genotypes of grain amaranth (*Amaranthus* spp.) were evaluated for twelve quantitative traits for two years and the pooled data was analyzed. The mean, range, genotypic and phenotypic coefficient of variation, heritability in broad sense and genetic advance were calculated. Path coefficient analysis was carried out using correlation coefficients to know the yield contributing traits having true associations with seed yield. High heritability coupled with high genetic advance for yield per day to maturity, yield per day to harvest index, panicle girth and seed yield per plant was observed. All the traits except days to seed fill possessed positive association with grain yield. Harvest index was positively correlated with days to maturity. Harvest index, aerial biomass per plant and days to maturity also had high phenotypic and genotypic direct effects on seed yield per plant, revealing that indirect selection for these traits would be effective in improving seed yield.

Venkatesh *et al.* (2014) studied on one hundred genotypes of grain amaranth to estimate correlation and path co-efficient among 10 quantitative traits including grain yield in grain amaranth. At the phenotypic level, stem girth, number of leaves per plant, plant height, panicle length and seed weight exhibited significant positive correlation with grain yield. Path co-efficient analysis revealed maximum positive direct effect of seed weight (0.234), panicle length (0.221) and plant height (0.124) on grain yield. The study suggests that selection of varieties with higher seed weight, panicle length and plant height will help the breeder to select the genotypes which can give better grain yield.

Gerrano *et al.* (2015) thirty-two *amaranthus* genotypes have been collected and conserved in the gene bank of the ARC-Roodeplaat Vegetable and Ornamental Plant Institute, South Africa. Genetic correlation coefficient for the traits showed that there were significant correlations among some of the phenotypic traits. An extremely strong correlation was observed between leaf area and leaf area index and moderate correlation with panicle length, fresh biomass, dry biomass and yield per plant. Plant height was also positively correlated with fresh biomass and dry biomass. Yield per plant showed a moderate positive correlation with leaf area, leaf area index and plant height, and a strong correlation with fresh biomass and dry biomass.

Oduwaye *et al.* (2016) evaluated 18 *Amaranthus cruentus* and 11 *Amaranthus hypochondriacus* genotypes at two locations in Nigeria differing in temperature/precipitation to determine the influence of environment on genetic gain. Higher genotypic coefficient of variability, heritability estimates, and genetic advance was observed for the traits at Abeokuta (more wet) than Ibadan (more dry) conditions. Grain yield had positive association with the traits at the two locations except inflorescence length. Inflorescence length was positively associated with grain yield at Abeokuta and negatively associated at Ibadan. Path analysis indicated simultaneous improvement of grain yield with petiole length at Abeokuta but with petiole length and leaf area at Ibadan.

Tejaswini *et al.* (2017) studied correlation and path coefficient analysis using twenty-seven genotypes in grain amaranth species with nineteen yield and yield attributing characters was carried out in twenty-seven genotypes of vegetable amaranth in Randomized Block Design with three replications. Highly significant and positive correlation with foliage yield was observed with plant height, stem diameter, stem weight per plant, leaf length, leaf width, leaf area index, protein content, whereas

number of branches and number of leaves showed negative association with foliage yield. Path coefficient analysis revealed that the characters like plant height, protein content had high to moderate positive direct effect on foliage yield per plant and these traits recorded significant, positive correlation with foliage yield per plant. It clearly indicates that direct selection based on these characters would be effective for an increase in foliage yield.

Jangde *et al.* (2017) studied correlation and path coefficient analysis using twenty-three genotypes of amaranthus during *kharif* 2015-16 at Raipur. Analysis of variance revealed that mean sum of squares due to genotypes was highly significant for all the characters. Correlation coefficient correlation studies revealed that leaf yield kilograms per plot showed positive and significant correlation with number of leaves per plant and fresh stem weight for quantitative characters. Path coefficient analysis revealed that fresh steam weight (1.100) and number of leaves per plant (0.014) showed the highest positive direct effect on leaf yield.

Shrivastav *et al.* (2017) studied the seed yield per plant was found highly and positively correlation with inflorescence length, plant height and biological yield per plant. Seed yield per plant showed negative correlation with days to 50 per cent flowering and protein content and non-significant correlation with maturity. The characters showing significant positive correlation among yield and yield contributing characters would be highly effective and efficient in improving respective traits. Path analysis revealed biological yield per plant and harvest index as important components having high order of direct effect and biological yield per plant via days to maturity followed by harvest index via protein content, inflorescence length via plant height.

Sagar *et al.* (2018) studied genotypic correlation coefficients among growth, yield and quality parameters in twenty-five amaranthus genotypes foliage yield per plant was significantly and positively correlated with stem girth, number of leaves per plant, number of branches per plant, spike length, number of spikes per plant at both phenotypic and genotypic level. Yield per plant was also positively and significantly correlated with leaf area only at genotypic level.

Gelotar *et al.* (2018) reported that seed yield per plant was significant and positively correlated with days to flowering, plant height and length of inflorescence. Path co-efficient analysis indicated the highest positive direct effect on seed yield per plant by days to flowering, leaf area and 1000-seed weight.

Tiwari (2018) studied twenty-seven genotypes of grain amaranth were used to study correlation and path analysis which resulted days to maturity got significant positive correlation with seed yield, plant height, length of inflorescence and 10 ml seed weight (g). Plant height was also found to have significant positive correlation with seed yield and 10 ml seed weight. Length of inflorescence and 10 ml seed weight had significant and positive correlation with yield. In case of path analysis, days to maturity had positive direct effects on grain yield than 10 ml seed weight, length of inflorescence and plant height.

Rashad and Umakanta (2020) twenty promising genotypes of green amaranth during 2015 at Gazipur. Correlation study revealed that total biomass showed significant association with foliage yield per m². Hence, selection based on total biomass improve the foliage yield of green amaranth.

2.3 Genotype × Environment interaction and stability parameters

Sharma *et al.* (2001) studied phenotypic stability of 8 genotypes of grain amaranth (*Amaranthus hypochondriacus* L.) grown during 1997, 1998 and 1999. Genotypes showed significant genotype × environment interaction for days to maturity, plant height, panicle length, harvest index and grain yield. 'Amont' grain amaranth was stable with high mean performance for grain yield, harvest index and plant height, whereas 'Annapurna' for grain yield and panicle length.

Varalakshmi *et al.* (2002) studied genotype × environment interactions for some quantitative characters of 20 genotypes in grain amaranth (*Amaranthus hypochondriacus* L.). Significant linear component against pooled deviation for days to 50 per cent flowering, plant height and yield/plant indicated that the major component for differences in stability was due to linear regression and the performance can be predicted with some reliance under different environments. The grain yield/plant, IIHR-11, IIHR-22 and IIHR-46 were found to be responsive ($b < 1.0$) over the environments, hence more adaptable to normal growing conditions.

Varalakshmi (2003) studied stability parameters of 14 advanced breeding lines of vegetable amaranth (*Amaranthus tricolor* L.) were worked out during 1995, 1996, 1997 and 1998 for 5 quantitative characters under 3 environments. None of the lines tested was found to stable for all the characters studied. However, 'AV 20' for plant height, 'AV 29' for leaf weight and plant weight, 'AV 28' for stem weight 'AV 22' and 'AV 38' for leaf number were found to be stable.

Kishore *et al.* (2007) studied Joint regression analysis over eight environments in 8 genetically diverse amaranth genotypes during *kharif*. Sangla and Salooni indicated the presence of genotype $\times$ environment interaction for all the traits studied. On the basis of mean performance and stability parameters, genotype Suvarna was significantly superior with regard to seed yield, days to 50 per cent flowering and days to maturity in comparison to the local check. Considering the stability parameters in general, genotype Suvarna is by far the best genotype followed by Annapurna and PRA-I for cultivation in the higher regions of Himachal Pradesh.

Garcia Pereyra (2011) evaluated five genotypes of *Amaranthus hypochondriacus* L. and one of *A. cruentus* L. Study of genotype $\times$ environment interaction indicated that the evaluated materials tended to behave differently in the various localities and evaluated population densities.

Chatarmal and Kute (2013) evaluated 12 genotypes of grain amaranth in four different environments during *rabi* 2009. None of the genotypes was found to be stable for grain yield. RGAS-92-10-1 and RGAS-08-12 exhibited stability for length of inflorescences, whereas RGAS-92-10-1 was stable for plant height. RGAS-08-15 and RGAS-08-11 exhibited wider stability for early maturity. For days to 50 per cent flowering, RGAS-08-10 showed average stability. RGAS-08-15 exhibited stability for poor/stressed environment.

Oduwaye *et al.* (2013) study was carried out to examine the effect of genotype $\times$ environment interactions on the performance and stability of 30 amaranth accessions and to identify reference test environments in which to evaluate amaranth across four different environments situated at Ibadan and Abeokuta, in Southwest Nigeria. NG145 and NG205 produced the highest seed yields and was most stable accession at Ibadan. TIBET50, NG430 and NG174 were better adapted to Abeokuta, while NH161, NG174 and AM44 were better adapted to Ibadan.

Kumar and Yassin (2013) evaluated amaranth genotype at Karaikal, India, during November-February 2007-2008 for yield characters under very high (D_1), high (D_2), normal (D_3) and low (D_4) plant densities to identify stability parameters. Genotype Annapurna was stable for grain yield in all plant densities. Genotypes BGA 2, GA 2 and IC 415290 were stable for protein content and could be utilized for improvement of these traits. Similarly, SKNA 601 was stable for leaf area at 50 per cent

flowering in all plant densities. Among characters studied, length of the rachis per inflorescence and protein content were relatively stable in all plant densities.

Rekha Singh *et al.* (2015) studied on 40 genotypes of grain amaranth (*Amaranthus hypochondriacus* L.) for four environments at Allahabad during 2010-12. The pooled analysis of variance for biochemical characters over four environments was found non-significant for all biochemical characters.

Manikandan and Srimathi (2015) reported single plant seed yield was the lowest when crop was sown in summer and was higher with *kharif* crop. Similarly, the crop growth parameter was recorded maximum in *kharif* sown crop and was minimum in the crop sown in the summer. The total yield as well as the graded seed was the highest with *kharif* crop than the summer crop by 10.4 and 2 per cent respectively.

Oduwaye *et al.* (2016) evaluated 18 *Amaranthus cruentus* and 11 *Amaranthus hypochondriacus* genotypes at two locations in Nigeria differing in temperature/precipitation to determine the influence of environment on genetic gain. Genotype $\times$ environment was significant for all analyzed morphological parameters and for grain yield, 1000 seed weight and no. of days to 50 per cent flowering in *Amaranthus cruentus*. In *Amaranthus hypochondriacus* genotype $\times$ environment was significant for plant height, leaf area, inflorescence length, 1000 seed weight and grain yield.

Dewan *et al.* (2017) studied 20 genotypes of Stem amaranth to find genotype $\times$ environment interaction effects on the field performance at Genetics Farm of Sher-e-Bangla Agricultural university, Dhaka during 2013-14. Based on stable responses considering the higher yield character G-08 and G-18 could be selected for use in breeding program.

Pagi *et al.* (2017) studied to assess grain yield stability of thirteen genotypes in varied environments in three successive growing seasons and effects of genotype (G) and genotype $\times$ environment (GE) Result of study revealed that GGE biplot was effective to recognize stable and highest yield (1648.92 kg/ha) genotype as G5 followed by G6 (1457.24 kg/ha) and G3 (1268.62 kg/ha) genotypes while the genotype G7 had the lowest grain yield and was the least stable across varying environments.

Pan and Singh (2018) studied on 14 lines/varieties of vegetable amaranth (*Amaranthus tricolor* L.) to study the stability parameters during summer season (February-April) of 2008, 2010 and 2011 at Ranchi. The line HAMTH-15 (19.79 t/ha) was the top yielder of greens/ha, stable and suitable for favourable environment. The line was also better performing, stable and suitable for favourable environment for

length of internode (6.16 cm), length of lamina (9.23 cm) and width of lamina (6.34 cm) and for unfavourable environment for girth of stem (0.64 cm) and leaf-stem ratio (1.05). The line HAMTH-13 was also very promising, stable and suitable for unfavourable environment for yield of greens (17.43 t/ha).

Agida *et al.* (2020) study was carried out on 28 genotypes of grain amaranth in two different locations of South-West Nigeria. The field trials were undertaken from August to December 2013. There were significant ($p < 0.05$) differences in grain yield of the accessions. Accessions 74-43, RRC1351, RRC399, RRC8 and RRC551 produced higher grain yields in both locations compared to the rest of the accessions. The top high-yielding accessions included RRC1351 (1.9 t/ha), RRC399 (1.8 t/ha), 74-43 (1.7 t/ha), RRC8 (1.4 t/ha) and RRC551 (1.3 t/ha). Yield of grain amaranth was significantly lower in the more humid Ibadan than the less humid Ogbomoso.

III. MATERIAL AND METHODS

A field experiment was conducted to study “**Stability analysis in grain amaranth (*Amaranthus hypochondriacus* L.)**” during *rabi* 2019-20 at field unit of Centre for Crop Improvement, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar. Geographically, Sardarkrushinagar is situated at 24°N latitude and 72°E longitude with an elevation of 154.52 meters above the mean sea level. The meteorological data recorded during the period of investigation are presented in Appendix-I.

The details of the materials used, methods adopted and statistical analysis followed during the investigation are presented in this chapter.

3.1 Experimental materials

The experimental materials used for study comprised of 25 (Twenty-five) genotypes of grain amaranth were acquired from Center for Crop Improvement, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar, Dist. Banaskantha (Gujarat State). The details of genotypes listed in Table 3.1.

Table 3.1: List of Amaranth genotypes selected for study

Sr. No.	Genotypes	Sr. No.	Genotypes
1.	SKGPA-61	14.	BGA-7-1
2.	SKGPA-74	15.	CGA-18-1
3.	SKGPA-150	16.	CGA-18-2
4.	SKNA-401	17.	GA-1
5.	SKNA-808	18.	GA-2
6.	SKNA-903	19.	GA-3
7.	SKNA-1313	20.	SUVARNA
8.	SKNA-1406	21.	ANNPURNA
9.	SKNA-1407	22.	IC-469820
10.	SKNA-1503	23.	IC-506575
11.	SKNA-1508	24.	IC-436953
12.	SKNA-1510	25.	IC-279511
13.	SKNA-1701		

3.2: Experimental details

- | | | |
|------|------------------------------|--|
| (1) | Title of experiment | : “ Stability analysis in grain amaranth (<i>Amaranthus hypochondriacus</i> L.) ” |
| (2) | Location of Field experiment | : Center for Crop Improvement,
S. D. Agricultural University
Sardarkrushinagar-385 506 |
| (3) | Season and year | : <i>Rabi</i> 2019-20 |
| (4) | Date of sowing | : 1 st Environment – 11 th November, 2019
2 nd Environment – 21 st November, 2019
3 rd Environment – 2 nd December. 2019 |
| (5) | No. of genotype | : 25 (Twenty-five) |
| (6) | Experimental design | : RBD (Randomized Block Design) |
| (7) | No. of replications | : 3 (Three) |
| (8) | Spacing | : 45× 15 cm |
| (9) | Length of row | : 3.0 m (Single row per genotype) |
| (10) | Plant protection measure | : As per recommendation |
| (11) | Agronomic practices | : As per recommendation |

3.3 Observations recorded

The observations were recorded on individual plant basis on five randomly selected plants of the following characters in each replication and the statistical analysis was based on the averages.

3.3.1 Days to 50 per cent flowering

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

3.3.2 Number of branches per plants

The number of total branches in each of the five selected plants were counted and averaged was reported as number of branches/plants.

3.3.3 Length of inflorescence (cm)

The length of inflorescence of the plant was measured in centimeters from the base of the inflorescence to top of the inflorescence at the time of maturity and the mean was calculated.

3.3.4 Girth of inflorescence (cm)

The Girth of inflorescence was measured in centimeter from middle of the inflorescence at the time of maturity.

3.3.5 Leaf area per plant (cm²)

Five plants from each replication were randomly selected and measure leaf area of leaf with the help of Leaf area meter and then average of leaf area per plant was counted.

3.3.6 Stem diameter (mm)

The diameter of stem was measured in millimeter from one centimeter of the soil surface (ground level).

3.3.7 Plant height (cm)

Height of the plant was measure in centimeter from soil surface (ground level) to the top of the main inflorescence at the time of maturity and the mean was calculated.

3.3.8 Days to maturity

Number of days taken from the days of sowing to the physiological 80 per cent maturity of crop was recorded as days to maturity.

3.3.9 Biological yield per plant (g)

Biological yield represented total weight of whole plant except roots. Biological yield of tagged plants was recorded in gram.

3.3.10 Grain yield per plant (g)

Randomly selected five competitive plants was harvested and threshed. Seed will be cleaned and weighted and average on per plant basis were worked out for grain yield per plant in gram.

3.3.11 Harvest index (%)

Harvest index was calculated as per percent basis. It is a ratio of grain yield per plant and biological yield per plant.

$$\text{Harvest Index (\%)} = \frac{\text{Total grain yield per plant}}{\text{Total Biological yield per plant}} \times 100$$

3.3.12 Test weight (g/10ml)

A random sample of 10 ml bulk grain was taken from each treatment in each replication and weight in grams on electronic balance.

3.3.13 Protein content (%)

Protein content of the grinded seed sample was determined by Lowry's method (Lowry *et al.*, 1951).

3.4 Statistical analysis

The data of all the traits were compiled and mean value of 25 randomly selected plants of each genotype of each replication were used for statistical analyses. The computer facilities available at Department of Agricultural Statistics, C. P. College of Agriculture, S. D. Agricultural University, Sardarkrushinagar was utilized for this purpose. The following statistical parameters were worked out for presentation of the data on different quantitative attributes.

3.4.1 Analysis of variance

The data recorded for all the characters were subjected to analysis of variance with the formula suggested by Panse and Sukhatme (1978) for individual environments as well as pooled over environments.

(a) Analysis of variance for individual environment

The analysis of variance for individual environment had the format as given in Table 3.3 and the statistical model was as under.

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

Where,

Y_{ij} = Yield of the i^{th} genotype in j^{th} replication,

μ = General mean,

R_j = Effect of j^{th} replication,

G_i = Effect of i^{th} genotype,

E_{ij} = Random error associated due to i^{th} genotype in j^{th} replication, and

i = 1, 2, ..., g and j = 1, 2, ..., r.

For all the characters under study, the mean values of five randomly selected plants were used for statistical analysis. The data recorded for different characters were subjected to analysis of variance. Different components of variance viz., phenotypic, genotypic and environmental variances were estimated. Different parameters of genetic variability were computed by standard statistical procedures. The phenotypic and genotypic correlations were also estimated. The genotypic correlations were subjected to path coefficient analysis. The analysis of variance was done as suggested by Panse and Sukhatme (1978).

Table 3.2: Analysis of variance for individual environment

Sources	d.f.	Mean square	Expected mean square
Replications	(r-1)	MS ₁	$\sigma_e^2 + g \sigma_r^2$
Genotypes	(g-1)	MS ₂	$\sigma_e^2 + r \sigma_g^2$
Error	(r-1) (g-1)	MS ₃	σ_e^2
Total	(rg-1)	-	-

Where,

- r = Number of replications,
 g = Number of genotypes,
 σ_e^2 = Variance due to error,
 σ_r^2 = Variance due to replications,
 σ_g^2 = Variance due to genotypes, and
 MS_1, MS_2, MS_3 = Mean squares for replications, genotypes and error, respectively.

The standard error for mean (S.Em.) between treatments mean was calculated from ANOVA table.

$$S.Em. = \frac{MS_3}{r}$$

The critical difference to compare the mean values of various genotypes was calculated by using the following formula.

$$C.D. \text{ at } 5 \% = S.Em. \times [2]^{0.5} \times 't'$$

Where,

- $S.Em.$ = Standard Error of Mean, and
 $'t'$ = Tabulated value of 't' at 1 per cent or 5 per cent level at error degree of freedom.

The co-efficient of variation (C.V. %) was calculated by using the following formula.

$$C.V. (\%) = \frac{(MS_3)^{0.5}}{\bar{X}} \times 100$$

Where,

- $\bar{X}$ = Population mean, and
 MS_3 = Error mean sum of square.

(b) Pooled analysis of variance over environments

The pooled analysis of variance as given in Table 3.3 utilized model as:

$$Y_{ijk} = \mu + G_i + R_j + E_k + GE_{ik} + E_{ijk}$$

Where,

- Y_{ijk} = Yield of i^{th} genotype of j^{th} replication in k^{th} environment,
 μ = General mean,
 G_i = Effect of i^{th} genotype,
 R_j = Effect of j^{th} replication,
 E_k = Effect of k^{th} environment,
 GE_{ik} = Interaction effect of i^{th} genotype with k^{th} environment, and
 E_{ijk} = Random error effect associated with ijk^{th} observation.

Table 3.3: Pooled analysis of variance over environments

Sources	d.f.	Mean square	Expected mean square
Replications within environments	$E(r-1)$	-	-
Environments (E)	$(e-1)$	-	-
Genotypes (G)	$(g-1)$	MS_1	$\sigma_e^2 + r\sigma_{ge}^2 + rE\sigma_g^2$
Genotype $\times$ Environment ($G \times E$)	$(g-1)(E-1)$	MS_2	$\sigma_e^2 + r\sigma_g^2$
Pooled error	$E(r-1)(g-1)$	MS_3	σ_e^2

Where,

- r = Number of replications,
 g = Number of genotypes,
 e = Number of environments,
 σ_e^2 = Variance due to error,
 σ_g^2 = Variance due to genotypes,
 σ_{ge}^2 = Variance due to genotype $\times$ environment interaction,
 MS_1, MS_2, MS_3 = Mean square for genotypes, $G \times E$ interaction and pooled error, respectively.

The Genotype $\times$ Environment interaction ($G \times E$) mean squares were tested against pooled error. The variance due to replications, environments and genotypes were in turn tested against Genotype $\times$ Environment interactions mean squares. The estimates of standard error of mean, critical difference and co-efficient variation were obtained as shown below.

$$\begin{aligned}
\text{S. Em.} &= (MS_3/r_e)^{0.5} \\
\text{C.D. at 5 \%} &= \text{S.Em.} \times (2)^{0.5} \times t'_{0.05} \text{ at error d.f.} \\
\text{C.V. \%} &= \frac{(MS_3)^{0.5}}{\bar{X}} \times 100
\end{aligned}$$

3.4.2 Estimation of variance components, co-efficient of variation, heritability and genetic advance

(i) Mean

It is computed by dividing the sum of all observations in a sample by their number.

$$\bar{X} = \frac{\sum X_{ij}}{n}$$

Where,

$\bar{X}$ = General mean,

X_{ij} = Any observation in i^{th} replication and j^{th} genotype, and

n = Number of observations.

(ii) Range

It is the difference between highest value and lowest value in a particular character. The genotypic, phenotypic and environmental components were estimated as explained by Johnson *et al.* (1955).

$$\text{Range} = \text{Maximum value} - \text{Minimum value}$$

(iii) Analysis of variance component

The mean squares due to genotypes and error were used for the calculation of variance components by manipulation of expected mean squares (Johnson *et al.*, 1955) as shown below.

(a) Individual environment

$$\begin{aligned}
\sigma_e^2 &= MS_3 \\
\sigma_g^2 &= (MS_2 - MS_3) / r \\
\sigma_p^2 &= \sigma_g^2 + \sigma_e^2
\end{aligned}$$

Where,

$$\sigma_p^2 = \text{Variance due to phenotypes.}$$

(b) Pooled over environment

$$\begin{aligned}
\sigma_e^2 &= MS_3 \\
\sigma_{ge}^2 &= (MS_2 - MS_3)/r \\
\sigma_g^2 &= (MS_1 - MS_2)/rE \\
\sigma_p^2 &= \sigma_g^2 + (\sigma_{ge}^2/E) + (\sigma_e^2/rE)
\end{aligned}$$

Where,

$$\sigma_{ge}^2 = \text{Variance due to } G \times E \text{ interaction.}$$

(iv) Genotypic and phenotypic co-efficient of variation

The genotypic and phenotypic co-efficients of variation which measures the magnitude of variation present in a particular character was estimated for individual and pooled over environments by the formula suggested by Burton (1952).

$$\text{Genotypic co-efficient of variation (GCV) in per cent} = \frac{\sigma_g}{\bar{X}} \times 100$$

$$\text{Phenotypic co-efficient of variation (PCV) in per cent} = \frac{\sigma_p}{\bar{X}} \times 100$$

Where,

$$\begin{aligned}
\bar{X} &= \text{General mean,} \\
\sigma_g &= \text{Genotypic standard deviation, and} \\
\sigma_p &= \text{Phenotypic standard deviation.}
\end{aligned}$$

GCV and PCV were categorized as low, moderate and high by following Shivasubramanian and Menon (1973). It is as follows

$$\begin{aligned}
0-10 \% &= \text{Low} \\
10-20 \% &= \text{Moderate} \\
20 \% \text{ and above} &= \text{High}
\end{aligned}$$

(v) Estimation of heritability

The broad sense heritability was calculated for combined analysis by using the formula suggested by Allard (1960).

$$\text{Heritability (\%)} = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Heritability percentage was categorized as demonstrated by Robinson *et al.* (1966).

0-30 %	=	Low
30-60 %	=	Moderate
60 % and above	=	High

(vi) Genetic advance expressed as percentage of means

Expected genetic advance could be calculated by using the methodology suggested by Allard (1960) at 5 per cent selection intensity using the constant 'K' as 2.06.

$$G.A. = h^2_{(b)} \times K \times \sqrt{\sigma_p^2}$$

Where,

G.A.	=	Genetic advance,
$h^2_{(b)}$	=	Heritability (broad-sense),
K	=	Selection intensity at 5 per cent = 2.06 and
$\sqrt{\sigma_p^2}$	=	Variance due to phenotype.

The expected genetic advance expressed as percentage of mean was calculated by using the following formula (Johnson *et al.*, 1955).

$$G.A. \text{ as \% of mean} = \frac{G.A.}{\bar{X}} \times 100$$

Where,

G.A.	=	Expected genetic advance and
$\bar{X}$	=	Mean of character under study.

The genetic advance as per cent mean was categorized as suggested by Johnson *et al.* (1955).

0-10 %	=	Low
10-20 %	=	Moderate
20 % and above	=	High

3.4.3 Estimation of correlation co-efficient

The phenotypic, genotypic and environmental correlation co-efficients were worked for all possible pairs of thirteen characters using the data pooled over environment. Analysis of covariance between all possible pairs of thirteen characters was performed as per Panse and Sukhatme (1985) as given in Table 3.5.

Table 3.4: Analysis of covariance components

Sources	d.f.	Sum of product	Mean sum of product	Expected mean sum of product
Replications in environments	$e(r-1)$	SP_1	MSP_1	-
Genotypes (g)	$(g-1)$	SP_2	MSP_2	$COV_{xy(e)} + rCOV_{xy(ge)} + rECO_{xy(g)}$
Environments (E)	$(e-1)$	SP_3	MSP_3	$COV_{xy(e)} + rCOV_{xy(ge)} + rgCOV_{xy(E)}$
$G \times E$	$(g-1)(e-1)$	SP_4	MSP_4	$COV_{xy(e)} + rCOV_{xy(ge)}$
Pooled error	$e(r-1)(g-1)$	SP_5	MSP_5	$COV_{xy(e)}$

Where,

$COV_{xy(g)}$, $COV_{xy(e)}$, $COV_{xy(ge)}$ and $COV_{xy(e)}$ are genotypic, environmental, $G \times E$ interaction and error covariance between character x and y, respectively.

(i) Analysis of covariance components

The covariance components were estimated by equating the expected mean sum of products with their observed values.

$$COV_{xy(e)} = \sigma_{xy(e)} = MSP_5$$

$$COV_{xy(g)} = \sigma_{xy(g)} = (MSP_2 - MSP_4)/rE$$

$$COV_{xy(ge)} = \sigma_{xy(ge)} = (MSP_4 - MSP_5)/r$$

$$COV_{xy(p)} = \sigma_{xy(p)} = COV_{xy(g)} + COV_{xy(ge)}/E + COV_{xy(e)}/rE$$

Where,

$$COV_{xy(p)} = \text{Phenotypic covariance between character x and y.}$$

(ii) Estimation of correlation co-efficient

The formula suggested by Al-Jibouri *et al.* (1958) was utilized for calculating the phenotypic (r_p), genotypic (r_g) and environmental (r_e) correlation co-efficients for all possible pairs of fourteen characters.

The genotypic correlation is chiefly caused by pleiotrophy and linkage action of genes and was estimated by:

$$r_g = \sigma_{xy(g)} / (\sigma_{xg} \times \sigma_{yg})^{0.5}$$

The environmental correlation, which is not, strictly speaking, the correlation of environmental deviation but also with non-additive genetic deviation was estimated by:

$$r_e = \sigma_{xy(e)} / (\sigma_{xe} \times \sigma_{ye})^{0.5}$$

The genetic and environmental causes of correlation combine together to give the phenotypic correlation and was measured by:

$$r_p = \sigma_{xy(p)} / (\sigma_{xp} \times \sigma_{yp})^{0.5}$$

The phenotypic correlation co-efficient was tested against tabulated values of 'r' with (g-2) degree of freedom as per the procedure suggested by Fisher and Yates (1963).

Test of significance of correlation coefficient

Comparison of sample 'r' with population value.

$H_0 : \rho = 0$ (both the variables are not linearly associated)

$H_a : \rho \neq 0$

$$\begin{aligned} t_{(n-2)} &= r - \rho / \text{SE of } r \quad \text{SE of } r = \sqrt{\frac{1-r^2}{n-2}} \\ &= \frac{r}{\sqrt{1-r^2}} \times \sqrt{n-2} \quad \text{under } H_0 : \rho = 0 \end{aligned}$$

Where,

r = Correlation coefficient, and

n = Number of pairs of observation.

The genotypic and phenotypic correlation coefficients were worked out of all possible pairs and were tested against standardized tabulated values at 5 and 1 per cent level of significance.

3.4.4 Path coefficient analysis

The cause and effect, interrelationship between two variables cannot be estimated from simple correlation coefficient analysis. Therefore, the path coefficient analysis was carried-out according to the method suggested by Wright (1921) and used by Dewey and Lu (1959). Genotypic correlation coefficients of twelve variables with grain yield per plant were used to estimate the path coefficients for the direct effects of various independent characters on seed yield per plant. The path coefficients were obtained by solving a set of simultaneous equations as below.

$$\begin{aligned}
r_{1y} &= \mathbf{P}_{1y} + \mathbf{r}_{12}\mathbf{P}_{2y} + \mathbf{r}_{13y}\mathbf{P}_{3y} + \dots\dots\dots\mathbf{r}_{1i}\mathbf{P}_{iy} \\
r_{2y} &= \mathbf{P}_{2y} + \mathbf{r}_{21}\mathbf{P}_{1y} + \mathbf{r}_{23y}\mathbf{P}_{3y} + \dots\dots\dots\mathbf{r}_{2i}\mathbf{P}_{iy} \\
r_{3y} &= \mathbf{P}_{3y} + \mathbf{r}_{31}\mathbf{P}_{1y} + \mathbf{r}_{32y}\mathbf{P}_{2y} + \dots\dots\dots\mathbf{r}_{3i}\mathbf{P}_{iy} \\
&\vdots \\
&\vdots \\
&\vdots \\
&\vdots \\
&\vdots \\
r_{iy} &= \mathbf{P}_{iy} + \mathbf{r}_{i1}\mathbf{P}_{1y} + \mathbf{r}_{i2}\mathbf{P}_{2y} + \dots\dots\dots\mathbf{r}_{(i-1)i}\mathbf{P}_{iy}
\end{aligned}$$

Where,

- r_{1y} to r_{iy} = Genotypic correlation co-efficient between casual factor 1 to i and dependent character y (yield), (i = 13),
 r_{12} to $r_{(i-1)i}$ = Genotypic correlation co-efficient between casual characters, and
 $\mathbf{P}_{1y}$ to $\mathbf{P}_{iy}$ = Direct effects of characters 1 to i on character y (path co-efficients).

The above equation was written in a matrix form as under:

Matrix-A

Matrix-C

Matrix-B

$$\begin{pmatrix} r_{1y} \\ r_{2y} \\ r_{3y} \\ \vdots \\ \vdots \\ \vdots \\ \vdots \\ r_{iy} \end{pmatrix} = \begin{pmatrix} 1 & r_{12} & r_{13} & \dots\dots\dots & r_{1i} \\ r_{21} & 1 & r_{23} & \dots\dots\dots & r_{2i} \\ r_{31} & r_{23} & 1 & \dots\dots\dots & r_{3i} \\ \vdots & \vdots & \vdots & & \vdots \\ \vdots & \vdots & \vdots & & \vdots \\ \vdots & \vdots & \vdots & & \vdots \\ \vdots & \vdots & \vdots & & \vdots \\ r_{i1} & r_{i2} & r_{i3} & & r_{in} \end{pmatrix} \times \begin{pmatrix} \mathbf{P}_{1y} \\ \mathbf{P}_{2y} \\ \mathbf{P}_{3y} \\ \vdots \\ \vdots \\ \vdots \\ \vdots \\ \mathbf{P}_{iy} \end{pmatrix}$$

Then, $\mathbf{B} = \mathbf{C}^{-1} \times \mathbf{A}$

Where,

$$\mathbf{C}^{-1} = \begin{pmatrix} C_{11} & C_{12} & C_{13} & \dots & C_{1i} \\ C_{21} & C_{22} & C_{23} & \dots & C_{2i} \\ C_{31} & C_{32} & C_{33} & \dots & C_{3i} \\ | & | & | & & | \\ | & | & | & & | \\ | & | & | & & | \\ C_{i1} & C_{i2} & C_{i3} & \dots & C_{ii} \end{pmatrix}$$

The direct effect were calculated as follows :

$$P_{1y} = \sum_i C_{11} r_{iy}$$

$$P_{2y} = \sum_i C_{21} r_{iy}$$

$$P_{3y} = \sum_i C_{31} r_{iy}$$

$$\begin{matrix} | \\ | \\ | \\ | \end{matrix} \quad \begin{matrix} | \\ | \\ | \\ | \end{matrix} \quad \begin{matrix} \\ \\ \\ \end{matrix} \\ P_{iy} = \sum_i C_{i1} r_{iy}$$

The indirect effects were obtained by multiplication of path co-efficient connecting the casual effect with yield and genotypic correlation between two corresponding casual characters.

The residual effect was calculated with the following formula.

$$\text{Residual effect (x)} = (1-R^2)^{0.5}$$

Where,

$$R^2 = \sum_p P_{iy}^2 + 2 \sum_i \sum_j P_{iy} P_{jy} r_{ij}$$

$$i = 1 \text{ to } 10$$

$$j = 1 \text{ to } 10$$

$$i \neq j$$

Where,

$$P = \text{Number of casual characters}$$

3.4.5 Genotype × Environment interaction and stability parameters

The mean values recorded for thirteen characters in respect of 25 genotypes for three environments as well as pooled over environments are given in Appendix-II. The same were used for the analysis of variance for phenotypic stability.

(a) Analysis of variance for phenotypic stability

Phenotypic stability of a genotype could be judged in two different ways (i) conventional pooled analysis of variance and (ii) regression analysis according to Eberhart and Russel (1966). Consistent high performance together with (i) the regression of each genotype in an experiment on an environmental index and (ii) a function of squared deviations from this regression would provide estimates of the desired stability parameters.

The statistical analysis for genotype × environment interaction and stability parameters were carried out according to the method of Eberhart and Russell (1966) to calculate the analysis of variance, which is presented in Table 3.6.

Where,

r, e and g indicate number of replications, environments and genotypes, respectively. The term σ_e^2 represents mean squares due to pooled error.

For 'F' test, the mean square due to pooled deviation (MS_3) was first tested against pooled error.

$$F = \frac{MS_3}{\text{Pooled error m.s.}}$$

The appropriate 'F' test for testing the significance of difference among genotypes mean was obtained as:

$$F = \frac{MS_1}{MS_3}$$

To test the genetic differences among varieties for their regression on the environment index, the following 'F' ratio was work out.

$$F = \frac{MS_2}{MS_3}$$

(b) Stability parameters

The stability parameters for the various characters were computed following the methodology of Eberhart and Russell (1966). For each genotype, stability is described by three parameters viz., mean performance, the regression of mean performance on an environmental index and the mean square deviation from this regression. Eberhart and Russell (1966) suggested that ideal genotype is one which has a high mean ($\bar{X}$), unit regression co-efficient ($b_i = 1$) and the least deviation from regression ($S^2d_i = 0$).

Table 3.5: Analysis of variance for phenotypic stability as per Eberhart and Russell (1966) model

Source	d.f.	S.S.	M.S.
Genotypes	(g-1)	$\frac{1}{e} \sum_i y_{i.}^2 - (\sum_{ij} y_{ij})^2 / ge$	MS ₁
Environments	(e-1)	$\frac{1}{g} \sum_j y_{.j}^2 - (\sum_{ij} y_{ij})^2 / ge$	-
G × E	(g-1)(e-1)	$\sum_{ij} y_{ij}^2 - \sum_i y_{i.}^2 / e - \sum_j y_{.j}^2 / g + (\sum_{ij} y_{ij})^2 / ge$	-
Environments (Linear)	1	$\frac{1}{g} (\sum_j y_{.j} I_j)^2 / \sum_j I_j^2$	-
G × E (Linear)	(g-1)	$\sum_i [(\sum_j y_{ij} I_j)^2 / \sum_j I_j^2] - \text{Environments (linear) S.S.}$	MS ₂
Pooled deviation	g(e-2)	$\sum_{ij} \delta_{ij}^2$	MS ₃
Deviation of individual genotype	(e-2)	$\sum_j y_{.j}^2 - \frac{(\sum_i y_{ij})^2}{n} - \frac{(\sum_{ij} y_{ij} I_j)^2}{\sum_j I_j^2}$	-
Pooled error	e(r-1)(g-1)	$\sum_{ij} e_{ij}^2$	MS _e

These parameters are defined in a linear model as follows:

$$Y_{ij} = \mu_i + b_i I_j + \delta_{ij}$$

Where,

- Y_{ij} = Mean performance of i^{th} genotype in j^{th} environment,
 μ_i = i^{th} genotype mean over all the environment,
 b_i = Regression co-efficient that measures the response of the i^{th} genotype to changing environments,

δ_{ij} = Deviation from regression of the i^{th} genotype in the j^{th} environment,

I_j = Environmental index, obtained as a mean of all the genotypes at the j^{th} environment minus grand mean, such that $\sum I_j = 0$, and

$$I_j = (\sum_i Y_{ij}/g) - (\sum_i \sum_j Y_{ij}/ge).$$

Where,

E = Number of environments.

The stability parameter, regression co-efficient was estimated as under:

$$b_i = \sum_j Y_{ij} I_j / \sum_j I_j^2$$

The mean square deviation ($S^2 d_i$) was calculated as under:

$$S^2 d_i = [\sum_j \delta_{ij}^2 / (e-2)] - [\sigma^2 e / r]$$

Where,

$\sigma^2 e$ = The estimate of pooled error

e = Number of environments

$$\sum_j \delta_{ij}^2 = \frac{[\sum_j Y_{ij}^2 - Y_i^2] - (\sum_i Y_{ij} I_j)^2}{\sum_j I_j^2}$$

The significance of the deviation from regression for each genotype was tested by the appropriate test as suggested by Eberhart and Russell (1966).

$$F = \frac{\sum_j \delta_{ij}^2 / (e-2)}{\text{Pooled error m.s.}}$$

The standard error of regression was calculated by using the formula :

$$S.E.(b_i) = \left[\frac{\text{M.S. due to pooled deviation of } i^{\text{th}} \text{ genotype}}{\sum_j I_j^2} \right]^{0.5}$$

The significance of each regression co-efficient was tested from unity as under.

$$T = \frac{1 - b_i}{S.E.(b_i)}$$

With $g(e-2)$ degree of freedom.

IV. RESULTS AND DISCUSSION

Knowledge of the degree of yield and yield attribute variations in high temperature environments was shown to be highly useful in identifying genotypes that are extensively adapted. Grain yield per plant was discovered to be a quantitatively inherited trait, and there is considerable interaction between genotype and environment. Some crop varieties are widely adapted, whereas others are not. Plant breeders can examine the adaptation of a genotype to a certain environment by testing genotypes on different dates of sowing *i.e.*, sowing time. The knowledge on $G \times E$ interaction is important for developing a more stable variety.

Yield is a complicated character that is impacted by several yield contributing factors. As a result, it was required to assess the nature and size of the relationship between these characteristics, as well as their direct and indirect effects on grain yield per plant.

During rabi, 2019-20, 25 genotypes of *Amaranthus hypochondriacus* L. were evaluated in Randomized Block Design at the Center for Crop Improvement, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar to study the variability, correlation, and path among the traits and stability parameters. Data on days to 50 per cent flowering, days to maturity, plant height, length of inflorescence, girth of inflorescence, stem diameter, number of branches per plant, leaf area, biological yield/plant, grain yield/plant, harvest index, test weight and protein content were recorded. The results of present investigation entitled “**Stability analysis in grain amaranth (*Amaranthus hypochondriacus* L.)**” are presented in the following heads.

- 4.1 Analysis of variance for individual environment and pooled over environment
- 4.2 Mean performance and range of phenotypic variation
- 4.3 Estimation of genetic parameters for individual environment and pooled over environment
- 4.4 Estimation of correlation co-efficients on the basis of pooled over environment
- 4.5 Path co-efficient analysis
- 4.6 Genotype $\times$ Environment interaction and stability analysis

The results for each of the above aspects are provided in detail in the following paragraphs.

4.1 Analysis of variance for individual environment and pooled over environment

Tables 4.1 and 4.2 provide the analysis of variance for all thirteen distinct characteristics investigated in three environments and pooled across environments.

For all characteristics, the analysis of variance indicated very high significant differences across the accessions. The variations between accessions in three habitats, as well as those pooled across environments, were very significant for all of the characteristics studied, suggesting the presence of broad genetic diversity for several traits in the genetic material under examination. Significant difference among all the genotypes under study has been reported by Venkatesh *et al.* (2014) and Shah *et al.* (2018).

4.2 Mean performance and range of phenotypic variation

The mean values for different genotypes for various characters in individual environments as well as across the environments have been presented in Appendix- II.

A study of Appendix-II revealed that genotypes performed well in E₁, followed by E₂, and had the lowest values for almost all of the characters in E₃. None of the genotypes performed consistently for any of the characters across all three environments. This indicated that genotypes differed in their performance for yield and other quantitative characters.

4.2.1 Days to 50 per cent flowering

The pooled data over all three environments for days to 50 per cent flowering ranged from 34.78 (IC-506575) to 65.00 (SUVARNA) days. The average mean was 50.28 days. Pooled data revealed that early flowering was exhibited by IC-506575 (34.78 days) followed by IC-436953 (35.33 days) and ANNPURNA (35.89 days). The pooled coefficient of variation for three environments was 3.22 per cent.

4.2.2 Days to maturity

The pooled data over all three environments for days to maturity ranged from 98.56 (IC-436953) to 130.89 (SUVARNA) days. The average mean was 117.37 days. Pooled data revealed that early maturity was exhibited by IC-436953 (98.56 days) followed by IC-279511 (99.22 days) and ANNPURNA and IC-506575 (99.33 days). The pooled coefficient of variation for three environments was 1.61 per cent.

Table 4.1: Analysis of variance (Mean sum of square) for different characters in grain amaranth for individual environments

ENVIRONMENT-I														
Sources of variation	d.f.	DF	DM	PH	LI	GI	SD	NB	LA	BY	GY	HI	TW	PC
Replication	2	0.48	12.41	81.67	20.14	6.96	5.23	0.37	6318.32	94.36	9.96	6.68	0.25	0.14
Genotype	24	319.57**	480.49**	2574.28**	214.77**	31.68**	32.22**	14.05**	1032965.05**	1951.91**	235.21**	339.44**	0.19*	1.13**
Error	48	2.94	5.23	29.64	8.94	3.41	1.75	0.14	15879.44	33.92	4.71	15.21	0.09	0.29
ENVIRONMENT-II														
Sources of variation	d.f.	DF	DM	PH	LI	GI	SD	NB	LA	BY	GY	HI	TW	PC
Replication	2	2.97	4.21	67.69	0.11	0.08	0.88	0.35	5191.04	8.13	3.24	25.76	0.32	0.34
Genotype	24	161.32**	528.43**	2323.50**	269.23**	10.71**	14.76**	17.55**	242241.42**	979.69**	31.29**	300.84**	1.28**	1.09**
Error	48	2.00	2.50	21.66	8.23	1.88	0.47	0.11	4594.17	26.30	1.94	26.79	0.20	0.36
ENVIRONMENT-III														
Sources of variation	d.f.	DF	DM	PH	LI	GI	SD	NB	LA	BY	GY	HI	TW	PC
Replication	2	8.01	3.45	67.65	25.81	4.27	0.67	0.00	6177.76	9.00	0.92	19.76	0.17	1.31
Genotype	24	212.75**	117.02**	2497.14**	268.37**	45.00**	15.06**	7.79**	214945.80**	530.08**	12.64**	268.00**	1.65**	2.08**
Error	48	2.94	3.38	27.64	10.32	1.57	0.68	0.05	4176.15	14.71	0.69	18.20	0.32	0.60

* and ** : Significant at 5 and 1 per cent levels of significance, respectively

DF : Days to flowering, DM : Days to maturity, PH : Plant height (cm), LI : Length of inflorescence (cm), GI : Girth of inflorescence (cm), SD : Stem diameter (mm), NB : Number of branches per plant, LA : Leaf area per plant (cm²), BY : Biological yield per plant (g), GY : Grain yield per plant (g), HI : Harvest index (%), TW : Test weight (g/10 ml) and PC : Protein content (%).

Table 4.2: Pooled analysis of variance (Mean square) over environments for different characters in grain amaranth

POOLED ENVIRONMENT														
Sources of variation	d.f.	DF	DM	PH	LI	GI	SD	NB	LA	BY	GY	HI	TW	PC
Environment	2	2247.39**	9049.67**	11245.06**	1056.81**	284.09**	342.40**	2.97**	5722117.71**	23067.58**	2638.04**	421.37	73.90**	28.00**
Genotype	24	661.96**	907.49**	6880.65**	510.24**	53.84**	53.79**	38.22**	1125174.37**	2529.17**	167.64**	458.38*	2.14**	2.59**
G × E	48	5.28	36.41	85.71	40.35	5.59	1.37*	0.19**	60829.65**	155.42	18.58**	74.98	0.16	0.28**
Pooled Error	144	2.62	3.70	26.31	9.16	2.28	0.96	0.10	8216.58	24.97	2.44	20.06	0.20	0.41

* and ** : Significant at 5 and 1 per cent levels of significance, respectively

DF : Days to flowering, DM : Days to maturity, PH : Plant height (cm), LI : Length of inflorescence (cm), GI : Girth of inflorescence (cm), SD : Stem diameter (mm), NB : Number of branches per plant, LA : Leaf area per plant (cm²), BY : Biological yield per plant (g), GY : Grain yield per plant (g), HI : Harvest index (%), TW : Test weight (g/10 ml) and PC : Protein content (%).

4.2.3 Plant height

The pooled data over all three environments for plant height ranged from 48.20 (IC-436953) to 147.13 (SKGPA-61) cm. The average mean was 102.18 cm. Pooled data revealed that maximum plant height was exhibited by SKGPA-61 (147.13 cm) followed by GA-2 (127.87 cm) and GA-3 (124.11 cm). The pooled coefficient of variation for three environments was 5.02 per cent.

4.2.4 Length of inflorescence

The pooled data over all three environments for length of inflorescence ranged from 34.07 (SKGPA-74) to 58.26 (SKGPA-61) cm. The average mean was 46.84 cm. Pooled data revealed that maximum length of inflorescence was exhibited by SKGPA-61 (58.26 cm) followed by GA-2 (58.09 cm) and SKNA-1701 (57.89 cm). The pooled coefficient of variation for three environments was 6.46 per cent.

4.2.5 Girth of inflorescence

The pooled data over all three environments for girth of inflorescence ranged from 15.96 (IC-506575) to 27.59 (SKNA-808) cm. The average mean was 20.25 cm. Pooled data revealed that maximum girth of inflorescence was exhibited by SKNA-808 (27.59 cm) followed by SKNA-903 (23.49 cm) and IC-279511 (23.04 cm). The pooled coefficient of variation for three environments was 7.47 per cent.

4.2.6 Stem diameter

The pooled data over all three environments for stem diameter ranged from 5.61 (IC-436953) to 13.81 (SKNA-808) mm. The average mean was 10.52 mm. Pooled data revealed that maximum stem diameter was exhibited by SKNA-808 (13.81 mm) followed by SUVARNA (13.64 mm) and SKNA-1701 (13.33 mm). The pooled coefficient of variation for three environments was 9.34 per cent.

4.2.7 Number of branches per plant

The pooled data over all three environments for number of branches per plant ranged from 1 to 6.82 (IC-279511). The average mean was 2.00. Pooled data revealed that maximum number of branches per plant was exhibited by IC-279511 (6.82) followed by IC-506575 (6.33) and ANNPURNA (5.91). The pooled coefficient of variation for three environments was 15.87 per cent.

4.2.8 Leaf area

The pooled data over all three environments for leaf area ranged from 164.78 (IC-506575) to 1422.00 (SKGPA-61) cm². The average mean was 731.73 cm². Pooled data revealed that maximum leaf area was exhibited by SKGPA-61

(1422.00 cm²) followed by SKNA-808 (1344.89 cm²) and GA-2 (1243.22 cm²). The pooled coefficient of variation for three environments was 12.39 per cent.

4.2.9 Biological yield per plant

The pooled data over all three environments for biological yield per plant ranged from 14.80 (IC-436953) to 75.93 (SKNA-1406) g. The average mean was 48.02 g. Pooled data revealed that maximum biological yield per plant was exhibited by SKNA-1406 (75.93 g) followed by SKNA-1701 (69.29 g) and SKNA-808 (69.22 g). The pooled coefficient of variation for three environments was 10.22 per cent.

4.2.10 Grain yield per plant

The pooled data over all three environments for grain yield per plant ranged from 3.61 (IC-436953) to 19.16 (SKGPA-61) g. The average mean was 11.56 g. Pooled data revealed that maximum grain yield per plant was exhibited by SKGPA 61 (19.16 g) followed by SKNA-1701 (19.10 g) and CGA-18-1 (16.69 g). The pooled coefficient of variation for three environments was 13.39 per cent.

4.2.11 Harvest index

The pooled data over all three environments for harvest index ranged from 7.45 (SUVARNA) to 39.07 (ANNPURNA) per cent. The average mean was 25.04 per cent. Pooled data revealed that maximum harvest index was exhibited by ANNPURNA (39.07 %) followed by IC-469820 (35.58 %) and SKNA-903 (35.23 %). The pooled coefficient of variation for three environments was 17.89 per cent.

4.2.12 Test weight

The pooled data over all three environments for test weight ranged from 5.52 (SUVARNA) to 7.61 (ANNPURNA) g. The average mean was 6.88 g. Pooled data revealed that maximum test weight was exhibited by ANNPURNA (7.61 g) followed by IC-279511 (7.49 g) and IC-469820 (7.48 g). The pooled coefficient of variation for three environments was 6.56 per cent.

4.2.13 Protein content

The pooled data over all three environments for harvest index ranged from 11.20 (IC-436953) to 13.61 (SUVARNA and BGA-7-1) per cent. The average mean was 12.79 per cent. Pooled data revealed that maximum protein content was exhibited by SUVARNA and BGA-7-1(13.61 %) followed by GA-1 (13.46 %) and GA-2 (13.42 %). The pooled coefficient of variation for three environments was 5.05 per cent.

4.3 Estimation of genetic parameters for individual environments and pooled over environment

The estimates of genotypic variance (σ^2g), phenotypic variance (σ^2p) and environmental variance (σ^2e), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2) in broad sense and genetic advance as percent of mean were estimated for all the thirteen characters under individual environment (E_1 , E_2 and E_3) and pooled estimate of components of variance and genetic parameters are presented in table 4.3 and 4.4, respectively.

4.3.1 Genotypic, phenotypic and environmental components of variation

The genotypic and phenotypic variances for different characters under different environments are presented in table 4.3. In the individual environments (E_1 , E_2 and E_3) genotypic (σ^2g), phenotypic (σ^2p) and environmental component (σ^2e) were found high for leaf area followed by plant height, biological yield per plant, days to maturity, harvest index, days to 50 per cent flowering, grain yield per plant and length of inflorescence except grain yield per plant moderate in E_2 and low in E_3 whereas, moderate values showed girth of inflorescence and stem diameter in E_3 . The characters viz., number of branches per plant, test weight and protein content manifested low estimates of genotypic, phenotypic and environmental variances.

Highest estimates of genotypic and phenotypic variance were obtained for days to 50 per cent flowering, grain yield per plant and biological yield per plant in E_1 than E_2 and E_3 . Days to maturity obtained higher genotypic and phenotypic variance in E_1 and E_2 than E_3 . The phenotypic variance was slightly higher than the genotypic variance for most of the characters.

Pooled estimates of genotypic and phenotypic variance over three environments are present in table 4.4. In across environments analysis, higher values of phenotypic and genotypic component of variances were noted for leaf area (132323.01 and 124106.42) followed by plant height (787.9 and 761.59), biological yield per plant (303.22 and 278.24), days to maturity (104.12 and 100.42), days to 50 per cent flowering (75.88 and 73.15), length of inflorescence (64.83 and 55.67) and harvest index (68.77 and 48.70) whereas, moderate value showed grain yield per plant (20.80 and 18.36). The remaining characters manifested low estimates of genotypic and phenotypic variances. The maximum variability which was found due to genotype indicating their stability and minimum influence by environment.

Table 4.3: Mean, range, variability parameters, heritability and genetic advance for thirteen characters in individual environment in grain amaranth

Sr. No.	Characters	Genetic parameters								
		Mean	Range	σ^2_p	σ^2_g	σ^2_e	PCV (%)	GCV (%)	h^2 (%)	GAM (%)
Environment-I										
1	Days to 50 per cent flowering	44.76	25.33-61.66	108.48	105.54	2.93	23.27	22.95	97.29	46.64
2	Days to maturity	104.69	83.66-125.33	163.65	158.42	5.23	12.22	12.02	96.80	24.37
3	Plant height (cm)	116.17	59.73-167.33	877.85	848.21	29.64	25.50	25.07	96.62	50.75
4	Length of inflorescence (cm)	47.59	25.53-58.13	77.54	68.61	8.93	18.50	17.40	88.47	33.71
5	Girth of inflorescence (cm)	22.10	17.73-30.93	12.84	9.43	3.41	16.21	13.89	73.42	24.52
6	Stem diameter (mm)	12.83	6.50-19.76	11.91	10.16	1.75	26.90	24.85	85.31	47.27
7	Number of branches per plant	2.05	1.00-7.20	4.78	4.64	0.14	106.55	104.94	96.99	212.88
8	Leaf area (cm ²)	1050.67	220.00-2281.66	354907.98	339028.54	15879.44	56.70	55.42	95.53	111.58
9	Biological yield per plant (g)	67.39	20.46-105.13	673.25	639.33	33.92	38.50	37.52	94.96	75.32
10	Grain yield per plant (g)	18.07	3.73-34.14	81.54	76.83	4.71	49.96	48.50	94.22	96.97
11	Harvest index (%)	27.32	6.02-53.86	123.29	108.08	15.21	40.64	38.05	87.66	73.39
12	Test weight (g/10 ml)	7.88	7.17-8.26	0.13	0.03	0.09	4.53	2.36	27.03	2.52
13	Protein content (%)	13.04	11.69-14.64	0.57	0.28	0.29	5.79	4.07	49.47	5.90
Environment-II										
1	Days to 50 per cent flowering	50.38	37.00-64.00	55.10	53.10	2.00	14.73	14.46	96.37	29.24
2	Days to maturity	124.10	100.00-136.66	177.81	175.31	2.50	10.74	10.67	98.59	21.81
3	Plant height (cm)	93.43	40.80-140.53	788.93	767.28	21.65	30.06	29.65	97.25	60.22
4	Length of inflorescence (cm)	50.15	33.20-69.60	95.22	87.00	8.22	19.46	18.60	91.36	36.62
5	Girth of inflorescence (cm)	20.41	17.06-26.00	4.83	2.94	1.88	10.76	8.40	60.97	13.51
6	Stem diameter (mm)	10.13	5.51-13.41	5.24	4.76	0.47	22.59	21.55	91.01	42.35
7	Number of branches per plant	2.17	1.00-7.66	5.93	5.81	0.11	112.01	110.93	98.07	226.29
8	Leaf area (cm ²)	573.11	132.33-1219.00	83809.92	79215.75	4594.17	50.51	49.11	94.52	98.35
9	Biological yield per plant (g)	46.83	15.66-87.00	344.10	317.80	26.30	39.61	38.07	92.36	75.36

Table 4.3 Contd....

Table 4.3 Contd....

Sr. No.	Characters	Genetic parameters								
		Mean	Range	σ^2_p	σ^2_g	σ^2_e	PCV (%)	GCV (%)	h^2 (%)	GAM (%)
10	Grain yield per plant (g)	10.61	4.43-18.38	11.73	9.78	1.94	32.28	29.49	83.45	55.49
11	Harvest index (%)	25.21	11.04-58.11	118.14	91.35	26.79	43.11	37.91	77.32	68.67
12	Test weight (g/10 ml)	6.88	5.48-8.00	0.56	0.36	0.20	10.91	8.75	64.28	14.45
13	Protein content (%)	13.24	10.98-14.04	0.61	0.24	0.36	5.88	3.72	40.12	4.86
Environment-III										
1	Days to 50 per cent flowering	55.70	40.66-69.33	72.88	69.93	2.94	15.33	15.01	95.96	30.30
2	Days to maturity	123.30	109.33-132.33	41.26	37.88	3.38	5.21	4.99	91.8	9.85
3	Plant height (cm)	96.93	36.26-134.73	850.80	823.16	27.63	30.09	29.6	96.75	59.97
4	Length of inflorescence (cm)	42.76	27.26-62.53	96.34	86.01	10.32	22.95	21.69	89.28	42.21
5	Girth of inflorescence (cm)	18.22	10.00-28.88	16.05	14.48	1.57	21.98	20.88	90.21	40.85
6	Stem diameter (mm)	8.61	3.10-11.58	5.48	4.80	0.68	27.18	25.43	87.58	49.04
7	Number of branches per plant	1.78	1.00-5.60	2.63	2.58	0.05	90.86	90.07	98.27	183.93
8	Leaf area (cm ²)	571.40	126.66-1100.00	74432.70	70256.55	4176.15	47.75	46.39	94.39	92.84
9	Biological yield per plant (g)	32.50	5.33-59.53	186.50	171.79	14.71	42.03	40.33	92.11	79.75
10	Grain yield per plant (g)	6.36	1.83-9.23	4.67	3.98	0.69	34.00	31.39	85.24	59.70
11	Harvest index (%)	22.59	5.26-52.72	101.47	83.27	18.20	44.59	40.4	82.07	75.39
12	Test weight (g/10 ml)	5.89	3.91-6.87	0.76	0.45	0.32	14.84	11.34	58.39	17.85
13	Protein content (%)	12.10	10.30-13.50	1.10	0.49	0.60	8.66	5.81	45.04	8.03

Where,

σ^2_g , σ^2_p and σ^2_e are the genotypic, phenotypic and environmental variance, respectively

GCV % and PCV % are genotypic and phenotypic co-efficient of variance, respectively

h^2 (%) and GAM are broad sense heritability and genetic advance expressed as per cent of mean, respectively

Table 4.4: Mean, range, variability parameters, heritability and genetic advance for thirteen characters in pooled over environments in grain amaranth

Sr. No.	Characters	Genetic parameters								
		Mean	Range	σ^2_p	σ^2_g	σ^2_e	PCV (%)	GCV (%)	h^2 (%)	GAM (%)
1	Days to 50 per cent flowering	50.28	34.77-65.00	75.88	73.25	2.62	17.32	17.02	96.54	34.44
2	Days to maturity	117.36	98.55-130.88	104.12	100.42	3.70	8.69	8.54	96.44	17.26
3	Plant height (cm)	102.17	48.20-147.13	787.90	761.59	26.31	27.47	27.01	96.66	54.70
4	Length of inflorescence (cm)	46.83	34.06-58.25	64.83	55.67	9.16	17.19	15.93	85.87	30.40
5	Girth of inflorescence (cm)	20.25	15.96-27.58	8.02	5.73	2.29	13.98	11.82	71.45	20.58
6	Stem diameter (mm)	10.52	5.61-13.81	6.84	5.87	0.97	24.85	23.02	85.86	43.95
7	Number of branches per plant	2.00	1.00-6.82	4.34	4.24	0.10	103.96	102.74	97.67	209.17
8	Leaf area (cm ²)	731.73	164.77-1422.00	132323.01	124106.42	8216.59	49.71	48.14	93.79	96.04
9	Biological yield per plant (g)	48.90	14.80-75.93	303.22	278.24	24.98	35.61	34.11	91.76	67.31
10	Grain yield per plant (g)	11.68	3.61-19.15	20.80	18.36	2.45	39.05	36.68	88.24	70.98
11	Harvest index (%)	25.04	7.44-39.06	68.77	48.70	20.07	33.12	27.87	70.82	48.31
12	Test weight (g/10 ml)	6.88	5.52-7.61	0.42	0.22	0.20	9.41	6.75	51.38	9.96
13	Protein content (%)	12.79	11.20-13.61	0.66	0.24	0.42	6.35	3.85	36.72	4.80

Where,

σ^2_g , σ^2_p and σ^2_e are the genotypic, phenotypic and environmental variance, respectively

GCV % and PCV % are genotypic and phenotypic co-efficient of variance, respectively

h^2 (%) and GAM are broad sense heritability and genetic advance expressed as per cent of mean, respectively

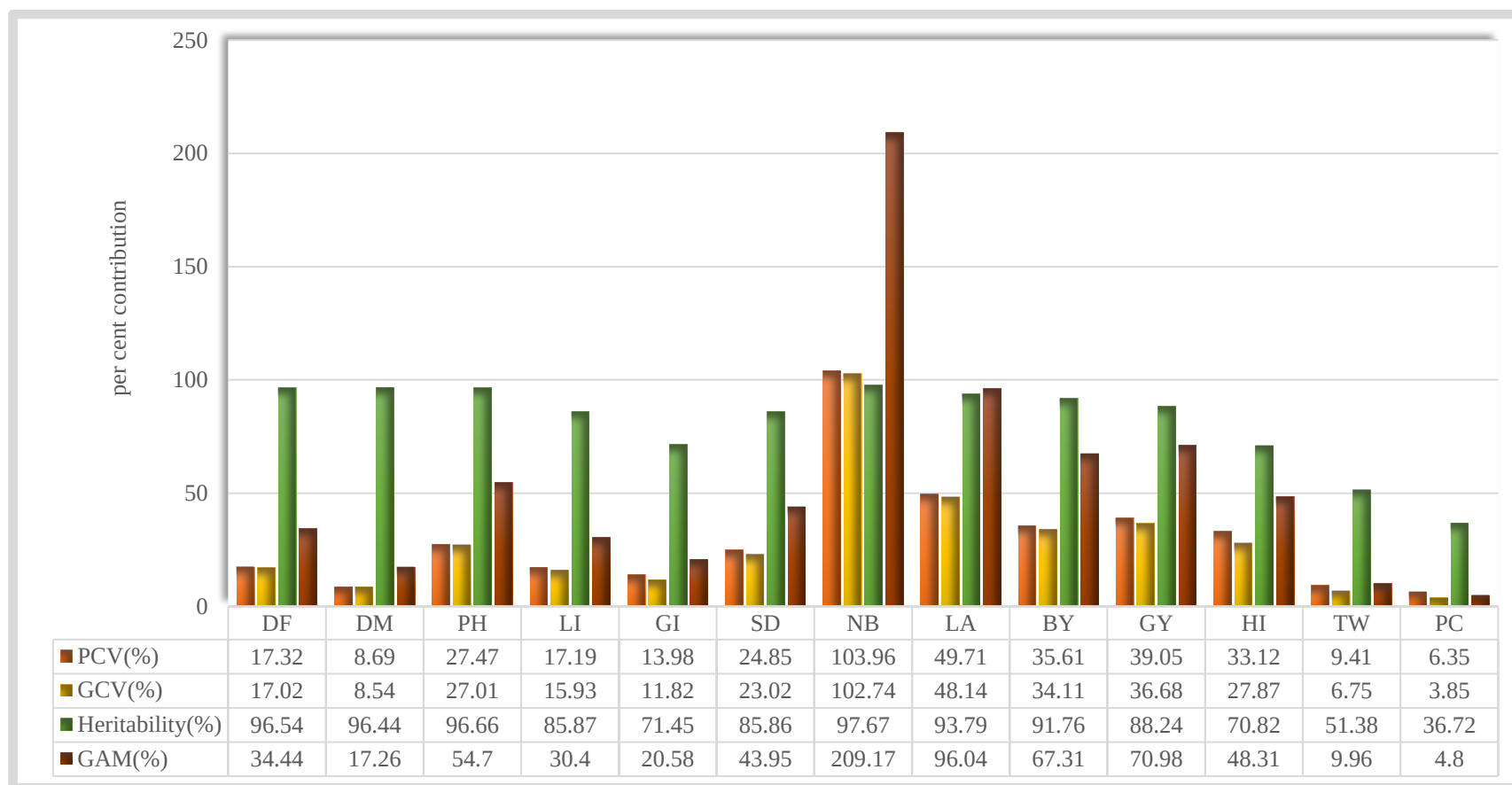


Fig 1: Graphical comparison of GCV (%), PCV (%), heritability (%) and expected genetic advance as per cent of mean for thirteen characters in grain amaranth

DF : Days to flowering, DM : Days to maturity, PH : Plant height (cm), LI : Length of inflorescence (cm), GI : Girth of inflorescence (cm), SD : Stem diameter (mm), NB : Number of branches per plant, LA : Leaf area per plant (cm²), BY : Biological yield per plant (g), GY : Grain yield per plant (g), HI : Harvest index (%), TW : Test weight (g/10 ml) and PC : Protein content (%).

4.3.2 Genotypic and phenotypic co-efficient of variation

The estimates of genotypic and phenotypic components of variance given in the 4.3.1 section reflected the large amount of variation found within populations for various traits. However, because these estimates are linked to a squared unit of measurement for some characters, they cannot be used to compare the relative degree of variability for various characters. This may be achieved by computing the genotypic co-efficient of variance GCV (%) and the phenotypic co-efficient of variance PCV (%). The genotypic and phenotypic co-efficient of variation for all the traits within individual environment and pooled over basis are summarized in Table 4.3 and 4.4, respectively.

Co-efficient of variation was calculated at respective phenotypic and genotypic levels. Phenotypic co-efficient of variation was higher in magnitude than that of genotypic for all the characters in individual as well as pooled over environments. This might be due to environmental effect. Similar results were reported by Sheelamary *et al.* (2016), Kumar and Murthy (2017), Shrivastav *et al.* (2017), Shah *et al.* (2018) and Tiwari (2018). For the majority of characteristics, the GCV (%) was close to the PCV (%), indicating a lower effect of environment and a higher involvement of genetic factors in trait expression. The higher the co-efficient of variation, the greater the possibility of enhancing these characteristics through phenotypic selection

The value of genotypic and phenotypic co-efficient of variation in all individual environments (Table 4.3) revealed that in E₁ high GCV (%) and PCV (%) were observed for number of branches per plant followed by leaf area, grain yield per plant, harvest index, biological yield per plant, stem diameter, plant height and days to 50 per cent flowering whereas moderate for length of inflorescence, girth of inflorescence and days to maturity, respectively. The relatively low values of GCV (%) and PCV (%) were observed for protein content and test weight.

In E₂ high GCV (%) and PCV (%) were observed for number of branches per plant followed by leaf area, harvest index, biological yield per plant, grain yield per plant, plant height and stem diameter whereas moderate for length of inflorescence, days to 50 per cent flowering and days to maturity, respectively. The relatively low values of GCV (%) and PCV (%) were observed for test weight, girth of inflorescence and protein content.

In E₃ high GCV (%) and PCV (%) were observed for number of branches per plant followed by leaf area, harvest index, biological yield per plant, grain yield per plant, plant height, stem diameter, length of inflorescence and girth of inflorescence whereas

moderate for days to 50 per cent flowering and test weight, respectively. The relatively low values of GCV (%) and PCV (%) were observed for protein content and days to maturity.

The value of genotypic and phenotypic co-efficients of variation across the environments (Table 4.4) revealed that high GCV (%) and PCV (%) were observed for number of branches per plant (102.74 and 103.96) followed by leaf area (48.14 and 493.71), grain yield per plant (36.68 and 39.05), biological yield per plant (34.11 and 35.61), harvest index (27.87 and 33.12), plant height (27.01 and 27.47) and stem diameter (23.02 and 24.85). These findings were in agreement with the report of Vyas (2000) for grain yield per plant, number of branches per plant and harvest index, Patel (2011) and Venkatesh *et al.* (2014) for grain yield per plant and plant height, Ahmmed *et al.* (2012) for number of branches per plant, Yadav *et al.* (2014) and Sheelamary *et al.* (2016) for grain yield per plant, Shrivastav *et al.* (2017) for harvest index, biological yield/plant, Gelotar (2018) for number of branches per plant, leaf area, grain yield per plant and plant height, Kumar *et al.* (2018) for number of branches per plant.

The moderate genotypic and phenotypic co-efficient of variation were observed in days to 50 per cent flowering (17.02 and 17.32), length of inflorescence (15.93 and 17.19) and girth of inflorescence (11.82 and 13.98). Similar kind of results were reported by Venkatesh *et al.* (2014) for days to 50 per cent flowering, Shrivastav *et al.* (2017) for length of inflorescence.

Relatively low GCV (%) and PCV (%) were observed for days to maturity (8.54 and 8.69), test weight (6.75 and 9.41) and protein content (3.85 and 6.35). These finding were in agreement with Venkatesh *et al.* (2014) for days to maturity and protein content, Shrivastav *et al.* (2017) for protein content and test weight.

4.3.3 Estimates of heritability and expected genetic advance

Tables 4.3 and 4.4 provide estimates of heritability as a percentage in the broad sense for all of the characters under study in both individual and pooled environments.

All the traits showed high heritability in all the environments except for test weight low in E₁ (27.03) and moderate in E₃ whereas, moderate heritability for protein content in all three environments. The higher value of heritability indicates that the selection would be more effective to bring about improvement in these characters. The lower heritability indicates less chances of improvement through selection.

At 5.00 per cent selection intensity, the expected genetic advance was calculated as a percent of the mean for thirteen characters. Table 4.3 for individual environments and Table 4.4 for pooled across environments show the expected genetic advance (% mean) as for different characters. In all individual as well as pooled over environment the expected genetic advance as per cent of mean was found high for number of branches per plant, leaf area, grain yield per plant, biological yield per plant, harvest index, stem diameter, plant height, days to 50 per cent flowering, length of inflorescence, girth of inflorescence and days to maturity except girth of inflorescence moderate in E₂ and low for days to maturity in E₃ and moderate in pooled over environments. Lower genetic advance as per cent mean was found for protein content and for test weight in E₁ and pooled over environments.

In pooled over environments, high heritability was associated with high genetic advance (% mean) for number of branches per plant (97.67 and 209.17), plant height (96.66 and 54.7), days to 50 per cent flowering (96.54 and 34.44), biological yield per plant (91.76 and 67.31), leaf area (93.79 and 96.04), grain yield per plant (88.24 and 70.98), length of inflorescence (85.87 and 30.4), stem diameter (85.86 and 43.95) girth of inflorescence (71.45 and 20.58) and harvest index (70.82 and 48.31). These findings were in agreement with the report of Vyas (2000) for grain yield per plant and number of branches per plant, Verma *et al.* (2001) for grain yield per plant and plant height, Patel (2004) and Ahmmed *et al.* (2012) for number of branches per plant, Akaneme *et al.* (2013) for days to 50 per cent flowering, Yadav *et al.* (2014) days to 50 per cent flowering, inflorescence length and plant height Venkatesh *et al.* (2014) for grain yield per plant, Shrivastav *et al.* (2017) for plant height, biological yield per plant, harvest index, length of inflorescence, Gelotar (2018) for plant height, length of inflorescence, grain yield per plant and days to 50 per cent flowering.

High heritability combined with high genetic advance as a percentage of mean suggests that these traits were governed by additive gene action and that these characters might be improved by selection.

High heritability was associated with moderate genetic advance (% mean) for days to maturity (96.44 and 17.26). Similar results were reported by Kumar and Murthy (2017) for days to maturity.

Whereas, test weight (51.38 and 9.96) and protein content (36.72 and 4.8) showed high heritability with lower genetic advance (% mean). Similar results were reported by Shrivastav *et al.* (2017) for test weight and protein content. It revealed that presence

of non-additive gene action and influence of environment in the expression of these traits and thus, simple selection would be less effective for improvement of these characters.

4.4 Estimation of correlation co-efficient on the basis of pooled over environment

Yield is a complicated character that is the outcome of a multiplicative interaction between multiple yield components (Grafius, 1956), and thus requires a thorough understanding of the character association produced by each character on grain yield before launching on any breeding programme.

Correlation studies give accurate information on the nature and extent of relationships between characters. These relationships might be positive or negative. Negative associations are limiting factors in high-yield selection. It is consequently critical to identify the characters that are positively correlated to yield. The study of genetic correlation provides us with an understanding of the extent to which the characters are controlled by the same set of genes. If the correlation is high, pleiotropy becomes important, whereas independent inheritance of traits may be perceived if the correlation is low.

Genotypic correlations reveal the existence of real associations, whereas, the phenotypic correlations may occur by chance. Significant phenotypic correlations without significant genotypic associations are of no value. If the genotypic correlation is significant and phenotypic is not, it means that the existing real association is masked by environmental effect. This indicates the importance of genotypic correlation compared to phenotypic correlation. Plant breeders would greatly benefit from information on the association of economically valuable characteristics since it will help in evaluating the reliability of simultaneously improving two or more characters.

The genotypic correlation co-efficient were greater than the phenotypic co-efficient (Table 4.5). These findings are in general agreement with the findings of Shukla and Singh (2003), Ahmmed *et al.* (2012), Patial *et al.* (2014), Shrivastav *et al.* (2017) and Sagar *et al.* (2018) This revealed that there was a high degree of genotypic association between two variables; however, its phenotypic expression may be altered by environmental factors. In a few situations, the phenotypic correlation was somewhat greater than the genotypic correlation, suggesting that non-genetic factors inflated the genetic correlation values due to environmental factors having less influence.

4.4.1 Grain yield per plant

The character grain yield per plant was positively and highly significantly correlated with days to 50 per cent flowering ($r_g = 0.4064$, $r_p = 0.3268$ and $r_e = 0.3874$),

days to maturity ($r_g = 0.6267$, $r_p = 0.3590$ and $r_e = 0.0596$), plant height ($r_g = 0.8529$, $r_p = 0.5154$ and $r_e = 0.0175$), stem diameter ($r_g = 0.5675$, $r_p = 0.3419$ and $r_e = 0.0588$), leaf area ($r_g = 0.6017$, $r_p = 0.5104$ and $r_e = 0.4418$) and biological yield per plant ($r_g = 0.7019$, $r_p = 0.5532$ and $r_e = 0.4272$) at genotypic, phenotypic and environmental levels, respectively. Whereas, girth of inflorescence ($r_g = 0.4267$ and $r_p = 0.0852$) significantly and positively correlated at genotypic and phenotypic levels, respectively. Highly significant and positive correlations were also observed by Dutta *et al.* (2002) for plant height, length of inflorescence, days to maturity and days to 50 per cent flowering, Shukla and Singh (2003) for plant height at genotypic level. Ahmmed *et al.* (2012) for stem diameter and plant height. Patial *et al.* (2014) for days to 50 per cent flowering, days to maturity, biological yield per plant and plant height. Venkatesh *et al.* (2014) for plant height at phenotypic level. Oduwaye *et al.* (2016) for days to 50 per cent flowering, plant height, leaf area and stem diameter. Shrivastav *et al.* (2017) for length of inflorescence, plant height and biological yield per plant. Gelotar *et al.* (2018) for days to 50 per cent flowering, plant height and length of inflorescence. Harvest index ($r_g = -0.1721$) and test weight ($r_g = -0.0409$) were found non-significant and negatively correlated at genotypic level. Number of branches ($r_g = -0.7353$, $r_p = -0.4794$ and $r_e = -0.1494$) was found significance but negative correlated at genotypic, phenotypic and environmental levels, respectively.

4.4.2 Days to 50 per cent flowering

Days to 50 per cent flowering was highly significance and positively correlated with days to maturity ($r_g = 1.0329$ and $r_p = 0.8458$), plant height ($r_g = 0.8604$ and $r_p = 0.8020$), girth of inflorescence ($r_g = 0.5125$ and $r_p = 0.2786$), stem diameter ($r_g = 0.9297$ and $r_p = 0.8359$), leaf area ($r_g = 0.8386$ and $r_p = 0.7033$), biological yield per plant ($r_g = 0.9246$ and $r_p = 0.7294$) and protein content ($r_g = 0.6217$ and $r_p = 0.3830$) at genotypic and phenotypic levels, respectively. Whereas, length of inflorescence ($r_g = 0.3642$ and $r_p = 0.1921$) was non significance and positively correlated at genotypic level. Shrivastav *et al.* (2017) also reported days to 50 per cent flowering had positive and highly significant correlation with days to maturity, plant height, biological yield and protein content.

4.4.4 Plant height

Plant height was highly significance and positively correlated with plant height ($r_g = 0.9856$ and $r_p = 0.0.7792$), length of inflorescence ($r_g = 0.6051$ and $r_p = 0.2831$), stem diameter ($r_g = 0.9519$ and $r_p = 0.7846$), leaf area ($r_g = 0.9280$ and $r_p = 0.6502$),

biological yield per plant ($r_g = 1.0019$ and $r_p = 0.7213$) and protein content ($r_g = 0.7289$ and $r_p = 0.3450$) at genotypic and phenotypic levels, respectively. Whereas, girth of inflorescence ($r_g = 0.5343$) was highly significance and positively corelated at genotypic level. Shrivastav *et al.* (2017) also reported plant height had positive and highly significant correlation with length of inflorescence and biological yield per plant.

4.4.5 Length of inflorescence

Length of inflorescence was highly significance and positively corelated with stem diameter ($r_g = 0.4760$ and $r_p = 0.2331$), leaf area ($r_g = 0.6086$ and $r_p = 0.2752$), biological yield per plant ($r_g = 0.7320$ and $r_p = 0.3248$) and harvest index ($r_g = 0.4221$) at genotypic and phenotypic levels, respectively. Whereas, test weight ($r_g = 0.3719$) and protein content ($r_g = 0.3949$) were non significance and positively corelated at genotypic level. Shrivastav *et al.* (2017) also reported length of inflorescence had positive and highly significant correlation with biological yield per plant, teat weight and protein content.

4.4.6 Girth of inflorescence

Girth of inflorescence was highly significance and positively corelated with stem diameter ($r_g = 0.7369$ and $r_p = 0.3908$), leaf area ($r_g = 0.7161$ and $r_p = 0.3142$) and biological yield per plant ($r_g = 0.7508$ and $r_p = 0.2764$) at genotypic and phenotypic levels, respectively.

4.4.7 Stem diameter

Stem diameter was highly significantly and positively corelated with leaf area ($r_g = 0.8926$ and $r_p = 0.6765$), biological yield per plant ($r_g = 0.9445$ and $r_p = 0.7829$) and protein content ($r_g = 0.4817$ and $r_p = 0.3042$) at genotypic and phenotypic levels, respectively.

4.4.8 Number of branches per plant

Number of branches per plant was highly significant and positively corelated with harvest index ($r_g = 0.7228$ and $r_p = 0.3502$) and test weight ($r_g = 0.6494$ and $r_p = 0.4769$) at genotypic and phenotypic levels, respectively. Shrivastav *et al.* (2017) also reported number of branches per plant had positive and highly significant correlation with harvest index and test weight.

4.4.9 Leaf area

Leaf area was highly significantly and positively corelated with biological yield per plant ($r_g = 0.9756$ and $r_p = 0.6553$) at genotypic and phenotypic levels, respectively. Whereas, protein content ($r_g = 0.3082$ and $r_p = 0.1795$) was non-significant but positively corelated at genotypic and phenotypic levels, respectively.

Table 4.5: Genotypic (r_g), phenotypic (r_p) and environmental (r_e) correlation co-efficients among thirteen characters in grain amaranth

Characters		DM	PH	LI	GI	SD	NB	LA	BY	HI	TW	PC	GY
DF	r_g	1.0329**	0.8604**	0.3642	0.5125**	0.9297**	-0.8847**	0.8386**	0.9246**	-1.1003**	-0.933**	0.6217**	0.4064**
	r_p	0.8458**	0.802**	0.1921	0.2786*	0.8359**	-0.8330**	0.7033**	0.7294**	-0.4601**	-0.5677**	0.383**	0.3268**
	r_e	0.046	0.1907	-0.3343**	-0.2189	0.2832*	0.0278	0.3757**	0.2437*	0.3469**	0.4686**	0.0069	0.3874**
DM	r_g		0.9856**	0.6051**	0.5343**	0.9519**	-0.9566**	0.928**	1.0019**	-0.9788**	-0.8396**	0.7289**	0.6267**
	r_p		0.7792**	0.2831*	0.1836	0.7846**	-0.8389**	0.6502**	0.7213**	-0.4392**	-0.5611**	0.345**	0.359**
	r_e		-0.0358	-0.2225	-0.2671*	0.2805*	-0.4523**	0.0878	0.2044	-0.0461	-0.1313	-0.1085	0.0596
PH	r_g			0.7679**	0.4272**	0.8892**	-0.9276**	0.9306**	0.9927**	-0.684**	-0.6146**	0.5328**	0.8529**
	r_p			0.5493**	0.271*	0.7545**	-0.8547**	0.7552**	0.7435**	-0.3343**	-0.3841**	0.2785*	0.5154**
	r_e			0.1183	0.0317	0.0118	0.0492	0.2792*	0.0886	-0.0221	0.168	-0.1687	0.0175
LI	r_g				-0.228	0.476**	-0.621**	0.6086**	0.732**	0.4221**	0.3719	0.3949	1.323**
	r_p				0.0726	0.2331*	-0.4032**	0.2752*	0.3249**	-0.1245	-0.0225	0.2783*	0.3668**
	r_e				0.3401**	-0.2354*	0.2271*	-0.1732	-0.1846	-0.4649**	-0.452**	0.1829	-0.4379**
GI	r_g					0.7369**	-0.4362**	0.7161**	0.7508**	-0.5725**	-0.8002**	-0.0844	0.4267**
	r_p					0.3908**	-0.2351*	0.3142**	0.2764*	-0.2031	-0.3996**	0.0691	0.0852
	r_e					-0.1132	0.2654*	-0.1234	-0.2093	-0.0215	-0.0424	0.1771	-0.1544
SD	r_g						-0.9007**	0.8926**	0.9445**	-0.9781**	-0.9179**	0.4817**	0.5675**
	r_p						-0.7916**	0.6765**	0.7829**	-0.4646**	-0.4952**	0.3042**	0.3419**
	r_e						-0.0407	0.152	0.4600**	-0.0547	0.3227**	0.0886	0.0588
NB	r_g						-0.8255**	-0.9226**	0.7228**	0.6494**	-0.5302**	-0.7353**	
	r_p						-0.6523**	-0.7237**	0.3502**	0.4769**	-0.3025**	-0.4794**	
	r_e						-0.0821	-0.2054	-0.0447	0.1151	0.1643	-0.1494	
LA	r_g								0.9756**	-0.9059**	-0.8115**	0.3082	0.6017**
	r_p								0.6553**	-0.1958	-0.3367**	0.1795	0.5104**
	r_e								0.1461	0.3244**	0.3135**	0.0515	0.4418**
BY	r_g									-0.8969**	-0.834**	0.5545**	0.7019**
	r_p									-0.4138**	-0.3988**	0.2503*	0.5532**
	r_e									-0.1145	0.1534	-0.0437	0.4272**
HI	r_g										1.192**	-0.2609*	-0.1721
	r_p										0.5961**	-0.1297	0.4169**
	r_e										0.268*	-0.0669	0.7077**
TW	r_g											-0.2793*	-0.0409
	r_p											-0.0354	0.0935
	r_e											0.1758	0.2113
PC	r_g												0.4943**
	r_p												0.047
	r_e												-0.2522*

* and ** : Significant at 5 and 1 per cent levels of significance, respectively

DF : Days to flowering, DM : Days to maturity, PH : Plant height (cm), LI : Length of inflorescence (cm), GI : Girth of inflorescence (cm), SD : Stem diameter (mm), NB : Number of branches per plant, LA : Leaf area per plant (cm²), BY : Biological yield per plant (g), GY : Grain yield per plant (g), HI : Harvest index (%), TW : Test weight (g/10 ml) and PC : Protein content (%).

4.4.10 Biological yield

Biological yield was highly significantly and positively correlated with protein content ($r_g = 0.5545$ and $r_p = 0.2503$) at genotypic and phenotypic levels, respectively.

4.4.11 Harvest index

Biological yield was highly significantly and positively correlated with protein content ($r_g = 0.5545$ and $r_p = 0.2503$) at genotypic and phenotypic levels, respectively.

4.4.12 Test weight

Test weight had negative and significant correlation at genotypic ($r_g = -0.2793$ and $r_p = 0.2503$) and negative and non-significant correlation found at phenotypic level ($r_p = -0.0354$) with protein content.

4.5 Path co-efficient analysis

Path coefficient analysis partitioned the observed genotypic and phenotypic correlation coefficients between yield and its components into direct and indirect effects. The selection of the traits contributing directly to the yield will be beneficial for the breeder in changing the genetic architect of the crop plant for promoting the yield potential of the crop. Path analysis is the effective statistical tool to determine the direct and indirect contributions of different characters towards yield.

Path coefficient is a standardized partial regression coefficient which separates the correlation coefficient into its components of direct and indirect effects. Thus, it helps in examining the relative contribution of both the direct and indirect effects of independent variables on dependent variable.

In general, the genotypic, direct effect as well as indirect effects were slightly higher in magnitude as compared to phenotypic direct and indirect effects. Direct and indirect effects of twelve casual variables on grain yield per plant are presented in Table 4.6 and depicted diagrammatically are shown in Fig. 2.

4.5.1 Days to 50 per cent flowering v/s grain yield per plant

The positive and significant genotypic correlation ($r_g = 0.4063$) was observed between days to 50 per cent flowering and grain yield per plant. It's direct effect was positive (17.0382) while, indirect effect through plant height (20.1327), biological yield per plant (18.2997), girth of inflorescence (1.9352), and length of inflorescence (0.505) were positive for this trait. Indirect effect through leaf area (-29.654), number of branches per plant (-11.899), stem diameter (-5.5413), protein content (-6.7544) days to maturity (-2.3222) harvest index (-1.0733) and test weight (-0.2423) were negative. Dutta *et al.* (2002) reported that grain yield had significance and positive

association with days to 50 per cent flowering. Oduwaye *et al.* (2016) and Gelotar *et al.* (2018) reported high and positive direct effect of days to 50 per cent flowering on grain yield.

4.5.2 Days to maturity v/s grain yield per plant

The positive and significant genotypic correlation ($r_g = 0.6266$) was observed between days to maturity and grain yield per plant. Direct effect of days to maturity with grain yield per plant was negative (-17.5983) while, indirect effect through leaf area (-32.815), number of branches per plant (-12.868), stem diameter (-5.6737), protein content (-7.954), harvest index (-0.9540) and test weight (-0.2181) were negative. Dutta *et al.* (2002) reported that grain yield had high and positive association with days to maturity. Patial *et al.* (2014), Shrivastav *et al.* (2017) and Tiwari (2018) reported negative direct effect of days to maturity on grain yield.

4.5.3 Plant height v/s grain yield per plant

The positive and significant genotypic correlation ($r_g = 0.8528$) was observed between plant height and grain yield per plant. Its direct effect was positive (23.3991) while, indirect effect through biological yield per plant (19.6474), days to 50 per cent flowering (14.6597), girth of inflorescence (1.6138), and length of inflorescence (1.0648) were positive for this trait. Dutta *et al.* (2002) reported that grain yield had high and positive association with plant height. Dutta *et al.* (2002) reported that grain yield had high and positive association with days to 50 per cent flowering. Shukla and Singh (2003), Venkatesh *et al.* (2014) and Tejaswini *et al.* (2017) found same results for plant height. Tiwari (2018) reported positive direct effect of plant height on grain yield.

4.5.4 Length of inflorescence v/s grain yield per plant

The positive and significant genotypic correlation ($r_g = 1.3230$) was observed between length of inflorescence and grain yield per plant. Its direct effect was positive (1.3866) while, indirect effect through biological yield per plant (14.4876) plant height (17.9684), days to 50 per cent flowering (6.2058), and test weight (0.0966) were positive for this trait. Dutta *et al.* (2002) reported that grain yield had high and positive association with length of inflorescence. Oduwaye *et al.* (2016) and Tiwari (2018) reported positive direct effect of length of inflorescence on grain yield.

4.5.5 Girth of inflorescence v/s grain yield per plant

The positive and significant genotypic correlation ($r_g = 0.4266$) was observed between girth of inflorescence and grain yield per plant. Its direct effect was positive (3.7777) while, indirect effect through biological yield per plant (14.8605), plant height

(9.9959), days to 50 per cent flowering (8.7326), and protein content (0.9229) were positive for this trait.

4.5.6 Stem diameter v/s grain yield per plant

The positive and significant genotypic correlation ($r_g = 0.5674$) was observed between stem diameter and grain yield per plant. It's direct effect was negative (-0.9603) while, indirect effect through leaf area (-31.563), number of branches per plant (-12.115), protein content (-5.2565), days to maturity (-2.131), harvest index (-0.9532) and test weight (-0.2384) were negative.

4.5.7 Number of branches per plant v/s grain yield per plant

The negative and significant genotypic correlation ($r_g = 0.4266$) was observed between number of branches per plant and grain yield per plant. It's direct effect was positive (13.4505) while, indirect effect through leaf area (29.1917), protein content (5.7859) stem diameter (5.3687), days to maturity (2.1416), harvest index (0.7045) and test weight (0.1687) were positive for this trait.

4.5.8 Leaf area v/s grain yield per plant

The positive and significant genotypic correlation ($r_g = 0.6016$) was observed between leaf area and grain yield per plant. It's direct effect was negative (-35.362) while, indirect effect through, number of branches per plant (-11.103), stem diameter (-5.32), protein content (-3.3629), days to maturity (-2.0774), harvest index (-0.8828) and test weight (-0.2108) were negative. Oduwaye *et al.* (2016) reported high and negative direct effect of leaf area on grain yield.

4.5.9 Biological yield v/s grain yield per plant

The positive and significant genotypic correlation ($r_g = 0.7018$) was observed between biological yield per plant and grain yield per plant. It's direct effect was positive (19.792) while, indirect effect through plant height (21.7758), days to 50 per cent flowering (15.7535), girth of inflorescence (2.8364) and length of inflorescence (1.015) were positive for this trait. Patial *et al.* (2014) and Shrivastav *et al.* (2017) reported positive direct effect of biological yield on grain yield.

4.5.10 Harvest index v/s grain yield per plant

The negative and non-significant genotypic correlation ($r_g = -0.1720$) was observed between harvest index and grain yield per plant. It's direct effect was positive (0.9746) while, indirect effect was positive for all characters except days to 50 per cent flowering

Table 4.6: Path co-efficient analysis in pooled environment direct and indirect effect of twelve causal variables on grain yield per plant in pooled environments

Characters	DF	DM	PH	LI	GI	SD	NB	LA	BY	HI	TW	PC	GY
DF	17.0382	-2.3122	20.1327	0.505	1.9362	-5.5413	-11.899	-29.654	18.2997	-1.0723	-0.2423	-6.7844	0.4063
DM	17.5983	-2.2386	23.0627	0.839	2.0184	-5.6737	-12.868	-32.815	19.8293	-0.954	-0.2181	-7.954	0.6266
PH	14.6597	-2.2064	23.3991	1.0648	1.6138	-5.3002	-12.476	-32.909	19.6474	-0.6666	-0.1596	-5.8138	0.8528
LI	6.2058	-1.3546	17.9684	1.3866	-0.8618	-2.8371	-8.3524	-21.52	14.4876	0.4114	0.0966	-4.3079	1.323
GI	8.7326	-1.1961	9.9959	-0.3163	3.7777	-4.3922	-5.8676	-25.325	14.8605	-0.558	-0.2079	0.9229	0.4266
SD	15.8404	-2.131	20.8075	0.66	2.7838	-5.9603	-12.115	-31.563	18.6941	-0.9532	-0.2384	-5.2565	0.5674
NB	-15.073	2.1416	-21.704	-0.861	-1.6479	5.3687	13.4505	29.1917	-18.26	0.7045	0.1687	5.7859	-0.7353
LA	14.2876	-2.0774	21.7758	0.8438	2.7054	-5.32	-11.103	-35.362	19.3088	-0.8828	-0.2108	-3.3629	0.6016
BY	15.7535	-2.2429	23.2282	1.015	2.8364	-5.6297	-12.41	-34.499	19.792	-0.8741	-0.2166	-6.0514	0.7018
HI	-18.747	2.1912	-16.004	0.5853	-2.1627	5.8295	9.7221	32.0327	-17.752	0.9746	0.3096	2.8475	-0.172
TW	-15.898	1.8797	-14.382	0.5157	-3.0233	5.4714	8.7353	28.696	-16.506	1.1618	0.2597	3.0476	-0.0408
PC	10.5943	-1.632	12.4682	0.5475	-0.3195	-2.8715	-7.1326	-10.899	10.977	-0.2544	-0.0725	-10.911	0.4943

* and ** : Significant at 5 and 1 per cent levels of significance, respectively

DF : Days to flowering, DM : Days to maturity, PH : Plant height (cm), LI : Length of inflorescence (cm), GI : Girth of inflorescence (cm), SD : Stem diameter (mm), NB : Number of branches per plant, LA : Leaf area per plant (cm²), BY : Biological yield per plant (g), GY : Grain yield per plant (g), HI : Harvest index (%), TW : Test weight (g/10 ml) and PC : Protein content (%).

(-18.747), biological yield per plant (-17.752), plant height (-16.004) and girth of inflorescence (-2.1627) were negative in magnitude. Patial *et al.* (2014) and Shrivastav *et al.* (2017) reported positive direct effect of harvest index on grain yield.

4.5.11 Test weight v/s grain yield per plant

The negative and non-significant genotypic correlation ($r_g = -0.0408$) was observed between test weight and grain yield per plant. It's direct effect was positive (0.2597) while, indirect effect was positive for all characters except days to 50 per cent flowering (-15.898), biological yield per plant (-16.506), plant height (-14.3820) and girth of inflorescence (-3.0233) were negative in magnitude. Oduwaye *et al.* (2016), Gelotar *et al.* (2018), Tiwari (2018), reported high and positive direct effect of test weight on grain yield.

4.5.12 Protein content v/s grain yield per plant

The positive and significant genotypic correlation ($r_g = 0.4943$) was observed between protein content and grain yield per plant. It's direct effect was negative (-10.911) while, indirect effect was negative for all characters except days to 50 per cent flowering (10.5943), biological yield per plant (10.977), plant height (12.4682) and length of inflorescence (0.5475) were negative in magnitude. Shrivastav *et al.* (2017) reported negative direct effect of protein content on grain yield.

The direct effect of any component character on grain production per plant provides an indication of the reliability of indirect selection to be made through that character to increase yield. If the co-efficient correlation and direct impacts are both high and positive, then the correlation describes the actual relation and character selection will be effective. If the correlation co-efficient is positive but the direct effect is negative or negligible, the indirect causal factors must be evaluated simultaneously for selection in such situations.

The residual effect determines how best the causal factors account for the variability of the dependent factors, the grain yield per plant in this case if, the value of residual effect is moderate or high, it indicates that decides the character studied are some other attributes which contributes for yield.

Based on the results of this study, correlation between grain yield with days to 50 per cent flowering, plant height, length of inflorescence, girth of inflorescence, number of branches per plant and biological yield per plant is due to direct and positive effect of a character whereas, direct and negative effect with the days to maturity, stem diameter, leaf area and protein content.

4.6 Genotype $\times$ Environment interaction and stability analysis

The crop in the field is a community of plant that should be genetically uniform, represents the true genotype. During a growing season the particular combinations of soil, climate and pests, plus the competition among crop plants and other crop species (weeds) forms a unique environment that interacts with the genotype resulting in an expression of the genotype, including yield. Hence, crop performance is a function of the genotype of the crop and the nature of the production environment. It generally happens that many varieties of different crops do not exhibit similarity in their performance when tested under different environmental conditions. This is because of the presence of genotype $\times$ environment interactions, which results in changes of relative ranking in term of yield and component traits of different genotypes and also alters the magnitude of differences between genotypes from one environment to another. The existence of genotype $\times$ environment interaction, inhibit genetic analysis of the performance and reduces the efficiency of crop improvement via plant breeding, largely because they confound comparisons among genotypes with the environments of test and creates uncertainty in the expression of the phenotype to its full genetic potential. Change in ranking makes, it difficult for the plant breeder to decide, which kind of genotype should be selected. Therefore, knowledge of the nature and magnitude of genotype $\times$ environment interaction has become essential to the plant breeder in taking the decisions concerning breeding methodology.

Stratification of environments has been practiced to minimize the genotype $\times$ environment interactions and also to enhance the precision in selection. However, even with this refinement of technique, the interactions of genotypes with environments within same year remain very large (Allard and Bradshaw, 1964). Sprague (1966) opined that the possibility of reducing Genotype $\times$ Environment interaction in field experiments is questionable in spite of knowing the factors responsible for such interactions.

4.6.1 Analysis of variance

The analysis of variance for stability for different characters, as per Eberhart and Russell (1966), model is given in Table 4.7. The mean sum of square due to genotypes, environments, environment (linear) and genotype $\times$ environment (linear) were tested against pooled deviation. The pooled deviation was tested against pooled error. The genotype showed significant differences for all the thirteen characters. Mean square due to environment and environment (liner) was highly significant for all the characters

except harvest index. This indicated that environment used was quite differ from each other. Genotype $\times$ environment interaction showed significant differences for stem diameter, number of branches per plant, leaf area, grain yield and protein content when tested against pooled error, indicating wide difference between environments and differential behavior of genotypes in different environments. These results are in agreement with Sharma *et al.* (2001), Varalakshmi *et al.* (2011), García-Pereyra (2011) and Oduwaye *et al.* (2016). Genotype $\times$ environment (liner) was observed significant for girth of inflorescence, stem diameter, number of branches, leaf area, grain yield per plant and protein content when tested against pooled deviation. Result of analysis of variance (mean square) for phenotypic stability revealed that variation of genotype $\times$ environment (liner) for stem diameter, number of branches, leaf area, grain yield per plant and protein content is higher and highly significant as compared to non-linear component. This indicated that major portion of interaction was in linear in nature and prediction over environments for stem diameter, number of branches, leaf area, grain yield per plant and protein content would be possible. High significance of pooled deviation for all the character except number of brancher per plant and protein content. Indicates the importance of nonlinear component in determining indication of the genotypes with environment.

4.6.2 Environmental indices

The environment index reveals the suitability of an environment at a specific location. According to Breeze (1969), estimates of the environment index can provide the basis for identifying the favourable environment for the expression of maximum potential of genotype. The positive and negative value of environmental index indicates the favourable and unfavourable situations, respectively for each character (De *et al.*, 1992).

The results of estimates of environmental index (I_j) given in Table 4.8, suggested that E_1 (Date of sowing 11th November 2019) was most favourable environment whereas, E_3 (Date of sowing 2nd December 2019) was most unfavourable environment for all character except days to 50 per cent flowering and days to maturity.

The E_2 (Date of showing 21st November 2019) was favourable for days to 50 per cent flowering, days to maturity, length of inflorescence, girth of inflorescence, number of branches per plant, harvest index, test weight and protein content.

Table 4.7: Analysis of variance (Mean square) for phenotypic stability for different characters in grain amaranth

Sources of variation	d.f.	DF	DM	PH	LI	GI	SD	NB	LA	BY	GY	HI	TW	PC
Genotype (G)	24	220.65**	302.49**	2293.55**	170.08**	17.94**	17.93**	12.74**	375058.12**	843.05**	55.88**	152.79*	0.71**	0.86**
Environment(E)	2	749.13**	3016.55**	3748.36**	352.27**	94.69**	114.13**	0.99**	1907372.53**	7689.20**	879.34**	140.45	24.63**	9.33**
G × E	48	5.28	36.41	85.71	40.35	5.59	1.37*	0.19**	60829.65**	155.42	18.58**	74.98	0.16	0.28**
Environment (linear)	1	1498.26**	6033.11**	7496.72**	704.54**	189.39**	228.26**	1.98**	3814745.06**	15378.40**	1758.69**	280.91	49.27**	18.66**
G × E (linear)	24	6.35	29.90	89.63	34.60	7.76*	2.07**	0.34**	107419.23**	192.94	31.72**	79.67	0.18	0.41**
Pooled deviation	25	4.04**	41.20**	78.51**	44.26**	3.28**	0.65**	0.04	13670.46**	113.18**	5.22**	67.48**	0.14**	0.14
Pooled error	144	1	1	9	3	1	0	0	2739	8	1	7	0	0

* and ** : Significant at 5 and 1 per cent levels of significance, respectively

DF : Days to flowering, DM : Days to maturity, PH : Plant height (cm), LI : Length of inflorescence (cm), GI : Girth of inflorescence (cm), SD : Stem diameter (mm), NB : Number of branches per plant, LA : Leaf area per plant (cm²), BY : Biological yield per plant (g), GY : Grain yield per plant (g), HI : Harvest index (%), TW : Test weight (g/10 ml) and PC : Protein content (%).

Table 4.8: Estimates of environmental index (I_j) for different characters under different environments expressed as deviation of grand mean

Sr. No.	Characters	Environments		
		E_1	E_2	E_3
1	Days to 50 per cent flowering	-5.52	0.1	5.42
2	Days to maturity	-12.67	6.74	5.94
3	Plant height (cm)	14	-8.74	-5.24
4	Length of inflorescence (cm)	0.76	3.32	-4.07
5	Girth of inflorescence (cm)	1.85	0.16	-2.03
6	Stem diameter (mm)	2.31	-0.39	-1.91
7	Number of branches per plant	0.05	0.17	-0.22
8	Leaf area (cm ²)	318.94	-158.62	-160.33
9	Biological yield per plant (g)	18.49	-2.07	-16.4
10	Grain yield per plant (g)	6.39	-1.07	-5.32
11	Harvest index (%)	2.28	0.17	-2.45
12	Test weight (g/10 ml)	1	0	-0.99
13	Protein content (%)	0.25	0.45	-0.69

4.6.3 Stability parameters

According to Eberhart and Russell model (1966), a stable genotype is one which shows (i) high mean, (ii) regression co-efficient ($b_i = 1$) equal to unity and (iii) a mean square deviation from regression (S^2d_i) near to zero. Accordingly, three kinds of linear responses (b_i) viz., $b_i < 1$, $b_i = 1$ and $b_i > 1$ have been considered, and interpreted as $b_i = 1$, average stability and widely adaptable to different environments; $b_i > 1$, below average stability, increasing sensitivity to environmental changes and well adapted to favourable environment and $b_i < 1$, above average stability, greater tolerance to environmental changes; thereby genotypes would have specific adaptability to poor yielding environment. The stability parameters viz., mean performance, regression co-efficient ($b_i = 1$) and a mean square deviation from regression (S^2d_i) of 25 genotypes for eight characters were computed to assess relative stability over range of environments and are presented in Table 4.9. The character-wise results are described in the subsequent paragraphs.

4.6.3.1 Stem diameter

The deviation from regression (S^2d_i) was significant for four genotypes and hence these genotypes were unstable. Fifteen genotypes exhibited higher mean value than the general mean (10.52). Out of these, six genotypes had non-significant regression (b_i) and non-significant deviation from regression (S^2d_i) indicating average stability over different environments. SKGPA-61, SKGPA-150, SKNA-401, SKNA-903, SKNA-1503, SKNA-1508, SKNA-1510, SKNA-1701, BGA-7-1, CGA-18-1,

CGA-18-2, ANNPURNA, IC-469820, IC-506575 and IC-279511 genotypes had significant unit regression ($b_i < 1$) and non-significant S^2d_i were good for poor environment.

4.6.3.2 Number of branches per plant

The deviation from regression (S^2d_i) was significant for three genotypes and hence these genotypes were unstable. Two genotypes IC-506575 and IC-279511 exhibited higher mean value than the general mean (2) and had non-significant regression (b_i) and non-significant deviation from regression (S^2d_i) indicating average stability over different environments.

4.6.3.3 Leaf area

The deviation from regression (S^2d_i) was significant for seven genotypes and hence these genotypes were unstable. Fourteen genotypes exhibited higher mean value than the general mean (731.73). Out of these, six genotypes had non-significant regression (b_i) and non-significant deviation from regression (S^2d_i) indicating average stability over different environments. SKNA-903, SKNA-1503, SKNA-1701, BGA-7-1, CGA-18-1, SUVARNA, ANNPURNA, IC-469820, IC-506575, IC-436953 and IC-279511 genotypes had significant unit regression ($b_i < 1$) and non-significant S^2d_i were good for poor environment. The genotype SKGPA-150 had significant unit regression ($b_i > 1$) and non-significant S^2d_i were advised for better environment.

4.6.3.4 Grain yield per plant

The deviation from regression (S^2d_i) was significant for eleven genotypes and hence these genotypes were unstable. Fifteen genotypes exhibited higher mean value than the general mean (11.56). Out of these, six genotypes had non-significant regression (b_i) and non-significant deviation from regression (S^2d_i) indicating average stability over different environments. SKGPA-74, SKNA-1313, SKNA-1406, SKNA-1407, SKNA-1503, SUVARNA, ANNPURNA and IC-506575 genotypes had significant unit regression ($b_i < 1$) and non-significant S^2d_i were good for poor environment.

4.6.3.5 Protein content

The deviation from regression (S^2d_i) was significant for CGA-18-1 hence it was unstable. twelve genotypes exhibited higher mean value than the general mean (12.79). Out of these, ten genotypes had non-significant regression (b_i) and non-significant deviation from regression (S^2d_i) indicating average stability over different environments. SKGPA-150, SKNA-401, SKNA-808, SKNA-1510, SKNA-1701, GA-1

and GA-2 genotypes had significant unit regression ($b_i < 1$) and non-significant S^2d_i were good for poor environment.

Table 4.9: Stability parameters of various genotypes for different characters in grain amaranth

Sr. No.	Genotypes	Stem diameter (mm)			Leaf area (cm ²)		
		Mean	b_i	S^2d_i	Mean	b_i	S^2d_i
1	SKGPA-61	10.80	0.72**	-0.15	1422.00	2.69**	98114.27**
2	SKGPA-74	12.42	1.19	-0.01	834.22	1.41**	40388.70**
3	SKGPA-150	10.77	0.89**	-0.15	710.33	1.41**	6735.18
4	SKNA-401	10.33	0.97**	-0.31	992.11	2.75	5865.20
5	SKNA-808	13.81	1.32	0.02	1344.88	1.94	-637.87
6	SKNA-903	11.23	0.44	0.26	504.16	0.17**	-2052.55
7	SKNA-1313	11.61	1.10	0.25	1060.22	1.66	-2231.50
8	SKNA-1406	11.84	0.97*	1.54*	826.77	1.33	-237.40
9	SKNA-1407	12.67	1.06	0.03	1116.00	1.04	43233.92**
10	SKNA-1503	10.12	0.73**	-0.32	736.44	0.38**	255.96
11	SKNA-1508	10.71	0.78**	-0.002	630.11	0.13	60744.08**
12	SKNA-1510	9.96	0.52**	0.018	807.88	1.14**	10461.63*
13	SKNA-1701	13.32	0.97**	-0.33	893.27	0.67**	6651.62
14	BGA-7-1	10.19	0.75**	0.064	644.33	0.49*	3509.12
15	CGA-18-1	10.14	0.97**	-0.013	535.88	0.59**	-1797.04
16	CGA-18-2	10.63	0.79**	0.026	642.88	1.08**	9902.27*
17	GA-1	11.79	2.00**	1.63*	766.66	0.61*	8186.46*
18	GA-2	13.17	1.71	0.93	1243.22	2.72	309.04
19	GA-3	12.20	1.15	0.014	733.33	1.24	-2625.89
20	SUVARNA	13.64	2.46**	1.97**	818.88	0.10	2340.68
21	ANNPURNA	5.85	0.66**	-0.32	221.33	0.55**	-2702.52
22	IC-469820	5.95	0.25**	-0.33	235.88	0.045	-2532.24
23	IC-506575	7.73	0.80**	0.42	164.77	0.17**	-2493.59
24	IC-436953	5.61	0.83	2.75**	181.00	0.29**	-2702.87
25	IC-279511	6.48	0.85**	-0.17	226.55	0.30**	-2621.03
Mean		10.52			731.73		
S.Em.±		0.68			142.40		

Table 4.9 Contd....

Table 4.9 Contd....

Sr. No.	Genotypes	Grain yield per plant (g)			Protein content (%)		
		Mean	b _i	S ² d _i	Mean	b _i	S ² d _i
1	SKGPA-61	19.15	1.83	1.33	12.40	1.71**	0.015
2	SKGPA-74	6.95	0.70**	-0.66	12.41	1.22**	-0.116
3	SKGPA-150	13.41	1.23	-0.58	13.18	0.38*	-0.115
4	SKNA-401	15.04	1.33	1.50	13.07	0.86**	-0.08
5	SKNA-808	11.74	1.18	-0.49	12.45	0.04	-0.126
6	SKNA-903	13.83	1.25	0.37	12.42	1.87**	0.078
7	SKNA-1313	9.95	0.85**	-0.35	12.34	2.70**	-0.097
8	SKNA-1406	9.58	0.40**	-0.84	13.25	0.72	0.307
9	SKNA-1407	12.32	0.90**	0.12	12.78	0.61	0.113
10	SKNA-1503	10.85	0.60**	-0.63	12.88	1.15	-0.068
11	SKNA-1508	15.07	1.63**	4.00*	13.29	0.42	-0.059
12	SKNA-1510	14.00	1.52**	11.02**	12.75	0.82**	-0.081
13	SKNA-1701	19.10	2.25**	3.76*	12.58	0.17**	-0.141
14	BGA-7-1	13.74	1.52	0.06	13.61	0.24	0.066
15	CGA-18-1	16.69	1.58**	2.79*	12.57	0.80	0.536*
16	CGA-18-2	11.97	1.59**	11.97**	12.55	1.53**	-0.089
17	GA-1	12.76	1.12**	7.73**	13.45	0.14	-0.131
18	GA-2	16.33	1.88**	7.14**	13.41	0.85**	-0.14
19	GA-3	13.49	1.07**	6.60**	13.05	1.10	-0.073
20	SUVARNA	4.03	0.22*	-0.22	13.60	1.97	0.363
21	ANNPURNA	6.92	-0.09	0.40	12.91	0.59	0.037
22	IC-469820	6.43	-0.08	34.33**	12.97	0.73	-0.011
23	IC-506575	5.94	0.05	0.22	12.20	2.77**	-0.063
24	IC-436953	3.61	0.12	4.07*	11.20	0.29	0.157
25	IC-279511	8.96	0.26	15.85**	12.38	1.22**	-0.131
Mean		11.56			12.79		
S.Em.±		2.49			0.31		

Table 4.9 Contd....

Table 4.9 Contd....

Sr. No.	Genotypes	Number of branches per plant		
		Mean	b_i	S^2d_i
1	SKGPA-61	1	-	-0.036
2	SKGPA-74	1	-	-0.036
3	SKGPA-150	1	-	-0.036
4	SKNA-401	1	-	-0.036
5	SKNA-808	1	-	-0.036
6	SKNA-903	1	-	-0.036
7	SKNA-1313	1	-	-0.036
8	SKNA-1406	1	-	-0.036
9	SKNA-1407	1	-	-0.036
10	SKNA-1503	1	-	-0.036
11	SKNA-1508	1	-	-0.036
12	SKNA-1510	1	-	-0.036
13	SKNA-1701	1	-	-0.036
14	BGA-7-1	1	-	-0.036
15	CGA-18-1	1	-	-0.036
16	CGA-18-2	1	-	-0.036
17	GA-1	1	-	-0.036
18	GA-2	1	-	-0.036
19	GA-3	1	-	-0.036
20	SUVARNA	1	-	-0.036
21	ANNPURNA	5.91	5.82**	0.15*
22	IC-469820	5.57	3.64**	0.10*
23	IC-506575	6.33	5.99	0.021
24	IC-436953	5.43	4.06	0.68**
25	IC-279511	6.82	5.40	-0.001
Mean		2.00		
S.Em.±		0.26		

* and ** : Significant at 5 and 1 per cent levels of significance, respectively

When, $H_0: b_i = 1$ and $H_0: S^2d_i = 0$

$H_a: b_i \neq 1$ and $H_a: S^2d_i \neq 0$

A comprehensive analysis of stability parameters (Table 4.10) indicated that none of the genotypes were stable for all of the characters. The situation was similar in terms of average performance and responsiveness. As a result, any generalization about genotype stability and responsiveness for all characteristics was impossible. According to the stability analysis, the five genotypes have average stability and wider adaptability for grain yield per plant. They also have average, above-average, or below-average stability for other characters. Genotypes SKGPA-150, SKNA-401 and SKNA 808 are showing average stability for grain yield per plant as well as stem diameter, leaf area and protein content whereas, SKGPA-61 showing average stability for grain yield per plant along with stem diameter and protein content. SKNA-903 showing stability for leaf area, and protein content along with grain yield per plant. Whereas, BGA-7-1 showing stability for stem diameter and leaf area along with grain yield per plant.

Table 4.10: Stable genotypes for grain yield per plant along with stability for component traits

Genotypes	Mean	b_i	S^2d_i	Average stability for other characters
SKGPA-61	19.15	1.83	1.33	SD, PC
SKGPA-150	13.41	1.23	-0.58	SD, LA, PC
SKNA-401	15.04	1.33	1.50	SD, LA, PC
SKNA-808	11.74	1.18	-0.49	SD, LA, PC
SKNA-903	13.83	1.25	0.37	LA, PC
BGA-7-1	13.74	1.52	0.06	SD, LA

Where,

SD = Stem diameter (mm)

LA = Leaf area (cm²)

PC = Protein content (%)

Above study revealed that SKGPA-74, SKNA-1313, SKNA-1406, SKNA-1407, SKNA-1503, SUVARNA, ANNPURNA and IC-506575 showing stability for grain yield per plant in poor environmental conditions.

The stability study indicated that genotypes showed stability for grain yield per plant also exhibiting average, above, or below average stability for one or more yield components. It is thus proposed that while making selections, consideration should be given to the phenotypic stability of characters directly related to grain yield, and genotypes having average stability for different characters would be used to develop stable populations.

V. SUMMARY AND CONCLUSIONS

The current study was carried out on 25 genotypes to investigate variability, correlation, path co-efficient analysis, $G \times E$ interaction, and stability analysis in grain amaranth [*Amaranthus hypochondriacus* L.]. The experiment was set up in a randomized block design and replicated thrice in three different environments. i.e., date of sowing viz., 11th November, 21st November and 2nd December during *rabi* season of the year 2019-20 at Center for Crop Improvement, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar.

The analysis of variances revealed highly significant differences among the genotypes for all character studied for all environments and pooled. It indicates that genotypes were performed differently from each other for all the traits. All the characteristics in the genetic material under investigation demonstrating the presence of broad genetic variation for different characters.

Genotypes performed well in E_1 , followed by E_2 , and had the lowest values for almost all of the characters in E_3 . None of the genotypes performed consistently for any of the characters across all three environments. This revealed that genotypes differed in yield and other quantitative characters.

E_1 had the highest estimates of genotypic and phenotypic variance for days to 50 per cent flowering, grain yield per plant, and biological yield per plant than E_2 and E_3 . In the individual environments (E_1 , E_2 and E_3) genotypic (σ^2_g), phenotypic (σ^2_p) and environmental component (σ^2_e) were found high for leaf area followed by plant height, biological yield per plant, days to maturity, harvest index, days to 50 per cent flowering, grain yield per plant and length of inflorescence except grain yield per plant moderate in E_2 and low in E_3 whereas, moderate values showed girth of inflorescence and stem diameter. The phenotypic variance was slightly higher than the genotypic variance for most of the characters.

Leaf area had the highest phenotypic and genotypic component of variance values in the across environments analysis, followed by plant height, biological yield per plant, days to maturity, days to 50 per cent flowering, length of inflorescence, and harvest index. The maximum variability which was found due to genotype indicating their stability and minimum influence by environment.

For all characteristics in individual and pooled over environments, the phenotypic co-efficient of variation was greater in magnitude than the genotypic co-efficient of

variation. This might be due to an environmental factor. The GCV (%) was close to the PCV (%) for the majority of traits, indicating a lesser influence of environment and a greater role of genetic factors in trait expression. The high GCV (%) and PCV (%) were observed for number of branches per plant, leaf area, grain yield per plant, biological yield per plant, harvest index, plant height and stem diameter for all the individual environments. The higher the co-efficient of variation, the greater the possibility of enhancing these characteristics through phenotypic selection.

The greater the heritability value, the more effective the selection would be in improving these traits. The lower heritability suggests that there are less opportunities for improvement through selection. Heritability and expected genetic advance as a percentage of mean was found to be high in all individual as well as pooled over environment for number of branches per plant, leaf area, grain yield per plant, biological yield per plant, harvest index, stem diameter, plant height, days to 50 per cent flowering, length of inflorescence, girth of inflorescence, and days to maturity. High heritability combined with high genetic advance as a percentage of mean suggests that these traits were governed by additive gene action and that these characters might be improved by selection.

Correlation studies provide reliable information on the type and extent of character correlations. The existence of real associations is shown by genotypic correlations, but phenotypic correlations may occur by chance. These relationships might be positive or negative. If the genotypic correlation is significant but the phenotypic correlation is not, it implies that the existing true relationship is being masked by environmental effects. The character grain yield per plant was positively and highly significantly correlated with days to 50 per cent flowering, days to maturity, plant height, stem diameter, leaf area and biological yield per plant at genotypic, phenotypic and environmental levels, respectively. Whereas, girth of inflorescence significantly and positively correlated at genotypic and phenotypic levels, respectively. Hence, concentrate more on above parameters for improving grain yield per plant in grain amaranth.

Genotypic and phenotypic correlation coefficients between yield and its components were divided into direct and indirect effects using path coefficient analysis. correlation between grain yield with days to 50 per cent flowering, plant height, length of inflorescence, girth of inflorescence, number of branches per plant and biological yield per plant is due to direct and positive effect of a character

whereas, direct and negative effect with the days to maturity, stem diameter, leaf area and protein content.

The analysis of variance for stability for thirteen different character showed significant differences for all the characters. Mean square due to environment and environment (liner) was highly significant for all the characters except harvest index. Genotype $\times$ environment interaction showed significant differences for stem diameter, number of branches per plant, leaf area, grain yield and protein content when tested against pooled error, indicating wide difference between environments and differential behavior of genotypes in different environments. Genotype $\times$ environment (liner) was observed significant for girth of inflorescence stem diameter, number of branches, leaf area, grain yield per plant and protein content when tested against pooled deviation. Result of analysis of variance (mean square) for phenotypic stability stability revealed that variation of genotype $\times$ environment (liner) for stem diameter, number of branches, leaf area, grain yield per plant and protein content is higher and highly significant as compared to non-linear component. This indicated that major portion of interaction was in linear in nature and prediction over environments for all these traits would be possible. High significance of pooled deviation for all the character except number of brancher per plant and protein content. Indicates the importance of nonlinear component in determining indication of the genotypes with environment.

The estimations of the environmental index (I_j) showed that E_1 (day of sowing 11th November, 2019) was the most favourable environment. According to the stability analysis, the six genotypes have average stability and wider adaptability for grain yield per plant. They also have average, above-average, or below-average stability for other characters.

From all the genotypes under study SKGPA-150, SKNA-401 and SKNA 808 are showing average stability for grain yield per plant as well as stem diameter, leaf area and protein content whereas, SKGPA-61 showing average stability for grain yield per plant along with stem diameter and protein content. SKNA-903 showing stability for leaf area, and protein content along with grain yield per plant. Whereas, BGA-7-1 showing stability for stem diameter and leaf area along with grain yield per plant. In poor environmental conditions SKGPA-74, SKNA-1313, SKNA-1406, SKNA-1407, SKNA-1503, SUVARNA, ANNPURNA and IC-506575 showing stability for grain yield per plant.

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Appendix-I: Weekly meteorological data recorded during the crop season (November-2019 to March-2020)

Month and Year	Standard Week	Temperature (°C)		Relative Humidity (%)		Rainfall (mm)
		Max.	Min.	Morning	Evening	
November-2019	45	32.4	20.7	64	67	0.0
	46	31.4	18.4	61	64	5.0
	47	31.8	15.3	53	58	0.0
	48	29.9	17.4	56	54	0.0
December-2019	49	28.6	13.3	55	51	0.0
	50	27.1	9.5	49	42	4.0
	51	25.7	10.7	53	40	0.0
	52	25.8	6.9	48	26	0.0
January-2020	01	24.3	9.3	55	40	0.0
	02	24.0	8.0	52	38	0.0
	03	23.6	7.3	46	29	0.0
	04	27.8	10.4	47	28	0.0
	05	25.8	6.4	46	25	0.0
February-2020	06	27.6	8.4	52	28	0.0
	07	32.5	11.5	58	22	0.0
	08	35.3	12.1	62	20	0.0
	09	34.5	13.2	67	24	0.0
March-2020	10	32.1	13.0	68	42	0.0
	11	32.5	12.7	62	34	0.0
	12	35.5	16.9	66	36	0.0
	13	36.0	16.3	68	34	3.0

Source: Agricultural Meteorology Department, Chimanbhai Patel College of Agriculture, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar.

Appendix-II: Mean performance of genotypes for yield and yield contributing characters in grain amaranth for all individual and pooled over environment

Sr. No.	Genotypes	Days to 50% flowering				Days to maturity				Plant height (cm)			
		E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₁₃	Pooled
1	SKGPA-61	48.00	55.00	58.67	53.89	112.33	130.33	126.33	123.00	167.33	140.53	133.53	147.13
2	SKGPA-74	59.00	59.00	66.00	61.33	112.00	132.00	130.00	124.67	137.87	102.80	86.00	108.89
3	SKGPA-150	43.67	53.00	57.67	51.44	114.00	134.00	126.00	124.67	139.07	107.40	125.80	124.09
4	SKNA-401	49.67	53.00	56.33	53.00	104.00	133.67	126.33	121.33	134.27	103.73	96.00	111.33
5	SKNA-808	54.00	57.00	63.67	58.22	110.67	136.67	127.67	125.00	137.67	106.40	112.67	118.91
6	SKNA-903	37.67	45.00	48.00	43.56	91.00	109.00	126.00	108.67	105.27	68.73	89.87	87.96
7	SKNA-1313	47.00	53.33	64.00	54.78	111.00	126.33	124.00	120.44	117.80	103.93	129.20	116.98
8	SKNA-1406	50.00	53.67	58.00	53.89	112.33	129.67	126.67	122.89	137.27	104.07	105.00	115.44
9	SKNA-1407	47.00	53.33	57.33	52.56	104.00	129.33	127.67	120.33	119.20	109.07	113.40	113.89
10	SKNA-1503	48.67	53.00	56.67	52.78	111.33	133.33	122.33	122.33	137.87	106.73	98.00	114.20
11	SKNA-1508	48.33	49.67	57.33	51.78	113.67	133.33	123.00	123.33	121.93	97.20	111.67	110.27
12	SKNA-1510	43.00	49.33	54.33	48.89	100.33	130.33	123.00	117.89	114.47	83.93	81.67	93.36
13	SKNA-1701	49.00	51.00	60.67	53.56	108.67	133.33	123.67	121.89	123.00	124.73	121.80	123.18
14	BGA-7-1	49.00	51.33	60.00	53.44	111.33	129.00	122.67	121.00	123.07	103.00	108.80	111.62
15	CGA-18-1	47.00	52.00	58.00	52.33	100.00	133.33	127.00	120.11	109.80	93.53	100.53	101.29
16	CGA-18-2	42.33	49.00	56.33	49.22	102.33	132.00	124.00	119.44	141.47	106.40	111.07	119.64
17	GA-1	53.00	60.33	67.00	60.11	111.33	131.33	124.33	122.33	135.73	113.67	100.93	116.78
18	GA-2	57.67	55.67	58.67	57.33	124.33	133.67	130.33	129.44	145.47	122.47	115.67	127.87
19	GA-3	47.00	51.33	57.00	51.78	116.33	108.67	128.33	117.78	118.67	118.93	134.73	124.11
20	SUVARNA	61.67	64.00	69.33	65.00	125.33	135.00	132.33	130.89	111.20	88.13	111.20	103.51
21	ANNPURNA	29.00	37.00	41.67	35.89	84.00	102.67	111.33	99.33	70.67	51.20	45.80	55.89
22	IC-469820	29.00	39.00	41.67	36.56	83.67	102.00	115.33	100.33	59.73	46.87	47.27	51.29
23	IC-506575	26.00	37.67	40.67	34.78	84.00	101.67	112.33	99.33	66.80	40.80	54.87	54.16
24	IC-436953	25.33	38.33	42.33	35.33	84.33	102.00	109.33	98.56	65.47	42.87	36.27	48.20
25	IC-279511	27.00	38.67	41.33	35.67	85.00	100.00	112.67	99.22	63.27	48.67	51.60	54.51
Mean		44.76	50.39	55.71	50.28	104.69	124.11	123.31	117.37	116.17	93.43	96.93	102.18
Lowest		25.33	37.00	40.67	34.78	83.67	100.00	109.33	98.56	59.73	40.80	36.27	48.20
Highest		61.67	64.00	69.33	65.00	125.33	136.67	132.33	130.89	167.33	140.53	134.73	147.13
S.Em.±		0.99	0.82	0.99	1.33	1.32	0.91	1.06	3.48	3.14	2.69	3.04	5.35
C.D. at 5 %		2.81	2.32	2.82	3.77	3.76	2.60	3.02	9.91	8.94	7.64	8.63	15.20
C.V. %		3.83	2.81	3.08	3.22	2.18	1.28	1.49	1.64	4.69	4.98	5.42	5.02

Appendix-II Contd..

Appendix-II Contd..

Sr. No.	Genotypes	Length of inflorescence (cm)				Girth of inflorescence (cm)			
		E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
1	SKGPA-61	55.63	65.33	53.80	58.26	23.67	22.53	19.11	21.77
2	SKGPA-74	31.40	33.20	37.60	34.07	23.33	21.00	19.22	21.19
3	SKGPA-150	58.13	53.47	57.00	56.20	19.20	20.20	18.11	19.17
4	SKNA-401	47.20	55.80	43.07	48.69	20.20	19.53	17.67	19.13
5	SKNA-808	29.13	39.60	36.53	35.09	29.67	24.20	28.89	27.59
6	SKNA-903	48.50	43.00	40.33	43.94	30.93	21.20	18.33	23.49
7	SKNA-1313	53.67	57.40	40.73	50.60	18.80	19.87	16.22	18.30
8	SKNA-1406	56.27	53.42	39.00	49.56	24.80	20.60	17.89	21.10
9	SKNA-1407	43.87	53.73	49.13	48.91	21.93	20.47	21.33	21.24
10	SKNA-1503	42.47	54.00	39.00	45.16	17.73	19.47	16.44	17.88
11	SKNA-1508	49.67	54.67	55.47	53.27	19.80	19.80	18.67	19.42
12	SKNA-1510	51.67	56.53	41.83	50.01	20.53	18.87	21.00	20.13
13	SKNA-1701	55.60	55.53	62.53	57.89	24.07	20.53	22.67	22.42
14	BGA-7-1	48.80	50.80	45.13	48.24	20.87	19.20	15.78	18.61
15	CGA-18-1	43.73	50.27	51.33	48.44	20.57	21.20	14.56	18.77
16	CGA-18-2	46.93	51.20	52.53	50.22	21.80	20.67	19.33	20.60
17	GA-1	53.13	52.00	41.40	48.84	22.27	20.33	15.89	19.50
18	GA-2	58.00	69.60	46.67	58.09	20.43	20.47	21.89	20.93
19	GA-3	50.65	63.67	48.53	54.28	22.87	20.27	16.78	19.97
20	SUVARNA	25.53	44.87	38.80	36.40	21.40	26.00	20.67	22.69
21	ANNPURNA	47.40	45.07	27.27	39.91	21.60	17.80	14.67	18.02
22	IC-469820	44.00	38.60	33.40	38.67	18.27	19.47	14.56	17.43
23	IC-506575	53.60	36.60	27.87	39.36	18.27	17.07	12.56	15.96
24	IC-436953	47.07	36.00	27.60	36.89	25.60	17.80	10.00	17.80
25	IC-279511	47.93	39.53	32.53	40.00	24.00	21.80	23.33	23.04
Mean		47.60	50.16	42.76	46.84	22.10	20.41	18.22	20.25
Lowest		25.53	33.20	27.27	34.07	17.73	17.07	10.00	15.96
Highest		58.13	69.60	62.53	58.26	30.93	26.00	28.89	27.59
S.Em.±		1.73	1.66	1.86	3.67	1.07	0.79	0.72	1.37
C.D. at 5 %		4.91	4.71	5.27	10.43	3.03	2.25	2.06	3.88
C.V. %		6.28	5.72	7.51	6.46	8.36	6.72	6.88	7.47

Appendix-II Contd..

Appendix-II Contd..

Sr. No.	Genotypes	Stem diameter (mm)				Number of branches per plant				Leaf area (cm ²)			
		E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₁₃	Pooled
1	SKGPA-61	12.59	10.18	9.65	10.81	1.00	1.00	1.00	1.00	2281.67	1219.00	765.33	1422.00
2	SKGPA-74	15.35	11.49	10.42	12.42	1.00	1.00	1.00	1.00	1283.33	757.67	461.67	834.22
3	SKGPA-150	12.72	10.77	8.84	10.78	1.00	1.00	1.00	1.00	1162.00	417.00	552.00	710.33
4	SKNA-401	12.63	9.82	8.54	10.33	1.00	1.00	1.00	1.00	1872.00	620.00	484.33	992.11
5	SKNA-808	17.05	12.80	11.59	13.81	1.00	1.00	1.00	1.00	1965.00	1068.67	1001.00	1344.89
6	SKNA-903	12.48	10.43	10.78	11.23	1.00	1.00	1.00	1.00	559.33	494.83	458.33	504.17
7	SKNA-1313	13.93	11.80	9.11	11.62	1.00	1.00	1.00	1.00	1592.00	780.33	808.33	1060.22
8	SKNA-1406	14.49	10.35	10.68	11.84	1.00	1.00	1.00	1.00	1253.00	579.67	647.67	826.78
9	SKNA-1407	15.32	11.77	10.95	12.68	1.00	1.00	1.00	1.00	1449.33	798.67	1100.00	1116.00
10	SKNA-1503	11.77	9.94	8.65	10.12	1.00	1.00	1.00	1.00	859.00	637.00	713.33	736.44
11	SKNA-1508	12.69	9.94	9.52	10.72	1.00	1.00	1.00	1.00	674.33	430.00	786.00	630.11
12	SKNA-1510	11.35	9.28	9.27	9.97	1.00	1.00	1.00	1.00	1172.67	545.33	705.67	807.89
13	SKNA-1701	15.60	12.90	11.49	13.33	1.00	1.00	1.00	1.00	1107.50	718.33	854.00	893.28
14	BGA-7-1	11.75	10.41	8.43	10.20	1.00	1.00	1.00	1.00	801.00	510.67	621.33	644.33
15	CGA-18-1	12.23	10.22	7.98	10.15	1.00	1.00	1.00	1.00	724.67	420.67	462.33	535.89
16	CGA-18-2	12.64	9.83	9.43	10.63	1.00	1.00	1.00	1.00	988.67	550.33	389.67	642.89
17	GA-1	16.01	12.13	7.23	11.79	1.00	1.00	1.00	1.00	963.33	742.67	594.00	766.67
18	GA-2	16.81	13.41	9.31	13.18	1.00	1.00	1.00	1.00	2111.33	850.33	768.00	1243.22
19	GA-3	14.70	12.23	9.70	12.21	1.00	1.00	1.00	1.00	1129.33	530.00	540.67	733.33
20	SUVARNA	19.76	11.44	9.72	13.64	1.00	1.00	1.00	1.00	852.67	852.33	751.67	818.89
21	ANNPURNA	7.41	5.51	4.64	5.86	5.87	7.13	4.73	5.91	397.00	132.33	134.67	221.33
22	IC-469820	6.51	5.92	5.42	5.95	5.47	6.40	4.87	5.58	250.33	219.33	238.00	235.89
23	IC-506575	9.33	8.12	5.75	7.73	6.47	7.47	5.07	6.33	220.00	147.67	126.67	164.78
24	IC-436953	7.03	6.70	3.10	5.61	6.31	5.67	4.33	5.44	275.00	132.67	135.33	181.00
25	IC-279511	8.58	5.82	5.06	6.49	7.20	7.67	5.60	6.82	322.33	172.33	185.00	226.56
Mean		12.83	10.13	8.61	10.52	2.05	2.17	1.78	2.00	1050.67	573.11	571.40	731.73
Lowest		6.51	5.51	3.10	5.61	1.00	1.00	1.00	1.00	220.00	132.33	126.67	164.78
Highest		19.76	13.41	11.59	13.81	7.20	7.67	5.60	6.82	2281.67	1219.00	1100.00	1422.00
S.Em.±		0.76	0.40	0.48	0.68	0.22	0.20	0.12	0.26	72.75	39.13	37.31	142.40
C.D. at 5 %		2.17	1.13	1.35	1.93	0.62	0.55	0.35	0.73	206.87	111.27	106.09	404.90
C.V. %		10.31	6.77	9.58	9.34	18.48	15.55	11.94	15.87	11.99	11.83	11.31	12.39

Appendix-II Contd..

Appendix-II Contd..

Sr. No.	Genotypes	Biological yield per plant (g)				Grain yield per plant (g)			
		E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
1	SKGPA-61	69.87	87.00	45.87	67.58	30.46	18.38	8.63	19.16
2	SKGPA-74	68.53	37.33	45.73	50.53	11.61	5.86	3.41	6.96
3	SKGPA-150	74.47	56.60	31.60	54.22	21.16	12.51	6.59	13.42
4	SKNA-401	85.07	55.80	29.07	56.64	24.01	12.38	8.74	15.04
5	SKNA-808	97.33	50.80	59.53	69.22	19.51	10.00	5.73	11.75
6	SKNA-903	39.80	44.80	30.40	38.33	21.54	13.38	6.59	13.83
7	SKNA-1313	77.73	56.40	26.73	53.62	15.20	9.61	5.07	9.96
8	SKNA-1406	105.13	74.87	47.80	75.93	12.15	9.15	7.47	9.59
9	SKNA-1407	67.07	50.33	54.60	57.33	18.40	10.56	8.02	12.33
10	SKNA-1503	60.47	36.13	29.07	41.89	14.84	9.84	7.89	10.85
11	SKNA-1508	88.07	38.87	34.80	53.91	26.14	11.55	7.53	15.07
12	SKNA-1510	60.13	51.07	34.67	48.62	24.76	9.59	7.66	14.00
13	SKNA-1701	100.67	75.20	32.00	69.29	34.15	14.95	8.20	19.10
14	BGA-7-1	59.00	56.00	27.40	47.47	23.23	12.88	5.13	13.75
15	CGA-18-1	92.67	50.73	36.40	59.93	27.39	13.45	9.23	16.69
16	CGA-18-2	74.33	32.53	33.53	46.80	23.22	7.37	5.32	11.97
17	GA-1	91.67	54.20	21.13	55.67	19.11	13.92	5.27	12.76
18	GA-2	83.27	63.27	30.00	58.84	29.24	12.03	7.74	16.34
19	GA-3	68.20	51.93	43.80	54.64	21.16	10.14	9.18	13.49
20	SUVARNA	87.27	40.13	47.73	58.38	5.23	4.44	2.45	4.04
21	ANNPURNA	21.87	21.53	13.40	18.93	5.99	7.93	6.86	6.93
22	IC-469820	20.47	20.73	13.53	18.24	4.15	11.31	3.84	6.43
23	IC-506575	34.00	19.40	17.73	23.71	6.01	6.72	5.12	5.95
24	IC-436953	23.40	15.67	5.33	14.80	3.73	5.27	1.83	3.61
25	IC-279511	34.20	29.40	20.53	28.04	9.46	11.98	5.46	8.96
Mean		67.23	45.50	31.34	48.02	17.82	10.48	6.39	11.56
Lowest		20.47	15.67	5.33	14.80	3.73	4.44	1.83	3.61
Highest		105.13	87.00	59.53	75.93	34.15	18.38	9.23	19.10
S.Em.±		3.36	2.96	2.21	7.20	1.25	0.80	0.48	2.49
C.D. at 5 %		9.56	8.42	6.30	20.47	3.56	2.29	1.36	7.08
C.V. %		8.64	10.95	11.80	10.22	12.01	13.13	13.06	13.39

Appendix-II Contd..

Appendix-II Contd..

Sr. No.	Genotypes	Harvest index (%)				Test weight (g)				Protein content (%)			
		E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₁₃	Pooled
1	SKGPA-61	43.61	21.05	18.85	27.84	7.95	6.72	5.40	6.69	12.53	13.42	11.26	12.40
2	SKGPA-74	16.92	16.63	7.47	13.67	7.42	6.05	4.60	6.02	12.84	12.86	11.54	12.41
3	SKGPA-150	28.48	22.10	20.73	23.77	7.78	7.52	5.38	6.89	13.40	13.25	12.89	13.18
4	SKNA-401	28.24	22.15	30.27	26.89	8.12	7.07	5.62	6.94	13.48	13.31	12.44	13.08
5	SKNA-808	20.39	19.77	9.61	16.59	7.46	5.65	4.43	5.85	12.56	12.39	12.40	12.45
6	SKNA-903	53.87	29.99	21.83	35.23	8.10	7.37	5.80	7.09	13.25	12.97	11.06	12.43
7	SKNA-1313	19.45	17.08	19.04	18.52	7.70	7.33	6.16	7.06	13.18	13.42	10.43	12.34
8	SKNA-1406	11.56	12.43	15.67	13.22	7.72	6.53	5.52	6.59	13.94	13.15	12.66	13.25
9	SKNA-1407	27.44	20.91	14.70	21.01	8.26	6.57	5.65	6.83	12.55	13.38	12.43	12.78
10	SKNA-1503	24.51	27.19	27.22	26.31	8.08	6.35	5.80	6.74	12.97	13.58	12.12	12.89
11	SKNA-1508	29.74	29.78	21.59	27.03	7.85	6.55	6.49	6.96	13.62	13.30	12.96	13.29
12	SKNA-1510	41.45	18.86	22.72	27.67	8.10	6.54	6.44	7.03	12.78	13.28	12.22	12.76
13	SKNA-1701	33.95	19.90	25.84	26.56	7.80	6.52	6.28	6.87	12.62	12.68	12.47	12.59
14	BGA-7-1	40.11	23.00	18.73	27.28	8.07	6.99	6.87	7.31	13.33	14.01	13.50	13.61
15	CGA-18-1	29.64	26.57	25.43	27.22	7.84	6.67	5.85	6.79	12.15	13.46	12.13	12.58
16	CGA-18-2	31.22	22.69	16.41	23.44	8.09	6.70	5.85	6.88	12.76	13.38	11.51	12.55
17	GA-1	20.93	25.67	24.84	23.81	8.03	6.77	6.29	7.03	13.58	13.46	13.34	13.46
18	GA-2	35.23	19.10	26.83	27.06	7.84	6.81	5.92	6.86	13.60	13.83	12.83	13.42
19	GA-3	31.13	20.08	21.07	24.09	7.61	6.80	6.48	6.96	13.13	13.71	12.32	13.05
20	SUVARNA	6.03	11.05	5.27	7.45	7.17	5.48	3.92	5.52	14.64	14.04	12.14	13.61
21	ANNPURNA	27.42	37.05	52.73	39.07	8.05	7.97	6.82	7.61	12.74	13.45	12.56	12.92
22	IC-469820	20.40	58.12	28.24	35.58	7.99	7.61	6.86	7.48	13.43	13.08	12.42	12.98
23	IC-506575	17.75	34.70	28.98	27.14	7.88	7.78	6.38	7.35	12.68	13.63	10.31	12.21
24	IC-436953	16.16	33.63	33.99	27.93	8.06	7.56	6.00	7.20	11.69	10.99	10.93	11.20
25	IC-279511	27.37	40.76	26.65	31.59	7.97	8.00	6.49	7.49	12.61	12.99	11.54	12.38
Mean		27.32	25.21	22.59	25.04	7.88	6.88	5.89	6.88	13.04	13.24	12.10	12.79
Lowest		6.03	11.05	5.27	7.45	7.17	5.48	3.92	5.52	11.69	10.99	10.31	11.20
Highest		53.87	58.12	52.73	39.07	8.26	8.00	6.87	7.61	14.64	14.04	13.50	13.61
S.Em.±		2.25	2.99	2.46	5.00	0.18	0.26	0.33	0.24	0.31	0.35	0.45	0.31
C.D. at 5 %		6.40	8.50	7.00	14.22	0.50	0.74	0.93	0.67	0.88	0.99	1.27	0.88
C.V. %		14.28	20.53	18.88	17.89	3.87	6.52	9.57	6.56	4.11	4.55	6.42	5.05

CERTIFICATE

This is to certify that, I have no objection for supplying to any scientist only one copy or any part of this thesis at a time through reprographic process, if necessary for rendering reference service in a library or documentation centre.



(Savaliya Parth M.)

Place : SARDARKRUSHINAGAR

Date : 13th September, 2021