

**“GENETIC VARIABILITY AND GENETIC DIVERSITY STUDIES
FOR YIELD AND YIELD CONTRIBUTING CHARACTERS IN
QUINOA (*Chenopodium quinoa* Willd.) GENOTYPES”**

by

Miss. Shinde Sayali Satish

Reg. No. 018/030

A Thesis submitted to the
**MAHATMA PHULE KRISHI VIDYAPEETH,
RAHURI - 413 722, DIST. AHMEDNAGAR,
MAHARASHTRA, INDIA**

in partial fulfilment of the requirements for the degree
of

MASTER OF SCIENCE (AGRICULTURE)

in

**AGRICULTURAL BOTANY
(GENETICS AND PLANT BREEDING)**



DEPARTMENT OF AGRICULTURAL BOTANY

**POST GRADUATE INSTITUTE,
MAHATMA PHULE KRISHI VIDYAPEETH,
RAHURI - 413 722, DIST. AHMEDNAGAR,
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2020

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2020

CANDIDATE'S DECLARATION

I hereby declare that this thesis or part
there of has not been submitted
by me or other person to any
other University or Institute
for Degree or
Diploma

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Dated : / /2020

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This is to certify that the thesis entitled “**GENETIC VARIABILITY AND GENETIC DIVERSITY STUDIES FOR YIELD AND YIELD CONTRIBUTING CHARACTERS IN QUINOA (*Chenopodium quinoa* Willd.) GENOTYPES**”, submitted to the Faculty of Agriculture, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist.- Ahmednagar, Maharashtra (India), in partial fulfilment of the requirements for the degree of **MASTER OF SCIENCE (AGRICULTURE) in AGRICULTURAL BOTANY (GENETICS AND PLANT BREEDING)**, embodies results of piece of bonafide research work carried out by **Miss. SHINDE SAYALI SATISH** under my guidance and supervision and that no part of the thesis has been submitted to any other degree or diploma.

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ACKNOWLEDGEMENT

Though formal and dead words cannot carry the fragrance of emotions with them, still they are the sole available way of expressing emotions in such formal acknowledgements.

I bestow my deep sense of gratitude to my Research Guide and Chairman of Advisory Committee **Dr. S.V. Pawar**, Assistant Professor of Agricultural Botany, State Level Biotechnology Center, Mahatma Phule Krishi Vidyapeeth, Rahuri for his valuable suggestions, constructive criticism intellectual guidance and constant encouragement throughout the course of this investigation which helped me to complete this manuscript.

It is my proud privilege to offer and well devoted thanks to **Dr. K. P. Vishvanatha**, Honorable Vice Chancellor, MPKV, Rahuri, **Dr. A. L. Pharande**, Dean Faculty of Agriculture, Director of Instruction, MPKV, Rahuri; **Dr. P. N. Rasal**, Associate Dean, Post Graduate Institute, Mahatma Phule Krishi Vidyapeeth, Rahuri, for his directives and help during the experimentation of research work.

It is my proud privilege to record my sincere gratitude to **Dr. A. S. Jadhav**, Head, Department of Botany, for their valuable help and encouragement throughout the course of study

I have immense pleasure in expressing my profound sense of gratitude to members of my advisory committee- **Prof. M.T. Bhingarde**, Plant Breeder, AICRN on Potential Crops, Mahatma Phule Krishi Vidyapeeth, Rahuri. **Dr. S. R. Dhonde**, Assistant Maize Breeder AICRP on Maize MPKV Rahuri and **Dr. M. S. Shinde**, Assistant Sorghum Breeder, Sorghum Improvement Project, MPKV, Rahuri and **Dr. G. C. Shinde**, Assistant Professor of Botany, PGI, MPKV, Rahuri, for their continuous inspiration and help throughout the research work.

I express my sincere thanks to **Dr. A.J. Shivgaje**, Associate Professor of Statistics, Department of Agricultural Statistic, College of Agriculture Dhule, member of my advisory committee for his suggestions and **Dr. Swati Shinde**, Department of Statistics, PGI, MPKV, Rahuri, for valuable help during statistical analysis and for their timely help and co-operation during completion of my course and research work.

It is my proud privilege to record my sincere gratitude to Dr. A.S. Jadhav, Head, Department of Botany, Dr. A.P. Padhye, Dr. N.S. Kute, Dr. V.L. Amolic, Prof. A.H. Sonone, Dr. P.L. Kulwal, Dr. V.P. Chimote, Dr. A.A. Kale and other staff members of Botany Department, M.P.K.V., Rahuri for their valuable help and encouragement throughout the course of study.

I would like to express my sincere appreciation to my beloved seniors Miss. Ashwini Janjal, Miss. Snehal, Miss. Dipika Patil, Miss. Kirti Ladkat, Miss. Gayatri Chavan, Mr. Pranod Pawar, Mr. Nilesh Adsule, Mr. Swapnil Mane and Mr. Akash Shinde for their valuable guidance and help. I am thankful to all my batch mates Miss. Rachana Bhosale, Miss. Pradnya Pawar, Mr. Devendra Vanjare, Mr. Niranjan Deshmukh,

Mr. Tukaram Sadgar, Mr. Shubham Rathod, Mr. Somnath Yadav, Mr. Abhijeet Shelar, Mr. Raju Mahajan, Mr. Tushar Wagh, Mr. Deepak Bhosale, Mr. Manoj Suryawanshi, Miss. Rekha Gondake, Miss. Shirin Pandit, Miss. Akhansha Dhapate, Miss. Rutuja Manugade, Miss. Mohini Jadhav, Miss. Shubhangi Ghodake, Mr. Dayanand Waghmode and Mr. Dhanraj Rathod. I am also thankful to B.Sc. (Agriculture) friends Miss. Mukta Aghav, Miss. Komal Mohite, Miss. Aboli Bansode, Miss. Priya Shinde, Miss. Dhanshree Bhandare and Juniors Miss. Madhuri Mali, Miss. Shivani Bhosale, Miss. Poonam Gadade, Miss. Kranti Kamble whose excellent company affection and co-operation helped me in carrying out my study with joy and happiness

I have no word to express my feeling towards my family but I make mention of my father **Mr. Shinde Satish Baburao** and loving mother **Mrs. Shinde Bharati Satish**. I express my deep sense of appreciation towards my paternal and maternal grandparents and brother **Mr. Sangram Shinde (Bhaiya)** and **Mr. Saurabh Shinde** for their never-ending love, constant encouragement blessing and eternal moral support which have brought my educational career to this stage.

I offer thanks to all those who have helped me directly and indirectly during the course of my study. I thank all the family of MPKV, Rahuri for giving me this opportunity as well as providing facility in time to complete my research work. Last but not the least I thank Almighty for the wisdom and perseverance that he has bestowed upon me during this research project, and indeed, throughout my life.

Place : MPKV, Rahuri

(S.S. Shinde)

Date : / /2020

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LIST OF ABBREVIATIONS

-	:	Minus
%	:	Percentage
Σe	:	Environmental variance
Σg	:	Genotypic variance
Σp	:	Phenotypic variance
/	:	Per
+	:	Plus
<	:	Less than
=	:	Equal
>	:	Greater than
@	:	At the rate
C.D.	:	Critical difference
C.V.	:	Coefficient of variance
cm	:	Centimeters
D	:	Divergence distance
DC	:	Divergence classes
DC 1	:	Divergence class 1
DC 2	:	Divergence class 2
DC 3	:	Divergence class 3
DC 4	:	Divergence class 4
d. f.	:	Degrees of freedom
EC	:	Exotic collection
<i>et al.</i>	:	et all (and others)
etc.	:	Etcetera
F ₁	:	First filial generation
F ₂	:	Second filial generation
F ₃	:	Third filial generation
F ₄	:	Fourth filial generation
F ₅	:	Fifth filial generation
Ft.	:	Feet/Foot
g.	:	Gram
GA	:	Genetic advance

GCV	:	Genotypic coefficient of variation
h^2 (b.s.)	:	Heritability in broad sense
ha.	:	Hectare
IC	:	Indigenous collection
i.e.	:	That is
K	:	Differential constant
Kg	:	Kilo gram
No.	:	Number
PCA	:	Path coefficient analysis
PCV	:	Phenotypic coefficient of variation
<i>per se</i>	:	Actual
R	:	Residual effect
S.E.	:	Standard error
<i>Via</i>	:	Through
<i>viz.,</i>	:	Videlicet (namely)
X	:	General mean

ABSTRACT

“GENETIC VARIABILITY AND GENETIC DIVERSITY STUDIES FOR YIELD AND YIELD CONTRIBUTING CHARACTERS IN QUINOA (*Chenopodium quinoa* Willd.) GENOTYPES”

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AGRICULTURE BOTANY

2020

Research Guide	: Dr. S.V. Pawar
Department	: Agricultural Botany
Major discipline	: Genetics and Plant Breeding

An experiment entitled, “Genetic variability and genetic diversity studies for yield and yield contributing characters in quinoa (*Chenopodium quinoa* Willd.) was carried out at Agricultural Botany Research Farm, Mahatma Phule Krishi Vidyapeeth, Rahuri - 413 722, Dist. Ahmednagar, Maharashtra (India) during *Rabi* season, 2019. The present investigation was undertaken to evaluate thirty diverse quinoa genotypes to estimate genetic variability, heritability and genetic advance, correlation coefficient, path analysis and genetic diversity.

The study involving thirty genotypes of quinoa was sown in a randomized block design (RBD) with three replications. Observations were recorded for nine characters *viz.*, days to 50 per cent flowering, days to maturity, plant height, branches per plant, inflorescence per plant, inflorescence length, inflorescence width, yield per plant, seed volume weight/10 ml.

Greater amount of variability was observed among the genotypes for all characters studied. The magnitude of genotypic coefficient of variation was lower than phenotypic coefficient of variation.

The GCV and PCV both were observed high for inflorescence per plant. However, moderate amount of GCV and PCV observed for branches per plant, inflorescence length, inflorescence width and seed yield per plant. The estimates of

heritability (b.s.) ranged from 76.09 to 95.55 per cent. The highest heritability was observed for days to maturity (95.55 %) followed by inflorescence per plant (90.80 %), days to 50 % flowering (89.84 %), branches per plant (88.44 %), inflorescence length (87.06 %), inflorescence width (86.60 %), seed volume weight/ 10 ml (81.25 %), seed yield per plant (76.36 %) and plant height (76.09 %). Therefore, it can be concluded that environmental effects are least on the characters studied. High heritability coupled with high genetic advance as percent mean was observed for branches per plant, inflorescence per plant, inflorescence length, inflorescence width and seed yield per plant.

The seed yield per plant showed significant and positive relationship at genotypic and phenotypic level with plant height followed by branches per plant, inflorescence per plant, seed volume weight/10 ml, inflorescence width and inflorescence length respectively. The seed yield per plant showed significant and negative correlation with days to 50 per cent maturity at genotypic and phenotypic level respectively and days to maturity significant at genotypic and non significant at phenotypic level. Branches per plant, Inflorescence per plant, inflorescence length, inflorescence width, yield per plant, seed volume weight/10 ml showed highly positive association with each other.

The path analysis revealed the character inflorescence width showed highest direct positive effect on seed yield per plant followed by plant height, seed volume weight/10 ml inflorescence per plant, days to 50 per cent flowering. Exhibited high direct effects in the desirable direction and also confirmed their strong association with seed yield per plant indicating, the true and perfect relationship between them and it suggested that, direct selection based on these characters would help in selecting the high yielding genotypes in quinoa.

Genetic divergence in 30 genotypes of the quinoa was measured following Mahalanobis's (1936) D^2 statistics. The 30 genotypes were grouped into eleven clusters. Cluster I was the largest cluster with 11 genotypes followed by cluster II with 7 genotypes, cluster V, IX, XI with 2 genotypes while, cluster III, IV, VI, VII, VIII and X were monogenotypic. The calculated D^2 values varied from 2.37 to 12.05 (Table 4.7).

The maximum intra cluster distance was observed for cluster XI and inter cluster distance was maximum between cluster X and V. Highest mean values showed by cluster IX for characters inflorescence length, inflorescence per plant, plant height, branches per plant. Cluster V showed highest mean values for days to 50 % flowering and days to maturity.

Out of 9 characters studied, the days to maturity showed maximum contribution to divergence followed by inflorescence width, branches per plant, days to 50 % flowering, seed volume weight/10 ml, inflorescence length, plant height, seed yield/plant and inflorescence per plant. The remaining characters did not contribute to divergence. Based on inter-cluster distance, intra-cluster distance and per se performance the genotypes *viz.*, EC-896097, EC-896108, EC-896212, EC-896209 and IC-411824 can be used for future breeding programme.

1. INTRODUCTION

Over past decades, agriculture has achieved monumental increase in food production but these have been paralleled by serious overuse of non renewable inputs and natural resources, loss of biodiversity and changes in lifestyle. Today, out of more than 7000 species used for food only four crops *viz.*, rice, maize, wheat and potato contribute over 60 per cent of calories obtained by human. This dramatic shrinkage of food basket brought a negative impact on nutrition security and dietary diversity, which caused the health related problems like micronutrient deficiencies or “hidden hunger”. Hence there is an urgent need to include a much wider range of crop species in current agriculture system and for this purpose “Neglected and Underutilized Crops” or “Orphan Crops” can be appropriate solution for above problems (Prescott-Allen and Prescott-Allen, 1990 and Amaya *et al.*, 2014).

Quinoa (*Chenopodium quinoa* Willd.) is a annual herbaceous species belonging to family *Amaranthaceae*, but formerly placed in *Chenopodiaceae* family, domesticated staple food in Andean South America. It is principally a grain crop harvested and consumed in a manner similar to that for cereal grain, although its leaves are also used as potherb. Quinoa was domesticated ancient Andean civilization in region surrounding the Bolivian and Peruvian altiplano. Nevertheless cultivation of quinoa extends to south central zone of Chile in fragmented pattern.

The plant belongs to a complex of allotetraploid taxa ($2n = 4x = 36$) which includes *Chenopodium berlandieri subsp. berlandieri*, *Chenopodium berlandieri subsp. nuttalliae*, *Chenopodium hircinum*, and *Chenopodium quinoa* (Gomez-Pando, 2015; Matanguihan *et al.*, 2015). It belongs to the *Amaranthaceae* (formerly *Chenopodiaceae*) family which includes other economically important plant species like spinach (*Spinaca oleracea*) and sugarbeet (*Beta vulgaris*) (Giusti, 1970; Maughan *et al.*, 2004 and Kadereit *et al.*, 2003).

Quinoa is a dicotyledonous plant species, very different from monocotyledonous cereal grains. fast-growing plant, grows up to 2 m tall with alternate, coarsely toothed, triangular to ovate leaves and is similar in appearance to the common North American weed (*Chenopodium album* called as lamb’s quarter or goosefoot). Quinoa plant is C_3 species with 90 per cent self-pollinating (Gonzalez *et al.*, 2011). Each

inflorescence produce hundreds of small achenes, around 2 mm in diameter. Quinoa is an achene (a seed-like fruit with a hard coat) with diversified colours ranging from white or pale yellow to orange, red, brown and black. Quinoa has greater plasticity of adaptation to photoperiod, altitude, soil pH etc. It can be grown from sea level to 3,900 meters above mean sea level and pH range of 6 to 8.5 and temperature from sub-tropical to tropical and humid areas. The base temperature of quinoa is 30⁰C with optimum temperature of 15⁰C to 30⁰C and can tolerate maximum temperature of 50⁰C. Quinoa seems to be a quantitative short day species where the length of the vegetative period depends not only on the day length and latitude of the origin but also on altitude of origin (Rishi and Galwey, 1989).

It is cultivated in the world with an area of 126 thousand hectares with a production of 103 thousand tonnes. In India, quinoa was cultivated in an area of 440 hectares with an average yield of 1053 tonnes in 2014-15 (Srinivasa Rao, 2014). Quinoa was successfully introduced in India in early nineties. Andhra Pradesh, Rajasthan and Uttarakhand are the major quinoa growing regions in India. It is estimated that quinoa is being cultivated on near about 3300 ha in 11 districts of Rajasthan including Bikaner, Bhilwara and Udaipur *etc.* during 2018 (Anonymous, 2018). Grain yield is a complex character and depends on number of component characters which are quantitatively inherited. As such before initiating any breeding programme, a thorough knowledge of nature and magnitude of genetic variability and extent of association between yield and other components is very essential. Growing period of quinoa varied between 70 to 200 days and some entries did not mature in some locations. The experiment conducted to evaluate quinoa entries in America, Europe and Africa and reported that growing period of quinoa in Kenya was 65-98 days and all cultivars matured with seed yield of 4000 kg/ha. In Denmark and Sweden, growing period was 120-160 days but yields were low and few varieties only matured. The growing period in Greece was 110-160 days and the yield was 2000 kg/ha (Jacobsen *et al.*, 2003).

Quinoa shows disomic inheritance for most qualitative traits and its small seed has excellent carbohydrate, fat, protein content balance and protein content sustainability higher than that of major cereal grains varying between 7.5 to 22 per cent. One of the report of United Nations Organisation for Agriculture and Food (2015) clearly noted that, the quinoa grain is the only vegetable food that provides ideal balance of eight essential amino acids essential to the life of humans in optimum quantities and is

comparable with milk. It contains high amount of Ca, Fe, Zn, Cu and Mn. The oil content is 1.8 to 9.5 per cent and rich in essential fatty acids like linoleate and linolenate (55-65 % of lipid fraction). In addition, quinoa seed is rich in thiamine (0.4 mg), folic acid (78.1 mg), vitamin C (16.4 mg), riboflavin (0.39 mg) and carotene (0.39 mg) in 100 g seed respectively. The calorific value is 350 cal per 100 g grains and is greater than that of other cereal and legume foods. The digestibility of quinoa protein is more than 80 per cent. In addition to above nutritional factors, the quinoa grain is soft, gluten free, gets cooked quickly and has a pleasant taste. Quinoa also contains natural antioxidants like α -tocopherol (5.3 mg), γ -tocopherol (2.6 mg) in 100 g seed and phytoestrogens that prevent chronic diseases such as osteoporosis, breast cancer, heart diseases and other feminine problems caused by lack of oestrogen during the menopause. Hence FAO nominated 2013 as International year of Quinoa (Bhargava *et al.* 2006). Quinoa is qualified as a functional food (Filho *et al.*, 2017; Abugoch, 2009) because its nutritional quality is superior to other grains like rice and wheat (Vilcacundo and Hernandez, 2017; Navruz-Varli and Sanlier, 2016).

India with experience of four revolutions since independence i.e., green revolution in Agriculture (rice and wheat), white revolution (milk), pharma (medicine) and information technology that lead India to the path of debt laden to self sufficiency. But still India tops in malnutrition with over 70 per cent pregnant women, 45 per cent among children and nearly 52 per cent population are suffering with diabetes due to over dependence on few cereal foods (rice or wheat). It is eroding the productivity of country by 4-6 per cent Gross Domestic Product (GDP) (Srinivasa Rao, 2014). Quinoa can be introduced in India to check malnutrition as well as to increase foreign exchange.

Quinoa has a significant worldwide potential as a new cultivated crop species and as an imported commodity from South America. The main uses of quinoa are for cooking, baking etc, various products for people are allergic to gluten, animal feed, animal fodder and pellets, modified products such as breakfast cereals, pasta and cookies. Industrial uses of starch, protein and saponin and as a game cover crop. In developing countries of Africa and Asia quinoa may be a crop able to provide highly nutritious crop under dry conditions. Population demand an increase in food production along with sustainable agriculture. There is need for cultivation of crops that require minimum input, but can counter the nutritional deficiency prevalent in general population of this region in developing countries. Quinoa can be termed underutilized, especially for India since

inspite of its wide adaptability, rusticity and nutritional superiority, its commercial potential has remained untrapped. Quinoa's highly proteinaceous grain can help to make diets more balanced in this region and can play an important role in combating silent hunger among poor population in India who have little access to protein rich diet. Quinoa's ability to produce highly protein grains under ecologically extreme conditions makes it important for diversification of future agricultural system.

In addition, quinoa has been mentioned as a potential new crop for NASA's controlled ecological life support system (CELSS), which utilizes plants to remove carbon dioxide from the atmosphere and to generate food, oxygen, and water for the crew of space missions (Schlick and Bubenheim, 1996). Quinoa is considered a multipurpose agro industrial crop (Galwey, 1993). The seed may be utilized for human food and in flour products and in animal feedstocks because of its high nutritive value.

Very little research work has been done on the adoptability and standardisation of package of practices of quinoa in India. Bhargava *et al.*, (2006) studied about genetic variability and adaptation in North India and reported that entries originated from inter- Andean valleys of Bolivia that are white or yellow in colour with small size are more adoptable than other entries. Andhra Pradesh Academy of Rural Development (APARD), Hyderabad initiated central funded project "Project Anantha" to improve the production and productivity and in turn net profit of farmers of Anantapur and tested quinoa as alternate crop to ground nut. They reported that quinoa (yellow colour entry) has taken 90-120 days and produced average yield of 760 kg/ha (APARD, 2014).

The main aim of quinoa breeders is the development of cultivars with high grain yield and quality components adopted to diverse agro climatic region, inspite of the immense nutritive importance of crop, not much work has been done for its genetic improvement leading to lack of many important aspects. Breeding a crop for new, diverse and targeted environment requires use of range of genotypes since it allows us to qualify interspecific variability in the base population plays a very important role in any crop breeding programme. It becomes imperative to compute variable present in material and its partitioning into genotypic, phenotypic and environment once. Improvement of yield requires an in depth knowledge of magnitude of variation present in available germplasm. The success of breeding programme means development superior varieties/ hybrids depends on the magnitude of genetic variability and heretability present in the source material. The extent of of variability is measured by GCV and PCV which provides

information about relative amount of variation in different characters. Since the estimates of variability alone will not be much use for selection based on phenotypic basis, genetic gain should also be considered. Estimation of genetic diversity and identification of superior genotype which are highly diverse can assessed as parent in hybridization programme to produce superior varieties/ hybrids.

Genetic diversity is one of the criteria for parents selection in hybridization programme. Plant characteristics advantageous for the adaptation of quinoa to other growth regions of the world are available but are scattered throughout the existing germplasm. Further breeding of quinoa in new regions should concentrate on uniformity, early maturity, high yield, quality aspects, and industrial uses of the seed and of specific ingredients. The ideal variety of quinoa for seed production would be one maturing uniformly and early. A growing period of less than 150 days would normally be regarded as beneficial. Quinoa should also have a consistently high seed yield and a low saponin content, and it should be short and non branching to facilitate mechanical harvesting. Size, shape, and compactness of the inflorescence may be important for the rate of maturation. A large open inflorescence will dry quicker after rain and in morning dew than a small, compact one, but it may also be prone to seed scattering. The availability of transgressive segregant in any breeding programme depends upon the diversity between the parents involved. The quantification of genetic diversity through biometric procedures such as Mahalanobis D^2 statistic has made it possible to choose genetically diversified parents. Recent work indicated that the Mahalanobis generalized distance (D^2 statistic) may be an efficient tool in the quantitative estimation of genetic diversity (Mahalanobis, 1936). The divergence analysis has a definite role to play in an efficient choice of divergent parents for hybridization to exploit maximum heterosis or transgressive segregants for improving grain yield.

Keeping all these aspects in view, the present investigation in which “Genetic variability and genetic diversity studies for yield and yield contributing traits in quinoa (*Chenopodium quinoa* Willd.) genotypes.” 30 genotype of quinoa subjected to diversity analysis with sowing in rabi season, 2019 with following objectives:

1. To study the genetic variability for yield and yield contributing traits in Quinoa.
2. To study the genetic diversity in Quinoa.

2. REVIEW OF LITERATURE

Success of any breeding programme depends on the availability of variation and selection practiced. The selection of elite genotypes requires the knowledge of quantitative traits. The present investigation is aimed at finding out statistical parameters *viz.*, genetic variability, correlation, path analysis, heritability, genetic advance and genetic diversity. Regarding quinoa, very limited literature is available, however, in present chapter attempt has been made to review the results obtained by earlier authors in quinoa. Literature collected has been reviewed under following sub headings.

2.1 Genetic Variability, Heritability and Genetic Advance

2.2 Correlation

2.3 Path Analysis

2.4 Genetic Diversity

2.1 Genetic variability, Heritability and Genetic Advance

Bhargava *et al.* (2007) carried out an experiment using 29 germplasm line of *Chenopodium species* and reported that phenotypic coefficient of variation (PCV) value for all the traits were higher than the corresponding genotypic coefficient of variation (GCV) values. In broad sense heritability was high and exceeded 80 per cent for all the traits. Genetic advance as per cent of mean (GAM) was highest for yield (140.19 %), followed by dry weight per plant (133.62 %), inflorescence length (102.08 %) and primary branches per plant (94.66 %). Seed protein showed lowest gain among quality traits (32.69 %) while for morphological traits the lowest value was for days to flowering (15.65 %) which is moderate GAM.

Rao *et al.* (2009) evaluated 121 quinoa accession for analysis of variability in some agronomic traits at Arabian peninsula and concluded that the genotype Ames 22157 was the earliest to flower (47 days) and Ames 13761 was the tallest, measuring up to 118 cm at maturity. Seed yield was maximum in genotype Ames 13761 (2.58 t/ha).

Miranda *et al.* (2012) studied agronomical and nutritional traits of six quinoa genotypes in three distinctive geographical zones of Chile and reported that plant morphology, particularly panical length and width, were significantly different between the northern and central-southern groups. They also observed that the central and

southern genotypes did not differ significantly ($P < 0.05$) for seed diameter and showed the lowest value for 1000 seed weight, whereas Ancovinto genotype showed lowest value of seed diameter (1.44 mm) and the highest value of 1000 seed weight (4.72 g). Protein content in quinoa genotypes was observed between 11.13 and 16.18 per cent.

Mhada *et al.* (2014) performed the variability analysis on a collection of seventy accessions for two successive years in Morocco. They evaluated twenty-three quinoa quantitative and qualitative characters for the genetic variability, relationship among the accessions and their statistical analysis showed highly significant differences between accessions for all the quantitative traits. Most plants were in midrange between 50 and 150 cm. There was also significant variation among accessions for harvest index and grain yield per plant, which varied from 8.0 to 67.0 per cent and 14.0 to 195.9 g, respectively.

Szilagyi and Jornsgard (2014) studied quinoa varieties for seed yield and some morphological traits and reported that under irrigated condition, seed yield range from 1.70 to 2.96 t/ha with Jason Red. Days to maturity ranges from 130 to 140 day and late maturity genotypes like Jacobson grew taller than the one that matured as early as Jason Red. The results also showed that the harvest index ranged from 44.52 -57.03 per cent with an average of 50.20 per cent.

Benlhabib *et al.* (2016) studied 72 accessions of quinoa and reported impressive transgressive segregation was measured for seed yield (22.42 g/plant), while plant height and maturity had higher heritabilities (73 and 89 % , respectively).

Curti *et al.* (2016) studied a set of 34 quinoa population in Argentina and concluded that traits like main stem branches, plant height and panicle length shown wide range of variability with coefficient of variation (CV) of 93.7, 44.2, 41.2 per cent, respectively.

De Santis *et al.* (2016) conducted an experiment on thirty *Chenopodium spp.* germplasm lines and reported that the harvest index, seed yield per plant and seed yield showed the wide range of variability (CV = 86.6, 75.5 and 72.7 %, respectively) followed by the dry matter yield and biological yield per plant (CV= 49.3 and 47.3 %, respectively). Heritability estimates were relatively high for almost all of the traits, except for plant height at maturity and seed protein (33 and 57 %, respectively). Genetic advance as per cent of mean (GAM) was maximum for seed yield per plant (118.8 %), followed by seed yield (11.5 %) and harvest index (109.3 %). Seed protein showed the

lowest GAM (8.27 %) while, for the morphological traits the lowest GAM was observed for days to flowering (18.0 %) which is moderate GAM.

Vasconcelos *et al.* (2016) analysed genetic parameters and productivity of quinoa genotypes in two different environments and reported a significant difference among genotypes from the analysis of variance. High heritability (80.01 %) with low GCV (2.19 %) were observed for the maturity period whereas plant height was recorded with moderate heritability (71.68 %) and GCV (15.05 %) in combined analysis.

Al-Naggar *et al.* (2017) performed an experiment on five quinoa genotypes for two successive seasons. Experimental results revealed that quinoa genotypes varied greatly in days to flowering (56.6 to 60.8 days), days to maturity (127.7 to 134.1 days), inflorescence length (11.1 to 16.0 cm), plant height (48.8 to 57.0 cm), seed yield per plant (14.8 to 29.9 g) and test weight (1.8 to 3.6g) under severe water stress. Maximum predicted genetic advance from selection was achieved from inflorescence per plant (101.87 %) followed by primary branches per plant (68.04 %), test weight (62.10 %) and seed yield per plant (56.02 %) under severe water stress.

Maliro *et al.* (2017) evaluated eleven diverse varieties of quinoa in Malawi and reported that highest yielding genotype was Black Seeded (2050 kg/ha) followed by Multi Hued (1603 kg/ha) and BioBio (1446 kg/ha). Ecuadorian was slowest to reach at maturity (112 to 119 days), while mean maturity period length for rest of the genotypes was lies between 101 and 103 days.

Naneli *et al.* (2017) explored seven quinoa genotypes at two different locations (Tokat and Amasya) and concluded significant differences among the genotypes in terms of the characters observed. Number of panicles per plant showed maximum coefficient of variation (CV) in both the regions (4.67 and 4.69, respectively). The difference among the genotypes in terms of main panicle length was found to be significant at 1 per cent in both loci, ranging between 12.5 to 34.0 cm at Tokat location and 13.4 to 35.5 cm at Amasya location. From the combined analysis, the maximum grain yield was obtained from Ames genotype (460.5 kg/ha) and lowest from the Black genotype (133.8 kg/ha).

Reguera *et al.* (2018) evaluated three quinoa cultivars (Salcedo INIA, Titicaca and Regalona) at different locations (Spain, Peru and Chile) and reported that most of the morphological traits varied with the location and among cultivars. Titicaca showed the shortest time to flowering and maturity at both locations (Chile and Spain),

followed by Regalona. Salcedo-INIA presented the longest time to flower and mature (95 and 184 days, respectively) in Spain and Chile. The range of total protein content was found between 14 and 17 per cent among the cultivars.

2.1.2 Genetic variability, heritability and genetic advance in related crops

Bezawele et al. (2006) studied total 66 finger millet accessions constituted of 64 landraces and 2 standard varieties and evaluated for 15 morphoagronomic characters in randomized complete block design with three replications of Aresi-negele research sub centre in Ethiopia during 2004. The main cropping season objects were to access variability and association of characters. For all characters phenotypic and genotypic coefficient of variation varied in order of 8.05-31.23 per cent and 6.22-24.21 per cent in both cases for days to maturity and grain yield/plant, respectively. Existence of variability for characters studied in finger millet and potential characters used in genetic improvement.

Kusuma et al. (2007) observed high GCV and PCV for panicle length, dry weight of panicle, dry weight of stem, harvest index and seed yield in grain amaranth. Low PCV and GCV were reported for days to 50 % flowering and days to maturity whereas moderate PCV and GCV for plant height and girth. High heritability and GAM recorded for panicle length, dry weight of panicle and dry weight of stem, while, moderate heritability and GAM for days to 50 % flowering, maturity and stem girth. However, high heritability and moderate GAM were reported for plant height, harvest index and grain yield.

Sumathi et al. (2010) conducted a field trial 47 pearl millet genotypes and reported that the phenotypic coefficient of variation (PCV) was greater than genotypic coefficient of variation (GCV) for all the characters studied. This shows the influence of the environmental effect on the characters. The traits, number of tillers per plant, ear head length, root-shoot ratio and seed yield showed moderate PCV and GCV, while, the traits, days to 50 % flowering, plant height, ear head breadth, root length and shoot length showed low PCV and GCV. High heritability was observed for all the traits under study. High heritability combined with high genetic advance (as per cent of mean) was observed for ear head length and seed yield and these characters were controlled by additive gene effects.

Varalakshmi and Devaraju (2010) conducted an experiment to study the genetic variability in Indian spinach (*Basella alba* L.) with eleven germplasm lines. They

reported that phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the traits studied. Moderate heritability along with high genetic advance also observed for leaf weight and total plant weight, indicating the presence of additive gene action.

Smitha and Krishnakumar (2011) evaluated genetic variability in twenty three grain amaranth accessions and reported that the genotype GA 31 exhibited maximum plant height (138 cm) and yield per plant (209 g). Highest number of branches per plant (18) and grain yield per plant (128g) was observed in “GA-25”. The study showed that phenotypic coefficient was higher than genotypic coefficient of variation for most of the traits and it was ranged from 12.64 to 49.83 per cent. High genotypic coefficient of variation with high heritability and genetic advance were recorded for grain yield and plant height at flowering.

Ahammed *et al.* (2012) observed the highest PCV (87.85 %) and GCV (81.67 %) for primary branches per plant while the lowest PCV (10.28 %) for plant height and the lowest GCV (7.51 %) for leaf width in variability study on amaranthus. Heritability estimates in broad sense were higher for leaf weight per plant (91.10 %) followed by leaves per plant (86.83%), primary branches per plant (86.42%), stem weight per plant (82.56%) and yield per hectare (78.70%). Leaf weight per plant, stem weight per plant and yield per hectare exhibited high heritability (91.10, 82.56 and 78.70 %) along with high genetic advance (49.38, 134.12 and 56.00 %), respectively.

Chander Parkash (2012) conducted a research on sixty indigenous and exotic germplasm lines of bathua (*Chenopodium album*) for estimation of genetic variability. The research results revealed that the phenotypic coefficients of variation were higher than genotypic coefficients of variation for all the characters. The estimates of genotypic coefficient of variation were higher for number of leaves per plant (46.75 %), followed by leaf width (47.07 %) and leaf yield per plant (46.43 %). High heritability estimates coupled with high genetic advance were observed for traits, i.e. plant height, number of leaves per plant, leaf length, leaf width and leaf yield.

Sravanthi *et al.* (2012) studied forty germplasm lines of *Amaranthus species*. They showed significant GCV among the genotypes for all the characters viz., days to 50 % flowering (33.4 %), plant height (28.15 %), number of branches per plant

(26.10 %), inflorescence length (63.81 %), days to 80 % maturity of seed (20.13 %), test weight (37.54 %), protein content (18.53 %), dry matter content (64.00 %) and seed yield per plant (44.59 %). The result also showed high estimates of heritability along with high GAM for all the tested characters.

Akaneme and Ani (2013) evaluated five accessions of the *Amaranthus hybridus* in the field and observed high PCV and GCV for plant height and 50 % flowering, whereas low PCV and GCV for stem diameter and test weight. Low heritability observed for plant height, 50 per cent flowering and stem diameter whereas high heritability for test weight.

Hasan *et al.* (2013) reported that the differences between GCV and PCV were high for leaf length and stem diameter indicating the vulnerability of traits to environmental influences in amaranthus. High GCV and PCV were observed for leaf weight (77.54 and 80.14 %, respectively). They also noticed high heritability with high genetic advance for number of leaves, leaf weight and marketable yield.

Ramesh *et al.* (2013) evaluated ten genotypes in *Amaranthus hypochondriacus* L. and reported high PCV and GCV for leaf area at 50 % flowering, length of inflorescence, grain yield, carbohydrates and protein content. Medium PCV and GCV observed for plant height, days to 50 % flowering and diameter of the inflorescence whereas high heritability and GAM for all the traits.

Subi and Idris (2013) evaluated fifteen genotypes of pearl millet (*Pennisetum glaucum* L. R. Br.) and observed highly significant differences for genotypes and genotypes $\times$ seasons interaction for days to 50 % flowering and days to maturity. In general phenotypic coefficients of variation (PCV) estimates were higher than genotypic coefficients of variation (GCV) estimates for all the studied characters in all genotypes displaying the influence of environment effect on the studied characters. The combined results for heritability showed that the high estimates of heritability and genetic advance were scored for days to 50 % flowering and days to maturity indicating that these characters were under the control of additive genetic effects.

Parveen *et al.* (2014) found that phenotypic coefficients of variation in *amaranthus species*, was higher than genotypic coefficients of variation for all the characters and this indicate high influence of environment on the expression of these traits. PCV was highest for the character leaves per plant at 60 days and lowest for number of branches per plant in 90 days. Leaves per plant in 60 days (51.41 %) and

number of branches per plant in 90 days (39.12 %) showed high estimates of GCV. Length of petiole in 60 days (18.98 %) and Leaf width in 60 days (18.66 %) showed moderate estimates of GCV.

Sarker *et al.* (2014) conducted a trial on forty three vegetable amaranth (*Amaranthus tricolor* L.) genotypes and reported high range of variability with high genotypic variance for like plant height, leaves per plant, diameter of stem base, leaf area and foliage yield per plot. Slight differences between genotypic and phenotypic variances and genotypic and phenotypic coefficient of variations were also observed for all the traits.

Venkatesh *et al.* (2014) carried out an experiment on one hundred genotypes of grain amaranth for analysis of variability and heritability. They reported that highest value of PCV and GCV for grain yield per plant (63.08% and 55.96%, respectively) followed by stem girth (50.94 and 47.86 %, respectively), panicle length (37.57 and 31.67 %, respectively) and plant height (31.76 and 25.73 %, respectively). All the traits studied exhibited high heritability. High genetic advance as per cent of mean was observed for days to 50 % flowering.

Yadav *et al.* (2014) evaluated genotypic variability and character association in twenty seven grain amaranth genotypes and reported that traits *viz.*, plant height, petiole length, leaf blade length, inflorescence length, test weight, daysto 50 % flowering and days to physiological maturity show moderate GCV and PCV values. The characters like leaf blade width, lateral spikelet length and grain yield per plant showed high GCV and PCV values. Genotypic coefficient of variation for different characters ranged from 11.60 to 42.73 per cent. The highest GCV was recorded with grain yield per plant (42.73 g) followed by leaf blade width. The lowest GCV was observed for test weight (11.70 g).

Sheelamary and Phogat (2016) conducted an experiment using 100 genotypes of grain amaranthus for analysis of variability and reported wide range of variability for the traits days to 50 % flowering (51-75 days), plant height (32.0-115.6 cm) and inflorescence length (16.4-61.6 cm). Seed yield per plant (95.18 %) was recorded with highest PCV followed by lateral spikelet length (47.30 g), plant height (42.03 %), inflorescence length (39.74 %), hundred seed weight (28.58 %) and days to 50 % flowering (27.06 %). The extent of heritability was high for all the characters

whereas genetic advance as Percentage of mean was recorded high for the characters days to 80 % maturity (50.50 %) and 100 seed weight (33.12 %).

Anuradha *et al.* (2017) analysis of variance of 25 finger millet advanced breeding lines revealed significant variation for all the traits studied. The present findings implies the presence of larger variability for yield and other related traits which can be exploited in finger millet improvement.

Diwan *et al.* (2017) conducted an experiment on ten genotypes of *Amaranthus tricolor* and observed high magnitude of GCV as well as PCV for traits leaf weight (35.01 and 35.63 g), leaf length (19.69 and 24.50 %) and internodal length (18.46 and 22.99 %) suggested the substantial improvement on spp., through selection for these traits. They also reported high heritability coupled with high genetic advance for number of leaves per plant, leaf width and leaf weight indicating that most likely the heritability is due to additive gene effects and selection may be effective.

Lokeshkumar and Murthy (2017) conducted an investigation on 105 genotypes of grain amaranth at Hebbal, University of Agricultural Sciences, Bengaluru. The analysis of variance revealed significant difference among the genotypes for most of the traits except the traits like panicle width and 1000 seed weight. Genotypes showed wide range of variation from 29 to 44 days for 50 per cent flowering, 79 to 100 days for maturity period, 23.37 to 140.72 cm for plant height and 7.33 to 32.33 g for grain yield per plant. Low GCV and PCV observed for plant height, dry weight of stem, total dry weight, dry weight of panicle, dry weight of leaf, harvest index, plant height and grain yield had high heritability with high genetic advance.

Devaliya *et al.* (2018) comprised 68 diverse genotypes of finger millet (*Eleusine coracana* (L.) Gaertn). The data on 13 quantitative traits were recorded to assess the magnitude of genetic variability, heritability and genetic advance for yield and yield contributing traits. In the present investigation, values of phenotypic coefficients of variability were greater than genotypic coefficients of variability for all the traits studied. High heritability along with high genetic advance (% of mean) observed for grain yield per plant, number of productive tillers per plant, straw yield per plant and main earhead length, indicating involvement of additive gene action for these traits and phenotypic selection based on these traits in the segregating generations would likely to be more effective.

Patel *et al.* (2018) thirty two genotypes of little millet were studied for genetic variability at Hill Millet Research Station in randomized block design for different morphological and biochemical traits. In the present study the high heritability coupled with high genetic advance was observed for number of productive tillers per plant, grain yield per plant, straw yield per plant, 1000 seed weight, protein content, ash content, fat content, calcium content, iron content and fiber content which, indicated that these characters are largely governed by additive genes and selection for improvement of such characters could be rewarding. The hybridization program between the divergent mutant lines GE 2-2 or GE 3-4 with GG 3-1 is expected to give promising and desirable segregants in subsequent generations. Traits such as days to 50 % flowering and days to maturity had major contributions to the induced genetic divergence.

Tiwari *et al.* (2018) performed a research work on fifty four genotypes of grain amaranth including four checks for variability analysis and reported that differences among the entries were highly significant for days to 50 % flowering, days to maturity, plant height, inflorescence length, and non-significant for test weight and seed yield per plant.

Singamsetti *et al.* (2018) in a field study evaluated 13 elite entries of finger millet to assess the magnitude of genetic variability, heritability and genetic advance for yield and yield attributing traits. The analysis of variance revealed that there were significant differences among the entries for all the traits studied. The genetic parameters revealed that moderate to high variability coupled with high heritability and high genetic advance as per cent of mean were observed for days to 50 % flowering, plant length (cm), number of tillers per plant, number of fingers per ear and main ear length (cm) suggesting the predominance of additive type of gene action in controlling these traits. These results indicating the operation of additive gene action in the inheritance of these traits and improvement of these characters is possible through simple selection

2.2 Correlation coefficient analysis

Galton (1889) developed basic concept of correlation, later elaborated, and discussed by Fisher (1918) and Wright (1921) in plant breeding programmes. In genetic studies, plant breeders are generally concerned with two types of correlation i.e. (1) phenotypic correlation (11) genotypic correlation. The association between two characters that can be observed directly is the phenotypic correlation. It is the artefact

of both genotypic and environmental effect on the expression and ultimate association of two characters. Association of characters, which is statistically determined by correlation coefficient, has been quite useful as a basis of selection. Improvement of any crop needs better understanding of association between yield and yield attributes. Correlation coefficients can range from (-1) to (+1). The value of -1 represents a perfect negative correlation while +1 represents a perfect positive correlation. Selection for one character would result in association of characters, which is statistically determined by correlation coefficient, has been quite useful as a basis of selection. Improvement of any crop needs better understanding of association between yield and yield attributes. This relation suggests the advantage of a scheme for more than one character at a time. If negative correlation exists between components of yield, then selection is to be done for intermediate combination for improvement of yield.

2.2.1 Correlation studies in quinoa

Jacobsen *et al.* (1996) reported that the grain yield had a positive association with plant height, length and diameter of inflorescence, and maturity period. Selection for lateness has resulted in more genotypes that are productive.

Rojas (2003) analysed 1512 accessions of quinoa for their diversity and reported significant correlation among branches per plant, panicle length, and panicle per plant suggesting that plants with good branching habit tend to develop a large number of long inflorescences. Panicle length was also positively associated with plant height indicating that lines with greater plant height also developed longer panicles. The positive correlations also observed between days to maturity and plant height ($r : 0.56$) while, harvest index showed negative and significant association with days to maturity ($r : -0.55$).

Spehar and Santos (2005) reported that inflorescence length and diameter were positively associated with grain yield, which indicates that selection by these characters may result in genotypes that are more productive. Positive correlation between plant height and inflorescence length suggests that high grain held can be attained by selecting for stem/inflorescence ratio. Stem diameter was also positively correlated with grain yield and biological yield.

Bhargava *et al.* (2007) reported that grain yield per plant showed positive and significant correlation with plant height ($r = 0.507$), test weight ($r = 0.491$), dry weight per plant ($r = 0.486$), primary branches per plant ($r = 0.417$) and harvest index

($r = 0.267$). Grain protein showed moderate to low genotypic correlation with all the morphological traits, including grain yield per plant ($r = 0.017$) indicating that all these traits negatively influence protein content in the seed. Traits like days to flowering, days to maturity, plant height, primary branches per plant, panicle length and dry weight per plant showed positive association amongst themselves.

Fuentes and Bhargava (2011) noticed high correlation between stem diameter and plant weight, stem diameter and plant height, plant weight and plant height, plant weight and inflorescence length, plant height and inflorescence length and leaf length and leaf width. Harvest index showed negative association with stem diameter, plant height, inflorescence length, inflorescence width and inflorescences per branch.

Mhada *et al.* (2014) also observed highest positive significant correlation between the seed yield and biological yield ($r = 0.67$) followed by days to maturity and plant height at harvest ($r = 0.64$), days to flowering and plant height ($r = 0.40$) and seed yield and days to early flowering ($r = 0.34$). Negative correlation was found between harvest index and fresh biomass ($r = -0.52$).

Szilagyi and Jornsgard (2014) also reported that the seed yield had significant and positive association with plant height, days to maturity, biological yield and harvest index in quinoa. The maximum value of correlation coefficients was recorded for days to maturity ($r = 0.863$) and the minimum value was exhibited for harvest index ($r = 0.492$) with seed yield. Besides this, they noticed negative correlation of harvest index with days to maturity.

Benlhabib *et al.* (2016) also reported that seed yield was positively correlated with panicle length and biomass.

Curti *et al.* (2016) also reported that out of the 136 correlation coefficients evaluated, 30 showed highly significant associations ($P = 0.01$) with an ($r = 0.4$) and 21 exhibited significant associations ($P = 0.05$) with a 0.35 ($r = 0.49$)

De Santis *et al.* (2016) also reported genotypic correlation among the various traits in quinoa. Seed yield per plant had positive correlation with days to flowering, test weight, biological yield per plant and harvest index. Harvest index was positively correlated to days to flowering and 1000 seed weight while negatively correlated to plant height ($r = -0.22$ and -0.55 , respectively) at flowering and maturity. Seed protein content showed significant negative association with almost all of the morphological traits except plant height at both flowering and maturity.

Long Nguyen (2016) also concluded that particle length is a yield component in quinoa and significant variation in this parameter may entail significant grain yield differences in quinoa.

Maliro *et al.* (2017) evaluated eleven diverse varieties of quinoa in Malawi and reported that there were strong positive correlation between seed yield and characters like plant height ($r = 0.74$), days to maturity ($r = 0.76$) and biological yield ($r = 0.87$) in irrigated condition. Plant height was strongly correlated to seed yield ($r = 0.74$), biological yield ($r = 0.80$) and days maturity ($r = 100.76$) but showed no association with the harvest index.

2.2.2 Correlation studies in related crops

Shukla and Singh (2003) conducted an experiment on character association studies in grain amaranth (*Amranthus spp.*) taking sixty-six genotypes at Lucknow. They have concluded that the genotypic correlation was generally higher than the corresponding phenotypic correlation. At the phenotypic level, significant and positive association was observed between plant height and number of primary branches per plant and number of nodes per plant and leaf size. Leaf size was positively associated with all the characters except inflorescence length.

Kusuma *et al.* (2007) evaluated sixty-four accessions of grain amaranth (*Amaranthus spp.*) for quantitative traits and noticed that genotypic correlations were slightly higher than the phenotypic correlations. Seed yield exhibited significant and positive association with panicle length, number of spikes per panicle, dry weight of panicle, dry weight of stem and harvest index.

Pan *et al.* (2008) reported that the genotypic correlation coefficients were higher in magnitude than the phenotypic correlation coefficients in *Amaranthus species*. Leaves per plant, stem diameter, stem weight per plant, leaf weight per plant and plant height exhibited highly significant positive correlation with yield per hectare both at genotypic and phenotypic level.

Ahammed *et al.* (2012) was observed highly significant positive correlation of traits like leaves per plant, stem diameter, stem weight per plant, leaf weight per plant and plant height 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.

Chander Parkash (2012) concluded that the genotypic correlation coefficients were in general higher in magnitude than the corresponding phenotypic correlation coefficients in bathua. All the characters were positively correlated with leaf yield but significant and positive correlation with leaf yield were shown only by plant height and number of leaves per plant.

Shankar *et al.* (2012) reported that yield per plot had a significant positive correlation with leaf length ($r = 0.44$), leaf width ($r = 0.51$), stem weight ($r = 0.98$), leaf weight ($r = 0.94$), number of leaves per plant and shoot weight ($r = 0.98$).

Hasan *et al.* (2013) carried out an experiment to study the correlation coefficient of 17 stem (*Amaranthus tricolor* L.) genotypes. The genotypic correlation coefficients were higher than the phenotypic correlation coefficients but difference between them, was in general low indicating that the environmental effects did not have much influence on the characters.

Khurana *et al.* (2013) conducted an experiment for correlation study of quantitative characters and concluded that plant height was positively correlated with number of branches per plant (0.649), leaf length (0.3381), leaf width (0.4195), number of leaves per plant (0.525), leaf area index (0.560) and total green yield. While number of leaves per plant was positively correlated with leaf area index (0.921) and total green yield (0.953). Leaf area index was positively correlated with total green yield (0.966). Total green yield exhibited highly significant and positive correlation with plant height, number of branches per plant, leaf length, leaf width, number of leaves, and leaf area index both at genotypic and phenotypic levels.

Yadav *et al.* (2014) reported that at genotypic level, seed yield per plant showed highly significant positive correlation with days to 80 % maturity ($r = 0.696$) and plant height ($r = 0.403$) and significant positive correlation with days to 50 % flowering ($r = 0.38$) whereas rest of the characters showed non-significant correlation in grain amaranth genotypes.

Sarker *et al.* (2014) found that the biological yield had significant positive correlation with leaf area ($r = 0.326$), shoot weight ($r = 0.999$) and stem base diameter ($r = 0.368$) in vegetable amaranth.

Venkatesh *et al.* (2014) carried out an experiment on 100 genotypes of grain amaranth for character association. They computed phenotypic correlation coefficient among ten characters of grain amaranth and concluded that grain yield is

positively and significantly associated with number of leaves per plant ($r = 0.760$), stem girth ($r = 0.455$), plant height ($r = 0.531$) and panicle length ($r = 0.525$).

Hailu *et al.* (2015) from a correlation study reported less value of phenotypic correlation coefficient than the genotypic correlation coefficient in most of the characters. The green leaf yield per plant showed a positive and significant relationship with the majority of the traits except lateral inflorescence, which had negative significant association with green leaf yield in vegetable amaranth.

2.3 Path coefficient analysis

Path coefficient analysis is simply a standardized partial regression coefficient which splits the correlation coefficient into the measure of direct and indirect effects. It helps to elucidate the intrinsic nature of the observed association for complex characters like yield. Wright (1921) coined the term path coefficient and gave the theory of path analysis on the basis of standardized partial regression analysis. Li (1956) gave a detailed account of both basic and applied aspect of path coefficient analysis by means of formulating a path diagram of cause effect relationship showing the inter-relationship of variables under study. Dewey and Lu (1959) for the first time applied the technique of path coefficient to plant breeding and reported that it provides important information about the specific forces acting to produce a particular correlation. They partitioned the total correlation coefficient into direct and indirect effect and assigned the values of path coefficient contributing to yield which help to ascertain with much more precision and clarity the complex association in the selection programme.

2.3.1 Path analysis in quinoa

Bhargava *et al.* (2007) reported that the test weight (1.057) had highest positive direct relationship with seed yield, followed by total chlorophyll (0.559) and branches per plant (0.520). Some traits showing high negative direct effect were leaf carotenoid (-0.749), seed size (-0.678) and days to flowering (-0.377). Among the quality traits, seed protein showed negative indirect effect on seed yield through all the traits barring harvest index and seed carotenoid, though the values of indirect effects were small.

2.3.2 Path analysis in related crops

Shukla *et al.* (2010) reported that the agronomic traits, plant height (0.12), stem diameter (0.21), leaves per plant (0.45) had substantial positive direct effects on

foliage yield, while, characters like branches per plant (-1.22) and leaf size (-0.27) showed negative direct effect on foliage yield in vegetable amaranth (*Amaranthus tricolor*).

Varalakshmi and Devaraju (2010) noticed that the leaf number had the maximum direct positive effect on total plant weight, followed by leaf length. Indirect effects of other characters through these characters were also seen to be positive. Thus, emphasis should be on indirect selection through leaf characters like leaf number, leaf length and leaf weight for yield improvement in *Basella spp.*

Chander Parkash (2012) from a path analysis study, observed that the number of leaves had highest direct effect (0.6279) on leaf yield, followed by leaf length (0.1728) and suggested that direct selection could be made for these characters for improving leaf yield. Further, plant height showed maximum positive indirect effect (0.2084) *via* number of leaves towards leaf yield hence simultaneous selection for number of leaves per plant and plant height can be made for the improvement of leaf yield in bathua.

Hasan *et al.* (2013) from the result of path analysis indicated that stem weight had maximum direct effect on marketable yield followed by leaf weight and leaf number in vegetable amaranth.

Khurana *et al.* (2013) reported that the number of leaves per plant had highest positive direct effect (0.4933) on total green yield followed by leaf area index (0.4268), leaf length (0.0986), plant height (0.0915), leaf width (0.0487) and protein content (0.0208) in amaranth. The indirect effect of leaf area index on total green yield was highest (0.4543) in positive direction *via* number of leaves per plant.

Sarker *et al.* (2014) based on path coefficient values, reported that direct selection through three traits i.e., leaf area, diameter of stem base and leaf weight would significantly improve the foliage yield of vegetable amaranth.

Venkatesh, *et al.* (2014) carried path coefficient analysis in grain amaranth and revealed maximum positive direct effect of number of leaves per plant (0.575) on grain yield followed by seed weight (0.234), panicle length (0.221) and plant height (0.124). This result suggests that selection of varieties with higher number of leaves, seed weight and panicle length will help to select the genotypes which can give better grain yield.

Hailu *et al.* (2015) observed positive direct effects of leaf area, leaf width and plant height on biological yield per plant in vegetable amaranth.

2.4 Genetic Diversity

Genetic diversity is the genetic differences as observed between the individuals or genetic stocks with respect to individual trait or an array of traits. It is a result of inheriting genetic variation present in the germplasm. The knowledge of nature and degree of genetic divergence is useful in selecting the desirable parents for breeding programme. The genetic divergence enables the evaluation of genotypes without crossing and grouping the genetic material into few clusters in a significant pattern.

Mahalanobis (1936) described D^2 statistics as a tool for quantitative estimates of genetic divergence between the populations. Rao (1952) suggested more flexible method, which would replace the measurement of large number of characters, all of which contribute in some degree towards discrimination by relatively few measurements. Application of original concept of D^2 statistics of Mahalanobis (1928) for assessment of genetic diversity in plant breeding was suggested by Rao (1952). Allard (1961) studied relationship between diversity and consistence of performance in different levels of environment with three distinct genetic diversity levels. They found that genetic diversity and productivity were complete related and many other factors determined the productivity of mixed population. The genetic diversity and stability were correlated irrespective of components involved. Moll *et al.* (1962) reported genetic diversity and its reflection in expression of heterosis in maize. Murthy and Arunachalan (1966) revealed that geographical distribution and genetic diversity could not be directly related in any of the crops.

2.4.1 Genetic diversity in quinoa crop

Risi and Galwey (1989) measured the discrete and continuous characteristics related to plant morphology and pigmentation and the duration of developmental phases in a diverse collection of quinoa germplasm. A hierarchical cluster analysis of all characteristics confirmed that the variety amarilla de Marangani was unusual, but otherwise did not produce clear clusters. Accessions from near sea level I Chile formed a particularly homogenous group. The impossibility of describing the variation in term of a few axes or clusters means that a vast range of combinations of characteristics is available to breeders.

Rojas (2003) determined genetic diversity of quinoa and evaluated morphological traits and agronomical performance were evaluated during 1992-1993 and 1993-1994. About 92 per cent of the accessions were readily classified into seven groups identified by cluster analysis. The Mahalanobis distance D^2 method was used to show their statistical differences. Even incorrectly classified accessions were identified and reassigned to more appropriate group.

Bhargava *et al.* (2007) evaluated twenty nine germplasm lines of *Chenopodium quinoa* and two of *Chenopodium berlandieri subsp. nuttalliae* for 12 morphological and 7 quality traits for two test seasons. The 19 traits were analyzed for cluster and principal component analysis. All the germplasm lines were grouped into six clusters based on average linkage method. Cluster III had high values for seed yield and most of the quality traits but showed a small seed size. The dendrogram separated the two lines of *C. berlandieri subsp. nuttalliae* from the quinoa lines.

Rodriguez *et al.* (2009) evaluated comparative analysis of genetic and morphological diversity among quinoa accessions of south of Chile and highland accessions, 14 accession of quinoa collected in Araucania and Los angeles region, 3 Andean accession and one commercial cultivars were analyze with this tools, it was possible to indentify molecular differences and similarities that might be associated with morphological traits such as grain color, panical color and phenology.

Mhada *et al.* (2014) the present work has been carried out to evaluate the diversity of a collection of 78 quinoa accessions. Twenty-three quantitative and qualitative characters were used for the evaluation of genetic diversity and the relationship between the accessions, and also for the establishment of a core collection in Morocco. Hierarchical cluster analysis rearranged the 78 quinoa accessions into four main groups and ten sub-clusters. Clustering was found in associations with days to maturity and also with plant size and seed-size traits

2.4.2 Diversity in other related crops

Singh and Gupta (1979) studied genetic diversity using D^2 analysis in 34 bajara (*Pennisetum typhoides* L.) strains obtained from different parts of country, was in two different environments differing in level of fertility. Thirteen characters involving leaf, tiller, seed and other yield characters were used. There was considerable diversity in the material analysed. The diversity was more fully expressed in normal environment with fertilizer as compared to the environment without fertilizer.

Sherief and Shivshankar (1992) studied 225 genotypes of foxtail millet subjected to multivariate analyses through Mahalanobis D^2 statistical analysis. Analysis suggested the existence of considerable divergence among the material. D^2 statistic resulted in 33 clusters. Genetic divergence has not been found to be related with geographical diversity.

Yadav *et al.* (1994) fifty two pearl millet accessions of Indian and exotic origin were evaluated for genetic divergence. The accessions were grouped in ten clusters. Cluster I had approximately half of all the accessions. The genotypes in cluster I were early and had higher threshing ratio and seed weight, while those in clusters IV and V showed quick early growth. The clustering pattern indicated that the geographic diversity was not necessarily related with genetic diversity. Seedling vigour, productive tillers and plant height have been identified as potent variables which can be used as parameters while selecting diverse parents for hybridization programmes.

Vadivoo *et al.* (1998) analyzed 36 genotypes of finger millet (*Eleusine coracana*) with varying seed colors revealed a wide range of protein and calcium contents. Mahalanobis D^2 analysis grouped 36 genotypes into 8 cluster. Clustering pattern failed to indicate any relationship between genetic diversity and geographical diversity. Based on genetic divergence performance CO13, MS174 suitable for use as parent in hybridization programme.

Shanmuganathan *et al.* (2006) evaluated genetic diversity in pearl millet (*Pennisetum glaucum*) with 104 germplasm accessions of different origin. Analysis of variance indicated significant variances among the accessions for all the characters studied. Based on the D^2 analysis all the accessions were grouped into twelve clusters. Cluster I retain the maximum accessions of 82 and nine clusters retained only one accession each. The intra cluster distance ranged from 0.00 to 6.71 and the inter cluster distance was recorded highest between cluster XI and cluster XII. Cluster XII exhibited maximum mean value for five characters. Based on the relative contribution, plant height contributed more towards genetic divergence.

Obah (2009) evaluated 16 accessions of *A. hybridus* in field experiment at the biological garden of the University of Lagos. Data was collected on 22 quantitative and visually assessed characters which include leaf length, leaf width, number of days to 1st floral budding, days to 50 % flowering, seed length and width and 500 seed weight. Data was analyzed using various statistics which included mean, standard deviation, correlation and cluster analysis. Results showed a wide range of diversity in most of

quantitative characters assessed with variability in plant height ranging from 74.30 -181 cm, leaf length from 13.90-29.40 cm and leaf width from 7.00 - 12.40 cm. The accessions were further classified into four district groups with the accessions in each group demonstrating similar characteristics. Accessions within groups are closely placed in the dendrogram and showed promise for used in cultivar development. The district group could serve as breeding line for genetic improvement of *A. hybridus* through cross breeding.

Kumar *et al.* (2010) conducted an experiment with 140 diverse genotypes of finger millet (*Eleusine coracana* L. Gaertn.). The data on 10 quantitative traits, non-hierarchical Euclidean cluster analysis, all the 140 genotypes of the present study were grouped into ten non-overlapping clusters. Maximum number of genotypes (31) were included in cluster I followed by 28 genotypes in cluster V, 19 genotypes in cluster III, 14 genotypes each in clusters II and VIII, 11 genotypes in cluster VII, 10 genotypes in cluster IV, 7 genotypes in cluster VI, 5 genotypes in cluster IX, while there was only one genotype in cluster X. The inter-cluster distance varied from 16.85 between clusters X and I to 1.94 between clusters III and VIII. Genetic diversity was observed to be independent of the geographical origin of the genotypes. Selection based on these characters would be effective for future pearl millet crop improvement programme.

Shukla, *et al.* (2010) in the present study, 39 strains of vegetable amaranth (*Amaranthus tricolor*) were evaluated for eight morphological and seven quality traits for two test seasons to contributed 67.55 per cent of the variability. Cluster analysis grouped the strains into six clusters that displayed a wide range of diversity for most of the traits. Cluster analysis has proved to be an effective method in grouping strains that may facilitate effective management and utilization in crop-breeding programmes. The diverse strains falling in different clusters were identified, which can be utilised in different hybridisation programmes to develop high foliage yielding varieties rich in nutritional components. study the extent of genetic divergence among the strains. Multivariate analysis showed that the first four principal components have contributing in emergence effective genetic diversity.

Pandey and Singh (2011) studied the extent and magnitude of genetic divergence for 14 characters among 98 genotypes of grain amaranth (*Amaranthus hypochondriacus* L.) for the purpose of identifying more diverse parents which are expected to induce maximum variability. Based on genetic divergence statistics, genotypes were grouped into 18 clusters in which cluster I contained maximum number

of genotypes (42), Cluster II (11), Cluster III (7), Cluster IV and V (5 in each case) and Cluster VI has 4 genotypes. Cluster VII, VIII, IX, X have (3 in each), cluster XI, XII, XIII, XIV (2 in each) and clusters XV, XVI, XVII and XVIII (1 in each case).

Karad and Patil (2013) screened a set of sixty-five finger millet (*Eleusine coracana* L.) accessions for twelve morphological characteristics to study nature and magnitude of genetic divergence using Mahalanobis D^2 statistics during *kharif* 2009 and *kharif* 2010. Wide range of variation was observed for all the twelve characters under study. D^2 statistic indicated that the genotypes studied were genetically diverse. Based on genetic distances the 65 genotypes under study were grouped into five clusters. Cluster I contains highest 50 genotypes, followed by cluster II (11 genotypes) and cluster III (2 genotypes). The cluster IV and V were monogenotypic. In overall, D^2 analysis suggested KOPN 161, KOPN 370, VL 149, KOPN 387, PR 202, PES 110, KOPN 495, KOPN 892 and KOPN 926 were the most diverse parents could be utilized to improve, widen the genetic base and would be used as parents in breeding programme to enhance the productivity of finger millet.

Wolie and Belete (2013) conducted genetic divergence analysis based on multivariate analysis using Mahalanobis D^2 statistics, which grouped finger millet germplasms in to eight clusters. The maximum intra cluster D^2 was obtained in cluster VIII ($D^2 = 7.568$) and highest intercluster distance was between VII and cluster VIII ($D^2 = 1280$). The analysis showed also germplasms collected from the same geographic area were placed into different cluster groups and those collected from different geographic regions were placed in the same cluster.

Suryanarayana *et al.* (2014) evaluated 35 diverse genotypes of finger millet (*Eleusine coracana* L.) to know the genetic variability and divergence existing in the material. On the basis of non-hierarchical Euclidean cluster analysis, all the 35 genotypes of the present study were grouped into six non-overlapping clusters. The clustering pattern revealed that the genotypes originating from different geographical regions got themselves grouped into different clusters, indicated that the geographic biodiversity is not the responsible factor in determining genetic biodiversity. Among the characters plant height followed by seed yield per plant, main ear length contributed maximum towards the total divergence.

Gerrano *et al.* (2015) evaluated thirty two amaranthus genotypes in field plantings for quantitative morphological traits using a randomized complete block design (RCBD) across two seasons. Cluster analysis grouped the genotypes into six different

groups and a singleton based on their genetic similarity. The clustering of the genotypes based on their genetic similarity will help in the identification of diverse parents for use in the breeding programme.

Kumari and Singh (2015) carried out an experiment with thirty five genotypes of finger millet to study the nature and magnitude of divergence using Mahalanobis D^2 statistics, in randomized block design with three replication. The data for eleven important quantitative traits recorded from the genotypes raised. The 35 genotypes of finger millet were grouped into six clusters using Tocher's method. The genotypes in cluster IV and cluster VI, exhibited high degree of genetic diversity. Cluster III was suitable for grain yield per plant, 1000-grain weight, grain yield of main panicle and harvest index. Days to fifty per cent flowering and grain yield per plant contributed maximum towards genetic divergence.

Devaliya *et al.* (2017) conducted an experiment with 68 diverse genotypes of finger millet (*Eleusine coracana* (L.) Gaertn). The data on 13 quantitative traits were recorded to assess the magnitude of genetic divergence for yield and yield contributing traits. In the present investigation, D^2 statistic indicated that the genotypes studied were genetically diverse. D^2 analysis suggested genotypes belonging to the distinct cluster (VIII and III) could be used in hybridization programme for enhance the productivity of finger millet.

Mahanthasha *et al.* (2017) studied genetic divergence in finger millet with 11 characters which partitioned the 48 germplasm lines into eight clusters. Among the 11 quantitative traits studied, the most important trait contributing to the divergence was grain yield per plant followed by main ear width, total number of basal tillers per plant, total number of fingers on the main ear and finger width. Usefulness of parents has been identified based on genetic divergence for improving finger millet. Higher yielding clusters were VI, II and IV.

Negi *et al.* (2017) studied the genetic divergence among 35 finger millet genotypes for fourteen morphological characters using Mahalanobis D^2 statistics during *kharif*, 2014. Considering cluster mean and genetic distance the crossing of entry of clusters IV with entries of cluster V and those genotypes of cluster VI would be fruitful for obtaining transgressive segregants for developing high yielding and better quality finger millet varieties.

Rawat *et al.* (2018) carried out an experiment to assess the nature and magnitude of genetic variability and divergence among 200 finger millet accessions

including four check varieties viz., PRM-1, PRM-2, VL-352 and GPU-28 and also to identify diverse parents for use in further breeding programmes. Mahalanobis D^2 statistics grouped all the 200 accessions of finger millet into fifteen clusters. The accession IC-476030 was identified as early maturing with higher seed yield per plant. Therefore, the identified accession can be used in the crossing programme for developing an ideal high yielding variety that can perform better under low temperature conditions at mid and high hills of Uttarakhand.

Singh *et al.* (2018) conducted an experiment to evaluate the genetic divergence among 40 pearl millet germplasm using Mahalanobis D^2 statistics for thirteen different traits under rainfed condition for five years pooled data. D^2 clustering grouped the genotypes into eleven clusters. Based on cluster means, cluster II was suitable for early flowering and early maturity and cluster IV had highest grain yield per plant. The maximum contribution to genetic divergence was exhibited by number of productive tillers per followed by single plant yield, days to maturity, plant days to fifty per cent flowering, spike length, plant height, harvest index, test weight spike girth, reproductive period, ear exertion distance, yield and number of leaves per plant. Hence selection for these characters may be useful.

Dhanalakshmi *et al.* (2019) conducted a field experiment to estimate the nature of genetic diversity existing in 99 barnyard millet genotypes including two commercial check varieties viz., MDU1 and CO (KV) 2 under sodic soil condition. Mahalanobis D^2 analysis grouped the genotypes into 13 clusters with respect to 12 biometrical traits. Cluster I was the largest, consisting of 39 genotypes followed by cluster XIII with 35 genotypes. Cluster XII and XI had 4 and 3 genotypes, respectively. The remaining (9) clusters II, III, IV, V, VI, VII, VIII, IX and X included only 2 genotypes per cluster. Cluster XI recorded the highest intra-cluster distance followed by cluster XIII. The maximum inter-cluster distance was observed between clusters I and XI followed by clusters VIII and XI. The traits grain yield per plant and plant height contributed maximum to the genetic diversity. Thus, selection of genotypes as parents from these genetically diversified clusters for breeding programmes could result in heterotic hybrids and could generate good amount of genetic variability in barnyard millet genotypes under the sodic soil condition.

3. MATERIAL AND METHOD

The present investigation “Genetic variability and genetic diversity studies for yield and yield contributing traits in Quinoa (*Chenopodium quinoa* Willd.) genotypes” was conducted at Agricultural Botany Research Farm, Post Graduate Institute, MPKV, Rahuri-413 722 Dist. Ahmednagar, Maharashtra during *Rabi* season, 2019. The details of the material used and statistical procedure followed during the course of investigation are described in this chapter.

3.1 Experimental Material

The experimental material for the study consisted of 30 genotypes of Quinoa obtained from AICRN on Potential Crops, Mahatma Phule Krishi Vidyapeeth Rahuri- 413 722 Dist. Ahmednagar, Maharashtra (India). The list of thirty genotypes are presented in Table 3.1.

Table 3.1. List of 30 genotypes of quinoa

Sr. No.	Genotypes	Sr. No.	Genotypes	Sr. No.	Genotypes
1.	EC-896059	11.	EC-896109	21.	EC-896210
2.	EC-896083	12.	EC-896112	22.	EC-896212
3.	EC-896086	13.	EC-896114	23.	EC-896215
4.	EC-896087	14.	EC-896115	24.	EC-896229
5.	EC-896088	15.	EC-896116	25.	EC-896237
6.	EC-896089	16.	EC-896202	26.	EC-896271
7.	EC-896097	17.	EC-896203	27.	EC-896275
8.	EC-896098	18.	EC-896206	28.	EC-507139
9.	EC-896105	19.	EC-896207	29.	EC-507747
10.	EC-896108	20.	EC-896209	30.	IC-411824

3.2 Experimental Method

3.2.1 Experimental Design

The experiment was conducted in a randomized block design (RBD) with three replications with spacing 30cm x 10cm. All the cultural practices such as fertilizer application, interculturing, weeding etc., were followed to raise good crop.

3.2.2 Sowing and cultural practices

The land was prepared by ploughing followed by two cross harrowing. The plot size for quinoa was 0.60 m x 3.00 m. Fertilizer dose applied to quinoa was 25t/ha FYM, phosphobacteria 2kg/ha, 60 kg/ha N ,40 kg/ha P₂O₅ and 20kg/ ha K as basal

dose. The seeds were sown on 19th Nov 2019. The thinning operation was carried out 20 days after sowing. Other cultural practices were carried out as per recommendation.

3.3 Observations Recorded

Following observations were recorded on five randomly selected plants, from each treatment in each replication and averages were worked out.

3.3.1 Days to 50 per cent flowering (No.)

The number of days from sowing to flowering were recorded when 50 % of the plants from plots came to flowering and average number of days for 50 % flowering was estimated

3.3.2 Days to maturity (No.)

Days required to physiological maturity were recorded from sowing to harvest of crop for each genotype and average were calculated.

3.3.3 Plant height (cm)

Five plants randomly selected from each genotype and plant height in cm is measured with scale. Average was worked out as plant height in centimeter.

3.3.4 Branches per plant (No.)

Branches per plant were measured at full vegetative growth of the plant. The mean were worked out randomly selected five plants from each treatment.

3.3.5 Inflorescence per plant (No.)

Inflorescences per plant were measured at full vegetative growth of the plant. The mean were worked out randomly selected five plants from each treatment.

3.3.6 Inflorescence length (cm)

The length of inflorescence were measured from the tip of inflorescence to emergence of inflorescence start on stem. It were measured in centimeters and calculated the mean from randomly selected five plant from each treatment.

3.3.7 Inflorescence width (cm)

Width of inflorescence were measured of the main inflorescence at physiological maturity. It were measured in centimeters and calculated the mean from randomly selected five plants from each treatment.

3.3.8 Seed yield/ plant (g)

The plants were harvested separately from the randomly selected five plants and seed weight was worked out and expressed in gram per plant.

3.3.9 Seed volume weight (g/ 10 ml)

After harvesting of the quinoa crop, seeds was filled in 10 ml test tube at the 10 ml mark level these seeds were taken on paper and weight were recorded in grams.

3.4 Statistical Analysis

The mean values of five randomly selected observational plants for twelve different characters were used for statistical analysis. The following statistical parameters were calculated for presentation of data on different quantitative attributes.

3.4.1 Analysis of Variance (ANOVA)

Sr. No.	Sources of Variation	D.F.	MSS	Expected mean sum of squares
1.	Replications	r-1	Ms _r	$\sigma^2_e + t \sigma^2_r$
2.	Treatments	t-1	M _s t	$\sigma^2_e + r \sigma^2_t$
3.	Error	(r-1)(t-1)	M _s e	σ^2_e
	Total	(rt-1)		

The analysis of variance was done as suggested by Panse and Sukhatme (1995).

Where,

r = Number of replications

t = Number of treatments

e = error

3.4.2 Genotypic Coefficient of Variation (GCV)

It was estimated by the formula suggested by Burton (1952).

$$GCV = (\sqrt{\sigma^2_g} / \bar{x}) \times 100$$

Where,

σ^2_g = V_g = Genotypic variance

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

3.4.3 Phenotypic Coefficient of Variation (PCV)

It was estimated by the formula suggested by Burton (1952).

$$PCV = (\sqrt{\sigma^2_p} / \bar{x}) \times 100$$

Where,

σ^2_p = V_p = Phenotypic variance

$\bar{X}$ = General mean of the character.

As suggested by Robinson *et al.* (1949) variability estimates were categorized as,

Low	= Below 10 %
Moderate	= 10-20 %
High	= Above 20 %

3.4.4 Heritability Percentage (Broad sense)

Heritability Percentage in broad sense was calculated as given by Burton (1952).

$$h^2(b.s) = V_g / V_p \times 100$$

OR

$$h^2(b.s) = \sigma^2_g / \sigma^2_p \times 100$$

Where,

$h^2(b.s)$ = Heritability Percentage in broad sense

σ^2_g = (V_g) = genotypic variance

σ^2_p = (V_p) = phenotypic variance

As suggested by Robinson *et al.* (1949) heritability estimates were categorized as,

Low	= Below 30 %
Moderate	= 30-60 %
High	= Above 60 %

3.4.5 Genetic Advance

Genetic advance was calculated by the formula given by Johnson *et al.* (1955).

$$GA = K \times (\sigma^2_g / \sigma^2_p) \times \sqrt{\sigma_p}$$

OR

$$GA = K \times h^2 \times \sqrt{\sigma_p}$$

Where,

K = Selection differential which is 2.06 at 5 per cent selection intensity.

σ^2_g (V_g) = Genotypic variance.

σ^2_p (V_p) = Phenotypic variance.

$\sqrt{V_p}$ or σ_p = Phenotypic standard deviation.

As suggested by Robinson *et al.* (1949) genetic advance as per cent mean estimates were categorized as,

Low = Below 10 %

Moderate = 10-20 %

High = Above 20 %

3.4.6 Correlation

To understand the association among the characters, genotypic and phenotypic correlation coefficients were worked out by adopting the method described by Singh and Chaudhary (1977).

3.4.6.1 Phenotypic Correlation Coefficient

$$r_p = \text{covariance}(X, Y)_p / \sqrt{\text{Variance } X(p) \text{ Variance } Y(p)}$$

Where,

r_p = Phenotypic correlation coefficient between character X and Y.

3.4.6.2 Genotypic Correlation Coefficient

$$r_g = \text{covariance}(X, Y)_g / \sqrt{\text{Variance } X(g) \text{ Variance } Y(g)}$$

Where,

r_g = Genotypic correlation coefficient between character X and Y.

Significance of correlation coefficients was tested by using ‘t’ test given by Panse and Sukhatme (1995).

3.4.7 Path Coefficient Analysis

Path coefficient analysis was done according to the procedure suggested by Dewey and Lu (1959).

If, Y is the effect and X_1 is the cause, the path coefficient for the path from cause X_1 to the effect Y is $\sigma X_1 / \sigma Y$.

Direct and indirect effects were worked out by using genotypic correlations as below:

$$\text{Direct effect of } X_1 \text{ on } y = P_{X_1 Y}$$

Where,

$$P_{X_1 Y} = \text{Path coefficient of } X_1 \text{ on } Y.$$

Similarly, direct effects of other attributes on yield were worked out.

$$\text{Indirect effect of } X_1 \text{ viz. } X_2 \text{ on } Y = P_{X_2 Y} r_{X_1 X_2}$$

Where,

$$P_{X_2 Y} = \text{Path coefficient of the component character } X_2 \text{ on } Y.$$

$$r_{X_1 X_2} = \text{Genotypic correlation between } X_1 \text{ and } X_2.$$

Similarly, indirect effects in all possible combinations were calculated for all component characters.

The residual effect (R) was calculated as below;

$$R = [1 - (PX_1 \cdot rX_1Y) - (PX_2 \cdot rX_2Y) - \dots - (PX_n \cdot rX_nY)]^{1/2}$$

Where,

$PX_1, PX_2, \dots, PX_n$ = Direct effects of respective characters on yield.

rX_1, rX_2, rX_n = Correlation coefficient between respective characters and yield.

Scales for path coefficients

Values of direct (or) indirect effects	Rate (or) scale
0.00 to 0.09	Negligible
0.10 to 0.19	Low
0.20 to 0.29	Moderate
0.30 to 0.99	High
> 1.00	Very high

3.4.8 Genetic Distance (D^2)

3.4.8.1 D^2 analysis

The analysis of divergence was carried out by D^2 statistic of Mahalanobis (1936) as described by Rao (1952). Analysis of variance for the individual characters studied was worked out as per R.B.D. to test the significance of differences among the genotypes. The Characters exhibiting significant differences were only used for further Analysis of D^2 statistic.

The generalized distance between two populations was defined by Mahalanobis (1936) as:

$$D^2 = \sum \lambda_{i,j} \cdot d_i \cdot d_j$$

Where,

$\lambda_{i,j}$ = Reciprocal matrix to the common dispersion matrix.

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

d_j = Difference between the mean values of two populations for j^{th} character

Estimation of D^2 values from the above formula is very complicated in the present study.

Since, it requires the inversion of a thirteenth order determinant and then the evaluation of $B(BH) / 2$ terms whose sum is D^2 . It was found convenient to work with a set of uncorrelated characters construed from the original measurements. D^2 with such transformed variables reduces to the evaluation of a simple sum of squares. Transformation was done by Singh and Chaudhary using pivotal condensation method (1977).

The coefficients for the transformation were obtained by dividing the first row of the reduced matrix by the square root of the corresponding pivotal condensation elements.

3.4.8.2 Wilk's criteria

After testing the differences between populations for the characters, a simultaneous test of significance of difference in the values of a number of correlated variables with regard to the Pooled effect of the ten characters considered together was carried using Wilks criteria,

was estimated using the relationship that,

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

Where,

$|E|$ = Determinant of the experimental error sum of squares and sum of products matrix

$|E+V|$ = Determinant of the experimental error sum of squares and sum of products plus population sum of squares and product matrix.

Significance of A was estimated by X as

$$X^2_{pq} = -m \log A$$

Where,

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

$n = N_1 + \dots + N_K - 1$, = Total number of observations – 1

p = Number of characters

$q = K - 1$

K = Number of varieties

3.4.9 Determination of Gene Constellations

Tocher's method as described by Rao (1952) was followed for cluster formation. No formal rules can be laid down for finding the clusters because a cluster is

not a well-defined term. The only criterion appears to be that any two groups belonging to the same cluster should be at least on an average shows a smaller D^2 than those belonging to two different clusters. A simple device suggested by K. D. Tocher is to start with two closely associated groups and find a third group which has the smallest average D^2 from the first two. Similarly, the fourth is chosen to have the smallest D^2 from the first three and so on. If at any stage the average D^2 value of a group from those already listed appears to be high, then this group does not fit in with the former groups and is therefore taken outside the former cluster. The groups of the first cluster are then omitted and the rest are treated similarly. It is also useful to calculate the change in average D^2 within a cluster due to the inclusion of an additional group. If the changes are appreciable then the newly added group has to be considered as outside the cluster.

3.4.10 Average Intra and Inter Cluster D^2 and D Values

3.4.10.1 Average intra cluster D^2

$$D^2 = \Sigma D^2_i / n$$

Where,

D_i is the sum of distance between all possible combinations (n) of the population included in a cluster.

3.4.10.2 Average inter cluster D^2

$$D^2 = \Sigma \text{distance between the population of cluster } i \text{ and } j. / n_i n_j$$

Where,

n_i = number of populations in the cluster i .

n_j = number of populations in the cluster j .

3.4.10.3 Average intra and inter cluster distance

$$D = \sqrt{D^2}$$

3.4.11 Cluster Means

Cluster means were calculated for individual character on the basis of mean performance of the genotype included in the clusters.

3.4.12 Per cent Contribution of the Characters

In all the combination, each character was ranked on the basis of $\Sigma i = y_{ij} - y_{ik}$ values. Rank 1 was given to the highest mean difference and last rank to the lowest mean difference. The Percentage contribution was calculated on the basis of number of times a character appeared first rank in all the combinations (Singh and Chaudhary, 1977).

4. RESULTS AND DISCUSSION

The present investigation on “ Genetic variability and genetic diversity studies for yield and yield contributing traits in Quinoa (*Chenopodium quinoa* Willd.) genotypes. was undertaken with view to know genetic variability, correlation, path analysis and genetic diversity among 30 genotypes. Experiment was conducted at Agricultural Botany Research Farm, Post Graduate Institute, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar, Maharashtra (India) during *Rabi* season 2019. The results obtained on various parameters are presented in this chapter.

- 4.1 Analysis of variance (ANOVA)
- 4.2 Mean performance of quinoa genotypes
- 4.3 Genetic variability estimates, heritability and expected genetic advance
 - 4.3.1 Genotypic and phenotypic coefficients of variation
 - 4.3.2 Heritability
 - 4.3.3 Genetic advance as per cent of mean (GAM)
- 4.4 Correlation coefficient analysis
- 4.5 Path coefficient analysis
- 4.6 Genetic diversity

4.1 Analysis of Variance

The analysis of variance (Table 4.1) revealed that the mean sum of squares due to genotypes for nine characters *viz.*, days to 50 per cent flowering, days to maturity, plant height, n branches per plant, inflorescence per plant, inflorescence length, inflorescence width, seed volume weight/ 10 ml and seed yield per plant. The characters studied were significant, which indicated presence of appreciable amount of variability among the quinoa genotypes.

Table 4.1. Analysis of variance for different characters in quinoa

Sr. No.	Characters	Mean sum of square		
		Replication (2)	Treatment (29)	Error (58)
1.	Days to 50 per cent flowering (No.)	1.86	33.86**	1.23
2.	Days to maturity (No.)	1.15	113.19**	1.73
3.	Plant height (cm)	7.88	220.82**	20.94
4.	Branches per plant (No.)	3.09	121.70**	5.08
5.	Inflorescence per plant (No.)	1.42	123.10**	4.02
6.	Inflorescence length (cm)	3.52	40.68**	1.92
7.	Inflorescence width (cm)	2.20	31.41**	1.54
8.	Seed volume weight/10 ml (g)	0.04	1.12**	0.08
9.	Seed yield per plant (g)	3.38	38.28**	3.58

*, ** significant at 5 and 1 per cent, respectively

4.2 Mean Performance of the Genotypes

The mean performance of 30 genotypes of quinoa for 9 characters is given in Table 4.2.

4.2.1 Days to 50 per cent flowering (No.)

The general mean for days to 50 per cent flowering was 48.79 days. The variation for days to 50 per cent flowering ranged from 43.33 to 55.33 days. Ten genotypes flowered significantly earlier and twenty were late than general mean among 30 genotypes, EC-896209 (43.33 days) was earliest to flower followed by EC-896114 (43.66 days) and IC-411824 (43.66 days) While, genotype EC-896108 (55.33 days) was late in flowering followed by EC- 896212 (55.00 days) and EC-507139 (52.00 days).

4.2.2 Days to maturity (No.)

The general mean for number of days to maturity was 105.09 days. The variation for days to maturity ranged from 100.66 to 122.33 days. The nineteen genotypes showed significantly early maturity and eleven were late when compare with general mean. The genotype EC- 896209 (100.66 days) followed by EC-896114 (100.66 days) and IC-411824 (101.33 days) were early in maturity. Genotypes EC-896212 (122.33 days) and EC-896108 (122.33 days) were comparatively late in maturity.

Table 4.2 Mean performance of different quinoa genotypes for yield attributes

Sr No	Name of genotype	Days to 50 % flowering (No.)	Days to maturity (No.)	Plant height (cm)	Branches/ plant (No.)	Inflorescence /plant (No.)	Inflorescence length (cm)	Inflorescence width (cm)	Seed volume weight/ 10 ml (g)	Seed yield /plant (g)
1.	EC 896059	46.33	103.33	143.26	29.61	26.53	25.16	20.23	6.48	21.73
2.	EC 896083	47.58	104.40	142.93	28.20	24.10	24.06	20.00	6.31	19.36
3.	EC 896086	48.76	101.86	131.33	20.66	17.13	17.14	14.30	5.98	15.66
4.	EC 896087	49.66	109.00	150.80	32.00	27.13	20.70	16.28	7.04	20.36
5.	EC 896088	49.33	108.00	142.66	30.26	25.91	22.13	16.50	6.85	17.56
6.	EC 896089	49.33	101.23	144.40	28.53	23.86	23.90	16.05	7.04	20.50
7.	EC 896097	50.00	102.00	168.93	37.42	30.90	23.39	17.39	7.30	25.76
8.	EC 896098	49.33	101.66	155.43	30.13	25.43	21.20	16.43	6.83	20.60
9.	EC 896105	50.33	102.33	149.00	32.10	28.26	22.20	18.03	6.55	19.86
10.	EC 896108	55.33	122.33	145.26	29.40	25.07	19.36	15.43	6.50	21.06
11.	EC 896109	49.66	102.66	148.53	31.76	27.60	20.93	16.28	7.02	21.81
12.	EC 896112	49.00	103.33	146.33	28.00	24.03	21.90	16.73	6.92	19.72
13.	EC 896114	43.66	100.66	139.66	28.13	24.10	25.67	21.10	6.05	22.33
14.	EC 896115	49.33	103.66	132.08	24.26	19.56	23.29	18.73	7.21	18.10
15.	EC 896116	46.66	103.33	149.23	31.56	25.76	16.86	16.80	6.99	25.20
16.	EC 896202	44.00	101.66	152.50	31.86	25.96	17.94	17.96	6.17	23.52
17.	EC 896203	47.33	103.00	149.26	31.50	26.25	21.10	16.40	6.98	20.23
18.	EC 896206	46.66	102.33	146.18	28.47	24.36	19.86	15.55	6.08	20.50
19.	EC 896207	49.33	103.66	153.13	31.90	26.20	22.11	15.33	6.57	19.13
20.	EC 896209	43.33	100.66	174.20	42.86	37.37	24.73	20.06	7.50	25.60
21.	EC 896210	49.00	107.33	134.66	26.03	20.96	17.33	14.29	6.42	16.36
22.	EC 896212	55.00	122.33	145.66	31.40	26.63	22.46	19.42	6.67	21.03
23.	EC 896215	50.33	106.66	141.15	31.60	26.73	23.46	18.36	6.47	20.80
24.	EC 896229	50.00	106.00	144.26	31.73	26.00	24.06	18.63	6.50	20.63
25.	EC 896237	50.33	106.66	142.33	31.26	27.73	23.33	18.70	6.58	21.40
26.	EC 896271	50.00	106.00	150.40	36.73	31.66	24.58	19.46	7.08	20.93
27.	EC 896275	49.33	108.00	145.00	29.33	24.63	21.60	16.46	6.54	20.47
28.	EC 507139	52.00	101.33	148.33	35.63	30.13	22.40	17.53	6.73	20.46
29.	EC 507747	49.06	106.00	153.43	40.56	35.78	25.23	19.16	7.52	20.69
30.	IC 411824	43.66	101.33	164.00	43.03	38.29	27.60	21.73	7.33	25.36
	Mean	48.79	105.09	147.81	31.53	26.80	22.20	17.64	6.74	20.89
	S.E ±	00.64	0.76	2.64	1.30	1.16	0.80	0.72	0.16	1.09
	C.D (5%)	1.46	1.73	6.03	2.97	2.64	1.83	1.63	0.37	2.49
	C.V(%)	2.27	1.25	3.10	7.15	7.48	6.24	7.03	4.20	9.06

4.2.3 Plant height (cm)

The general mean for plant height was 147.81 cm. The plant height ranged from 131.33 to 174.20 cm. The sixteen genotypes were dwarf and fourteen were taller as compared to general mean. The genotype EC-896209 (174.20 cm) was the tallest genotype followed by EC-896097 (168.93 cm) and IC-411824 (164.00 cm). Genotype EC-896086 (131.33 cm) was dwarf followed by EC-896115 (132.08 cm).

4.2.4 Branches per plant (No.)

The general mean for branches per plant was 31.53. The variation for branches per plant ranged from 20.66 to 43.03. Sixteen genotypes produced less branches per plant and fourteen genotypes showed significantly higher branches per plant when compared to the general mean. The genotype IC-411824 (43.03) possessed highest number of branches per plant followed by EC-896209 (42.86). Genotype EC-896086 (20.66) had least number of branches followed by EC-896115 (24.26) and EC-896112 (28.00).

4.2.5 Inflorescence per plant (No.)

The general mean for inflorescence per plant was 26.80. The variation for inflorescence per plant ranged from 17.13 to 38.29. Twenty genotypes produced less number of inflorescence and ten genotypes showed significantly higher inflorescence per plant over general mean. The genotype IC-411824 (38.29) showed highest number of inflorescence per plant followed by EC-896209 (37.37) and EC-507747 (35.78). Genotype EC-896086 (17.13) had least inflorescence per plant followed by EC-896115 (19.56) and EC-896210 (20.96).

4.2.6 Inflorescence length (cm)

The general mean for inflorescence length was 22.20 cm. The variation for inflorescence length ranged from 16.86 to 27.60 cm. Fifteen genotypes showed short inflorescence length and fifteen genotypes showed significantly long inflorescence length as compared to general mean. The genotype IC-411824 (27.60 cm) had longest inflorescence length followed by EC-866114 (25.67 cm). While, genotype EC-896119 (16.86 cm) had shortest inflorescence length followed by EC-896086 (17.14 cm), EC-896210 (17.63 cm) and EC-896202 (17.94 cm).

4.2.7 Inflorescence width (cm)

The general mean for peduncle length was 17.64 cm. The variation for inflorescence width ranged from 14.29 to 21.73 cm. Sixteen genotypes showed short inflorescence width and remaining fourteen genotypes showed significantly long inflorescence width as compared to general mean. The genotype IC-411824 (21.73 cm) had longest inflorescence width followed by EC-896114 (21.10 cm), while genotype EC-896210 (14.29 cm) had shortest inflorescence width followed by EC-896086 (14.30 cm).

4.2.8 Seed volume weight/ 10 ml (g)

The general mean for seed volume weight/ 10 ml was 6.74 g. The variation for seed volume weight/ 10 ml per plant ranged from 5.98 to 7.52 g. Sixteen genotypes showed numerically high seed volume weight/ 10 ml and fourteen genotypes had less seed volume weight/ 10 ml than general mean. The genotype EC-507747 (7.52g) had the highest seed volume weight/ 10 ml followed by EC-896209 (7.50 g) and IC-411824 (7.33 g). Genotype EC-896086 (5.98 g) recorded least seed weight/ 10 ml followed by EC-896114 (6.05 g), EC-896206 (6.08 g), EC-896202 (6.17g) and EC-896083 (6.31 g).

4.2.9 Seed yield per plant (g)

The general mean of seed yield per plant was 20.89 g. The variation for seed yield per plant ranged from 15.66 to 25.76 g. The eighteen genotypes produced lower and twelve genotypes showed significantly higher seed yield per plant than the general mean. The genotype EC-896097 (25.76 g) had the highest seed yield per plant followed by EC-896209 (25.60 g) and IC-411824 (25.36 g). Genotype EC-896086 (15.66 g) had the lowest seed yield followed by EC-896210 (16.36 g) and EC-896088 (17.56 g).

4.3 Parameters of Genetic Variability

Meagre information on the nature and extent of genetic variability and characters association are available on quinoa (Bhargava *et al.*, 2007; De Santis *et al.*, 2016 and Mhada *et al.*, 2014). Much of the germplasm of quinoa available in the country has not properly evaluated hence, in the present study, 30 genotypes of quinoa were assessed for their genetic potential in respect of yield and its components. The extent of genetic variability available in a crop is a pre-requisite for its improvement, due to the fact that efficiency of selection depends mainly on it. In a crop improvement programme,

efficiency of selection of suitable parents depends on the amount of genetic variability present in a crop. The extent of variability in a crop population for a character is assessed by measuring genotypic and phenotypic coefficients of variation. Genetic variability parameters such as range, phenotypic coefficient of variation, genotypic coefficient of variation (Burton and Devane, 1953), broad sense heritability (Lush, 1949) and expected genetic advance as per cent mean (Johnson *et al.*, 1955) were estimated using adjusted trait mean of each of the germplasm.

Heritability is a good index of transmissibility of a character from parent to their offspring. The concept of heritability is important in determining whether the phenotypic differences among the individuals are genetical or due to the result of environmental factors. The role of genetic factors in expression of phenotype is indicated by heritability. The expected genetic gain from selection in a population is calculated by working out the genetic advance. Heritability along with genetic advance gives best picture or the efficiency of selection.

Range of variability, estimates of genotypic and phenotypic coefficient of variation, heritability Percentage in broad sense, genetic advance and genetic advance expressed as Percentage of mean are presented in (Table 4.3).

4.3.1 Genetic Variability

In present investigation wide range of variation was observed for all the characters studied. Highly significant differences were observed in thirty genotypes for plant height (131.33-174.20), inflorescence per plant (17.13-38.29), branches per plant (20.66-43.03) days to maturity (100.66-122.33), days to 50 per cent flowering (43.33-55.33), seed yield per plant (15.66-25.76) while, rest of characters had narrow range of variability. Highest CV showed by seed yield per plant (9.06) followed by inflorescence per plant (7.48), branches per plant (7.15), inflorescence width (7.03), inflorescence length (6.24), seed volume weight/ 10 ml (4.20), plant height (3.10), days to 50 % flowering (2.27), days to maturity (1.25).

The findings were quite similar to as reported by Szilagyi and Jornsgard (2014). De Santis *et al.* (2016) also observed a wide range of variability for seed yield per plant and biological yield per plant. Bhargava *et al.* (2007) observed the highest coefficient of variation (CV) for biological yield followed by seed yield, panicle length,

plant height. A wide range of variability was reported for plant height, panicle length and seed yield per plant in grain amaranth by Tiwari *et al.* (2018). Similar results in grain amaranth were also reported by Lokeshkumar and Murthy (2017); Diwan *et al.* (2017); Venkatesh *et al.* (2014); Ramesh *et al.* (2013) and Sravanthi *et al.* (2012) for different traits. Variation for important yield contributing characters indicated great scope to make selections for desirable estimates.

This indicated a great scope for exploitation for these traits. A wide range of variability for these traits in quinoa were reported by Curti *et al.* (2016) for main stem branches, plant height and panicle length. Mhada *et al.* (2014) reported significant variation among accessions for grain yield/plant. Similar result reported by De Santis *et al.* (2016) for seed yield. Al-Naggar *et al.* (2017) revealed that quinoa genotypes varied greatly in days to flowering, days to maturity, plant height, inflorescence length, seed yield per plant and test weight. Naneli *et al.* (2017) reported maximum coefficient of variation for number of panicle.

Coefficients of variation were calculated at respective phenotypic and genotypic levels. The magnitudes of phenotypic coefficients of variation (PCV) were greater than genotypic coefficients of variation (GCV) for all the characters with narrow difference indicating minute environmental influence on character expression. It is observed that, GCV and PCV for most of the traits were either high or moderate. The estimates of GCV and PCV from present investigation are given in Table 4.3. The estimates of genotypic coefficient of variation (GCV) reflect the total amount of genotypic variability present in material. However, the proportion of this variability that is transmitted from parents to the progeny is reflected by heritability. Lush (1949) gave the concept of broad sense heritability. It determines the efficiency with which we can utilize the genotypic variability in a breeding programme. The estimates of heritability were arbitrarily categorized in three major groups, i.e. high heritability (above 60 %), moderate heritability (30-60 %) and low heritability (below 30 %) (Robinson *et al.*, 1949). The estimates of heritability from present investigation are presented in Table 4.3.

Table 4.3. Parameters of genetic variability in 30 genotypes in quinoa

Sr. No.	Character	Mean	Range	GCV (%)	PCV (%)	ECV(%)	h² % (B.S)	Genetic Advance	Gen. Adv. as % of Mean
1.	Days to 50 % flowering (No.)	48.79	43.33-55.33	6.76	7.13	2.27	89.84	6.44	13.20
2.	Days to maturity (No.)	105.09	101.33- 122.33	5.80	5.93	1.25	95.55	12.27	11.68
3.	Plant height (cm)	147.81	131.33- 174.20	5.52	6.33	3.10	76.09	14.67	9.92
4.	Branches per plant (No.)	31.53	20.66-43.03	19.77	21.03	7.15	88.44	12.08	38.31
5.	Inflorescence per plant (No.)	26.80	17.13-38.29	23.50	24.66	7.48	90.80	12.37	46.13
6.	Inflorescence length (cm)	22.20	17.14-27.60	16.19	17.35	6.24	87.06	6.91	31.12
7.	Inflorescence width (cm)	17.64	14.30-21.73	17.88	19.21	7.03	86.60	6.05	34.27
8.	Seed volume weight/10 ml (g)	6.74	5.98-7.52	8.74	9.69	4.20	81.25	1.09	16.22
9.	Seed yield per plant (g)	20.89	15.66- 25.76	16.28	18.63	9.06	76.36	6.12	29.31

The relative role of genetic factors in expression of phenotypes can be obtained from calculation of heritability (Falconer, 1960). The expected genetic gain from the selection applied in a population can be measured by genetic advance. High heritability along with high genetic advance gives the best efficiency for selection.

When heritability is moderate to high with larger magnitude of expected genetic advance for a particular character, it is said to be governed by additive gene action but if the results are opposite and either of the condition like high heritability with low genetic advance or low heritability with low genetic advance is observed for any given character, then presence of non-additive gene action may be suspected.

Heritability decides resemblance of progeny with their parents (Falconer, 1960), while genetic advance provides the knowledge about expected gain for a particular character after selection. In general, in self-pollinated crops, characters with high heritability possess high genetic advance, but when phenotypic variation in the population is low, genetic advance also tends to be low and *vice-versa*. This shows that variation and heritability are very much important for any breeding programme.

4.3.1.1 Days to 50 per cent flowering (No.)

Low genotypic and phenotypic coefficient of variation was recorded by days to 50 % flowering (6.76 and 7.13%), it indicates that there is limited scope for selection for this character high heritability (89.84 %) coupled with moderate genetic advance as per cent of mean (13.20 %) was showed for the characters days to 50 % flowering.

The results of present study are in accordance with the findings of Bhargava *et al.* (2007) and De Santis *et al.* (2016) both reported high heritability coupled with moderate genetic advance as Percentage of mean for this trait in quinoa. Kusuma *et al.* (2007) Low PCV and GCV were reported for days to 50 % flowering in grain amaranth.

4.3.1.2 Days to maturity (No.)

Low genotypic and phenotypic coefficient of variation was recorded by days to maturity (5.80 and 5.93 %, respectively), it indicates that there is limited scope for selection for this character

High heritability (95.55 %) coupled with moderate genetic advance as per cent of mean (11.68 %) was showed for the characters days to maturity.

Benlhabib *et al.* (2016) observed high heritability for days to maturity in quinoa. Kusuma *et al.* (2007) Low PCV and GCV were reported for days to maturity in grain amaranth. These results are in contrary with the reports of Bhargava *et al.* (2007), moderate GCV, PCV and high heritability values along with high genetic advance in Percentage of mean for days to maturity in their findings on quinoa and Lokeshkumar and Murthy (2017) also showed contrary results, reported high heritability couples with high genetic advance in relative crop grain amaranth for this trait. This might be due to enviornmental influence or material used for experiment.

4.3.1.3 Plant height (cm)

Low genotypic and phenotypic coefficient of variation was recorded by plant height (5.52 and 6.33 %, respectively), it indicates that there is limited scope for selection for this character

High estimates of heritability (76.09 %) coupled with low genetic advance as per cent mean (9.92 %) showed by plant height and this indicates predominance of non additive gene action for control of this trait and heterosis breeding for plant height will be more effective.

Similar results observed in studies of Lokeshkumar and Murthy (2017) and reported low GCV, PCV and high heritability in relative crop grain amaranth for this trait. Venkatesh *et al.* (2014) observed high heritability in relative crop grain amaranth. These results are in contrary with the reports of Bhargava *et al.* (2007), in quinoa and Sravanthi *et al.* (2012) in amaranthus, this might be due to environmental influence.

4.3.1.4 Branches per plant (No.)

The branches per plant showed moderate GCV (19.77 %) and high PCV (21.03 %).

High estimates of heritability (88.44 %) coupled with high genetic advance as per cent mean for branches per plant (38.31 %). This indicates predominance of additive gene action for control of this trait and selection for branches per plant will be more effective.

The results of present study are in accordance with the findings of Bhargava *et al.* (2007) and Al-Naggar *et al.* (2017) both showed high heritability values along with high genetic advance in Percentage of mean for primary branches per plant in quinoa. Sravanthi *et al.* (2012) and Venkatesh *et al.* (2014) also showed similar results for heritability (high) with Genetic advance as per cent mean (high) in amaranthus.

4.3.1.5 Inflorescence per plant (No.)

High GCV and high PCV showed by number of inflorescence per plant (23.50 and 24.66 %, respectively), it indicates that there is ample scope for selection for this character.

High estimates of heritability (90.80 %) coupled with high genetic advance as per cent mean (46.13 %) showed by number of inflorescence per plant. This indicates predominance of additive gene action for control of this trait and selection for inflorescence per plant will be more effective.

4.3.1.6 Inflorescence length (cm)

Moderate GCV and moderate PCV showed by inflorescence length (16.19 and 17.35 %, respectively).

Inflorescence length showed high heritability (87.06 %) coupled with high genetic advance as per cent mean (31.12 %) for inflorescence length. This indicates predominance of additive gene action for control of this trait and selection for inflorescence length will be more effective.

The results of present study are in accordance with the findings of Bhargava *et al.* (2007) in quinoa and Lokeshkumar and Murthy (2017) and Venkatesh *et al.* (2014) also reported high heritability and genetic advance in relative crop grain amaranth for this trait. Kusuma *et al.* (2007) High heritability and GAM recorded for panicle length in grain amaranth. Sravanthi *et al.* (2012) and Venkatesh *et al.* (2014) similar results observed for for heritability (high) with Genetic advance as per cent mean (high) in amaranthus.

4.3.1.7 Inflorescence width (cm)

Moderate GCV (17.88 %) and moderate PCV (19.21 %) showed by inflorescence width, it indicates that there is ample scope for selection for this character.

Inflorescence width showed high heritability (86.60 %) with high genetic advance as per cent mean (34.27 %). This indicates predominance of additive gene action for control of this trait and selection for inflorescence width will be more effective

The results of present study are in accordance with the findings of Venkatesh *et al.* (2014) and Diwan *et al.* (2017) for heritability (high) with Genetic advance as per cent mean (high) in amaranthus. Kusuma *et al.* (2007) shows similar results for components of variation moderate PCV and GCV for panicle girth in grain amaranth.

4.3.1.8 Seed volume weight (g/ 10 ml)

Low GCV and low PCV exhibited by seed volume weight/10 ml (8.74 and 9.69 %, respectively).

High heritability seed volume weight/ 10 ml (81.25 %) with moderate genetic advance as per cent mean (16.22 %).

4.3.1.9 Seed yield per plant (g)

Moderate GCV (16.28 %) and moderate PCV (18.63 %) showed by seed yield per plant.

High heritability (76.36 %) with high genetic advance as per cent mean (29.31 %) showed by seed yield per plant. This indicates predominance of additive gene action for control of this trait and selection for seed yield per plant will be more effective.

Al-Nagger *et al.* (2017) Maximum predicted genetic advance from selection was achieved for seed yield per plant (56.02 %) suggesting existence of high variability among the studied genotypes bunt is considered to be governed by additive gene action hence; substantial improvement for this character could be achieved through direct selection. These results are in close harmony with the findings of Bhargava *et al.* (2007) for quinoa and Lokeshkumar and Murthy (2017) and Venkatesh *et al.* (2014) for relative crop grain amaranth. Al-Nagger *et al.* (2017) maximum predicted genetic advance from selection was achieved from inflorescence per plant (101.87 %) followed by primary branches per plant (68.04 %), test weight (62.10 %) and seed yield per plant (56.02 %) under severe water stress.

Sravanthi *et al.* (2012) and Venkatesh *et al.* (2014) similar results observed for heritability (high) with Genetic advance as per cent mean (high) in

amaranthus for majority of characters. The phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all characters. This indicates the effect of environmental factors on these characters. These results are in confirmation with the finding of Bhargava *et al.* (2007), who found that PCV as higher than the GCV values for all characters.

The difference between GCV and PCV were minimum for all the characters suggesting less influence of environment in the expression of these characters and one may rely upon the phenotypic values for direct selection. Genotypic and phenotypic variance was greater than environmental variance for all characters indicated that influence of environment on expression of these traits was lower or negligible. Hence selection for these characters would be effective.

In present study, high heritability coupled with high genetic advance as per cent of mean was for the characters *viz.*, inflorescence per plant, branches per plant, inflorescence width, inflorescence length, seed yield per plant, suggested that these characters are under the influence of additive gene action. Since genetic advance is a function of selection intensity, heritability and phenotypic standard deviation, high genetic advance obtained for these traits is mainly because of high heritability and high phenotypic standard deviation as the selection intensity is constant in present study.

4.4 Correlation Coefficient Analysis

A wide range of variation in quantitative characters provides the basis for selection in plant breeding programmes, whereas, the information on inter relationship among such quantitative traits facilitate the choice of suitable breeding method to be applied and selecting the parents for improving the crop.

Yield improvement is the main objectives in most of crop improvement programmes. It is believed that yield is determined by the action of several independent yield determining components characters. A positive correlation between yield and component characters is desirable as it could help in simultaneous improvement of both the traits.

The genotypic and phenotypic correlations indicate the extent of relationship between two variable characters under study of the two measures, genotypic correlation coefficient provides a close measure of association between characters and

gives an indication of characters which may be useful for overall improvement in the crop. They may also help to identify the characters that have little or no importance in the selection programme. In any event, they provide basic information useful to the breeder (Johnson *et al.*, 1995). The phenotypic correlations also help in formulating the selection index useful for crop improvement through simultaneous selection.

The genotypic correlation coefficients between yield and its related components are presented in Table 4.4.

4.4.1 Correlation of Seed Yield with its Component

The seed yield per plant showed significant and positive relationship at genotypic and phenotypic level with plant height ($r_g = 0.785$ and $r_p = 0.760$) followed by branches per plant ($r_g = 0.705$ and $r_p = 0.708$), inflorescence per plant ($r_g = 0.682$ and $r_p = 0.681$), seed volume weight/ 10 ml ($r_g = 0.590$ and $r_p = 0.247$), inflorescence width ($r_g = 0.520$ and $r_p = 0.500$) and inflorescence length ($r_g = 0.235$ and $r_p = 0.365$) respectively. The seed yield per plant showed significant and negative correlation with days to 50 per cent maturity ($r_g = -0.4932$ and $r_p = -0.291$) both at genotypic and phenotypic level respectively and days to maturity ($r_g = -0.226$) and $r_p = -0.106$) significant at genotypic and non-significant at phenotypic level.

The association between seed yield and its component traits in this study are accordance with the findings of Bhargava *et al.* (2007) reported that grain yield per plant showed positive and significant correlation with plant height ($r = 0.507$), dry weight per plant ($r = 0.486$), primary branches per plant ($r = 0.417$). Mhada *et al.* (2014) also observed highest positive significant correlation between the seed yield and biological yield ($r : 0.67$) followed by and plant height at harvest ($r : 0.64$) and plant height ($r : 0.40$). Benlhabib *et al.* (2016) also reported that seed yield was positively correlated with panicle length. De Santis, *et al.* (2016) also seed yield per plant had positive correlation with test weight, biological yield per plant. Jacobsen *et al.* (1996) reported that the grain yield had a positive association with plant height, length and diameter of inflorescence in quinoa. Spehar and Santos (2005) reported that inflorescence length and diameter were positively associated with grain yield. Stem diameter was also positively correlated with grain yield and biological yield Kusuma *et al.* (2007), Yadav *et al.* (2014) and Venkatesh *et al.* (2014) concluded positive correlation of plant height and panicle length

with seed yield in their research on grain amaranth. Szilagyi and Jornsgard (2014) also reported that the seed yield had significant and positive association with plant height, biological yield and harvest index in quinoa. Long Nguyen (2016) also concluded that panicle length is a yield component in quinoa and significant variation in this parameter may entail significant grain yield differences in quinoa. Maliro *et al.* (2017) reported that there were strong positive correlation between seed yield and characters like plant height ($r : 0.74$), days to maturity ($r : 0.76$) and biological yield ($r : 0.87$) in irrigated condition. Plant height was strongly correlated to seed yield ($r : 0.74$), biological yield ($r : 0.80$).

4.4.2 Correlation between Yield Components

4.4.2.1 Days to 50 per cent flowering (No.)

Days to 50 per cent flowering had positive significant correlation with days to maturity ($rg = 0.729$ and $rp = 0.682$) both at genotypic and phenotypic level. It showed significant negative correlation with plant height ($rg = -0.329$ and $rp = -0.236$) both at genotypic and phenotypic level respectively. Branches per plant ($rg = -0.232$ and $rp = -0.182$), inflorescence per plant ($rg = -0.240$ and $rp = -0.189$) and inflorescence width ($rg = -0.499$ and $rp = -0.216$), inflorescence length ($rg = -0.0265$ and $rp = -0.084$) showed negative significant correlation at genotypic level and negative non significant correlation phenotypic level. It showed negative and non-significant correlation with seed volume weight/10 ml ($rg = -0.019$ and $rp = -0.001$) both at genotypic and phenotypic level respectively

These results are in accordance with the findings of Bhargava *et al.* (2007) for days to maturity.

4.4.2.2 Days to maturity (No.)

Days to maturity had negative significant correlation with plant height ($rg = -0.244$ and $rp = -0.167$) and inflorescence length ($rg = -0.214$ and $rp = -0.086$) at genotypic level but negative non significant correlation at phenotypic level. The following characters showed negative but non significant correlation both at genotypic and phenotypic level, branches per plant ($rg = -0.119$ and $rp = -0.094$), inflorescence per plant ($rg = -0.115$ and $rp = -0.086$), inflorescence width ($rg = -0.158$ and $rp = -0.042$) and seed volume weight/10 ml ($rg = -0.091$ and $rp = -0.085$), respectively.

Table 4.4. Estimates of genotypic (above diagonal) and phenotype correlation coefficients (below diagonal) among seed yield and yield contributing characters in thirty quinoa genotypes

Sr. No.	Character	Days to 50 % flowering	Days to maturity	Plant height (cm)	Branches/ plant (No.)	Inflorescences/ plant (No.)	Inflorescence length (cm)	Inflorescence width (cm)	Seed volume weight (g/10 ml)	Seed yield/ plant (g)
1.	Days to 50 % flowering (No.)	1.000	0.729**	-0.329**	-0.232*	-0.240*	-0.265*	-0.499**	-0.019	-0.493**
2.	Days to maturity (No.)	0.682**	1.000	-0.244*	-0.119	-0.115	-0.214*	-0.158	-0.091	-0.226*
3.	Plant height (cm)	-0.236*	-0.167	1.000	0.841**	0.813**	0.248*	0.190	0.738**	0.785**
4.	Branches/plant (No.)	-0.182	-0.094	0.087	1.000	0.991**	0.523**	0.477**	0.821**	0.705*
5.	Inflorescences/ plant (No.)	-0.189	-0.086	0.830**	0.975**	1.000	0.599**	0.542**	0.806**	0.682**
6.	Inflorescence length (cm)	-0.084	-0.086	0.373**	0.534**	0.564**	1.000	0.745**	0.496**	0.235**
7.	Inflorescence width (cm)	-0.216*	-0.042	0.369**	0.544**	0.571**	0.837**	1.000	0.268**	0.520*
8.	Seed volume weight (g/10 ml)	-0.001	-0.085	0.442**	0.487**	0.462**	0.298**	0.188	1.000	0.590**
9.	Seed yield/plant (g)	-0.291*	-0.106	0.760**	0.708**	0.681**	0.365**	0.500**	0.247*	1.000

*and ** significant at P= 5 and P = 1 level of significance, respectively

These results are in agreement with the outputs of Bhargava *et al.* (2007) and Szilagyi and Jornsgard (2014) results are similar for correlation with the character days to 50 % flowering.

4.4.2.3 Plant height (cm)

Plant height had positive highly significant correlation with branches per plant ($r_g = 0.841$) at genotypic level and positive non significant ($r_p = 0.087$) at phenotypic level. Plant height had positive highly significant correlation with inflorescence per plant ($r_g=0.813$ and $r_p=0.830$), inflorescence length ($r_g = 0.248$ and $r_p = 0.373$), seed volume weight/10 ml ($r_g=0.738$ and $r_p=0.442$) at both genotypic and phenotypic level. Inflorescence width had positive and non significant level ($r_g=0.190$) at genotypic level but significant at phenotypic level ($r_p=0.369$).

Showed results were very similar to the finding of Bhargava *et al.* (2007a) for primary branches per plant, panicle length and biological yield. Spehar and Santos (2005) observed correlation between plant height and inflorescence length suggests that high grain held can be attained by selecting for stem/inflorescence ratio. Rojas (2003) panicle length was also positively associated with plant height indicating that lines with greater plant height also developed longer panicles. Fuentes and Bhargava (2011) noticed high correlation between plant height and inflorescence length.

4.4.2.4 Branches per plant (No.)

Branches per plant showed highly significant positive correlation with inflorescence per plant ($r_g= 0.991$ and $r_p=0.975$) , inflorescence length ($r_g=0.523$ and $r_p= 0.534$), Inflorescence width ($r_g= 0.477$ and $r_p=0.544$) and seed volume weight per plant ($r_g=0.821$ and $r_p=0.487$) both at genotypic and phenotypic level respectively.

These results are in accordance with the findings of Bhargava *et al.* (2007a) for almost all the traits. Rojas (2003) also reported significant correlation among branches per plant, panicle length and panicle per plant suggesting that plants with good branching habit tend to develop a large number of long inflorescences.

4.4.2.5 Inflorescence per plant (No.)

Inflorescence per plant showed highly significant and positive correlation ($r_g= 0.599$ and $r_p= 0.564$), Inflorescence width ($r_g= 0.542$ and $r_p= 0.571$), seed volume

weight/10 ml ($r_g=0.806$ and $r_p= 0.462$) both at genotypic and phenotypic level respectively.

4.4.2.6 Inflorescence length (cm)

Inflorescence length showed highly significant and positive correlation with inflorescence width ($r_g= 0.745$ and $r_p= 0.837$) and seed volume weight / 10 ml ($r_g = 0.496$ and $r_p= 0.298$) both at genotypic and phenotypic level respectively.

These results are in agreement with the outputs of Risi and Galwey (1989); Spehar and Santos (2005) Benlhabib, *et al.*, (2016). and Rojas (2003) also observed similar results panicle length was positively associated with plant height indicating that lines with greater plant height also developed longer panicles.

4.4.2.7 Inflorescence width (cm)

Inflorescence width showed significant and positive correlation with seed volume weight per /10 ml ($r_g= 0.268$) at genotypic level and positive and non significant ($r_p= 0.188$) at phenotypic level.

Showed results were very similar to the findings of Fuentes and Bhargava (2011) noticed high correlation between stem diameter and plant weight.

4.4.2.8 Seed volume weight / 10 ml (g)

The character seed volume weight/10 ml had positive and significant correlation at genotypic and phenotypic level with seed yield/plant ($r_g=0.590$ and $r_p=0.247$), respectively.

4.5 Path Analysis

Path analysis is partial coefficient, which splits correlation coefficient into direct and indirect effects. In present investigation, path analysis was done as per the procedure given by Dewey and Lu (1959) to know the direct and indirect effects of various characters. Correlation along with path analysis proves more reliable for use in breeding programme.

Yield is a complex character and the result of several component traits. Some characters contribute directly towards yield, whereas, others indirectly affect the yield. Hence, there is necessary to study direct and indirect effects of various characters on yield.

Table 4.5 Estimates of genotypic direct (diagonal) and indirect effects (above and below diagonal) of component characters on seed yield in thirty quinoa genotypes. Residual effect (R) = 0.276

Sr. No.	Character	Days to 50 % flowering	Days to maturity	Plant height (cm)	Branches/ plant (No.)	Inflorescences/ plant (No.)	Inflorescence length (cm)	Inflorescence width (cm)	Seed volume weight (g/10 ml)	Genotypic correlation with Seed yield/ plant (g)
1.	Days to 50 % flowering (No.)	0.018	-0.037	-0.275	0.195	-0.096	0.186	-0.477	-0.008	-0.493**
2.	Days to maturity (No.)	0.013	-0.050	-0.204	0.100	-0.046	0.151	-0.151	-0.039	-0.226*
3.	Plant height (cm)	-0.006	0.012	0.836	-0.707	0.325	-0.175	0.182	0.318	0.785**
4.	Branches/plant (No.)	-0.004	0.006	0.702	-0.842	0.400	-0.368	0.456	0.354	0.705**
5.	Inflorescences/pl ant (No.)	-0.004	0.006	0.679	-0.842	0.400	-0.422	0.518	0.347	0.682**
6.	Inflorescence length (cm)	-0.005	0.011	0.207	-0.440	0.239	-0.704	0.713	0.214	0.235*
7.	Inflorescence width (cm)	-0.009	0.008	0.159	-0.402	0.217	-0.525	0.956	0.116	0.520**
8.	Seed volume weight (g/10ml)	0.000	0.005	0.616	-0.691	0.322	-0.349	0.257	0.431	0.590**

The inter-relationship of the characters as revealed by the path coefficient analysis using genotypic correlation is presented in (Table 4.5).

4.5.1 Direct Effects of Component Characters on Seed Yield

In present study, the character inflorescence width (0.956) showed highest direct positive effect on seed yield per plant followed by plant height (0.836), seed volume weight /10ml (0.431), inflorescence per plant (0.400), days to 50 per cent flowering (0.01). Thus, direct selection for these traits will be beneficial in yield improvement programme. The characters branches per plant (-0.842), inflorescence length (-0.704), days to maturity (-0.050), showed negative direct effect on seed yield per plant.

Venkatesh *et al.* (2014) also reported positive direct effect of seed weight, and plant height these results were similar. Khurana *et al.* (2013) reported that leaf length (0.099), plant height (0.092) had highest positive direct effect on total green yield were similar and but inflorescence length were in contrast, which showed direct negative effect on seed yield per plant. These results might be due to difference in material used or environmental effects on grain yield in quinoa. Most of the characters were in accordance with the findings of Bhargava *et al.* (2007a) but character *viz.*, plant height, was in contrast, which showed direct negative effect on seed yield per plant. These results might be due to difference in material used or environmental effects. Venkatesh *et al.* (2014) also reported positive direct effect of seed weight, panicle length and plant height on grain yield in grain amaranth. Khurana *et al.* (2013) reported that the number of leaves per plant had highest positive direct effect (0.493) on total green yield followed by leaf area index (0.427), leaf length (0.099), plant height (0.092) and leaf width (0.049) in amaranth. The indirect effect of leaf area index on total green yield was highest (0.454) in positive direction *via* number of leaves per plant.

4.5.2 Indirect Effect of Component Characters on Seed Yield

4.5.2.1 Days to 50 per cent flowering (No.)

Days to 50 % inflorescence appearance was reported to have highest positive indirect effect on seed yield per plant through branches per plant (0.195) followed by inflorescence length (0.186). It showed negative indirect effect *via*

inflorescence width (- 0.477), plant height (-0.275), inflorescence/ plant (-0.096), days to maturity (-0.037) and seed volume weight / 10 ml (-0.008).

4.5.2.2 Days to maturity (No.)

Its maximum indirect positive effect was observed *via* inflorescence length (0.151) followed by branches per plant (0.100), days to 50 % flowering (0.013). Its maximum indirect negative effects was observed *via* plant height (-0.204) followed by inflorescence length (-0.151), inflorescence per plant (-0.046), seed volume weight /10 ml (-0.039).

4.5.2.3 Plant height (cm)

Its maximum indirect positive effect was observed *via* inflorescence per plant (0.325) seed volume weight/10 ml (0.318) followed by inflorescence width (0.182), days to maturity (0.012). Its indirect negative effects was observed *via* branches per plant (-0.707) followed by, inflorescence length (-0.175) and days to 50 % flowering (-0.006).

4.5.2.4 Branches per plant (No.)

Its maximum indirect positive effect was observed *via* plant height (0.702) followed by inflorescence width (0.456), inflorescence per plant (0.400), seed volume weight/10 ml (0.354), days to maturity (0.006). Its maximum indirect negative effects was observed *via* inflorescence length (-0.368) followed by days to 50% maturity (-0.004).

4.5.2.5 Inflorescence per plant (No.)

Its maximum indirect positive effect was observed *via* plant height (0.679) followed by inflorescence width (0.518), seeds volume weight/ 10 ml (0.347) and days to maturity (0.006). Its maximum indirect negative effects was observed *via* branches per plant (-0.842), followed by inflorescence length (-0.422), days to 50 per cent flowering (-0.004).

4.5.2.6 Inflorescence length (cm)

Its maximum indirect positive effect was observed *via* inflorescence width (0.713) followed by number of inflorescence per plant (0.239), seed volume weight/ 10 ml (0.214), plant height (0.207) and days to maturity (0.011). Its maximum indirect negative effects was observed *via* branches per plant (-0.440) followed by days to 50 per cent flowering (-0.005).

4.5.2.7 Inflorescence width (cm)

Its maximum indirect positive effect was observed *via* inflorescence / plant (0.217) followed by plant height (0.159), seed volume weight/10 ml (0.116) and days to maturity (0.008) Its maximum indirect negative effects was observed *via* inflorescence length (-0.525) followed by branches per plant (-0.402) and days to 50 per cent flowering (-0.009).

4.5.2.8 Seed volume weight g /10 ml

Its maximum indirect positive effect was observed *via* plant height (0.616) followed by inflorescence per plant (0.322), inflorescence width (0.257) and days to maturity (0.005). Its maximum indirect negative effects was observed *via* branches per plant (-0.691) followed inflorescence length (-0.349) and days to 50 per cent flowering (-0.000).

Bhargava *et al.* (2007b) reported from the path analysis that test weight (1.057) had highest positive direct relationship with seed yield, followed by total chlorophyll (0.559) and branches per plant (0.520). Some traits showing high negative direct effect were leaf carotenoid (-0.749), seed size (-0.678) and days to flowering (-0.377).

Direct effect of any character on yield gives an idea about low reliable selection which can be made for a particular character to bring improvement in the yield. If the correlation between a casual factor and the direct effect is more or less in magnitude, it explains the free relationship between the characters and direct selection through these traits will be effective.

However, if the final correlation coefficient is positive and the direct effect is negative or negligible than the indirect casual factors are to be considered simultaneously for selection.

The days to 50 per cent flowering showed maximum indirect positive effect *via* branches per plant followed by inflorescence length. The days to maturity showed maximum indirect positive effect was observed *via* inflorescence length followed by branches per plant and days to 50 % flowering. The plant height showed indirect positive effect was observed *via* seed volume weight/10 ml followed by inflorescence width, days to maturity. The branches per plant showed maximum indirect positive effect

was observed *via* plant height followed by inflorescence width seed volume weight /10 ml, inflorescence/plant, days to maturity. The inflorescence per plant showed indirect positive effect was observed *via* plant height followed by inflorescence width, seeds volume weight/10 ml and days to maturity. The inflorescence length showed indirect positive effect was observed *via* inflorescence width followed by inflorescence per plant, seed volume weight/10 ml, plant height and days to maturity. The inflorescence width showed indirect positive effect was observed *via* inflorescence per plant followed by plant height seed volume weight/10 ml and days to maturity. Seed volume weight / 10 ml showed indirect positive effect was observed *via* plant height followed by inflorescence per plant, inflorescence width and days to maturity.

In present study, the character inflorescence width showed highest direct positive effect on seed yield per plant followed by plant height, seed volume weight/10 ml, inflorescence per plant, days to 50 per cent flowering. Thus, direct selection for these traits will be beneficial in yield improvement programme. The characters branches per plant, inflorescence length, days to maturity, showed negative direct effect on seed yield per plant.

4.6 Genetic Divergence

Selection of elite genotypes with high performance for yield and yield contributing component with suitable genetic divergence among them is the most important and difficult job in starting any hybridization programme. It would be possible to identify desirable genotypes from the genetic variability estimated, but it is difficult to expect any extraordinary result from their progeny unless we have knowledge about divergence between them.

Genetic diversity between genotypes was calculated by distance statistic (D^2) given by Mahalanobis (1936) which acts as an important tool for plant breeder. The degree of divergence between biological population at genotypic level and the relative contribution of different components to the total divergence at both intra and inter cluster levels can be evaluated by this method. Rao (1952) first time suggested the application of this technique for the assessment of genetic diversity in plant breeding. It is used in plant breeding for classifying the genetic stocks, based on genetic divergence between populations.

4.6.1 Cluster Formation

Cluster formation was done by following Tocher's method as described by Rao (1952). The 30 genotypes were grouped into eleven clusters. Cluster I with 11 genotypes followed by clusters II with 7 genotypes, cluster V, IX and XI with 2 genotypes each. While, remaining all other clusters *viz.*, III, IV, VI, VII, VIII and X were solitary. (Table 4.6).

Table 4.6. Distribution of 30 genotypes of quinoa into eleven clusters

Clusters	No. of genotypes included	Genotypes
I	11	EC-896215, EC-896271, EC-896229, EC-896237, EC-896275, EC-896088, EC-896210, EC-896087, EC-896203, EC-896109, EC-896112.
II	7	EC-896059, EC-896083, EC-896206, EC-896086, EC-896105, EC-896115, EC-896098.
III	1	EC-507747
IV	1	EC-896097
V	2	EC-896108, EC-896212
VI	1	EC-896089
VII	1	EC-507139
VIII	1	EC-896207
IX	2	EC-896209, IC-411824
X	1	EC-896114
XI	2	EC-896116, EC-896202

4.6.2 Genetic Distance (D^2)

Genetic divergence in 30 genotypes of quinoa was measured by Mahalanobis (1936) D^2 statistics. The calculated D^2 values varied from 1.94 to 12.05 (Table 4.7). This high range for D^2 values indicate high amount of genetic diversity present in the genotypes. The lowest value was between the cluster V while, the highest was between cluster V and X.

Table 4.7. Average intra (bold) and inter cluster D values for eleven clusters in thirty quinoa genotypes

Cluster No	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	2.29	3.33	3.10	3.81	7.82	3.43	3.45	2.75	4.38	5.56	4.52
II		2.56	4.92	3.65	9.91	3.15	3.70	3.27	3.95	3.89	3.64
III			0.00	4.89	7.55	4.52	3.95	3.89	4.61	7.00	5.98
IV				0.00	9.97	2.53	3.47	2.58	4.22	6.06	4.84
V					1.94	10.19	9.71	8.88	10.68	12.05	10.31
VI						0.00	3.04	2.37	4.37	5.20	5.19
VII							0.00	3.19	5.17	6.11	5.26
VIII								0.00	4.39	5.85	5.13
IX									2.11	4.36	4.06
X										0.00	3.92
XI											2.70

The basic concept behind the formation of clusters is to get intra and inter cluster distance. This acts as index for selection of parents with diverse origin. The intra and inter cluster values are means derived from D^2 values of cluster elements. The crossing between the genotypes in different clusters with high inter cluster D^2 values will prove to be more correct approach to get desirable results.

4.6.3 Intra and Inter-cluster Distance

The averages inter and intra cluster 'D' values are presented in Table- 4.7. The averages inter and intra cluster 'D' values are presented in Table 4.7. The maximum intra cluster distance was registered between cluster XI (2.70) followed by cluster II (2.56), I (2.29), IX (2.11), V (1.94) and rest of cluster had zero intra cluster distance as they have only one genotype (monogenic). The high intra cluster distance values revealed the presence of genetic diversity between genotypes which were grouped together in those clusters. The maximum inter cluster distance showed by cluster X and cluster V (12.05) followed by cluster IX and V (10.68), cluster XI and V (10.31) and cluster VI and V (10.19). The minimum D^2 values observed between cluster VIII and VI (2.37) followed by cluster VI and IV (2.53), cluster (VIII and IV) (2.58) and cluster VIII and I (2.75).

Considering the intra cluster distance, cluster XI had maximum intra cluster distance followed by cluster II suggesting that genotypes present in these clusters might have different genetical architecture (Table 4.7). However, lowest intra cluster distance was observed in cluster V indicating that genotypes present in these cluster might have genetical similarities with one another and appeared to have evolved from the common gene pool. Cluster III, IV, VI, VII, VIII and X showed no intra cluster distance due to its monogenotypic nature.

In present investigation grouping of genotypes into 11 clusters suggested the presence of substantial amount of genetic diversity in the material under investigation. Wide range of diversity was reported by earlier workers.

While evaluating quinoa genotypes, Rojas (2003) to determine genetic diversity of quinoa. About 92 per cent of the accessions were readily classified into seven groups identified by cluster analysis. The Mahalanobis distance D^2 method was used to show their statistical differences. Even incorrectly classified accessions were identified and reassigned to more appropriate group. Bhargava *et al.* (2007b) all the germplasm lines were grouped into six clusters based on average linkage method. Cluster III had high values for seed yield and most of the quality traits but showed a small seed size. Mhada *et al.* (2014) hierarchical cluster analysis rearranged the 78 quinoa accessions into four main groups and ten sub-clusters. Clustering was found in associations with days to maturity and also with plant size and seed-size traits. divergence. Cluster III exhibited higher mean for days to 50 per cent flowering, plant height, primary branches per plant, secondary branches per plant. Pandey and Singh (2011) 98 genotypes of grain amaranth (*Amaranthus hypochondriacus* L.) genotypes were grouped into 18 clusters in which cluster I contained maximum number of genotypes (42), Cluster II (11), Cluster III (7), Cluster IV and V (5 in each case) and Cluster VI has 4 genotypes. Cluster VII, VIII, IX, X have (3 in each), cluster XI, XII, XIII, XIV (2 in each) and clusters XV, XVI, XVII and XVIII (1 in each case). Gerrano, *et al.* (2015) thirty two *Amaranthus* genotypes grouped into six different groups and a singleton based on their genetic similarity. The clustering of the genotypes based on their genetic similarity will help in the identification of diverse parents for use in the breeding programme.

4.6.4 Cluster Means for Different Characters

The mean performances of cluster values of twelve characters are presented in Table 4.8. A considerable inter cluster variation in respect of cluster was observed among the various clusters for nine characters studied.

4.6.4.1 Days to 50 per cent flowering (No.)

The genotypes in cluster IX were early for days to 50 per cent flowering (43.50 days) followed by cluster X (43.67 days). Whereas, genotypes present in cluster V (55.17 days) and cluster VII (52.00 days) were late for days to 50 per cent flowering.

4.6.4.2 Days to maturity (No.)

On the basis of cluster means it was found cluster X (100.67 days) matured earliest followed by cluster IX (101.00 days). Cluster V (122.33 days) and cluster were comparatively late in maturity followed by cluster I (106.06 days).

4.4.6.3 Plant height (cm)

Cluster mean for plant height was maximum for cluster IX (169.10 cm) followed by cluster IV (168.93 cm). The cluster X (139.67 cm) and cluster II (142.89 cm) recorded comparatively less in height.

4.4.6.4 Branches per plant (No.)

Cluster IX (42.95) recorded maximum branches per plant followed by cluster III (40.47). The cluster II (27.64) and cluster X (28.13) recorded less branches per plant respectively.

4.4.6.5 Inflorescence per plant (No.)

Cluster mean for inflorescence per plant was maximum for cluster IX (37.83) followed by cluster III (35.78), cluster IV (30.90) and cluster VII (30.13). The cluster II (23.63) had minimum inflorescence per plant followed by cluster cluster VI (23.87).

4.4.6.6 Inflorescence length (cm)

Cluster IX (26.17 cm) recorded highest cluster mean for inflorescence length followed by cluster X (25.68 cm). Cluster XI (17.40 cm) and cluster V (20.92 cm) show comparatively low value of inflorescence length.

Table 4.8. Mean values of the eleven clusters for nine characters in thirty Quinoa genotypes

Cluster No.	Days to 50 % flowering (No.)	Days to maturity (No.)	Plant height (cm)	Branches/ plant (No.)	Inflorescences/ plant (No.)	Inflorescence length (cm)	Inflorescence width (cm)	Seed volume weight (g/10ml)	Seed yield/ plant (g)
I	49.45	106.06	145.04	30.93	26.24	21.95	17.10	6.77	20.03
II	48.34	102.80	142.89	27.64	23.63	21.85	17.61	6.49	19.40
III	49.07	106.00	153.43	40.57	35.78	25.23	19.17	7.52	20.69
IV	50.00	102.00	168.93	37.42	30.90	23.40	17.40	7.30	25.77
V	55.17	122.33	145.47	30.40	25.85	20.92	17.43	6.59	21.05
VI	49.33	101.23	144.40	28.53	23.87	23.90	16.05	7.05	20.50
VII	52.00	101.33	148.33	35.63	30.13	22.40	17.53	6.74	20.47
VIII	49.33	103.67	153.13	31.90	26.30	22.11	15.33	6.58	19.13
IX	43.50	101.00	169.10	42.95	37.83	26.17	20.90	7.42	25.48
X	43.67	100.67	139.67	28.13	24.10	25.68	21.10	6.06	22.33
XI	45.33	102.50	150.87	31.72	25.87	17.40	17.38	6.58	24.36

4.4.6.7 Inflorescence width (cm)

Cluster X (21.10 cm) recorded highest cluster mean for inflorescence width followed by cluster IX (20.90 cm), cluster III (19.17 cm). Cluster VIII (15.33 cm) and cluster VI (16.05 cm) show comparatively low value of inflorescence width.

4.4.6.8 Seed volume weight / 10 ml (g)

Cluster mean for seed volume weight / 10 ml was maximum for cluster III (7.52 g) followed by cluster IX (7.42 g). Whereas, minimum seed volume weight / 10 ml were in cluster X (6.06 g) followed by cluster II (6.49 g).

4.4.6.9 Seed yield per plant (g)

Cluster IV (25.77 g) and cluster IX (25.48 g) exhibited highest seed yield per plant. The lowest seed yield per plant was observed for cluster VIII (19.13 g) followed by cluster II (19.40 g) and cluster I (20.03 g).

4.7 Per cent Contribution of 12 Characters for Divergence

All the 30 genotypes of quinoa were studied for 9 characters and the data collected was used to determine divergence (Table 4.9). According to wilks test, Out of 9 characters studied, the days to maturity (28.97 %) showed maximum contribution towards divergence. It was followed by inflorescence width (20.00 %), no of branches per plant (14.94 %), days to 50 % flowering (14.48 %) , seed volume weight/10 ml (7.13 %), inflorescence length (5.98), plant height (5.52 %), seed yield per plant (2.30 %) and number of inflorescence per plant (0.69 %).

Table 4.9. Per cent contribution of 9 characters for divergence

Sr. No.	Source	Times ranked first	Contribution (%)
1.	Days to 50 % flowering (No.)	63	14.48
2.	Days to maturity (No.)	126	28.97
3.	Plant height (cm)	24	5.52
4.	Branches per plant (No.)	65	14.94
5.	Inflorescence per plant (No.)	3	0.69
6.	Inflorescence length (cm)	26	5.98
7.	Inflorescence width (cm)	87	20.00
8.	Seed volume weight /10 ml (g)	31	7.13
9.	Seed yield per plant (g)	10	2.30
		Total	100

The magnitude of contribution by inflorescence per plant and seed yield per plant was low.

5. SUMMARY AND CONCLUSION

The present investigation, “Genetic variability and genetic diversity studies for yield and yield contributing traits in Quinoa (*Chenopodium quinoa* Willd.) genotypes” was undertaken with following objective.

1. To study the genetic variability for yield and yield contributing traits in Quinoa.
2. To study the genetic diversity in Quinoa.

Thirty genotypes of quinoa collected from AICRN on Potential Crops, MPKV, Rahuri-413 722, Dist. Ahmednagar, Maharashtra (India). The experiment was laid out in a randomized block design with three replications during *Rabi* 2019. The observations were recorded on yield and yield attributing characters *viz.*, days to 50 per cent flowering, days to maturity, plant height, branches per plant, inflorescence per plant, inflorescence length, inflorescence width, seed volume weight/ 10 ml and seed yield per plant.

Wide range of variation was observed for all characters under study. Analysis of variances exhibited significant treatment mean square for all the characters studied. It revealed the presence of considerable amount of variability evaluated.

5.1 Mean Performance

Highly significant differences among 30 genotypes were obtained. The the earliest days to 50 % flowering and days to maturity showed by EC-896209, EC-896114 and IC-411824. The genotypes EC-896209 and IC-411824 recorded higher plant height. IC-411824 showed highest performance for branches per plant, inflorescence per plant, inflorescence length, inflorescence width followed by EC-896209. The highest yield per plant showed by EC-896097 followed by EC-896209 and IC-411824. The highest seed volume weight / 10 ml showed by EC507747 followed by EC-896209 and IC-411824.

5.2 Genetic Variability

The magnitudes of high GCV and high PCV for inflorescence per plant. Thus, this character provide good source of variation and hence inflorescence per plant useful in crop improvement programme in quinoa. However, moderate amount of GCV and PCV observed for branches per plant, inflorescence length, inflorescence width and seed yield per plant.

The highest heritability was observed for days to maturity followed by inflorescence per plant, days to 50 % flowering, branches per plant, inflorescence length, inflorescence width, seed volume weight/10 ml, seed yield per plant, and plant height. Therefore, it can be concluded that environmental effects are least on the characters studied.

The inflorescence per plant showed highest genetic advance as present mean followed by branches per plant, inflorescence width, inflorescence length and seed yield per plant. Moderate genetic advance as per cent mean observed for seed volume weight /10 ml, days to 50 % flowering and days to maturity.

High heritability coupled with high genetic advance as per cent mean was observed for inflorescence per plant, branches per plant, inflorescence length, inflorescence width and seed yield per plant. It suggests the role of additive gene effect and direct selection is possible for all these characters. there is scope for improvement of these characters having high heritability coupled with genetic advance in breeding programme. High heritability coupled with moderate genetic advance as per cent mean was observed for days to 50 % flowering, days to maturity and seed volume weight/10 ml. While plant height showed the high broad sense heritability accompanied with low genetic advance this indicates that heritability is due to non-additive gene action and heterosis breeding will be effective for improvement of this character.

5.3 Correlation

In present study seed yield per plant had positive and significant correlation with plant height, branches per plant, inflorescence per plant, inflorescence length, inflorescence width, seed volume weigh/10 ml both at genotypic and phenotypic level. It had negative and highly significant correlation with days to maturity and days to 50 per cent flowering both at genotypic and phenotypic level except days to maturity at phenotypic level. This indicates the dependency of these characters on each other.

Days to 50 % flowering showed positive and significant correlation with days to maturity. Plant height showed positively significant correlation with branches per plant, inflorescence per plant, inflorescence length, inflorescence width, seed volume weight/10 ml both at phenotypic and genotypic level. Branches per plant showed significant positive correlation with inflorescence per plant, inflorescence length, inflorescence width and seed volume weight/10 ml plant both at phenotypic and

genotypic level. Inflorescence per plant showed significant and positive correlation with inflorescence length. Inflorescence width, seed volume weight/10 ml both at phenotypic and genotypic level. Inflorescence length showed highly significant and positive correlation with inflorescence width and seed volume weight/10 ml both at genotypic and phenotypic level. Inflorescence width showed significant and positive correlation with seed volume weight/10 ml at genotypic level and positive and non significant at phenotypic level. The character seed volume weight/10 ml had positive and significant correlation at genotypic and phenotypic level with seed yield/plant, respectively.

5.4 Path Analysis

The path analysis revealed the character inflorescence width showed highest direct positive effect on seed yield per plant followed by plant height, seed volume weight/10 ml, inflorescence per plant, days to 50 per cent flowering. Exhibited high direct effects in the desirable direction and also confirmed their strong association with seed yield per plant indicating, the true and perfect relationship between them and it suggested that, direct selection based on these characters would help in selecting the high yielding genotypes in quinoa. The characters branches per plant, inflorescence length, days to maturity, showed negative direct effect on seed yield per plant.

The days to 50 per cent flowering showed maximum indirect positive effect *via* branches per plant followed by inflorescence length. The days to maturity showed maximum indirect positive effect was observed *via* inflorescence length followed by branches per plant and days to 50 % flowering. The plant height showed indirect positive effect was observed *via* seed volume weight/10 ml followed by inflorescence width, days to maturity. The branches per plant showed maximum indirect positive effect was observed *via* plant height followed by inflorescence width seed volume weight /10 ml, inflorescence/plant, days to maturity. The inflorescence per plant showed indirect positive effect was observed *via* plant height followed by inflorescence width, seeds volume weight/10 ml and days to maturity. The inflorescence length showed indirect positive effect was observed *via* inflorescence width followed by inflorescence per plant, seed volume weight/10 ml, plant height and days to maturity. The inflorescence width showed indirect positive effect was observed *via* inflorescence per plant followed by plant height seed volume weight/10 ml and days to maturity. Seed volume weight/10 ml showed indirect positive effect was observed *via* plant height followed by inflorescence

per plant, inflorescence width and days to maturity. In present study residual effect at genotypic level was 0.276, which suggested that there might be few more component traits responsible to influence the green fodder yield/.plant than those studied (Table 4.5).

5.5 Genetic Diversity

In the present investigation D^2 values between all possible pairs of 30 genotypes ranged between 1.94 and 12.05. Total eleven clusters were formed using Tocher's method as described by Rao (1952). Cluster I was the largest cluster with 11 genotypes followed by cluster II with 7 genotypes, cluster V, IX, XI with 2 genotypes while, cluster III, IV, VI, VII, VIII and X were monogenotypic.

The maximum intra cluster distance was observed for the cluster XI followed by cluster II, I, IX and V suggesting that, genotypes present in these clusters might have different genetic architecture. The maximum intercluster distance was observed between cluster X and V followed by cluster IX and V indicating wide divergence among these clusters. This suggested that genotypes present in one cluster differ entirely from those parents in another cluster. The minimum inter cluster distance was observed between cluster VIII and VI.

Conclusions

From the above discussion it may be concluded that,

1. Analysis of variance revealed highly significant differences among the thirty genotypes for all the traits studied in quinoa indicating that all these traits are applicable to exploitation.
2. Based on mean performance of genotypes, the genotypes IC-411824, EC-896209, EC-507747, EC-896114 and EC-896097 were found superior for most of the characters.
3. The phenotypic variance and phenotypic coefficient of variation were slightly higher than the corresponding genotypic variance and genotypic coefficient for all the characters under study.
4. The significant treatment differences of 30 genotypes indicated good amount of variability for all the characters studied. In the present investigation inflorescence per plant showed high magnitude of GCV and PCV and characters like branches per plant, inflorescence length, inflorescence width and seed yield/ plant showed

moderate magnitude of GCV and PCV which shows good scope for their improvement through selection.

5. High heritability (b.s.) with high genetic advance as present mean was recorded for inflorescence per plant, branches per plant, inflorescence width, inflorescence length, seed yield per plant indicate that these traits were predominantly governed by additive gene action and selection of these traits would be more effective for desired genetic improvement.
6. Seed yield per plant exhibited positive correlation with plant height, branches per plant, inflorescence per plant, Inflorescence length, inflorescence width, seed volume weight per 10 ml.
7. In path analysis, the highest positive direct effect on seed yield per plant was through inflorescence width followed by plant height, seed volume weight/ 10 ml, inflorescence per plant and days to 50 % maturity. The characters, branches per plant, days to maturity and inflorescence length had high negative direct effect on seed yield per plant. By considering the overall indirect effect of all characters, plant height, n branches per plant, inflorescence per plant, seed volume weight/ 10 ml, inflorescence width, inflorescence length contributed indirectly towards seed yield per plant.
8. Path analysis showed direct selection based on character inflorescence width, plant height, seed volume weight /10ml, inflorescence per plant and days to 50 per cent flowering can help in the improvement of seed yield in quinoa.
9. All 30 genotypes under study were grouped into eleven clusters. The maximum intra cluster distance was observed for cluster XI and inter cluster distance was maximum between cluster X and V. Highest mean values showed by cluster IX for characters inflorescence length, inflorescence per plant, plant height, branches per plant. Cluster V showed highest mean values for days to 50 % flowering and days to maturity.
10. Out of 9 characters studied, the days to maturity showed maximum contribution towards divergence. It was followed inflorescence width, branches per plant (14.94 %), days to 50 % flowering, seed volume weight/10 ml, inflorescence length (5.98), plant height, seed yield per plant and inflorescence per plant.

11. Based on intercluster distance, intracluster distance and *per se* performance the genotypes viz., EC-896097, EC-896108, EC-896212, EC-896209 and IC-411824 can be used for future breeding programme.

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* Originals not seen

7. VITAE

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MASTER OF SCIENCE (AGRICULTURE)

in

**AGRICULTURAL BOTANY
(GENETICS AND PLANT BREEDING)**

2020

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