

**GENETIC DIVERSITY, CORRELATION AND PATH
ANALYSIS STUDIES IN CHICKPEA
(*Cicer arietinum* L.)**

**GADKAR UTKARSH GANESH
B.Sc. (Agriculture)**

**MASTER OF SCIENCE
IN
AGRICULTURE
(AGRICULTURAL BOTANY)
(GENETICS AND PLANT BREEDING)**



**DEPARTMENT OF AGRICULTURAL BOTANY
(GENETICS AND PLANT BREEDING)
COLLEGE OF AGRICULTURE, BADNAPUR
VASANTRAO NAIK MARATHWADA KRISHI VIDYAPEETH PARBHANI
– 431 402 (M.S.) INDIA
2022**

**“GENETIC DIVERSITY, CORRELATION AND PATH
ANALYSIS STUDIES IN CHICKPEA
(*Cicer arietinum* L.)”**

BY
GADKAR UTKARSH GANESH
B.Sc. (Agriculture)

A thesis submitted to
Vasant Rao Naik Marathwada Krishi Vidyapeeth, Parbhani
in partial fulfillment of the requirement for the degree of

**MASTER OF SCIENCE
IN
AGRICULTURE
(AGRICULTURAL BOTANY)
(GENETICS AND PLANT BREEDING)**



**DEPARTMENT OF AGRICULTURAL BOTANY
(GENETICS AND PLANT BREEDING)
COLLEGE OF AGRICULTURE, BADNAPUR
VASANTRAO NAIK MARATHWADA KRISHI VIDYAPEETH
PARBHANI – 431 402 (M.S.) INDIA**

2022

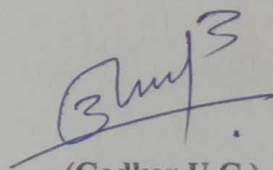
CANDIDATE'S DECLARATION

I hereby declare that the thesis entitled, "**GENETIC DIVERSITY, CORRELATION AND PATH ANALYSIS STUDIES IN CHICKPEA (*Cicer arietinum* L.)**", submitted by me is based on the actual work carried out by me under the guidance and supervision of **B. G. Kamble**. The extent of information derived from the existing literature have been duly cited and referenced. The existing research work or its any part is not submitted anywhere else for the award of any degree or diploma.

I also hereby declare that no sentence, equation, diagram, table, paragraph or section has been copied verbatim from previous work unless it is cited and duly referenced. There is no plagiarism; the work presented is original and own work of the researcher. No ideas, process, results or words of others have been presented as researcher's own work.

Place: Badnapur

Date: 30/11/2022



(Gadkar U.G.)

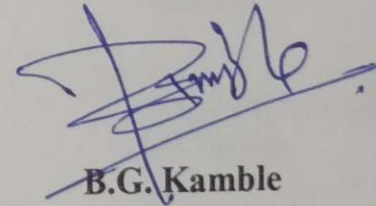
Reg.no.2020A07MB

CERTIFICATE – I

This is to certify that the thesis entitled, “**Genetic Diversity, Correlation and Path Analysis Studies in Chickpea (*Cicer arietinum* L.)**” submitted by **GADKAR UTKARSH GANESH** Reg. No. 2020A07MB in partial fulfillment of the requirements for the award of the degree of **MASTER OF SCIENCE (Agriculture)** in the subject of **AGRICULTURAL BOTANY (GENETICS AND PLANT BREEDING)** submitted to the Vasantao Naik Marathwada Krishi Vidyapeeth, Parbhani is a record of bonafide research work carried out by him under my guidance and supervision. The thesis or its any part has not previously formed the basis for the award of any degree, diploma or other similar title.

Place: Badnapur

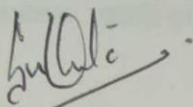
Date: 30/11/2022



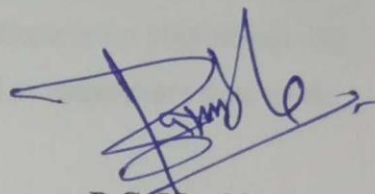
B.G. Kamble
Research Guide and Chairman
Advisory Committee

CERTIFICATE – II

This is to certify that the thesis entitled, “Genetic Diversity, Correlation and Path Analysis Studies in Chickpea (*Cicer arietinum* L.)” submitted by GADKAR UTKARSH GANESH Reg. No. 2020A07MB in partial fulfillment of the requirements for the award of the degree of MASTER OF SCIENCE (Agriculture) in the subject of AGRICULTURAL BOTANY (GENETICS AND PLANT BREEDING) to the Vasantao Naik Marathwada Krishi Vidyapeeth, Parbhani has been approved by the Student's Advisory Committee after viva voce examination of the student in collaboration with the External Examiner.

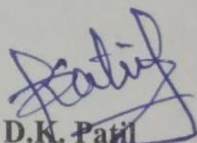
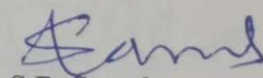
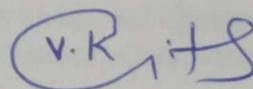
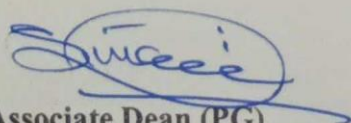


S. M. Umate
External Examiner



B.G. Kamble
Research Guide & Chairman
Advisory Committee

Advisory Committee:


D.K. Patil
Member
S.B. Sarode
Member
V. K. Gite
Member

Associate Dean (PG)
College of Agriculture,
VNMKV Parbhani.



Associate Dean and principal
College of Agriculture,
Badnapur.

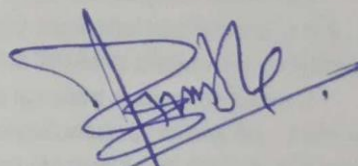
PLAGIARISM CLEARANCE CERTIFICATE

This is to certify that thesis entitled, "**Genetic Diversity, Correlation and Path Analysis Studies in Chickpea (*Cicer arietinum* L.)**" submitted by **GADKAR UTKARSH GANESH** Reg. No. 2020A07MB has been properly examined by URKUND: Anti plagiarism Software. The percentage of similarities found in the thesis is 2 %.

No sentence, equation, diagram, table, paragraph or section has been copied verbatim from previous work unless it is duly cited and referenced. The work presented is original and own work of the researcher (i.e. there is no plagiarism). No ideas, process, result or words of other have been presented as researcher's own work.

Place: Badnapur

Date: 30/11/22



B.G. Kamble

Research Guide and Chairman
Advisory Committee

Document Information

Analyzed document	U G Gadkar.docx (D151498816)
Submitted	2022-11-30 12:00:00
Submitted by	B G Kamble
Submitter email	kamble.jau@gmail.com
Similarity	2%
Analysis address	kamble.jau.vnmkv@analysis.urkund.com

Sources included in the report

SA	VNM Krishi Vidyapeeth / Utkarsh Gadkar Msc Thesis draft2022.pdf	 2
	Document Utkarsh Gadkar Msc Thesis draft2022.pdf (D151484627)	
	Submitted by: kamble.jau@gmail.com	
	Receiver: kamble.jau.vnmkv@analysis.urkund.com	

Entire Document

CHAPTER – I INTRODUCTION

CHAPTER – I

INTRODUCTION

Chickpea (*Cicer arietinum* L.), belongs to the family Fabaceae, sub-family Faboideae. It is a autogamous legume crop with chromosome no. $2n = 14$ or $2n = 16$. Others names for chickpea includes Gram, Bengal Gram, Garbanzo bean and Egyptian pea. The Bengal gram

seed is a quality source of proteins and carbohydrate, which add up to 80 % of the total dry weight of seed.

The root system in Gram is tap root with root nodules. Roots are robust and make its major portion up to 60 cm, although as deep as 2 m. The stem is generally herbaceous, may be shrubby and erect or spreading with much branching. The stem may be of dark green, bluish green or olive colour and has glandular pubescence. Leaves are stipulate, alternate, imparipinnate, glandular, pubescent with 3-8 pairs of leaflets and a top leaflet (rachis ending in a leaflet) pinnately compound and have pulvinate leaf base, leaflets ovate to elliptic. The flower of chickpea is complete, bisexual, zygomorphic, hypogynous, pentamerous solitary, axillary and polypetalous standard aestivation. Calyx is gamosepalous, lanceolate and densely covered with hairs. Corolla is polypetalous, papilionaceous having five petals, odd petal posterior, consisting of a posterior standard two lateral wings, two anterior ones forming a keel (enclosing stamens and pistil), vexillary aestivation. Stamens are ten in number in diadelphous (9 anthers are fused + 1 anther is free), condition of ovary is superior, sessile, inflated and pubescent. Fruits (pods) known as Legume. Pods are rhomboid ellipsoid, containing one/two or rarely three seeds and inflated, glandular-pubescent. Seed colour cream, yellow, brown, black, or green, rounded to angular, seed coat smooth or wrinkled. Generally Chickpea (*Cicer arietinum* L.) is divided into two type Kabuli and Desi. Desi type is distinguished by small, coloured, angular shaped seeds with high content of fibre

ACKNOWLEDGEMENT

"Words provide wings to our ideas but not always can words express our feelings in words or languages". No research work is possible alone, as it requires many minds and hands to beautify and to make it possible. Formal words cannot carry the fragrance of emotions with them; still they are only available means of expressing emotions."

No words would suffice to reveal the depth of my repeal and deep sense of gratitude to the Chairman of my Advisory Committee and Research Guide, *Dr. B. G. Kamble*, Associate Professor, Section Of Agricultural Botany, College Of Agriculture, Badnapur, VNMKV Parbhani. For guidance, constructive criticism, motivation, urge and zeal, lead me towards successful completion of my research work, I take this opportunity to express my deep and sincere feeling of gratitude to him for suggesting research topic, talented versatile advice and untiring efforts in preparation of the manuscript of this dissertation.

I wish to express my sincere thanks to *Dr. Indra Mani*, Hon. Vice-chancellor, VNMKV, Parbhani and *Dr. D.N. Gokhale*, Director, *Dr. P.G. Ingole* Ex- Director of Instruction and Dean Faculty of Agriculture, VNMKV, Parbhani and *Dr. D. P. Waskar* Director of Research, VNMKV, Parbhani and *Dr. R.D. Ahire* Associate Dean and Principal, College of Agriculture, Badnapur.

It is my great privilege and pleasure to record my deep sense of gratitude to the members of my advisory committee, *Dr. D. K. Patil*, principal scientist (plant breeding) & I/c agriculture research station, badnapur, VNMKV Parbhani. and *Dr. S. B. Sarode*, Scientist (plant breeding) agriculture research station, badnapur. and *Dr. V. K. Gite*, Scientist (plant breeding) agriculture research station, badnapur. for their valuable guidance and help during my course of investigation.

I extend my immerse pleasure to *Dr. V. K. Gite* for their help and guidance during my research work.

I wish to express my heartfelt, cordial, sincere and inherent thanks to my Department senior Shivajee Tengse, Nitin Gavhane, Anirudhha Madane and friends Sonali Gaikwad, Deepak, Bhagyashri, Kajal, Navnath Bhosle, Santosh, Ankush and my beloved juniors 2K21 Batch for their everlasting vibrant encouragement during carrying out this experimentation and untiring help was rendered with cheerful smiling gestures.

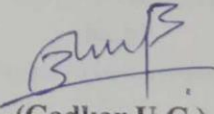
It gives me immense pleasure to acknowledge the vote of thanks to my juniors Nitin Shelke, uddhav parihar, eknath dubhalkar, akash jawle, tejas raywade, shubham jadhav, abhi kamble for their invaluable cooperation, endless help and moral support throughout this research programme.

I would like to take this opportunity to express my deepest and sincere gratitude to my family, Father Shree. Ganesh sopan gadkar, Mother Shreemati. Lalita ganesh gadkar and Brother sudarshan gadkar.

I am especially great to Jagananthi Gaware (Samarth Computers) And Sonu (jay malhar tea house). whose immense help made me possible to complete this manuscript.

Lastly, I express my regards to those whose names I have forgotten to mention here.

Place: Badnapur
Date: 30/11/22


(Gadkar U.G.)
Reg. No. 2020A07MB

CONTENTS

Sr. No.	Particulars	PageNo.
1.	Declaration by the Candidate	i
2.	Certificate – I	ii
3.	Certificate – II	iii
4.	Plagiarism Clearance Certificate	iv
5.	First Page of Plagiarism Report	v
6.	Acknowledgement	vi-vii
7.	List of Tables	viii
8.	List of Figures	ix
9.	List of Plates	x
10.	Abbreviations Used (if any)	xi
11.	Thesis Abstract	xii-xiv
12.	Chapter - I : Introduction	1-4
13.	Chapter - II : Review of Literature	5-24
14.	Chapter - III : Materials and Methods	25-38
15.	Chapter - IV : Results and Discussion	39-77
16.	Chapter - V : Summary and Conclusions	78-81
17.	Literature Cited	82 -92
18.	Curriculum Vitae	93

LIST OF TABLES

Table. No.	Particulars	Page No.
3.1	List of germplasms	26
4.1	Analysis of variance	40
4.2	Mean performance of germplasms	41-44
4.3	Estimates of variability parameters for ten different characters of chickpea	48
4.4	Composition of forty one chickpea germplasms into different clusters by Tocher's method	51
4.5	Average intra and inter cluster distance D^2 values	52
4.6	Average intra and inter cluster distance D values	53
4.7	Cluster means for yield and its components in chickpea	55
4.8	Per cent contribution of different characters to genetic diversity	57
4.9	Estimation of phenotypic (above diagonal) correlation coefficients	60
4.10	Estimation of genotypic (above diagonal) correlation coefficients	61
4.11	Direct and indirect effect of yield and its component character on grain yield at phenotypic level	66
4.12	Direct and indirect effect of yield and its component character on grain yield at genotypic level	67

LIST OF FIGURES

Figure No.	Title	In Between Pages
4.1	Formation of cluster by Tocher's method	52-53
4.2	Diagram showing the contribution towards Divergence	57-58
4.3	Diagram showing the phenotypic correlations of yield and its component characters in chickpea	64-65
4.4	Diagram showing the genotypic correlations of yield and its component characters in chickpea	67-68

LIST OF PLATES

Plate No.	Title	In Between Pages
3.1	A general experimental view for genetic diversity studies in chickpea	38-39

ABBREVIATIONS

%	:	Per cent
/	:	Per
C.D.	:	Critical Differences
cm	:	Centimetre
d.f.	:	Degree of freedom
e.g.	:	Example gratia (for example)
et.al.	:	Et alia (and others)
Etc.	:	Et cetra
Fig.	:	Figure
Ha	:	Hectare
i.e.	:	That is
j.	:	Journal
Kg	:	Kilogram
M	:	Million
M/ha	:	Million per hectare
m ²	:	Square meter
MS	:	Mean square
MSe	:	Error mean square
MT	:	Metric tonnes
q/ha	:	Quintal per Hectare
Sci.	:	Science
SE	:	Standard error
SE (d)	:	Standard error of difference
SE(m)	:	Standard error of Mean
Sr. No.	:	Serial number
Unpub.	:	Unpublished
Viz.,	:	Videlicet (namely)
Vs	:	Versus
σ	:	Standard Deviation
Σ	:	Summation

THESIS ABSTRACT

THESIS ABSTRACT

1. Title of the Thesis : **“Genetic Diversity, Correlation and Path Analysis Studies in Chickpea (*Cicer arietinum* L.)”**
 2. Name of the candidate : Gadkar Utkarsh Ganesh
 3. Name of Research Guide : B.G. Kamble
 4. Department : Agricultural Botany (Genetics and Plant Breeding)
 5. College/ University : College of Agriculture, Badnapur.
V. N. M. K. V. Parbhani
 6. Degree to be awarded : M. Sc. (Agriculture)
-

ABSTRACT

The current study, “Genetic Diversity, Correlation and Path Analysis Studies in Chickpea (*Cicer arietinum* L.)” was carried out to examine the magnitude of genetic diversity, correlation and path analysis for yield and yield contributing characters in forty one diverse genotypes of chickpea at College of Agriculture, Badnapur, in the Rabi season of 2021-22. Thirty six genotypes of chickpea along with five standard checks viz. Akash (BDNG-797), Digvijay, Vijay, Phule Vikram and JAKI 9218 were evaluated in RBD (randomized block design) with 2 replications. Observations were recorded for ten traits viz., days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight, seed yield per plant and harvest index.

The ANOVA differences were found statistically significant for most of the characters. The magnitude of the GCV and PCV (genotypic and phenotypic coefficients of variation) indicated that the experimental materials had a high amount of variability. In the current study, high estimates of the GCV and PCV (genotypic and phenotypic coefficient of variation) were seen for seed yield per plant followed

by number of pods per plant, 100 seed weight, plant height and number of secondary branches per plant. The highest broad sense heritability was observed for plant height followed by 100 seed weight, days to maturity, seed yield per plant, number of pods per plant, days to 50 % flowering, number of primary branches per plant, number of secondary branches per plant, number of seeds per pod and harvest index. The highest genetic advance as per cent of mean was noticed for the character number of pods per plant followed by plant height, seed yield per plant, 100 seed weight, days to maturity, days to 50% flowering, harvest index, number of secondary branches per plant, number of primary branches per plant and number of seeds per pod.

Based on D^2 values all the genotypes were grouped into twelve clusters with the varying number of genotypes in the clusters. The clustering pattern of these genotypes does not follow the geographical distribution. The maximum genetic distance (D) of 34.89 was found between the clusters VI and XII. The intra cluster distance (D^2) ranges from 68.72 to 90.06. The inter cluster distance (D^2) ranges from 49.00 to 1217.31. The maximum inter cluster distance ($D^2 = 1217.31$) was observed between cluster VI and cluster XII followed by cluster XII and VIII ($D^2 = 1069.94$), cluster VI and cluster X ($D^2 = 962.24$), cluster V and cluster VI ($D^2 = 919.90$) and cluster V and VIII ($D^2 = 860.24$). The minimum inter cluster distance ($D^2 = 49.00$) was between clusters III and VII.

The characters viz. number of pods per plant, 100 seed weight, harvest index, number of secondary branches per plant and plant height recorded highly positive significant correlation with seed yield at both genotypic and phenotypic level. This indicates the simultaneous improvement of these characters through selection.

From path coefficient analysis it is indicated that the characters viz., 100 seed weight, number of pods per plant, number of secondary branches per plant, days to 50% flowering, harvest index and number of primary branches per plant on seed yield in decreasing order of magnitude revealing that these were major yield contributing traits in chickpea.

The phenotypic coefficients of variation (PCV) were slightly higher than the genotypic coefficients of variation (GCV), indicating that the environment plays a role in governing these traits. Similarly, the magnitude of GCV and PCV was observed high for the characters viz., seed yield per plant followed by number of pods

per plant, 100 seed weight, plant height, number of secondary branches per plant and number of primary branches per plant. It indicates that the selection of desired germplasm for these traits may be worthwhile for improving seed yield in the future breeding programme.

Keywords: Chickpea, Genetic Diversity, Correlation, Path Analysis, and Phenotypic coefficient of variation and seed yield per plants.

CHAPTER – I
INTRODUCTION

CHAPTER – I

INTRODUCTION

Chickpea (*Cicer arietinum* L.), belongs to the family Fabaceae, sub-family Faboideae. It is a autogamous legume crop with chromosome no. $2n = 14$ or $2n = 16$. Others names for chickpea includes Gram, Bengal Gram, Garbanzo bean and Egyptian pea. The Bengal gram seed is a quality source of proteins and carbohydrate, which add up to 80 % of the total dry weight of seed.

The root system in Gram is tap root with root nodules. Roots are robust and make its major portion up to 60 cm, although as deep as 2 m. The stem is generally herbaceous, may be shrubby and erect or spreading with much branching. The stem may be of dark green, bluish green or olive colour and has glandular pubescence. Leaves are stipulate, alternate, imparipinnate, glandular, pubescent with 3-8 pairs of leaflets and a top leaflet (rachis ending in a leaflet) pinnately compound and have pulvinate leaf base, leaflets ovate to elliptic. The flower of chickpea is complete, bisexual, zygomorphic, hypogynous, pentamerous solitary, axillary and polypetalous standard aestivation. Calyx is gamosepalous, lanceolate and densely covered with hairs. Corolla is polypetalous, papilionaceous having five petals, odd petal posterior, consisting of a posterior standard two lateral wings, two anterior ones forming a keel (enclosing stamens and pistil), vexillary aestivation. Stamens are ten in number in diadelphous (9 anthers are fused + 1 anther is free), condition of ovary is superior, sessile, inflated and pubescent. Fruits (pods) known as Legume. Pods are rhomboid ellipsoid, containing one/two or rarely three seeds and inflated, glandular-pubescent. Seed colour cream, yellow, brown, black, or green, rounded to angular, seed coat smooth or wrinkled.

Generally Chickpea (*Cicer arietinum* L.) is divided into two type *Kabuli* and *Desi*. *Desi* type is distinguished by small, coloured, angular shaped seeds with high content of fibre and *Kabuli* type characterized by large, coloured, ram-head-shaped, seeds with low content of fibre.

The World Health Organization (WHO) recommends 80 g of pulses per capita per day, but the Indian Council of Medical Research (ICMR) recommends 70 g per capita per day. The protein content of pulses is two to three times more than that of cereal grains.

Not only do pulses have high protein content, but they also have a high concentration of some necessary amino acids, which are either absent or present in very little amounts in cereals. Also, several of the sulphur-containing necessary amino acids, such as methionine, which are deficient in pulses, are abundantly available in the cereals.

Chickpea seeds have an average protein content of 23%, a total carbohydrate content of 64%, 5.0% fat, 6.0% crude fibre and 2.0% ash. The mineral content is also high, containing phosphorus (P) (340mg/100g), calcium (Ca) (190mg/100g), magnesium (Mg) (140mg/100g), iron (Fe) (7mg/100g) and zinc (Zn) (3mg/100g) (Jukanti *et al.* 2012).

Chickpea is a nutrient-rich food, providing rich content (20% or higher of the Daily Value, DV) of protein, foliate dietary fibre and certain dietary minerals, such as iron and phosphorus in a 100 gram reference amount. Vitamin B6, thiamine, magnesium, and zinc contents are moderate, providing 10–16% of the Daily Value (DV). Compared to reference levels established by the UN Food and Agriculture Organization and World Health Organization (WHO), proteins in cooked and germinated chickpeas are rich in essential amino acids such as lysine, isoleucine, tryptophan, and total aromatic amino acids. A 100 gram serving of cooked chickpeas provides 164 kilocalories (690 kJ). Cooked chickpea are 60 per cent water, 9 per cent protein, 27 per cent carbohydrates, and 3 per cent fat 75 per cent of the fat content is unsaturated fatty acids for which linoleic acid comprises per cent of total fat (WHO).

Legumes have a unique place in Indian agriculture due to their ability to maintain and restore soil fertility, as well as their nutritious importance. Legumes improve soil health by biological nitrogen fixation in the roots, which is helped by the symbiotic bacteria *Rhizobium*. Among the legumes, chickpea is a prime *Rabi* crop in India. Chickpea ranks top in production and area among the pulses grown in the country.

Chickpea is exported from India to countries such as Algeria, Saudi Arabia, Sri Lanka, Pakistan, Arab EMTS and Gulf countries; however, it is imported from Tanzania, United States, Australia, Russia and Canada. (Anonymous, 2018-19).

During 2019-20, India had an area of 106 lakh ha with a 111 lakh tons of production and 1056 kg/ha. productivity, while Maharashtra had an area of 20.38 lakh ha with a 17.29 lakh tonnes of production and productivity of 849 kg/ha. Marathwada had an

area of 10.59 lakh ha with a 7.96 lakh tonnes of production and a 760.54 kg/ha productivity. (Anonymous, 2019-20).

In India area and production of chickpea is 9.85 million Ha and 11.99 million tonnes production with average productivity of 1217 kg/ha during 2020-2021. (Directorate of Economics & Statistics 2021).

In India Madhya pradesh has largest acreage and production followed by Rajasthan. The average yield of chickpea in India only 942 kg/ha. (Directorate of Economics & Statistics Report 2020-2021).

In Maharashtra Amravati district leads in chickpea production, with a share of 8%, followed by Ahmadnagar (7%), Akola (7%), Hingoli (6%), Washim (5%), Buldhana (5%), Latur (5%), Osmanabad (5%), Nagpur (5%), Jalgaon (5%), Nanded (5%) and other district in the state by 38%.

In Marathwada region highest area (9.89 lakh/ ha), production (7.96 lakh tonnes) and productivity (707 kg/ha) of the year chickpea was recorded in 2020-2021. The region is having 36.53 % contribution in the state area with 35.38 % production share of the state Average of last ten years. (Chief Statistician Commisionarate of Agriculture Report, Pune 2020-2021).

Even though Chickpea is widely grown in India, the productivity of chickpea in particular and pulses in general has stayed constant over the years. Therefore, knowledge of the nature and extent of genetic divergence is crucial and it is necessary to acutely analyse formulation of yield in diverse chickpea material. This in turn aids in developing the selection strategy and locating diverse parents which upon hybridization results in to wide range of gene combination.

Associations of one or more traits influenced by a number of genes are explored statistically by calculating correlation coefficients. Genotypic conjugation between characters is measured through genotypic correlation coefficient. While Wright's (1921) method of partitioning the correlation into direct and indirect effects by path coefficient analysis provides valuable information on the relative merit of the trait in the selection criteria. Genetic divergence among the parents is heritable is a crucial for cultivar improvement. In a breeding programme selection of parents is of utmost importance. Genetic diversity among the parents is essential for crop improvement because a crosses

involving genetically different parents is likely to produce high heterotic effects and more variation in segregating generations, which can be utilized for the crop advancement.

Genetic diversity or variability in plants impacts their potential for enhanced efficiency and thus their utilization for breeding programme, which may ultimately lead to increased food production. Genetic diversity knowledge helps in the recognition of gene stock, the tagging of germplasm and the initiation of core collections (Upadhyaya *et al.* 2007). The more genetically diverse parents have chosen for hybridization, the greater chances of enhancing the traits under consideration (Chowdhury *et al.* 2002).

In general, plant breeders choose the parents based on phenotypic divergence, but for efficient breeding, an understanding of the genetic divergence among the parents with regard to the desired traits is essential.

The Mahalanobis (1936) D^2 statistic is useful technique for calculating the divergence between two populations. Numerous investigations using this technique revealed that geographical diversity is not necessarily related to genetic diversity. It so provides clearer idea regarding the degree of divergence which is independent of size of sample and provides the criteria for selection of parental lines for future breeding programme.

Thus, the current study on chickpea (*Cicer arietinum* L.) was conducted to examine the Genetic Diversity, Correlation and Path Analysis in Chickpea (*Cicer arietinum* L.) in Forty One genotypes with the following objectives.

1. To study the genetic distinctiveness in chickpea.
2. To study association and path analysis for yield and yield contributing characters in chickpea.

CHAPTER – II
REVIEW OF LITERATURE

CHAPTER – II

REVIEW OF LITERATURE

The literature for current study, “**Genetic Diversity, Correlation and Path Analysis Studies in Chickpea (*Cicer arietinum* L.)**” has been reviewed under the following topics:

2.1 Genetic diversity:

2.2 Correlation and path analysis:

2.1 Genetic diversity:

The concept of D^2 statistic for estimating the divergence between two populations was established by Mahalanobis (1936). It produces a result depending on the degree of divergence and an independent sample size. It computes a generalized distance between any pairs of groups and divides breeding material into neat groups. Genetic diversity has a important role in the effective selection of parents for hybridization. The genetic variations observed between individuals and genetic stocks in relation to an single trait or array of traits is referred as genetic divergence.

Mahalanobis *et al.* (1936) applied D^2 statistic technique in the thorough study of anthropometric data of Uttar Pradesh dividing in 23 groups and 3 major clusters that were Brahmin (B-cluster) of the top of the Hindu social hierarchy comprising 9 groups, the Artisan (A-cluster) in the middle consisting of 4 groups and the Trival (T- cluster) at the 40 bottoms consisting of 10 groups.

Damber and Deshmukh (1984) reported considerable differences between clusters mean for seed size, yield plant, pods per plant and growth period, indicated that these traits were involved in divergence. Genetic diversity and genotypic diversity were unrelated.

2.1.1 Genetic diversity in chickpea:

Dasgupta *et al.* (1987) observed 22 varieties of *Cicer arietinum* L. and were grouped in to 5 clusters with 100 seed weight giving the maximum contribution to divergence. The clusters of *kabuli* type were diffrent from that of *desi* types and there was

no relationship seen between the clustering pattern and geographical distribution of the varieties.

Vijay Kumar *et al.* (1991) observed genetic diversity derived from data on 9 characters in 104 diverse genotype of Chickpea (77 *Desi* and 27 *Kabuli* types; both exotic and Indian material), grown during *rabi* 1985-86. Substantial diversity existed both within and between the 6 clusters, with the largest cluster containing 89 genotypes. Cluster pattern was not correlated with geographical origin or cultivar type.

Singh and Sareen (1993) reported that the data for days to 50 % flowering and seed yield were used for meteriglyps and index score analysis. The majority of *Kabuli* types were medium to late with average yield, whereas the *Desi* types were early and average yielding. D² analysis showed that maximum genetic distance was 10.55 (L 144 and C 214), 1366 (L144 and JG84) and 7.7 (L 532 and 132) over the 3 respective sowing dates.

Rao and Singh (1994) observed that the 25 genotypes clustered in to 3 group, 20 in group I, and 2 and 3 genotypes in groups II and III, respectively. The components days to days to maturity, .pods per plant and 100 seed weight accounted for the maximum divergence. Cluster I had the genotypes with pods per plant, medium seed size moderate yielders. Cluster II genotypes had wide plant spread, small seed size and high yield while cluster III had genotypes of poor yielding ability and small seeds. The genotypes JG 315, JG S6-S and JG 86-22 were recommended for use in crop improvement.

Pooran and Singh (1995) observed and grouped into six clusters. The genotype of cluster VI (C-235) and cluster IV (BG-273 and BG-276) were highly divergent it is suggested that varieties of cluster IV and cluster VI and cluster II and VI should be hybridized in breeding programme.

Deshmukh and Patil (1997) revealed fifty genotypes of Chickpea (*Cicer arietinum* L.) were grouped in to 11 clusters on the basis of Mahalanobis's D² analysis of data 7 yield related traits from trials conducted during *rabi* 1993-94. Data are tabulated on intra cluster and inter cluster distances.

Narendra Kumar (1997) studied sixty germplasm lines of Chickpea (*Cicer arietinum* L.) for 7 traits grouped into 5 clusters. The D² values between clusters varies from 8.0 to 38.2. Involving parents from cluster II and V in hybridization could produce

higher yielding varieties based on the mean performance, genetic distance and clustering patterns.

Sivakumar and Muthiah (2000) grouped cultivars into seven clusters. The highest differences were seen in clusters IV and VII while the lowest was among clusters IV and V. The inter cluster difference varied from 0 to 2.99. The highest inter cluster distance observed in cluster I having 108 genotype lines. Cluster III having *kabuli* types of chickpea genotypes was little diverse from the *desi* types. This was confirmed in the canonical root square analysis.

Nimbalkar and Harer (2001) studied forty genotypes into sixteen clusters. D^2 values among all possible pair of forty genotypes ranges between 12.62 to 3979.93. 10 of the 16 clusters were monogenotypic. The Cluster II had the most genotypes (12), after that clusters I (9) and IV (3). Cluster XVI and cluster III genotypes were more diverse than others. The main traits contributing to genetic diversity were pods per plant, plant height, and 100 seed weight (gram) based on variance of cluster means.

Gumber *et al.* (2002) observed the maximum heritability in number of pods per plant followed by number of secondary branches and 100 seed weight. Grain yield and seeds per pod had the highest estimation of the phenotypic coefficient of variation (PCV).

Jeena and Arora (2002) studied 28 genotypes and reported that cluster I content two genotypes each in cluster II and III, and monogenotypic clusters were II, V, VI, VII. Genotypes of similar origin in different clusters suggested the influence of human intervention and Eco geographical distribution. Excluding single genotype cluster all the other clusters were heterogeneous. A defined relationship between genetic diversity and geographic origin was not established.

Kashyap and Rastogi (2003) reported genetic diversity by D^2 statistical techniques for traits seed yield and its components in sixty chickpea genotypes. The germplasm lines grouped into six clusters, with cluster I (14 genotypes) having the highest intra- cluster distance. Cluster III and VI were observed as more genetically diverse.

Noor *et al.* (2003) observed days to maturity, number of secondary branches, days to flowering, and 100 seed weight these traits had medium to high genetic advance, whereas for other traits, low to high genetic advance seen along with low to medium heritability. The genotypes used in this study may limit the potential to improve these

characters through direct selection. It was concluded that improving chickpea cultivars with high seed yield and biological yield should be emphasized to improve seed yield.

Jeena *et al.* (2005) observed the eighty genotypes of chickpea. The maximum number of genotype lines was in cluster I (60 genotypes) after that cluster II (7 genotypes). It was observed geographical distribution and genetic divergence did not clearly related with each other. Based on inter cluster distances, crossing between BGM-419 and KPG 33 are expected to produce a broad spectrum of variability in segregating generation to isolate transgressive segregants for yield and its components.

Sandu *et al.* (2006) reported that the genotypes were grouped in to ten clusters, 3 of which were more genetically diverse than the others. Common genotypes were sorted out with in a cluster for combination of environments and pooled data over environments.

Dubey and Srivastava (2007) reported that the intra cluster distances varied from 0.00 to 18.55. The cluster III and I were largest with 12 and 13 genotypes each. The 6 cluster containing only one genotype was the most divergent. The inter cluster distance was minimum (7.81) among cluster II and cluster IV and was maximum at (56.55) among cluster III and cluster VI. These finding suggested that there was much divergence in the population of the forty genotypes and as also the hybridization between the cluster by varieties of their wide genetic diversity.

Dwevedi *et al.* (2009) carried out among the twenty five genotypes of chickpea to study the nature and degree of genetic variation using D^2 statistics technique. The data were recorded on 10 prime quantitative parameters from the germplasm accessions raised in RBD with 3 replication. The 25 genotypes were grouped into 6 clusters. The cluster I seen as largest cluster having 8 genotypes. Maximum inter cluster distance was seen among cluster III and VI, after that cluster I and VI. Among the all character studied harvest Index, 100 seed weight and number of pods per plant these three characters contributed most to the genetic divergence. Pods per plant had maximum PCV and GCV (Phenotypic and Genotypic Coefficient of Variation) , followed by biological yield per plant and 100 seed weight. A medium to high magnitude of heritability and genetic advance was observed for pods per pant, harvest index and biological yield. The genotypes KPJ 59, PBJ 1 and Pusa 329 were recognised as genetically diverse parents, which can be useful for future cultivar advancement programmes.

Sharma and Saini (2010) studied twenty eight genotypes of chickpea including checks which reported the presence of variability with high heritability for the yield and its contributing components.

Devendrappa *et al.* (2011) found that days to physiological maturity and seed yield per plant contributed the most to the total genetic diversity. Cluster VIII and cluster X had the highest inter-cluster distance, after that cluster IX and X, that had the highest diversity among them.

Khan and Khan (2011) examined 47 chickpea germplasm lines to study the nature and magnitude of genetic diversity. Days to 50% flowering, 100 seed weight, days to maturity, biological yield per plant, and grain yield per plant all showed maximum significant differences among genotypes. The highest GCV and PCV (phenotypic and genotypic coefficient of variation) was seen in seed yield per plant, and biological yield per plant respectively.

Singh *et al.* (2012) examined the sixty four chickpea genotypes that includes sixty interspecific derivatives, their parents and two standard checks, to study the nature and magnitude of genetic diversity using D^2 statistical technique. The maximum inter-cluster distance was seen between cluster VI and IX while the maximum intra cluster distance was seen among the genotypes of cluster VIII. Characters like seed yield, biological yield per plot and days to 50% flowering contributed most to the genetic diversgance.

Gul *et al.* (2013) examined 20 genotypes of *Cicer arientinum* L. in which broad sense (b.s.) heritability estimates were maximum for primary branches per plant, pods per plant, 100 seed weight, seed yield per plant and secondary branches per plant. The genetic advance was maximum for seed yield per plant, pods per plant, primary branches per plant and secondary branches per plant.

Jivani *et al.* (2013) investigated the degree of genetic variability, heritability and genetic advance and genetic divergence using 105 diverse genotypes of chickpea. The analysis of variance indicated the prevalence of sufficient genetic variation among the genotypes for all 11 traits. High heritability along with a high genotypic coefficient of variation and higher genetic advance as per cent of mean was seen for seed yield per plant, number of pods per plant biological yield per plant, harvest index and 100-seed

weight which showed that response to selection would be very high for these yield contributing components.

Yadav *et al.* (2015) evaluated forty-five promising chickpea genotypes. High GCV and PCV were recorded for plant height, primary branches per plant, pods per plant, 100-seed weight and seed yield per plant. The distinctness among GCV and PCV was very little in all these traits indicating negligible role of environment. The characters, which showed poor estimates for PCV and GCV were days to maturity, days to 50 per cent flowering and number of seeds per pod. In the present study, high heritability along with high genetic advance was recorded for seed yield per plant and primary branches per plant indicated the presence of a considerable amount of total variation due to genetic causes particularly the additive gene effects to be important for determining these traits. On the other hand, high heritability with moderate genetic advance was observed for number of primary branches, plant height and pods per plant indicating the influence of environment for these traits. Low heritability percentage coupled with low and moderate genetic advancement has been observed for days to maturity indicated that this trait was greatly influenced by environment biological yield, harvest index with seed yield per plant.

Jakhar *et al.* (2016) studied 40 genotypes of chickpea. 10 quantitative characters including grain yield were considered for the study. The character 100 seed weight was the highest contributor towards divergence 61.54% after that pods per plant 15.00%, days to 50% flowering and seed yield per plant 6.92%, secondary branches 4.23%, seeds per pod 2.18%, protein content 1.55% and number of primary branches 0.64%. The lowest contributors for divergence were the days to maturity and height of the plant (0.51%).

Alka Dev *et al.* (2017) tested sixty genotypes of chickpea in which the relative magnitude of difference between the PCV and GCV was lower for pods per plant, seeds per pod, 100 seed weight, number of nodules per plant and days to 50% flowering indicating that these traits were less affected by the environments. The estimates of broad sense heritability were highest for pod length, 100 seed weight, number of nodules per plant, days to 50% flowering and days to maturity.

Ambilwade *et al.* (2018) estimated genetic divergence in chickpea genotypes. The variation among genotypes was highly significant for plant height, number of primary

branches per plant, days to 50% flowering, days to maturity, number of secondary branches per plant, pods per plant, number of seeds per pod and harvest index.

Gediya *et al.* (2018) studied genetic diversity among 58 genotypes of chickpea, which were grouped into 16 clusters. Maximum genetic divergence was observed between cluster IX and XVI, followed by cluster IX and XIV, while closest proximity was noticed between cluster III and VIII. The characters viz., seed yield per plant, 100 seed weight, seeds per plant and pods per plant contributed much to the total genetic divergence. Based on cluster mean values, cluster XII was superior for seed yield per plant and harvest index; cluster XV for pods per plant, seeds per plant and first pod height and cluster X for 100 seed weight. For early flowering and maturing, cluster XIV was found superior, while cluster VII was best for protein content.

Thakur *et al.* (2018) assessed 100 genotypes in randomized complete block design with 2 replications in that study the analysis of variation showed highly significant differences among the genotype for all the characters studied viz., days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, total pods per plant, total number of seeds per pod, 100 seed weight (g), seed yield per plant (g) and harvest index (%) indicating thereby the wide range of genetic variability and scope of selection for these characters.

Aswathi *et al.* (2019) assessed the genetic variability for quantitative and qualitative traits in 52 chickpea genotypes. A significant variation was observed for all the characters. High phenotypic and genotypic coefficient of variation was observed for plant yield followed by 100 seed weight, number of pods per plant, number of seeds per pod, number of secondary branches and first pod height.

Janghel *et al.* (2019) studied 60 chickpea genotypes morphologically and classified them as per the guidelines for the conduct of DUS test of chickpea by the PPV & FRA, 2007, GOI. Among thirteen DUS traits recorded; 7 traits were found tri-morphic, 4 traits di-morphic and 2 traits polymorphic among 60 chickpea genotypes indicated the existence of a remarkable amount of genetic variability that has great potential to assign distinctive morphological profiles which could be used for varietal identification and further characterization.

Nadiya *et al.* (2019) reported that indigenous chickpea accessions were only from 3 governorates viz. the highest of seven accessions seed accessions were diverse concerning all seed characters studied, i.e. seed length (cm) and width (cm), 100-seed weight (gram) and seed colour. Seed length varied from 0.645 cm to 1.210 and seed width ranged from 0.505 cm to 1.005 cm. 100 seed weight were found to vary from 12.6 to 67.9 gram. Chickpea accessions were classified into 5 groups with scores from 1 to 5 based on simple 1 to complexity 5 of seed coat color pattern.

Ponnuru Akhil *et al.* (2019) estimated 15 characters to study genetic diversity using Mahalanobis D2 Statistics. Based on D2 values, 51 genotypes were grouped into 8 clusters. Cluster V consisted of a maximum of 18 genotypes, followed by Cluster VIII and cluster II, which had 11 and 9 genotypes, respectively.

Shedge *et al.* (2019) observed that the genotypes under study fall into 7 clusters. Cluster III was with the highest number of genotypes (11) followed by cluster II (10), clusters V (09), cluster VI (06) and IV and VII had one genotype. The maximum inter cluster distance ($D = 309.50$) was observed between cluster VII and cluster V, while the minimum inter cluster distance ($D = 41.46$) was observed between clusters IV and II. Considering all the traits, it was suggested that the genotypes in clusters VII and cluster V are suitable for the further breeding programmes having the most divergent.

Tamvar *et al.* (2019) studied 60 genotypes of chickpea. Genotypes were grouped into 5 clusters suggested the presence of wide genetic diversity among them. Among different 12 traits studied, protein content, 100-seed weight, number of secondary branches per plant, seed yield per plant, height at first pod, seed volume per weight, days to 50% flowering and number of primary branches per plant contributed very much towards genetic divergence. Based on inter-cluster distance, clusters III and IV followed by IV and V, and II and IV had maximum inter-cluster distance.

Bohare *et al.* (2020) studied genetic diversity in 49 genotypes of chickpea (*Cicer arietinum* L.) genotypes using Mahalanobis D2 Statistics. Based on D2 values, 49 genotypes were grouped into 17 clusters. Cluster III consisted of maximum 13 genotypes followed by Cluster I and cluster II which both had 10 genotypes. Inter cluster values varied from 4.31 to 26.36. The maximum inter cluster distance was recorded between cluster IX and XIII (26.36). Characters 100 seed weight (62.07%), days to 50% flowering

(17.94%) and canopy temperature depression (5.27%) contributed maximum towards diversity. Based on cluster mean values, cluster XIII was superior for yield per plot and 100 seed weight.

Chahande *et al.* (2020) studied 32 genotypes of chickpea (*Cicer arietinum* L.). 32 genotypes were grouped into 8 clusters. Cluster III consisted of maximum 9 genotypes, followed by Cluster II, cluster I and cluster IV, which had 8, 7 and 4 genotypes, respectively. Inter cluster values varied from 3.27 to 11.60. The maximum inter cluster distance was recorded between cluster IV and VI (11.60). Characters 100 seed weight (58.67%), days to maturity (13.91%) and days to 50% flowering (13.10) contributed maximum towards diversity. Based on cluster mean values, cluster IV was superior for 100 seed weight and seed yield per plant.

Shaikh *et al.* (2020) Assessment of genetic diversity existing in and within germplasm accessions for yield and its components to obtain superior recombinants which will be useful in understanding pattern of variation was performed utilizing the 36 genotypes and 4 standard checks of chickpea replicated twice. To study the nature and magnitude of genetic divergence using Mahalanobis (1936) D^2 statistics, phenotypic variances, coefficient of variation, heritability, genetic advance, correlation coefficient and path coefficient was estimated and cluster analysis was performed.

Kumar *et al.* (2021) evaluated chickpea genotypes for genetic divergence using Mahalanobis D^2 statistics. Cluster I had the most genotypes, with eleven, followed by cluster VI with eight, cluster III with seven and IV with five genotypes, while clusters II and V each had four genotypes. Cluster VII had a single genotype and was monogenic. Inter-cluster D^2 values varied from 30.73 to 204.05. Intra-cluster D^2 values varied from 0.00 to 25.16. Cluster V has the highest intra cluster distance followed by Cluster I and Cluster IV. Cluster II and VII (204.05) had the highest inter-cluster distance followed by Cluster II and V (170.79) and Cluster III and V (157.56).

Reddy *et al.* (2021) studied genetic diversity among 36 favorable genotypes of chickpea (*Cicer arietinum* L.) with help of Mahalanobis D^2 statistics. On the basis of D values, 36 genotypes were arranged into 5 clusters. The intra cluster distances were lower than inter-cluster distances, specifying that genotypes comprised within a cluster shows tendency to vary less apart from each other. Out of thirteen characteristics considered,

secondary branches per plant, number of pods per plant, seed yield per plant, harvest index and plant height, contributed very much in relation to genetic divergence.

Soumyashree et al. (2021) The present investigation was conducted for assessing genetic divergence among eighty nine chickpea genotypes. Based on D₂ values, the genotypes were grouped into seven clusters with highest inter cluster distance of 59.20 between Cluster I and VII. Cluster ranking, based on means showed Cluster IV at the top followed by Cluster II. With 72 genotypes, Cluster II was found to be largest, followed by Cluster III (6 lines), Cluster I (5 lines), while Cluster IV and VII had only 2 genotypes each. Intra cluster distance was highest in Cluster II (14.43) followed by Cluster III (6.22) whereas, inter cluster distance, varied between 12.89 (Cluster II and Cluster III) and 59.20 (Cluster I and Cluster VII).

Tengse *et al.* (2021) Chickpea genotypes and standard checks were replicated twice to measure genetic variety in and across germplasm groups for yield and its components in order to develop superior recombinants that would aid in the study of variation patterns. Mahalanobis (1936) D₂ statistics were used to determine phenotypic variances, coefficients of variation, heritability, genetic advance, and cluster analysis to study the nature and amount of genetic divergence. Data was gathered on eleven quantitative traits. Six clusters were formed from the sixty genotypes. Cluster I has the most genotypes, with 43. Clusters VI and IV had the greatest inter cluster distance, while cluster VI genotypes had the most intra cluster distance. The D (distance between clusters) ranged from 32.34% to 484.53. Cluster VI and cluster IV had the greatest inter cluster distance (D=484.53), followed by cluster VI and III (D=348.68), cluster VI and cluster I (D=327.59), cluster V and cluster III (D=315.96), and cluster IV and II (D=274.98). Clusters IV and IV had the smallest inter cluster distance (D=32.34). Clusters VI and IV had the highest value at the inter cluster level, followed by Clusters VI and III. The grouping means for different characters showed considerable differences among the clusters for all the characters.

2.2 Correlation and path analysis:

The concept of correlation was first put forward by Galton (1889) and later elaborated by Fisher (1918) and Wright (1921). The correlation coefficient is a statistical measure used to determine the degree and direction of a relationship between two or

more variables. It is symbolized by the letter "r." The correlation coefficients between all of the characteristics were calculated using the Searle (1961) method at the genotypic, phenotypic and environmental levels. Correlation studies improve comprehension of yield components which helps plant breeders during selection (Johnson *et al.*, 1955).

Basic concept of path coefficient was formulated by Sewall Wright in 1921. The correlation coefficient is a resultant of all paths connecting two variables, so the direct influence of a variable can be measured along a given path by standard deviation remaining in the effect after all other possible paths of influence are eliminated, while, the variation of the causes back of the given path is kept as great as ever regardless of their relations to other variables which have been made constant. Li (1956) focused on its importance and emphasized that practical implication of the method is greatly facilitated by formulation of a causal diagram.

Dewey and Lu (1959) applied the technique of path coefficient analysis for the first time in plant breeding using wheat grass (*Agropyron cristatum*) as a test genera and concluded that path coefficient method permits the separation of correlation into direct and indirect effects, a critical examination of specific forces acting to produce a given correlation and measures relative importance of each factor.

2.2.1 Correlation and path analysis in chickpea

Guler *et al.* (2001) investigated 5 chickpea lines for relationships between the yield and yield contributing components. In the evaluated traits, positive and significant relationships were recorded statistically between the seeds per pod and the pods per plant, between the seeds per plant and the pods per plant and the seeds per pod, between seed yield per plant and the pods per plant, the seeds per pod, the number of pods per plant; between the number of seeds per pod and seed yield per unit area; between the number of seeds per plant and seed yield per unit area. Negative and significant relationships were determined statistically between the number of pods per plant and 100 seed weight, between the number of seeds per pod and 100 seed weight, between the number of seeds per plant and 100 seed weight, between seed yield per unit area and 100 seed weight. The total determining coefficient related to 100 seed weight was 0.896 (89.6%) in the same model.

Jeena and Arora (2002) examined forty genotypes for yield and its contributing traits. Correlation between all the traits calculated and subjected to path analysis. The biological yield showed highest positive correlation with seed yield along with most positive direct effect on it. Major yield contributor traits from selection point of view were biological yield, number of pods per plant, 100 seed weight and first pod forming node.

Kumar *et al.* (2002) examined twenty four chickpea genotypes with eight quantitative traits in a randomized experiment. Results of correlation analysis showed that seed yield was positively associated with harvest index, number of pods per plant, biological yield and number of secondary branches per plant while negatively correlated with plant height. In all the yield components number of pods per plant positively associated with secondary branches per plant and biological yield per plant, while negatively related to 100-seed weight.

Saleem *et al.* (2002) examined interrelationships and path analysis of yield parameters in a set of 20 chickpea elite genotypes. Seed yield per plant was positively and significantly correlated with days to flowering, total weight of plant, number of pods per plant and 100-seed weight both at the genotypic and phenotypic levels. The correlation of secondary branches per plant with seed yield was negative and significant. pods per plant had maximum positive direct effect on seed yield. They concluded that pods per plant and 100 seeds weight could be employed as selection criterion to increase the yield.

Arora *et al.* (2003) examined 80 genotypes of chickpea for 18 traits including seed yield per plant. The correlation study showed that primary branches per plant expressed the highest significant positive relationship with seed yield per plant after that biological yield per plant, pods per plant, 100 seed weight, plant height, canopy spread, seeds per plant, secondary branches per plant and harvest index. Biological yield per plant had the highest positive direct effect on seed yield per plant followed by harvest index, pods per plant, 100 seed weight and seeds per pod.

Noor *et al.* (2003) investigated phenotypic and genotypic variances, heritability in broad sense (h^2), genetic advance, correlation and path analysis for yield and yield components in thirty chickpea genotypes under rainfed conditions. Moderate to high

genetic advance for days to flowering, days to maturity, secondary branches per plant, 100 seed weight, while low to moderate heritability observed with low genetic advance for other traits. Days to flowering, days to maturity, low seed weight exhibited high heritability coupled with high genetic advance hence cultivar advancement through these traits is possible by simple selection. It was concluded emphasis should be given on development of chickpea with higher seed weight and biological yield to improve grain yield. Correlation and path analysis showed that pods per plant and 100 seed weight were potential contributor to grain yield through direct effects.

Muhammad *et al.* (2004) examined variability, heritability, genetic advance, correlation coefficient and path coefficient for yield and its components in 24 advance lines of chickpea. High heritability with low G.A. of days to flowering, days to maturity and 100 seed weight showed the influence of dominant and episstatics genes for these characters. High heritability of secondary branches per plant and biological yield along with high G.A. revealed that additive gene effects are vital in determining these characters. Grain yield had positive and significant correlation with plant height, number of pods per plant, 100 seed weight and biological yield. High direct effects were contributed by biological yield and harvest index although the later had negative association with grain yield.

Renukadevi and Subbalaxmi (2006) estimated correlations and path coefficient analysis for 11 parameters including seed yield in 50 genotypes of chickpea (*Cicer arietinum* L.). Plant height, primary branches per plant, pods per plant, 100 seed weight, biological yield per plant and harvest index had positive and significant correlation with seed yield. The positive direct effect on seed yield was revealed by plant height, number of primary branches per plant, number of pods per plant, biological yield per plant, harvest index, days to maturity and soluble protein content. The studied eleven characters were responsible for majority variability in the seed yield.

Yucel *et al.* (2006) examined fifteen genotypes of *kabuli* type of chickpea. Investigation were done on the direct and indirect effects of yield components on seed yield per plant. Genotypic variance was the maximum for 100 seed weight followed by number of seeds per plant. Positive and significant ($P < 0.05$) relationship were determined between seed yield per plant and plant height, first pod height, secondary

branch, total pod and number of full pods and seeds per plant. This study suggests that seed and full pod numbers can be effective selection factors for improving seed yield per plant in *kabuli* type of chickpea.

Talebi *et al.* (2007) investigated the correlation and path analysis of the yield and yield components of thirty six genotypes of chickpea grown in dry land conditions. Based on statistical analysis, there was positive and significant correlation were found between 100 seed weight and plant height, between number of secondary branches and plant height, between days to heading and days to maturity, between days to maturity and number of primary and secondary branches, between seed yield and number of pods per plant and number of seeds per pod, between seed yield and biomass and harvest index were determined significantly. Negative and significant correlation were determined statistically between number of pods per plant and 100 seed weight, between seeds per pod and number of secondary branches. Harvest Index had the greatest direct effect on seed yield (PC = 0.901). Also, its indirect effect on seed yield was more positive through plant height, number of pods per plant, number of seeds per pod and biomass, but negative and low through days to heading and maturity, 100 seed weight and primary branches per plant. The selection for high seed yield should be based on biomass and harvest index.

Zena *et al.* (2008) investigated path coefficient analysis for enhance yield of chickpea thirty six genotypes of chickpea were tested in randomized block design (RBD) for total twelve quantitative characters including yield. Path coefficient analysis was carried out to examine the impact of various production parameters on the yield. The biological yield had recorded highest direct effect on the seed yield after that test weight, yield index, initial flowering period, maturity period, number of secondary branches per plant and number of seeds per pod respectively while 50% flowerings period has shown negative direct effect on the yield of gram.

Thakur and Sirohi (2009) examined 53 chickpea genotypes for correlation and path coefficient analysis. Correlation studies revealed that seed yield per plant exhibited stable positive association with biological yield per plant, number of pods per plant, number of primary branches per plant, plant height and harvest index at genotypic and phenotypic levels in individually as well as combined over seasons. Path analysis

indicated high positive and direct influence of biological yield per plant with seed yield per plant followed by harvest index and pods per plant in individual as well as combined over seasons.

Vaghela *et al.* (2009) investigated the correlation coefficient and path coefficient for yield and its components in chickpea. For majority of cases magnitude of genotypic correlation coefficients was greater than their corresponding phenotypic correlation coefficients for most of the traits. Seed yield per plant exhibited significant and positive correlation with biological yield, pods per plant, harvest index, seeds per pod, primary branches per plant and 100-seed weight at both genotypic and phenotypic levels. Path coefficient analysis indicated the highest positive direct effect of biological yield per plant followed by harvest index towards seed yield. The most important traits for selection criterion were biological yield per plant and harvest index were to enhance seed yield in chickpea cultivars.

Gohil and patel (2010) assessed 22 genotypes of chickpea that were genetically diverse under rainfed conditions to investigate the role of various characters to the yield. The genotypic correlation coefficients were higher than corresponding phenotypic ones for most of the traits combinations. 100-seed weight and harvest index had a significant positive association with seed yield. Number of pods per plant and number of seeds per pod had a positive association with seed yield. The maximum direct positive and negative contribution to seed yield was observed from biological yield per plant and days to maturity, respectively. The most significant characters which can be used in selection criterion to improve yield in chickpea under rainfed conditions were harvest index, 100-seed weight, pods per plant and earliness.

Kobraee *et al.* (2010) investigated correlation analysis and relationships between grain yield and quantitative traits in 3 chickpea cultivars and 3 sowing date. A 3 x 3 factorial experiment in RCBD format with 3 replications was conducted. The results indicated that both sowing date and cultivar had significant effect on grain yield and yield components. Early sowing in chickpea produced the highest plant height, distance of first pod from the earth surface, number of sub branches, number of pods per plant, number of seeds per plant, 100 seed weight, grain yield, biological yield and harvest index. There was significant difference between cultivars for grain yield. Results showed

that number of seeds per plant, number of pods per plant, plant height and biological yield had the highest positive correlation with grain yield. The number of seeds per plant had high and positive direct effects on seed yield.

Ali *et al.* (2011) estimated correlation for quantitative traits in chickpea. Correlation studies showed that biomass per plant, number of pods per plant, number of secondary branches per plant, number of seeds per pod and 100-seed weight were positive and significant at genotypic level but positive and highly significant at phenotypic level. Whereas number of days taken to flowering, number of days taken to maturity, primary branches per plant, secondary branches per plant were positively correlated with the grain yield per plant at genotypic and phenotypic levels. Plant height was negative and non-significantly correlated with grain yield per plant at both genotypic and phenotypic level.

Abhishek Kumar *et al.* (2012) investigated the genetic variability, character association and path analysis in early segregating population in chickpea. 100 seed weight followed by harvest index, pods per plant and seed yield per plant exhibited high estimates of heritability (b.s.) as well as genetic advance. Correlation coefficient analysis revealed that seed yield per plant exhibited significant and positive correlation with harvest index, 100 seed weight and number of pods per plant at both phenotypic and genotypic level. Direct selection for 100 seed weight and number of pods could be helpful in the improvement of chickpea breeding. Path analysis indicated that plant height, days to 50% flowering and number of pods per plant had high direct effect on seed yield at both phenotypic and genotypic levels.

Jivani *et al.* (2013) reported correlation and path coefficient analysis for seed yield per plant and its 10 contributing characters in 105 diverse chickpea genotypes. The seed yield per plant had significant and positive correlation with pods per plant, biological yield per plant and harvest index at genotypic as well as phenotypic level. Among all the component traits, biological yield per plant had significant and positive association with plant height, pods per plant and 100 seed weight. Path coefficient analysis recorded that the highest positive direct effect was seen for harvest index, after that biological yield per plant, number of pods per plant, and 100 seed weight towards

seed yield and were considered to be the most significant characters for selection for improvement of seed yield in chickpea.

Padmavathi *et al.* (2013) examined genetic variability, correlation and path analysis for yield and yield its component traits in 30 genotypes of *kabuli* type of chickpea. High genetic variability with high heritability and high genetic advance as per cent of mean was observed for primary branches per plant, biological yield per plant and seed yield per plant. Correlation studies showed that seed yield was significantly and positively correlated with plant height, primary branches per plant, secondary branches per plant, pods per plant, 100 seeds weight, harvest index and biological yield per plant. Path coefficient analysis indicated that biological yield per plant, number of pods per plant and harvest index had high positive direct effect on seed yield that indicated importance of these traits in improving of seed yield.

Gaur *et al.* (2014) reported that seed yield showed highly significant and negative correlation with plant height at phenotypic level and number of seeds per pod whereas, significant and negative correlation with number of branches per plant genotypic level and highly significant and negative correlation with number of pods per plant whereas, significant and negative correlation with number of seeds per pod number of pods per plant genotypic correlations were higher than phenotypic ones in magnitude for all the characters. The character which showed negative association at genotypic level also showed negative association at phenotypic level, and negative correlation with plant height number of pods per plant and number of seeds per pod path coefficient analysis indicated that the number of branches per plant 100-seed weight exhibited maximum direct effect on seed yield at genotypic level days to 80% maturity had positive but negligible direct effect whereas, days to flowering, plant height, number of pods per plant and number of seeds per pod exhibited negative direct effect on seed yield at genotypic level.

Bala *et al.* (2015) recorded significant and positive association of seed yield with pods per plant, harvest index, biological yield per plant and primary branches per plant.

Dhuria and Babbar (2015) evaluated 68 chickpea genotypes and reported that seed yield/plant was positive and significantly correlated with number of seed per pods, number of effective pods per plant, harvest index, total number of pods per plant,

biological yield per plant, days to maturity, number of secondary branches per plant and number of main branches per plant.

Chopdar *et al.* (2016) tested twenty genotypes of chickpea with 3 replications. Found that the seed yield per plant has a highly significant positive correlation with primary branches per plant, number of pods per plant, harvest index, number of seeds per pod, biomass per plant and 100 seed weight respectively. The expression of yield depends upon several yield contributing characters. The selection practiced for one trait may bring change in the other related traits.

Astereki *et al.* (2017) studied the correlation coefficients and path analysis between seed yield, morphological traits and yield components. Twenty five chickpea genotypes, including advanced lines and commercial varieties. The correlation coefficients indicated that there were significant and positive correlations between seed yield and number of pods per plant and harvest index in two years. Path analysis indicated that days to flowering, days to maturity, canopy height and width, number of pods per plant and flowering period directly and indirectly affected seed yield. Therefore, this study suggested that chickpea improvement program could be based on these traits, especially number of pods per plant and canopy height, according to positive direct effect on seed yield over two years, as selection criteria.

Singh *et al.* (2018) examined heritability, variability, and correlations between yield and yield components in fifteen chickpea genotypes for two years. Direct and indirect effects of yield components on seed yield per plant was recorded. Heritability for seed number, 100 seed weight, and full pods per plant were maximum than those for the other characters. Positive and significant ($P < 0.05$) relationships were seen among seed yield per plant and plant height, first pod height, secondary branches, total pod, number of full pods and number of seeds per plant. The path coefficient analysis based on seed yield per plant, as a dependent variable, showed that all of the other characters, except days to flowering, first pod height, and total pod number, exhibited high positive direct effects. Number of seeds and full pods showed the highest direct influence with 47.49% and 44.73%, respectively. Therefore, number of seed and full pod numbers can be good selection criterion for increasing seed yield per plant in Chickpea (*Cicer arietinum* L.).

Shara (2019) investigation was conducted to determine relationships among yield and some yield components using correlation and path coefficient analysis in chickpea grown under rainfed conditions. The character seed yield showed positive and highly significant correlation with most characters including plant height, number of branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight, dry matter weight, pods weight per plant, protein percentage and biological weight. The trait, dry matter weight per plant recorded the highest positive direct effect on seed yield reached 0.848, while the maximum positive indirect effect on seed yield recorded by weight of pods per plant.

Dawane *et al.* (2020) The present investigation was carried out for, Correlation studies and Path Coefficient Analysis in Chickpea (*Cicer arietinum* L.). Correlation studies showed that the traits viz. harvest index, number of pods per plant, 100 seed weight, number of seeds per pod and plant height exhibited positive and highly significant genotypic correlation with seed yield. This indicates that the simultaneous improvement of these characters through selection. Path coefficient analysis indicated that the characters viz number of primary branches per plant, plant height and days to 50 % flowering exhibited negative direct effect on seed yield per plant.

Shaikh *et al* (2020) studied phenotypic and genotypic path coefficient analysis studies in chickpea recorded that among all the component characters pods per plant showed the highest direct effect on seed yield followed by seeds per pod, 100 seed weight, secondary branches per plant, primary branches per plant while plant height, days to maturity and days to 50% flowering showed negative direct effect at phenotypic level.

Shaikh *et al* (2020) estimated phenotypic and genotypic correlation coefficients in yield and its component characters in chickpea recorded Seed yield per plant had positive significant correlation with number of pods per plant, number of seeds per pod, 100 seed weight, secondary branches per plant, harvest index and primary branches per plant.

Tengse *et al* (2021) The present investigation was carried out for correlation studies and path analysis in chickpea (*Cicer arietinum* L.). Correlation studies showed that the traits viz. harvest index, 100 seed weight, number of pods per plant and number of secondary branches per plant recorded a highly positive significant correlation with seed yield at both genotypic and phenotypic level and days to 50% flowering at genotypic

level with seed yield. From path coefficient analysis it is indicated that the characters viz., 100 seed weight, harvest index, number of pods per plant, days to 50% flowering and number of secondary branches per plant showed a positive direct effect on seed yield.

CHAPTER – III
MATERIALS AND METHODS

CHAPTER – III

MATERIALS AND METHODS

The current study, “**Genetic Diversity, Correlation and Path Analysis Studies in Chickpea (*Cicer arietinum* L.)**” was carried out at College of Agriculture, Badnapur, in the *Rabi* season of 2021-22. The detail description of the material used, methods implemented and statistical analysis followed during studies are described below.

3.1 Materials:

Experimental material comprising 41 elite germplasm lines of chickpea with wider variation for different traits were studied including 5 checks at College of Agriculture, Badnapur. The list of germplasm lines is given in Table 1.

3.2 Experimental design:

Thirty six genotypes of chickpea along with five standard checks viz. Akash (BDNG-797), Digvijay, Vijay, Phule Vikram and JAKI 9218 were evaluated in RBD (randomized block design) with 2 replications in the *Rabi* season of 2021-22. Genotypes were sown in one row of 4 m length with the spacing of 45 cm for row to row and 10 cm for plant to plant.

3.3 Cultural practices:

The land for the experiment was medium black which was brought to fine tilth. The fertilizer 25 kg N/ ha in the form of urea, 50 kg P₂O₅ in the form of SSP were applied as a basal dose at the time of sowing. In order to facilitate easy and better germination, a light irrigation is given after sowing. The operations like thinning, hoeing, weeding and plant protection measures were carried out regularly to insure satisfactory crop growth.

Table 3.1: List of forty one genotypes of chickpea

Sr. No.	Genotypes	Sr. No.	Genotypes
1.	BDNG 2018-8	22	ICC 14872
2.	BDNG 2018-13	23	ICC 85
3.	BDNG 2018-16	24	ICC 813
4.	BDNG 2017-1	25	ICC 8111-1
5.	BDNG 2018-15	26	ICC 8111-2
6.	BDNG 2017-23	27	ICC 1127
7.	AKG 1702	28	ICC G-27
8.	AKG 1506	29	ICC NG 113-1
9.	AKG 1709	30	ICC BG 73-1
10.	AKG 1402	31	ICC B 50
11.	AKG 1809	32	ICC NO 112
12.	AKG 1808	33	ICC B 88
13.	PHULE G 2012-10-17	34	ICC 0117676
14.	PHULE G 1221-2-6	35	ICC G 26
15	PHULE G 181609	36	ICC B 26
16	ICC NO 114	37	AKSAH (BDNG 797) (Ch.)
17	ICC 12735-1	38	JAKI 9218 (Ch.)
18	ICC 16348-2	39	VIJAY (Ch.)
19	ICC 16348	40	DIGVIJAY (Ch.)
20	ICC 06718	41	PHULE VIKRAM (Ch.)
21	ICC 261		

3.4 Experimental details:

1) Design	:	RBD
2) No. of replications	:	Two
3) Treatments	:	41(36 germplasm lines + 5 checks)
4) Plot size	:	One row of 4 meter length
5) Spacing	:	45 x 10 cm
6) Fertilizer dose	:	25:50:00NPK (kg/ha)
7) Season	:	<i>Rabi</i>
8) Locations	:	College of Agriculture, Badnapur.

3.5 Observations recorded

For recording of observations five competitive plants per genotype were selected at a random for characters in each replication and average for each was worked out for statistical analysis.

3.5.1 Days to 50% flowering

The number of days from sowing to the date when 50% plants in each plot flowered was recorded and the average number of days for 50% flowering was calculated.

3.5.2 Days to maturity

The number of days taken from the day of sowing to the day of maturity of crop was recorded as days to maturity.

3.5.3 Plant height (cm)

The plant height was recorded in centimetre at the time of harvesting by measuring the height of a plant from a ground level to the top of the main axis of top.

3.5.4 Number of primary branches per plant

The branches arising from main stem were considered as primary branches which were counted and recorded at the time of harvesting.

3.5.5 Number of secondary branches per plant

Fruiting branches arising from primary branches were recorded as secondary branches at the time of harvesting.

3.5.6 Number of pods per plant

The total number of pods was counted from five randomly selected plants at the maturity and average number is worked out.

3.5.7 Number of seeds per pod

This observation was recorded by taking the seeds of randomly selected five pods from a selected plant and the average of five plants was calculated.

3.5.8 100 seed weight (gram)

It was recorded by weighing randomly selected 100 seeds.

3.5.9 Seed yield per plant (gram)

The seed weight is obtained as a mean of five observational plants represent seed yield per plant.

3.5.10 Harvest index (%)

The harvest index was counted by the five randomly selected plants from the plot. it is in percentage estimated in percentage.

$$\text{Harvest index (\%)} = \frac{\text{Economic yield}}{\text{Biological yield}} \times 100$$

3.6 Statistical analysis:

3.6.1 Assessment of variability:

3.6.1.1 Analysis of variance:

The data collected on individual characters were subjected to the method of analysis of variance commonly applicable to the randomized block design (Panse and Sukhatme, 1967).

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

Where,

$$i = 1, 2, \dots, G$$

$$j = 1, 2, \dots, R$$

Y_{ij} = Observation on i th genotype in j th replication

μ = General mean

G_i = Effect of i th genotype

R_j = Effect of j th replication

E_{ij} = Random error associated with Y_{ij} observation

ANOVA Table:

Sources	Degree of Freedom	Mean of Sum	Expected Mean sum of squares
Replications	r-1	RMS	$\sigma_e^2 + \sigma_r^2$
Treatments	g-1	GMS	$\sigma_e^2 + \sigma_g^2$
Error	(r-1)(g-1)	EMS	σ_e^2

Where,

r = Number of replications

g = Number of genotypes

σ_r^2 = Variance due to replications

σ_g^2 = Variance due to genotypes and

σ_e^2 = Variance due to error

The genotype mean square (GMS) was tested against error mean square (EMS) by 'F' test for $n_1 = (g-1)$ and $n_2 = (r-1)(g-1)$ degrees of freedom, where, g = number of genotypes and r = number of replications. The characters showing significant differences were subjected to further analysis.

Estimation of S.E. and C.D.

$$\text{S.E. of mean (S.E.m)} = \sqrt{2^2_{e/r}}$$

$$\text{C.D.} = t \text{ at error d.f.} \times \text{S.E.m} \sqrt{2}$$

3.6.1.2 Estimation of mean and range:

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

$$\bar{X} = \frac{1}{n} \sum_{i=1}^n X_i$$

Where,

$\bar{X}$ = Mean of character

$\sum X_i$ = Total of all the observations for character

n = Number of observations

The lowest and highest values of the mean of each character represented the range.

3.6.1.3 Estimation of components of variation

The phenotypic and genotypic variances were calculated using the respective mean squares from the variance table (Johnson *et al.* 1955) as below.

Environmental variance (σ_e^2) = EMS

$$\text{Genotypic variance } (\sigma_g^2) = \frac{\text{GMS} - \text{EMS}}{r}$$

$$\text{Phenotypic variance } (\sigma_p^2) = \sigma_g^2 + \sigma_e^2$$

Where,

GMS = Genotypic mean sum of square

EMS = Error mean sum of squares

r = Number of replications

3.6.1.4 Estimation of coefficient of variation

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

3.6.1.4.1 Genotypic coefficient of variation (GCV)

$$\text{GCV (\%)} = \frac{\sigma_g^2}{\bar{X}} \times 100$$

Where,

σ_g^2 = Genotypic variance and,

$\bar{X}$ = Mean of character

3.6.1.4.2 Phenotypic coefficient of variation (PCV)

$$\text{PCV (\%)} = \frac{\sigma_p^2}{\bar{X}} \times 100$$

Where,

σ_p^2 = Phenotypic variance and,

$\bar{X}$ = Mean of character

GCV and PCV estimates were classified as Low : < 10 per cent, Medium: 10 to 20 per cent and High: > 20 per cent.

3.6.1.5 Estimation of heritability (b.s.)

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

$$h^2 = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where,

h^2 = Heritability

σ_g^2 = Genotypic variance

σ_p^2 = Phenotypic variance

The high, medium and low heritability estimates were classified based on the values given by Robinson (1966).

Low heritability = < 10 %

Moderate heritability = 10-30 %

High heritability = > 30 %

3.6.1.6 Genetic advance (G.A.)

Genetic advance (at 5 % selection intensity) was calculated using the formula given by Allard (1961).

i) Genetic advance (G.A.)

$$G.A. = k \times \frac{\sigma_g^2}{\sigma_p^2} \times \sqrt{\sigma_p^2}$$

Where,

σ_g^2 = Genotypic variance

σ_p^2 = Phenotypic variance

k = Selection differential (at 5 % selection = 2.06)

ii) G.A. as percentage of means (GAM)

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

Where,

G. A. = Genetic advance

$\bar{X}$ = Character mean

GA (As percentage of mean) was classified as

Low	: 10 per cent
Medium	: 10 to 20 per cent
High	: > 20 per cent

3.6.2 Genetic divergence D^2 analysis

The analysis of divergence was carried out by D^2 statistics proposed by Mahalanobis (1928, 1936) as described by Rao (1952). Analysis of variance for the individual character was worked out as per randomized block design analysis to test the significances of differences among the genotypes. The characters exhibited significant differences so all were used for further analysis of D^2 statistics. The analysis of covariance for character pair based on plant average was carried out (Cochran and Cox, 1957).

3.6.2.1 Wilk's criteria

After testing the differences among populations for characters, a simultaneous test of significance of difference between the mean value of several correlated variables about the pooled effect of nine characters considered together was carried out using Wilk's criteria ' Λ ' (Wilks, 1932) which was estimated using the relationship.

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

Where,

$|E|$ = The determinant of experimental error sum of squares and sum of products matrix

$|E + V|$ = The determinant of experimental error sum of squares and sum of products plus population sum of squares and product matrix

The significance of Wilk's criteria (Λ) was tested by χ^2 as,

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

Where,

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

$$n = N_1 + \dots + N_{k-1} \text{ (Total number of observations-1)}$$

p = Number of significant characters

q = k-1 (Number of genotypes -1)

K = Number of genotypes

3.6.2.2 Mahalanobis's generalized distance (D²)

The generalized distance between any two populations is defined as:

$$D^2 = \sum \sum \lambda_{ij} \sigma_i \sigma_j$$

Where,

λ_{ij} = Reciprocal matrix to the common dispersion matrix

σ_i = Difference between the mean value of the two populations for the *i*th character

σ_j = Difference between the mean value of the two populations for the *j*th character.

This quantity is estimated by D² statistic (Majumdar and Rao, 1958) as:

$$D^2 = \sum \sum S_{ij} \sigma_i \sigma_j$$

Where,

S_{ij} , σ_i , σ_j are the sample estimates of λ_{ij} , σ_i and σ_j respectively since this formula for computation requires the inversion of tenth order determinant and then evaluation of 10 (10+1) terms, whose sum is D².

3.6.2.3 Computation of D² values

For each combination, D² was calculated. Thus total 80(79)/2 = 3160 number of D² values were worked out.

3.6.2.4 Determination of population constellation

No rules can be laid down for finding the clusters because cluster is not well defined term. The only criteria appear to be that, any two groups belonging to the same cluster should be at least, on average show a smaller D² value than those belonging to two different.

The simple method suggested by Tocher (Rao, 1952) for cluster formation is to start with two closely related groups and find third group that has a smaller average D² value from the first two. Similarly, the fourth group is chosen to have smaller average D² values from the first three and so on. While proceeding further from cluster formation, at any stage, the average D² value of the group appears to be high

than those already listed, then this group does not fit in that format group and taken outside of that cluster.

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

3.6.2.5 Average intra-cluster distances

The intra cluster distances were calculated as,

$$\frac{\sum D_i^2}{n}$$

Where,

$\sum D_i^2$ = Sum of distances between all possible combinations

n = Number of genotypes included in a cluster

3.6.2.6 Average inter-cluster distances

The procedure followed for calculating inter-cluster distances was first to measure the distance between cluster-I and cluster-II, between cluster-I and cluster-III, and between cluster-I and cluster-IV and so on. Likewise, the clusters were taken one by one and the distances between other clusters were calculated. The average inter-cluster distances were calculated as,

$$\frac{\sum D_i^2}{(n_i \cdot n_j)}$$

Where,

n_i = Number of genotypes in cluster 'i'

n_j = Number of genotypes in cluster 'j'

3.6.2.7 Cluster diagram

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

With the help of D^2 values between the clusters, a diagram showing the relationship between different populations was drawn.

3.6.3 Correlations

Analysis of covariance was carried out by taking two characters at a time. The genotypic co-variance was calculated as per Johnson *et al.* (1955) as below:

Source	Degree of Freedom	Sum of squares	Mean sum of squares	Expectation of mean sum of squares
Replications	(r-1)	RP	RMP	$COVe_{1.2} + gCOV_{r1.2}$
Genotypes	(g-1)	GP	GMP	$COVe_{1.2} + rCOV_{g1.2}$
Error	(r-1) (g-1)	EP	EMP	$COVe_{1.2}$

Environmental covariance ($COV_{e1.2}$) = EMP

$$\text{Genotypic covariance } (COV_{g1.2}) = \frac{GMP - EMP}{r}$$

Phenotypic covariance ($COV_{p1.2}$) = ($COV_{g1.2}$) + ($COV_{e1.2}$)

Where,

GMP = Genotypic mean sum of product

EMP = Error mean sum of product

r = Replication

Appropriate variances and co-variances were used for calculating phenotypic and genotypic correlation coefficients (Johnson *et al.*, 1955).

The phenotypic correlation coefficient (r_p) was calculated as:

$$r_{p1.2} = \frac{COV_{p1.2}}{\sqrt{(\sigma_p^2)(\sigma_{p2}^2)}}$$

Where,

$r_{p1.2}$ = Phenotypic correlation coefficient between character 1 and 2

$COV_{.p1.2}$ = Phenotypic covariance between character 1 and 2.

$\sigma^2_{p1} . (\sigma^2_{p2})$ = Phenotypic variance of character 1 and 2 respectively.

The significance of the phenotypic correlation coefficient was tested by referring to Fisher and Yates (1943). The genotypic correlation coefficient (r_g) was calculated as:

$$r_{g1.2} = \frac{COV_{.g1.2}}{\sqrt{(\sigma^2_{g1}) . (\sigma^2_{g2})}}$$

Where,

$r_{g1.2}$ = Genotypic correlation coefficient between character 1 and 2

$COV_{.g1.2}$ = Genotypic covariance between character 1 and 2

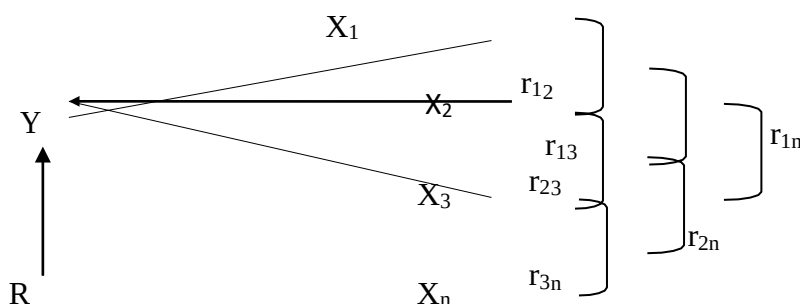
$(\sigma^2_{g1}) . (\sigma^2_{g2})$ = Genotypic variance of character 1 and 2 respectively.

The significance of correlation coefficients was tested from the statistical table of correlation coefficient at 1 and 5 per cent level of significance (Snedcor and Cochran, 1967).

3.6.4 Path coefficient analysis

To establish a cause and effect relationship the first step used was to partition genotypic and phenotypic correlation coefficient into direct and indirect effects by path analysis as suggested by Dewey and Lu (1959) and developed by Wright (1921).

The second step in path analysis is to prepare path diagram based on cause and effect relationship. In the present study, path diagram was prepared by taking yield as the effect i.e. function of various components like X_1 , X_2 , X_3 and these component showed following type of association with each other.



In path diagram the yield is the result of X_1 , X_2 , X_3 X_n and some

other undefined factors designated by R. The double arrow lines indicated

mutual association as measured by correlation coefficient. The single arrow represents direct influence as measured by path coefficient P_{ij} . Path coefficients were obtained by solving a set of simultaneous equation of the form as per Dewey and Lu (1959).

$$r_{ny} = P_{ny} + r_{n2} P_{2y} + r_{n3} P_{3y} + \dots$$

where,

r_{ny} = represents the correlation between one component and yield
 P_{ny} = represents path coefficient between that character and yield
 r_{n2} = represents correlation between that character and each of the other components in turn.

$$\begin{matrix} \text{Matrix A} \\ \left[\begin{matrix} r_{1y} \\ r_{2y} \\ r_{ny} \end{matrix} \right] \end{matrix} = \begin{matrix} \left[\begin{matrix} r_{11} & r_{12} & r_{13} \dots r_{1n} \\ r_{21} & r_{22} & r_{23} \dots r_{2n} \\ r_{n1} & r_{n2} & r_{n3} \dots 1 \end{matrix} \right] \end{matrix} \begin{matrix} \text{Matrix B} \\ \left[\begin{matrix} P_{1y} \\ P_{2y} \\ P_{ny} \end{matrix} \right] \end{matrix}$$

Where,

r_{12} = r_{21} and so on

r_{1y} = Correlation between one component character and seed yield

The 'B' matrix was inverted $[B]^{-1}$ and path coefficients (P_{ij}) were obtained as, i.e. $P_{ij} = (B)^{-1}.A$

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

$$\text{Indirect effects} = r_{ij} \times p_{iy}$$

Where,

i = 1 to 9

j = 1 to 9

P_{iy} = $P_{1y}, P_{2y}, \dots, P_{ny}$

Path coefficient (P_{ij}), correlation coefficient (r_{ij}) and residual factors

(R) were diagrammatically presented. The residual factor i.e. variation in yield unaccounted for by these associations was calculated with the following formula:

$$\text{Residual factor (R)} = (1 - R^2)$$

Where,

$$R^2 = P_{1y} r_{1y} + P_{2y} r_{2y} + \dots + P_{ny} r_{ny}$$

$$P_{1y}, P_{2y}, \dots, P_{ny} = \text{Direct path values}$$

$$r_{1y}, r_{2y}, r_{ny} = \text{Correlation coefficients.}$$



Plate 3.1 A general experimental view for genetic diversity studies in chickpea

CHAPTER – IV
RESULTS AND DISCUSSION

CHAPTER – IV

RESULTS AND DISCUSSION

The experimental results of the present investigation entitled “**Genetic Diversity, Correlation and Path Analysis Studies in Chickpea (*Cicer arietinum* L.)**” was undertaken with 41 genotypes of chickpea (*Cicer arietinum* L.) including five checks Viz. BDNG 797 (Akash), JAKI 9218, Vijay, Digvijay and Phule Vikram. The objective of experiment was to study genetic diversity, correlation and path analysis for yield and yield contributing characters in chickpea.

The results obtained for ten characters of 41 genotypes are discussed under following headings:

4.1 Analysis of variance:

4.2 Mean performance:

4.3 Genetic diversity:

4.4 Correlation:

4.5 Path analysis:

4.1 Analysis of variance:

The variation among genotypes were highly significant for days to 50% flowering, days to maturity, plant height, number of pods per plant, 100 seed weight, harvest index and seed yield per plant (Table 4.1) excluding number of primery and secondary branches and number of seed per pod.

Table 4.1: Analysis of variance for ten quantitative characters in chickpea.

Sources of Variation	d. f.	Mean sum of squares									
		Days to 50 % flowering	Days to maturity	Plant height (cm)	No. of Primary branches / plant	No. of Secondary branches / plant	No. of pods / plant	No. of seeds / pod	100 seed weight (g)	Harvest Index (%)	Seed yield / plant (g)
Replications	1	8.89	7.02	2.25	0.04	0.98	10.18	0.001	4.55	1.85	0.53
Genotypes	40	33.79**	60.20**	229.34**	0.28	8.61	788.41**	0.068	59.93**	25.22**	107.05*
Error	40	2.79	2.52	2.69	0.02	0.96	64.70	0.01	1.34	8.06	3.52

* Significant at 5 % level of significance

** Significant at 1 % level of significance

Table 4.2 Mean performance for ten quantitative characters in forty one genotypes of chickpea

Sr No.	Name of genotype	Days to 50 % Flowering	Days to maturity	Plant height (cm)	No. of Primary branches / plant	No. of Secondary branches / plant	No. of pods / plant	No. of seeds / pod	100 seed weight (g)	Harvest index (%)	Seed yield / plant (g)
1	BDNG 2018-8	51.00	111.50	54.38	2.45	8.80	76.70	1.10	24.75	42.61	18.77
2	BDNG 2018-13	54.50	114.00	54.85	2.30	8.40	78.30	1.20	28.90	42.32	23.58
3	BDNG 2018-16	54.00	113.50	60.35	2.10	9.20	58.30	1.30	32.16	40.99	19.37
4	BDNG 2017-1	50.50	111.00	59.54	2.00	12.20	73.10	1.10	25.00	38.59	20.49
5	BDNG 2018-15	52.50	111.50	60.65	2.30	7.90	65.40	1.60	26.70	35.37	15.69
6	BDNG 2017-23	53.00	115.00	55.18	2.30	9.90	56.10	1.10	22.55	35.23	12.96
7	AKG 1702	44.50	110.50	73.50	3.00	12.60	94.70	1.30	33.00	43.23	29.50
8	AKG 1506	54.00	111.00	47.90	2.50	13.00	102.2	1.20	25.40	38.02	26.81
9	AKG 1709	55.00	110.00	54.50	2.10	10.40	84.20	1.50	29.35	41.22	25.77
10	AKG 1402	47.00	109.00	54.63	2.10	10.90	86.70	1.35	31.45	42.70	28.76
11	AKG 1809	53.50	108.50	63.24	2.90	11.10	49.70	1.70	20.90	29.16	11.11
12	AKG 1808	54.00	106.00	55.44	1.90	9.30	88.70	1.00	25.50	39.82	23.35
13	PHULE G 2012-10-17	54.00	111.50	57.88	2.70	10.30	101.4	1.30	24.05	40.54	24.81

Table 4.2 contd.....

Sr No.	Name of genotype	Days to 50 % Flowering	Days to maturity	Plant height (cm)	No. of Primary branches / plant	No. of Secondary branches / plant	No. of pods / plant	No. of seeds / pod	100 seed weight (g)	Harvest index (%)	Seed yield / plant (g)
14	PHULE G 1221-2-6	54.00	108.00	50.44	2.20	8.80	89.80	1.20	21.25	41.00	22.69
15	PHULE G181609	57.00	109.00	59.66	2.50	11.20	110.0	1.40	22.00	38.35	32.48
16	ICC NO. 114	48.00	106.00	48.87	2.00	10.10	92.10	1.10	32.40	44.91	34.34
17.	ICC 12735-1	47.00	104.50	42.52	2.20	13.20	115.8	1.20	16.20	39.85	21.82
18	ICC 16348-2	53.00	104.50	43.34	2.40	9.30	70.90	1.10	24.00	40.65	20.88
19	ICC 16348	41.00	97.00	37.54	2.20	7.00	87.60	1.00	13.20	32.61	13.40
20	ICC 06718	49.00	108.00	35.02	2.40	9.30	57.90	1.40	27.40	33.76	16.90
21	ICC 261	53.00	106.50	18.15	2.30	7.90	55.90	1.60	19.65	37.81	11.73
22	ICC 14872	45.50	94.00	46.56	2.20	11.10	66.00	1.30	24.40	36.01	17.22
23	ICC 85	51.00	108.00	57.10	2.70	12.60	76.70	1.10	24.80	40.33	22.43
24	ICC 813	43.00	95.00	40.40	2.30	12.40	109.0	1.20	32.20	42.42	41.52
25	ICC 8111-1	45.50	106.50	45.62	3.10	14.30	67.60	1.10	36.00	40.22	35.50
26	ICC 8111-2	50.00	104.50	48.49	3.20	13.70	100.0	1.30	18.20	34.15	24.14

Table 4.2 contd.....

Sr. No.	Name of genotype	Days to 50 % flowering	Days to maturity	Plant height (cm)	No. of Primary branches / plant	No. of Secondary branches / plant	No. of pods / plant	No. of seeds / pod	100 seed weight (g)	Harvest index (%)	Seed yield / plant (g)
27	ICC 1127	44.00	95.00	39.67	2.50	13.90	105.9	1.00	15.95	33.47	16.93
28	ICC G-27	52.00	105.0	26.61	2.90	8.90	44.20	1.30	13.55	35.35	8.45
29	ICC NG 113-1	44.50	101.0	36.98	3.20	7.20	84.90	1.10	18.30	37.50	13.99
30	ICC BG 73-1	43.50	103.0	36.75	3.50	11.30	63.40	1.30	24.30	37.08	14.59
31	ICC B-50	47.50	104.0	46.85	3.10	9.50	45.50	1.20	28.75	42.03	20.49
32	ICC NO 112	50.00	103.0	33.00	2.40	10.00	60.50	1.00	19.40	32.65	13.65
33	ICC B-88	57.00	104.0	42.35	2.70	10.10	65.00	1.20	20.35	43.33	12.46
34	ICC 0117676	51.00	104.0	38.80	2.70	9.00	73.90	1.00	17.05	36.29	12.94
35	ICC G-26	55.00	104.5	50.44	2.50	16.10	64.30	1.60	20.90	39.66	14.25
36	ICC B-26	53.50	109.0	44.00	2.30	10.70	120.3	1.20	19.05	41.97	26.99
37	BDNG 797	54.00	114.5	40.60	2.10	9.50	78.60	1.40	18.50	38.08	18.05
38	JAKI 9218	52.50	116.5	38.40	2.70	14.10	77.50	1.00	21.80	42.12	23.25
39	Vijay	53.50	113.0	42.20	2.20	11.00	104.7	1.10	22.15	38.34	23.59

Table 4.2 contd.....

Sr. No.	Name of genotype	Days to 50 % Flowering	Days to maturity	Plant height (cm)	No. of Primary branches / plant	No. of Secondary branches / plant	No. of pods / plant	No. of seeds / pod	100 seed weight (g)	Harvest index (%)	Seed yield / plant (g)
40	Digvijay	51.00	113.00	44.20	2.50	10.20	77.90	1.30	22.20	39.96	20.48
41	Phule Vikram	49.00	111.50	54.90	2.40	9.70	100.3	1.00	22.40	41.52	27.08
	Mean	50.54	107.21	47.35	2.49	10.63	80.04	1.23	23.56	38.81	21.05
	C.V. %	3.30	1.48	4.52	6.35	9.25	10.04	7.96	4.91	7.31	12.17
	S.E. +/-	1.18	1.12	1.51	0.11	0.69	5.68	0.06	0.81	2.00	1.81
	C.D. 5%	3.37	3.21	4.33	0.32	1.98	16.25	0.19	2.33	5.73	5.18

4.2 Mean performance and the range of variability

Table 4.2 shows the mean values of the genotypes for the various characters studied, whereas Table 4.3 shows the estimations of the range of variability.

4.2.1 Days to 50 per cent flowering

The variation in days to 50 per cent flowering ranged between 41.00 to 57.00 days. Genotype ICC 16348 flowered in 41.00 days while highest 57.00 days were taken by PHULE G 181609 and ICC B-88. Mean value for this character was 50.54 days. Days to 50% flowering in BDNG 797 (54.00 days), Vijay (53.50 days), JAKI 9218 (52.50 days), Digvijay (51.000 days) and Phule Vikram (49.00 days). The genotype PHULE G 181609 and ICC B-88 recorded highest number of days to 50% flowering i.e. (57.00 days) followed by AKG 1709 and ICC G-26 (55.00 days), BDNG 2018-13 (54.50 days).

4.2.2 Days to maturity

The variation in days to maturity ranged between 94.00 days to 116.50 days. Genotype ICC 14872 matured in least number of 94.00 days while JAKI 9218 matured very late 116.50 days. Mean value for this character was 107.21 days. The genotypes viz. BDNG 797, JAKI 9218, Vijay, Digvijay and Phule Vikram recorded (114.50), (116.50), (113.00), (113.00) and (111.50 days) respectively. The genotype JAKI 9218 recorded highest days to maturity of (116.50 days) followed by BDNG 2017-23 recorded (115.00 days), BDNG 797 (114.50) and BDNG 2018-13(114.00) days.

4.2.3 Plant height (cm)

The variation in plant height ranged between 18.15 cm to 73.55 cm. The plant height was minimum in case of genotype ICC 261 (18.15 cm) while it was maximum in case of genotype AKG 1702 (73.55 cm). Mean value for this character was 47.35 cm. The genotypes viz. BDNG 797, JAKI 9218, Vijay, Digvijay, Phule Vikram had recorded (40.60 cm), (38.40 cm), (42.20 cm), (44.20 cm), and (54.90 cm) plant height (cm) respectively. While the genotype AKG 1702 recorded highest plant height (73.55 cm) followed by AKG 1809 (63.24 cm), BDNG 2018-15 (60.65 cm) and BDNG 2018-16 (60.37 cm) respectively.

4.2.4 Number of primary branches per plant

Primary branches per plant ranged from 1.90 to 3.50. The primary branches were least in genotype AKG 1808 (1.90) while it were maximum in genotype ICC BG 73-1 (3.50). Mean value for this character was 2.49. The genotypes viz. BDNG 797,

JAKI 9218, Vijay, Digvijay, Phule Vikram had recorded (2.10), (2.70), (2.20), (2.50), and (2.40) primary branches per plant respectively. The genotype ICC BG 73-1 recorded highest primary branches per plant i.e. 3.50 after that ICC G-27 and ICC 8111-2 (3.20), and ICC 8111-1 (3.10). respectively.

4.2.5 Number of secondary branches per plant

The variation in numbers of secondary branches per plant ranged from 7.00 to 16.10. The number of secondary branches were least in genotype ICC 16348 (7.00) while it were maximum in genotype ICC G-26 (16.10). Mean value for this character was (10.63). The genotypes viz. BDNG 797, JAKI 9218, Vijay, Digvijay, Phule Vikram had recorded (9.50), (14.10), (11.00), (10.20), and (9.70) number of secondary branches per plant respectively. The genotype ICC G-26 recorded highest secondary branches per plant i.e. (16.10) followed by ICC 8111-1 (14.30), check JAKI 9218 (14.10).

4.2.6 Numbers of pod per plant

Number of pods per plant ranged from 44.20 to 120.30. The genotype ICC G-27 recorded lowest i.e. (44.20) while ICC B-26 had maximum number of pods per plant i.e. (120.30). Mean value for this character was (80.04). The genotypes viz. BDNG 797, JAKI 9218, Vijay, Digvijay and Phule Vikram had recorded (78.60), (77.50), (104.70), (77.90) and (100.30) numbers of pod per plant respectively. The genotype ICC B-26 recorded highest pods per plant i.e. (120.30) followed by ICC 12735-1 (115.80), PHULE G 181609 (110.00) and ICC 8111-2 (105.90) respectively.

4.2.7 Numbers of seed per pod

Number of seeds per pod varied from 1.00 to 1.70 (AKG 1809) and the mean value for this character was (1.23). The genotypes viz. BDNG 797, JAKI 9218, Vijay, Digvijay and Phule Vikram had recorded (1.40), (1.00), (1.10), (1.30) and (1.00) number of seeds per pod respectively. Genotypes i.e. AKG 1809 (1.70), BDNG 2018-15 (1.60), ICC 261 (1.60), ICC G-26 (1.60) respectively.

4.2.8 100 seed weight (g)

The variation for 100 seed weight ranged between 13.20 g to 36.00 g. Genotype ICC 8111-1 (36.00 g) was highest while ICC 16348 (13.20 g) with lowest 100 seed weight. The mean value for this character was 23.56 g. Twenty genotypes were with more 100 seed weight than the mean performance. The genotypes viz. BDNG 797, JAKI 9218, Vijay, Digvijay and Phule Vikram had (18.50 g), (21.80 g), (22.15 g), (22.20 g) and (22.40 g) 100 seed weight respectively.

4.2.9 Harvest Index (%)

The variation for harvest index ranged from 29.16 % to 44.91 %. The genotype AKG 1809 showed lowest harvest index (29.16%) while genotype ICC NO 114 recorded highest harvest index (44.91%). Mean value for this character was (38.81%). Twenty Two genotypes were with more harvest index (%) than mean performance. The genotypes viz. BDNG 797, JAKI 9218, Vijay, Digvijay and Phule Vikram had (38.08 %), (42.12 %), (38.34%), (39.96 %) and (41.52 %) harvest index respectively.

4.2.10 Seed yield per plant (g)

The variation for seed yield per plant was varied between 8.45 g to 41.52 g. The genotype ICC G-27 had least seed yield per plant (8.45 g) while ICC 813 produced highest seed yield per plant (41.52 g). The mean value for this character was 21.05 g. Nineteen genotypes recorded more seed yield per plant than the mean value of seed yield per plant. The genotypes viz BDNG 797, JAKI 9218, Vijay, Digvijay and Phule Vikram had (18.05 g), (23.25 g), (23.59 g), (20.48 g) and (27.08 g) seed yield per plant respectively.

4.2.11 Genetic variability

Table 4.3 shows the parameters phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (b.s.) and genetic advance as a percent of mean for the various characters studied.

The genotypic variance, ranged from 0.03 to 361.85. The genotypic variance was highest for number of pods per plant (361.85) followed by plant height (112.37), seed yield per plant (50.24) and 100 seed weight (29.29). The phenotypic variance, ranged from (0.039 to 426.56). The pods per plant recorded maximum phenotypic variance (426.56) followed by plant height (116.97), seed yield per plant (56.81) and 100 seed weight (30.63).

Table 4.3: Estimates of variability parameters for ten quantitative characters in chickpea.

Sr. No.	Name of the characters	Range	Mean	σ^2_g	σ^2_p	GCV (%)	PCV (%)	h^2 (b.s.) (%)	G.A. % (5%)	G.A. % (1%)	G.A. as % of mean (5%)	G.A. as % of mean (1%)
1.	Days to 50 % flowering	41.00-57.00	50.54	15.50	18.29	7.78	8.46	84.70	7.46	9.56	14.77	18.93
2.	Days to maturity	94.00-116.50	107.21	28.83	31.36	5.00	5.22	92.00	10.60	13.59	9.89	12.67
3.	Plant height (cm)	18.15-73.55	47.35	112.3	116.9	22.38	22.83	96.10	21.40	27.43	45.19	57.92
4.	Number of primary branches per plant	1.90-3.50	2.49	0.13	0.15	14.48	15.81	83.90	0.68	0.87	27.31	35.00
5.	Number of secondary branches per plant	7.00-16.10	10.63	3.82	4.79	18.38	20.58	79.80	3.59	4.61	33.82	43.35
6.	Number of pods per plant	44.20-120.30	80.04	361.85	426.56	23.76	25.80	84.80	36.09	46.25	45.09	57.78
7.	Number of seeds per pod	1.00-1.70	1.23	0.030	0.039	13.97	16.08	75.50	0.31	0.39	25.00	32.05
8.	100 seed weight (g)	13.20-36.00	23.56	29.30	30.64	22.97	23.49	95.60	10.90	13.97	46.27	59.30
9.	Harvest index (%)	29.16-44.91	38.81	8.58	16.64	7.54	10.51	51.60	4.33	5.55	11.16	14.31
10	Seed yield per plant (g)	8.45-41.52	21.05	50.24	56.81	33.66	35.80	88.40	13.73	17.59	65.21	83.57

4.2.12 Genotypic and phenotypic coefficients of variation

Genotypic coefficient of variation (GCV) was maximum for seed yield per plant (33.66 %) after that number of pods per plant (23.76 %), 100 seed weight (22.97 %) and plant height (22.38 %). Phenotypic coefficient of variation (PCV) was maximum for seed yield per plant (35.80 %) followed by number of pods per plant (25.80 %), 100 seed weight (23.49 %) and plant height (22.83 %). The phenotypic coefficient of variation was generally greater than the the genotypic coefficient of variation.

4.2.13 Heritability, genetic advance and genetic advance as percent of mean

The estimates of heritability ranged from 51.60 % to 96.10 %. Maximum heritability was observed for plant height 96.10 % after that 100 seed weight 95.60 %, days to maturity 92.00 %, Seed yield per plant 88.40%, number of pods per plant 84.80%, days to 50 % flowering 84.70%, number of primary branches per plant 83.90%, number of secondary branches per plant 79.80 %, number of seeds per pod 66.70% and harvest index 51.60 %.

The estimates of genetic advance ranged from 0.31 % to 36.09 % at 5% level of significance and 0.39 % to 46.25 % at 1% level of significance. At 5% level of significance and at 1% level of significance the maximum estimate observed in case of number of pods per plant (36.09 %) and (46.25 %) followed by plant height (21.40 %) and (27.43 %), seed yield per plant (13.73 %) and (17.59 %), 100 seed weight (10.90 %) and (13.97 %), days to maturity (10.60 %) and (13.59 %), days to 50 % flowering (7.46 %) and (9.56 %), harvest index (4.33 %) and (5.55 %), number of secondary branches per plant (3.59 %) and (4.61 %), number of primary branches per plant (0.68 %) and (0.87 %), number of seeds per pod (0.31 %) and (0.39 %) respectively.

The estimates of genetic advance as percent of mean ranged from 9.89 % to 65.21 % at 5% level of significance and 12.67 % to 83.57 % at 1% level of significance. At 5% level of significance and at 1% level of significance the highest estimate recorded in case of seed yield per plant (65.21 %) and (83.57 %) followed by 100 seed weight (46.27 %) and (59.30 %), plant height (45.19 %) and (57.92 %), number of pods per plant (45.09 %) and (57.78 %), number of secondary branches per plant (33.82 %) and (43.35 %), number of primary branches per plant (27.31 %) and (35.00 %), number of seeds per pod (25.00%) and (32.05 %), days to 50% flowering (14.77 %) and (18.93 %), harvest index (11.16 %) and (14. 31 %), days to maturity

(9.89 %) and (12.67 %) respectively.

4.3 Genetic divergence

4.3.1 Mahalanobis's generalized distance (D^2)

For the pooled effect of the ten parameters tested, Wilk's criterion revealed significant differences between genotypes. As a result, additional analysis was performed to calculate D^2 values for all possible pairs of comparison among forty one genotypes. D^2 values calculated varied from 49.00 to 1217.31.

The Mahalanobis's D^2 statistics were estimated for all possible pairs of forty one genotypes based on ten character observations to determine the genetic diversity present among the genotypes under study.

4.3.2 Clustering pattern of the genotypes

Table 4.4 and Figure 4.1 shows the clustering pattern obtained based on the magnitude of D^2 values investigated.

These forty one genotypes were grouped into twelve clusters. The cluster I was with the highest number of genotypes (23) followed by cluster IV (08), clusters II , cluster III, cluster V, cluster VI, cluster VII, cluster VIII, cluster IX, cluster X, cluster XI and cluster XII had (01) genotype each respectively.

4.3.3 Intra and inter cluster divergence

The average intra and inter cluster D^2 and D values are presented in Table 4.5 and Table 4.6 shows cluster distance.

The intra cluster distance (D^2) ranges from 68.72 to 90.06. The inter cluster distance (D^2) ranges from 49.00 to 1217.31. The maximum inter cluster distance ($D^2 = 1217.31$) was observed between cluster VI and cluster XII followed by cluster XII and VIII ($D^2 = 1069.94$), cluster VI and cluster X ($D^2 = 962.24$), cluster V and cluster VI ($D^2 = 919.90$) and cluster V and VIII ($D^2 = 860.24$). The minimum inter cluster distance ($D^2 = 49.00$) was between clusters III and VII.

Table 4.4: Composition of forty one chickpea genotypes into different clusters**Tocher's method:**

Cluster No.	No. of genotypes	Genotypes included in the cluster
I	23	BDNG 2018-8, Phule Vikram, PHULE G 2012 10-17, PHULE G 1221-2-6, AKG 1808, AKG 1506, PHULE G 181609, ICC 16348-2, Digvijay, BDNG 2017-23, ICC 85, BDNG 2017-1, BDNG 2018-13, BDNG 2018-15, AKG 1709, JAKI 9218, AKG 1402, AKG 1809, ICC G-26, Vijay, ICC B-88, ICC 06718, BDNG 797.
II	01	ICC B-26
III	01	ICC NO 114
IV	08	ICC NO 112, ICC 0117676, ICC G-27, ICC 261, ICC NG 113-1, ICC 12735-1, ICC 8111-2, ICC BG 73-1.
V	01	BDNG 2018-16.
VI	01	ICC 16348.
VII	01	ICC B-50
VIII	01	ICC 1127
IX	01	ICC 14872
X	01	AKG 1702
XI	01	ICC 813
XII	01	ICC 8111-1

Table 4.5: Average intra and inter cluster (D^2) values in chickpea.

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XIII
I	68.72	129.27	124.76	212.86	142.56	446.47	119.68	418.20	131.79	220.52	228.31	367.11
II		0.00	305.20	86.86	396.40	164.09	305.55	179.83	151.78	484.88	346.70	701.72
III			0.00	404.40	71.23	733.86	49.00	668.22	182.79	117.72	84.64	117.94
IV				90.06	523.49	142.08	326.89	151.78	145.93	595.36	362.90	730.08
V					0.00	919.90	104.24	858.49	296.18	85.38	278.56	201.92
VI						0.00	665.64	54.91	280.56	962.24	628.00	1217.31
VII							0.00	603.68	141.85	132.48	100.20	113.64
VIII								0.00	200.51	825.99	516.20	1069.94
IX									0.00	290.02	125.44	397.60
X										0.00	242.42	180.10
XI											0.00	153.51
XII												0.00

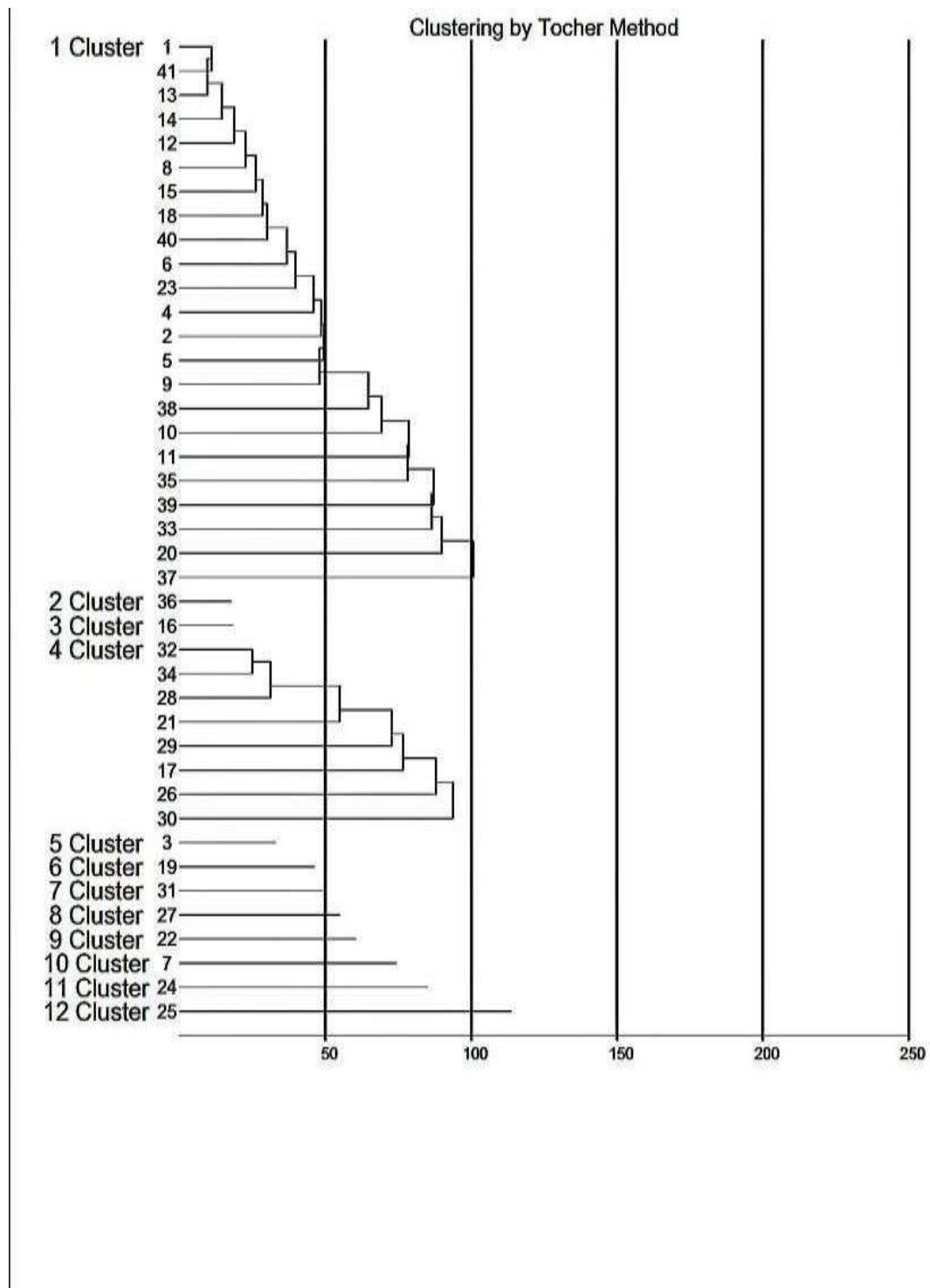


Fig. 4.1: Diagram showing formation of clusters by Tocher method.

Table 4.6: Average intra and inter cluster distance (D) values in chickpea.

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XIII
I	8.29	11.37	11.17	14.59	11.94	21.13	10.94	20.45	11.48	14.85	15.11	19.16
II		0.00	17.47	9.32	19.91	12.81	17.48	13.41	12.32	22.02	18.62	26.49
III			0.00	20.02	8.44	27.09	7.00	25.85	13.52	10.85	9.20	10.86
IV				9.49	22.88	11.92	18.08	12.32	12.08	24.40	19.05	27.02
V					0.00	30.33	10.21	29.30	17.21	9.24	16.69	14.21
VI						0.00	25.80	7.41	16.75	31.02	25.06	34.89
VII							0.00	24.57	11.91	11.51	10.01	10.66
VIII								0.00	14.16	28.74	22.72	32.71
IX									0.00	17.03	11.20	19.94
X										0.00	15.57	13.42
XI											0.00	12.39
XII												0.00

4.3.4 Cluster means for different characters

Table 4.7 shows the cluster means for the ten parameters. A considerable inter cluster variation was observed among the cluster means for the characters studied viz., days to 50 per cent flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, seed yield per plant, 100 seed weight and harvest index.

The cluster mean for days to 50 per cent flowering varied from (41.00) cluster VI to (54.00 days) cluster V. The cluster mean for days to maturity ranged from (94.00) cluster IX to (113.50 days) cluster V. The cluster mean for plant height ranged between (35.16) cluster IV to (73.55 cm) cluster X. The cluster mean for the number of primary branches per plant ranged between (2.00) cluster III to (3.10) cluster VII and cluster XII. The cluster mean for secondary branches per plant ranged between (7.00) cluster VI to (14.30) cluster XII.

The cluster mean for number of pods per plant was minimum in cluster VII (45.50) and it was maximum in cluster II (120.30). The cluster mean for number of seeds per pod was minimum in cluster VI and cluster VIII (1.00) and it was maximum in cluster IX and X (1.30). The cluster mean for 100 seed weight was minimum in cluster VI (13.20 g) and it was the maximum in cluster XII (36.00 g). The cluster mean for harvest index was maximum in cluster III (44.91%) and minimum in case of cluster VI (32.61%). The cluster mean for seed yield per plant was minimum in cluster VI (13.40 g) and it was maximum in cluster XI (41.52 g).

Table 4.7: Cluster means of different characters to genetic diversity in chickpea.

Clusters	Days to 50 % Flowering	Days to maturity	Plant height (cm)	No. of pri. Branches / plant	No. of sec. branches / plant	Numberof pods / plant	Number of seeds / pod	100 seed weight (g)	Harvest Index (%)	Seed yield / plant (g)
I	52.83	110.17	51.17	2.38	10.61	79.83	1.26	24.01	39.25	21.16
II	53.50	109.00	44.00	2.30	10.70	120.30	1.20	19.05	41.97	26.99
III	48.00	106.00	48.87	2.00	10.10	92.10	1.10	32.40	44.91	34.34
IV	48.88	103.94	35.16	2.80	10.15	74.83	1.23	18.33	36.34	15.16
V	54.00	113.50	60.37	2.10	9.20	58.30	1.30	32.16	41.00	19.37
VI	41.00	97.00	37.54	2.20	7.00	87.60	1.00	13.20	32.61	13.40
VII	47.50	104.00	46.85	3.10	9.50	45.50	1.20	28.75	42.03	20.50
VIII	44.00	95.00	39.67	2.50	13.90	105.90	1.00	15.95	33.48	16.93
IX	45.50	94.00	46.56	2.20	11.10	66.00	1.30	24.40	36.02	17.22
X	44.50	110.50	73.55	3.00	12.60	94.70	1.30	33.00	43.23	29.50
XI	43.00	95.00	40.40	2.30	12.40	109.05	1.20	32.20	42.43	41.52
XII	45.50	106.50	45.62	3.10	14.30	67.60	1.10	36.00	40.23	35.50

The application of D^2 analysis to determine the relative contribution of various plant characters to genetic divergence improved its utility. Table 4.8 and Fig. 4.2 shows the percentage contribution of the ten parameters studied to overall divergence.

It was observed that, seed yield per plant (42.20%) contributed highest for divergence. It was followed by plant height (16.83%), 100 seed weight (16.34%), days to maturity (6.83%), number of pods per plant (5.37%), number of primary branches (4.51%), number of secondary branches per plant (3.05%), harvest index (2.20%), number of seeds per pod (2.07%) and days to 50% flowering (0.61%).

Table 4.8: Per cent contribution of different characters to genetic diversity in chickpea

Sr. No.	Characters	No. of times appearing 1st in ranking	% contribution
1	Days to 50 % flowering	05	0.61%
2	Days to maturity	56	6.83%
3	Plant height (cm)	138	16.83%
4	Number of primary branches per Plant	37	4.51%
5	Number of secondary branches per Plant	25	3.05%
6	Number of pods per plant	44	5.37%
7	Number of seeds per pod	17	2.07%
8	100 seed weight (g)	134	16.34%
9	Harvest Index (%)	18	2.20%
10	Seed yield per plant (g)	346	42.20%
	Total	820	100%

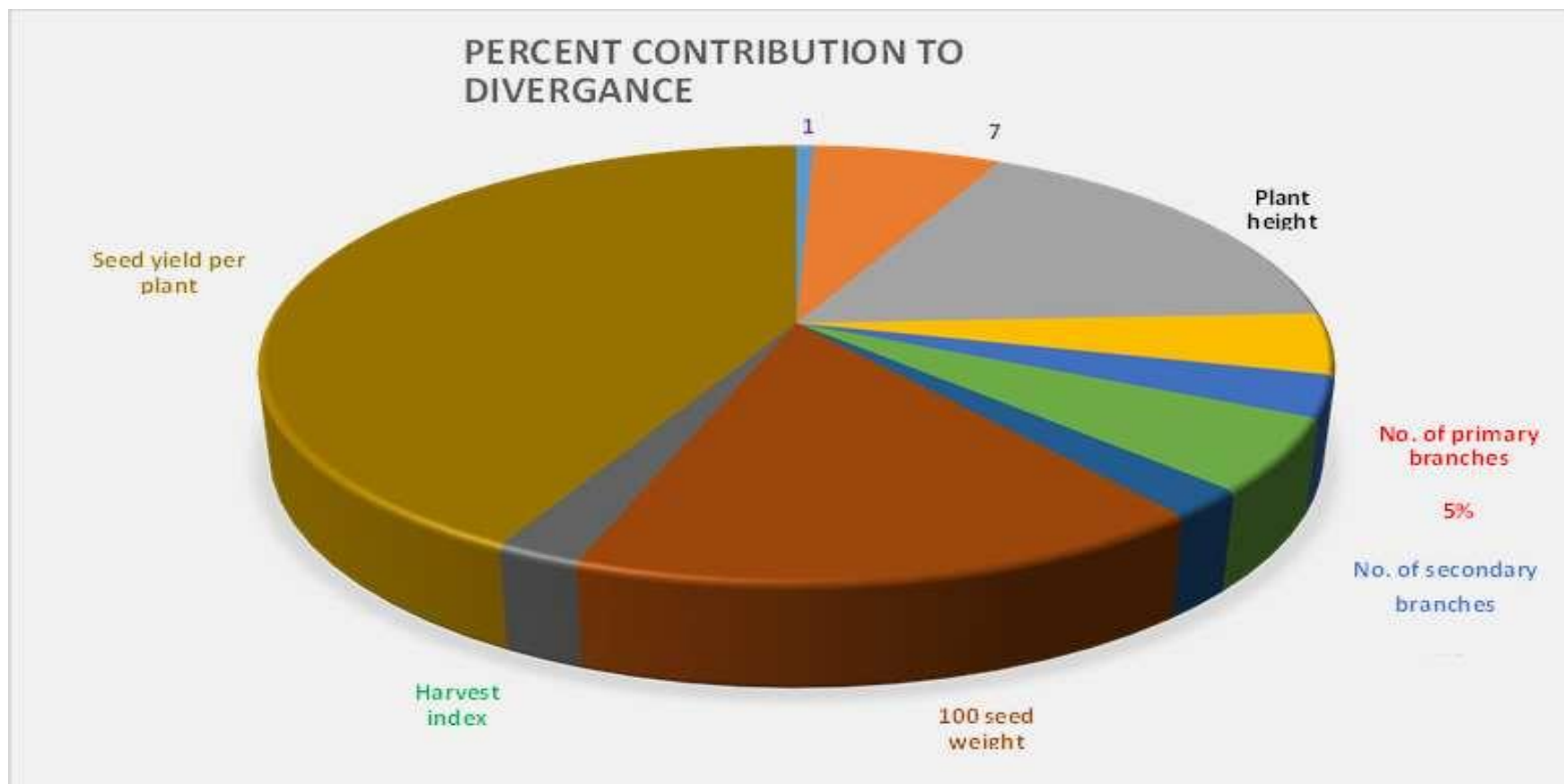


Fig. 4.2: Diagram showing the contribution towards divergence in chickpea

4.4 Correlation studies

Tables 4.9, 4.10 show the genotypic and phenotypic correlations for yield and its component characters studied. This chapter describes the only significant correlations, either positive or negative. In general, the genotypic correlation coefficients were higher than the phenotypic correlation coefficients.

4.4.1 Association of seed yield with its components

Seed yield per plant had significant positive correlation with number of pods per plant ($p=0.6488$; $g=0.6096$), 100 seed weight ($p=0.6065$; $g=0.6664$), harvest index ($p=0.5174$; $g=0.7310$), number of secondary branches per plant ($p=0.3623$; $g=0.3662$) and plant height ($p=0.3480$; $g=0.3649$) at both phenotypic and genotypic level.

4.4.2 Interrelationship of yield components

4.4.2.1 Days to 50 per cent flowering

Days to 50 per cent flowering showed significant positive correlation at both phenotypic and genotypic level with days to maturity ($p=0.5824$; $g=0.6581$) and number of seeds per pod ($p=0.2810$; $g=0.3477$). While it had the significant negative association with number of primary branches per plant ($p= -0.2471$; $g= -0.2971$) both at phenotypic and genotypic level.

4.4.2.2 Days to maturity

Days to maturity showed significant positive correlation both at phenotypic and genotypic level with plant height ($p=0.3944$; $g=0.4170$), harvest index ($p=0.2303$; $g=0.2391$) and 100 seed weight ($p=0.2213$; $g=0.3801$).

4.4.2.3 Plant height

The character plant height had positively significant correlation with 100 seed weight ($p=0.4754$; $g=0.5077$) and days to maturity ($p=0.3944$; $g=0.4170$) both at phenotypic and genotypic level and harvest index ($g=0.3349$) at genotypic level.

4.4.2.4 Number of primary branches per plant

The number of primary branches per plant showed significant negative correlation with days to 50 % flowering ($p=-0.2471$; $g=-0.2971$), at both phenotypic and genotypic level. While it had significant positive correlation with number of secondary branches ($p=0.2127$; $g=0.2186$).

4.4.2.5 Number of secondary branches per plant

The number of secondary branches per plant showed significant positive correlation at both phenotypic and genotypic level with number of pods per plant ($p=0.2815$; $g=0.2552$) and number of primary branches ($p=0.2127$; $g=0.2186$).

4.4.2.6 Number of pods per plant

The number of pods per plant showed significant positive correlation with harvest index ($p=0.2563$; $g=0.3527$) and number of secondary branches ($p=0.2815$; $g=0.2552$) both at phenotypic and genotypic level. While it had negative correlation with numbers of seeds per pod ($p= -0.2364$; $g= -0.3462$).

4.4.2.7 Number of seeds per pod

The number of seeds per pod showed significant positive correlation with days to 50% flowering ($p=0.2810$; $g=0.3477$) at both phenotypic and genotypic level. While it had significant negative correlation with numbers of pod per plant ($p= -0.2364$; $g= -0.3462$) and harvest index ($g= -0.2844$) at genotypic level.

4.4.2.8 100 seed weight

100 seed weight showed significant positive correlation with number of harvest index ($p=0.4736$; $g=0.6343$) and plant height ($p=0.4754$ $g=0.5077$) at both phenotypic and genotypic level.

4.4.2.9 Harvest index

Harvest index showed significant positive correlation with 100 seed weight ($p=0.4736$; $g=0.6343$), days to maturity ($p= 0.2303$; $g=0.3801$) and number of pods per plant ($p= 0.2563$; $g=0.3527$) both at phenotypic and genotypic level and number plant height ($g=0.3349$) at genotypic level. While significant negative correlation with number of seeds per pod ($g= -0.2844$) at genotypic level.

Table 4.9: Estimation of phenotypic (above diagonal) correlation coefficients in chickpea.

Characters	Days to 50 % Flowering	Days to maturity	Plant height (cm)	Number of primary branches / Plant	Number of secondary branches / plant	Number of pods/ plant	Number of seeds /pod	100 seed weight (g)	Harvest Index (%)	Seed yield / plant (g)
	1	2	3	4	5	6	7	8	9	10
Days to 50 % flowering	1.000	0.5824**	0.1877	-0.2471*	-0.0734	- 0.0971	0.2810*	-0.0857	0.0791	-0.1278
Days to maturity		1.000	0.3944**	-0.1376	-0.0412	-0.0299	0.1361	0.2213	0.2303*	0.0969
Plant height (cm)			1.000	-0.1068	0.1609	0.1750	0.1411	0.4754**	0.2072	0.3480**
Number of primary branches per plant				1.000	0.2127*	-0.2106	0.0402	-0.0837	-0.1271	-0.1476
Number of secondary branches per plant					1.000	0.2815*	0.0474	0.1183	0.1052	0.3623**
Number of pods per plant						1.000	-0.2364*	-0.0586	0.2563*	0.6488**
Number of seeds per pod							1.000	0.0837	-0.1188	-0.1316
100 seed weight (g)								1.000	0.4736**	0.6065**
Harvest index (%)									1.000	0.5174**
Seed yield per Plant (g)										1.000

* Significant at 5 % level of probability or level of significance.

** Significant at 1 % level of probability or level of significance.

Table 4.10: Estimation of genotypical (above diagonal) correlation coefficients in chickpea.

Characters	Days to50 % flowering	Days to maturity	Plant Height (cm)	Number of primary branches / plant	Number of secondary branches / plant	Numberof pods / plant	Number of seeds /pod	100 seed weight (g)	Harvest Index(%)	Seed yield /plant (g)
	1	2	3	4	5	6	7	8	9	10
Days to 50 % flowering	1.000	0.6581**	0.2139	-0.2971*	-0.0992	-0.1255	0.3477**	-0.0938	0.2148	-0.1400
Days to maturity		1.000	0.4170**	-0.1889	-0.920	-0.0667	0.1684	0.2391	0.3801**	0.0906
Plant height (cm)			1.000	-0.1203	0.1909	0.1743	0.1441	0.5077**	0.3349*	0.3649**
Number of primary branches per plant				1.000	0.2186*	-0.2417	0.0614	-0.0838	-0.2417	-0.1613
Number of secondary branches per plant					1.000	0.2552**	-0.0076	0.1639	0.0643	0.3662**
Number of pods per plant						1.000	-0.3462**	-0.0627	0.3527**	0.6096**
Number of seeds per pod							1.000	0.1234	-0.2844*	-0.2133
100 seed weight (g)								1.000	0.6343**	0.6664**
Harvest index (%)									1.000	0.7310**
Seed yield per Plant (g)										1.000

* Significant at 5 % level of probability or level of significance.

**Significant at 1 % level of probability or level of significance.

4.5 Phenotypic and Genotypic path coefficient analysis

Path coefficient analysis was used to determine the direct and indirect effects of each of the characters on seed yield per plant. The phenotypic and genotypic correlation coefficients, which are more important, are only partitioned into direct and indirect effects, as shown in Tables 4.11 and 4.12. Figures 4.3 and 4.4 shows phenotypic and genotypic path diagrams respectively.

4.5.1 Direct effect:

Among all the components, at phenotypic level 100 seed weight exhibited the highest positive direct effect ($p=0.6847$) on seed yield followed by number of pods per plant ($p=0.6766$), number of secondary branches per plant ($p=0.1033$), days to 50% flowering ($p=0.0443$), harvest index ($p=0.0328$) and number of primary branches per plant ($p=0.0327$). While plant height ($p= -0.1168$) and days to maturity ($p=-0.0094$) recorded negative direct effect.

At genotypic level 100 seed weight exhibited the highest positive direct effect ($g=0.8867$) on seed yield followed by number of pods per plant ($g=0.6922$), days to 50% flowering ($g=0.2045$), number of primary branches ($g=0.0839$) and number of secondary branches per plant ($g=0.0791$). While plant height ($g= -0.1901$), days to maturity ($g= -0.0634$) and harvest index ($g=-0.0555$) recorded negative direct effect.

4.5.2 Indirect effect

4.5.2.1 Days to 50% flowering

Days to 50% flowering had negative phenotypic and genotypic correlation ($p=-0.1278$; $g= -0.1400$) with seed yield per plant. It exhibited negative indirect effects through number of pods per plant ($p=-0.0657$; $g=-0.0868$) followed by 100 seed weight ($p=-0.0587$; $g=-0.0832$), plant height ($p=-0.0219$; $g=-0.0407$), number of primary branches ($p=-0.0081$; $g=-0.0249$), number of secondary branches ($p=-0.0076$; $g=-0.0078$), number of seeds per pod ($p=-0.0073$; $g=-0.0474$) and days to maturity ($p=-0.0055$; $g=-0.0417$). It showed positive indirect effect at phenotypic level through harvest index ($p=0.0026$) and negative at genotypic level ($g=-0.0119$). Thus these indirect causal factors are to be considered during selection process for improving seed yield per plant.

4.5.2.2 Days to maturity

Days to maturity had positive phenotypic and genotypic correlation ($p=0.0969$; $g=0.0906$) with seed yield per plant. It exhibited positive indirect effects through 100 seed weight ($p=0.1515$; $g=0.2120$) and days to 50% flowering

($p=0.0258$; $g=0.1346$). While negative indirect effect through plant height ($p=-0.0460$; $g=-0.0793$), number of pods per plant ($p=-0.0202$; $g=-0.0462$), number of primary branches ($p=-0.0045$; $g=-0.0158$), number of secondary branches ($p=-0.0043$; $g=-0.0073$), and number of seeds per pod ($p=-0.0035$; $g=-0.0230$) at both phenotypic and genotypic level. While it showed positive indirect effect through harvest index ($p=0.0076$) at phenotypic level and negative indirect effect at genotypic level ($g=-0.0211$).

4.5.2.3 Plant height

Plant height showed positive phenotypic and positive genotypic correlation ($p=0.3480$; $g=0.3649$) with seed yield per plant. It has positive indirect effect through 100 seed weight ($p=0.3255$; $g=0.4502$), number of pods per plant ($p=0.01184$; $g=0.1206$) and number of secondary branches per plant ($p=0.0166$; $g=0.0151$), days to 50% flowering ($p=0.0083$; $g=0.0467$) and negative indirect effect through days to maturity ($p=-0.0037$; $g=-0.0264$), number seeds per pod ($p=-0.0037$; $g=-0.0197$) and number of primary branches ($p=-0.0035$; $g=-0.0101$) at both phenotypic and genotypic level. While it showed positive indirect effect through harvest index ($p=0.0068$) at phenotypic level and negative indirect effect ($g=-0.0186$) at genotypic level.

4.5.2.4 Number of primary branches per plant

Number of primary branches per plant showed negative phenotypic and genotypic correlation ($p=-0.1476$; $g=-0.1613$) with seed yield per plant. It showed positive indirect effects at both phenotypic and genotypic level through number of secondary branches ($p=0.0220$; $g=0.0173$), plant height ($p=0.0125$; $g=0.0229$) and days to maturity ($p=0.0013$; $g=0.0120$). It showed negative indirect effects at both phenotypic and genotypic level through number of pods per plant ($p=-0.1425$; $g=-0.1673$), 100 seed weight ($p=-0.0573$; $g=-0.0743$), days to 50% flowering ($p=-0.0110$; $g=-0.0608$) and number of seeds per pod ($p=-0.0010$; $g=-0.0084$). While it showed negative indirect effect through harvest index ($p=-0.0042$) at phenotypic level and positive indirect effect ($g=0.0134$) at genotypic level.

4.5.2.5 Number of secondary branches per plant

Number of secondary branches per plant had positive phenotypic and genotypic correlation ($p=0.3623$; $g=0.3662$) with seed yield per plant. It showed positive indirect effects through number of pods per plant ($p=0.1905$; $g=0.1766$), 100 seed weight ($p=0.0810$; $g=0.1454$), number of primary branches ($p=0.0070$;

$g=0.0183$) and days to maturity ($p=0.0004$; $g=0.0183$) and negative indirect effect through number of plant height ($p=-0.0188$; $g=-0.0363$) and days to 50% flowering ($p=-0.0033$; $g=-0.0203$) at both phenotypic and genotypic level. It showed negative indirect effect at phenotypic level through number of seeds per pod ($p=-0.0012$) and positive at genotypic level through number of seeds per pod ($g=0.0010$). While it showed positive indirect effect through harvest index ($p=0.0035$) at phenotypic level and negative indirect effect ($g=-0.0036$) at genotypic level.

4.5.2.6 Number of pods per plant

Number of pods per plant had positive phenotypic and genotypic correlation ($p=0.6488$; $g=0.6096$) with seed yield per plant. It showed positive indirect effect through number of secondary branches per plant ($p=0.0291$; $g=0.0202$), number of seeds per pod ($p=0.0061$; $g=0.0472$) and days to maturity ($p=0.0003$; $g=0.0042$) and negative indirect effect through 100 seed weight ($p=-0.0401$; $g=-0.0556$), plant height ($p=-0.0204$; $g=-0.0331$), number of primary branches ($p=-0.0069$; $g=-0.0203$), days to 50% flowering ($p=-0.0043$; $g=-0.0257$) at both phenotypic and genotypic level. While it showed positive indirect effect through harvest index ($p=0.0084$) at phenotypic level and negative indirect effect ($g=-0.0196$) at genotypic level.

4.5.2.7 Number of seeds per pod

Number of seeds per pod had negative phenotypic and genotypic correlation ($p=-0.1316$; $g=-0.2133$) with seed yield per plant. Number of seeds per pod showed positive indirect effect through 100 seed weight ($p=0.0573$; $g=0.1094$), days to 50% flowering ($p=0.0125$; $g=0.0711$) and number of primary branches ($p=0.0013$; $g=0.0051$) and negative indirect effect through number of pods per plant ($p=-0.1599$; $g=-0.2396$), plant height ($p=-0.0165$; $g=-0.0274$) and days to maturity ($p=-0.0013$; $g=-0.0107$) at both phenotypic and genotypic level. It showed positive indirect effect through number of secondary branches per plant ($p=0.0049$) at phenotypic level and negative at genotypic level ($g=-0.0006$) and negative through harvest index ($p=-0.0039$) at phenotypic level and positive at genotypic level ($g=0.0158$).

4.5.2.8 100 seed weight

100 seed weight had positive phenotypic and genotypic correlation ($p=0.6065$; $g=0.6664$) with seed yield per plant. It showed positive indirect effect through number of secondary branches per plant ($p=0.0122$; $g=0.0130$) and negative indirect effect through plant height ($p=-0.0555$; $g=-0.0965$), number of pods per plant ($p=-0.0396$;

$g=-0.0434$), days to 50% flowering ($p=-0.0038$; $g=-0.0192$), number of primary branches per plant ($p=-0.0027$; $g=-0.0070$), number of seeds per pod ($p=-0.0022$; $g=-0.0168$) and days to maturity ($p=-0.0021$; $g=-0.0151$) at both phenotypic and genotypic level. It showed positive indirect effect through harvest index ($p=0.0155$) at phenotypic level and negative at genotypic level ($g=-0.0352$).

4.5.2.9 Harvest index

Harvest index had positive phenotypic and genotypic correlation ($p=0.5174$; $g=0.7310$) with seed yield per plant. It exhibited positive indirect effect through 100 seed weight ($p=0.3242$; $g=0.5625$), number of pods per plant ($p=0.1734$; $g=0.2441$), number of secondary branches per plant ($p=0.0109$; $g=0.0051$), days to 50% flowering ($p=0.0035$; $g=0.0439$) and number of seeds per pod ($p=0.0031$; $g=0.0388$) and negative effect through number of plant height ($p=-0.0242$ $g=-0.0637$), primary branches per plant ($p=-0.0042$; $g=-0.0203$) and days to maturity ($p=-0.0022$ $g=-0.0241$) at both phenotypic and genotypic level.

Table 4.11: Direct and indirect effect of yield and its component characters on grain yield at phenotypic level in chickpea.

Sr. No.	Characters	Days to 50 % flowering	Days to maturity	Plant height (cm)	Number of primary branches / plant	Number of secondary branches / plant	Number of pods / plant	Number of seeds / pod	100 seed weight (g)	Harvest index (%)	Total phenotypic correlation with seed yield / plant (g)
1.	Days to 50 % flowering	<u>0.0443</u>	0.0258	0.0083	-0.0110	-0.0033	-0.0043	0.0125	-0.0038	0.0035	-0.1278
2.	Days to maturity	-0.0055	<u>-0.0094</u>	-0.0037	0.0013	0.0004	0.0003	-0.0013	-0.0021	-0.0022	0.0969
3.	Plant height (cm)	-0.0219	-0.0460	<u>-0.1168</u>	0.0125	-0.0188	-0.0204	-0.0165	-0.0555	-0.0242	0.3480
4.	No. of primary branches per plant	-0.0081	-0.0045	-0.0035	<u>0.0327</u>	0.0070	-0.0069	0.0013	-0.0027	-0.0042	-0.1476
5.	No. of secondary branches per plant	-0.0076	-0.0043	0.0166	0.0220	<u>0.1033</u>	0.0291	0.0049	0.0122	0.0109	0.3623
6.	Number of pods per plant	-0.0657	-0.0202	0.1184	-0.1425	0.1905	<u>0.6766</u>	-0.1599	-0.0396	0.1734	0.6488
7.	Number of seeds per pod	-0.0073	-0.0035	-0.0037	-0.0010	-0.0012	0.0061	<u>-0.0260</u>	-0.0022	0.0031	-0.1316
8.	100 seed weight (g)	-0.0587	0.1515	0.3255	-0.0573	0.0810	-0.0401	0.0573	<u>0.6847</u>	0.3242	0.6065
9.	Harvest index (%)	0.0026	0.0076	0.0068	-0.0042	0.0035	0.0084	-0.0039	0.0155	<u>0.0328</u>	0.5174

Residual effect = 0.3742, Underlined figures indicate direct effect.

Table 4.12: Direct and indirect effect of yield and its component characters on grain yield at genotypic level in chickpea.

Sr. No.	Characters	Days to 50 % flowering	Days to maturity	Plant height (cm)	Number of primary branches / plant	Number of secondary branches / plant	Number of pods / plant	Number of seeds / pod	100 seed weight (g)	Harvest index (%)	Total genotypic correlation with seed yield / plant (g)
1.	Days to 50 % flowering	<u>0.2045</u>	0.1346	0.0437	-0.0608	-0.0203	-0.0257	0.0711	-0.0192	0.0439	-0.1400
2.	Days to maturity	-0.0417	<u>-0.0634</u>	-0.0264	0.0120	0.0058	0.0042	-0.0107	-0.0151	-0.0241	0.0906
3.	Plant height (cm)	-0.0407	-0.0793	<u>-0.1901</u>	0.0229	-0.0363	-0.0331	-0.0274	-0.0965	-0.0637	0.3649
4.	No. of primary branches per plant	-0.0249	-0.0158	-0.0101	<u>0.0839</u>	0.0183	-0.0203	0.0051	-0.0070	-0.0203	-0.1613
5.	No. of secondary branches per plant	-0.0078	-0.0073	0.0151	0.0173	<u>0.0791</u>	0.0202	-0.0006	0.0130	0.0051	0.3662
6.	Number of pods per plant	-0.0868	-0.0462	0.1206	-0.1673	0.1766	<u>0.6922</u>	-0.2396	-0.0434	0.2441	0.6096
7.	Number of seeds per pod	-0.0474	-0.0230	-0.0197	-0.0084	0.0010	0.0472	<u>-0.1365</u>	-0.0168	0.0388	-0.2133
8.	100 seed weight (g)	-0.0832	0.2120	0.4502	-0.0743	0.1454	-0.0556	0.1094	<u>0.8867</u>	0.5625	0.6664
9.	Harvest index (%)	-0.0119	-0.0211	-0.0186	0.0134	-0.0036	-0.0196	0.0158	-0.0352	<u>-0.0555</u>	0.7310

Residual effect = 0.2946, Underlined figures indicate direct effect

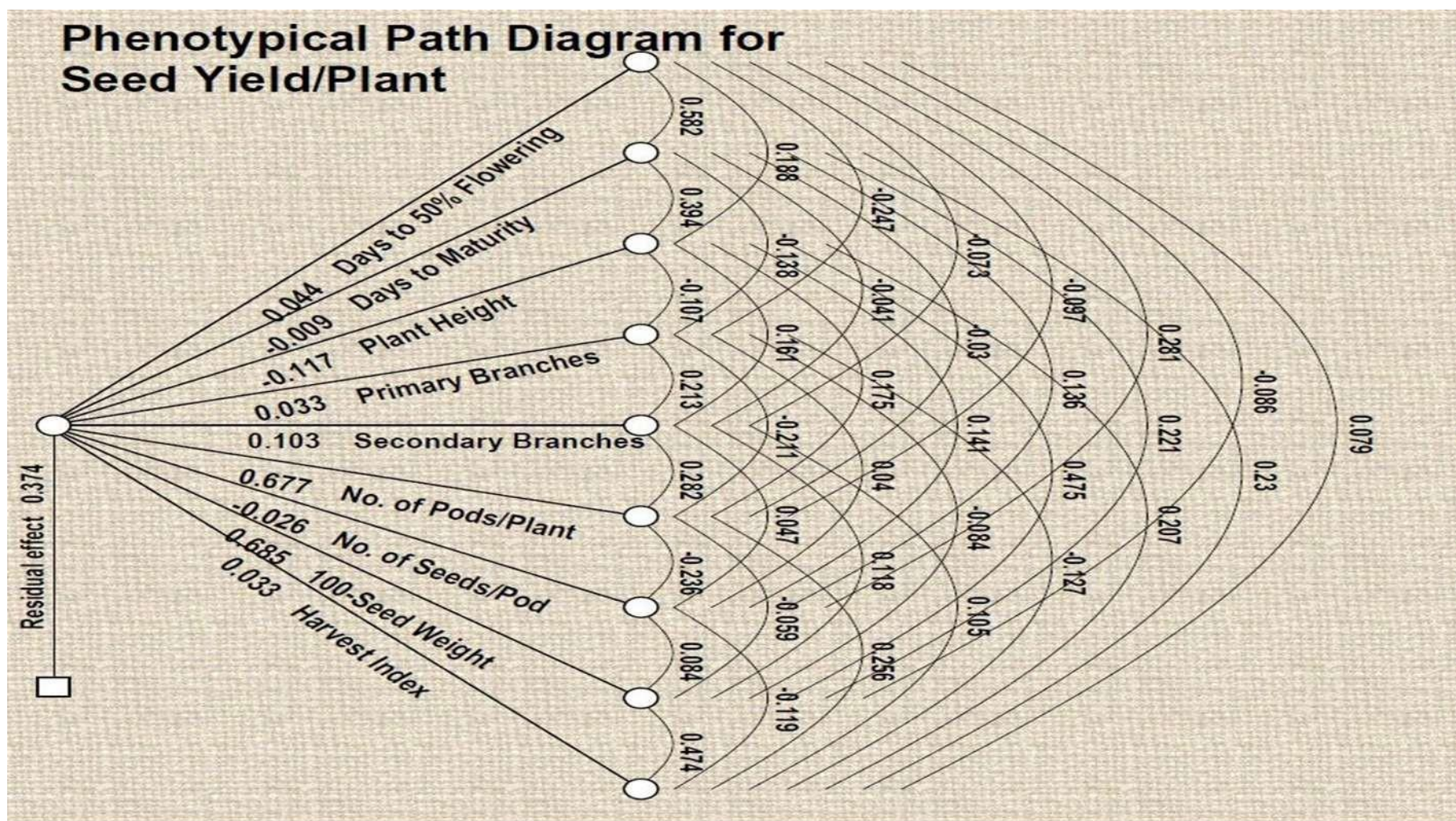


Fig. 4.3: Diagram showing the phenotypic path correlation of yield and its component characters of chickpea.

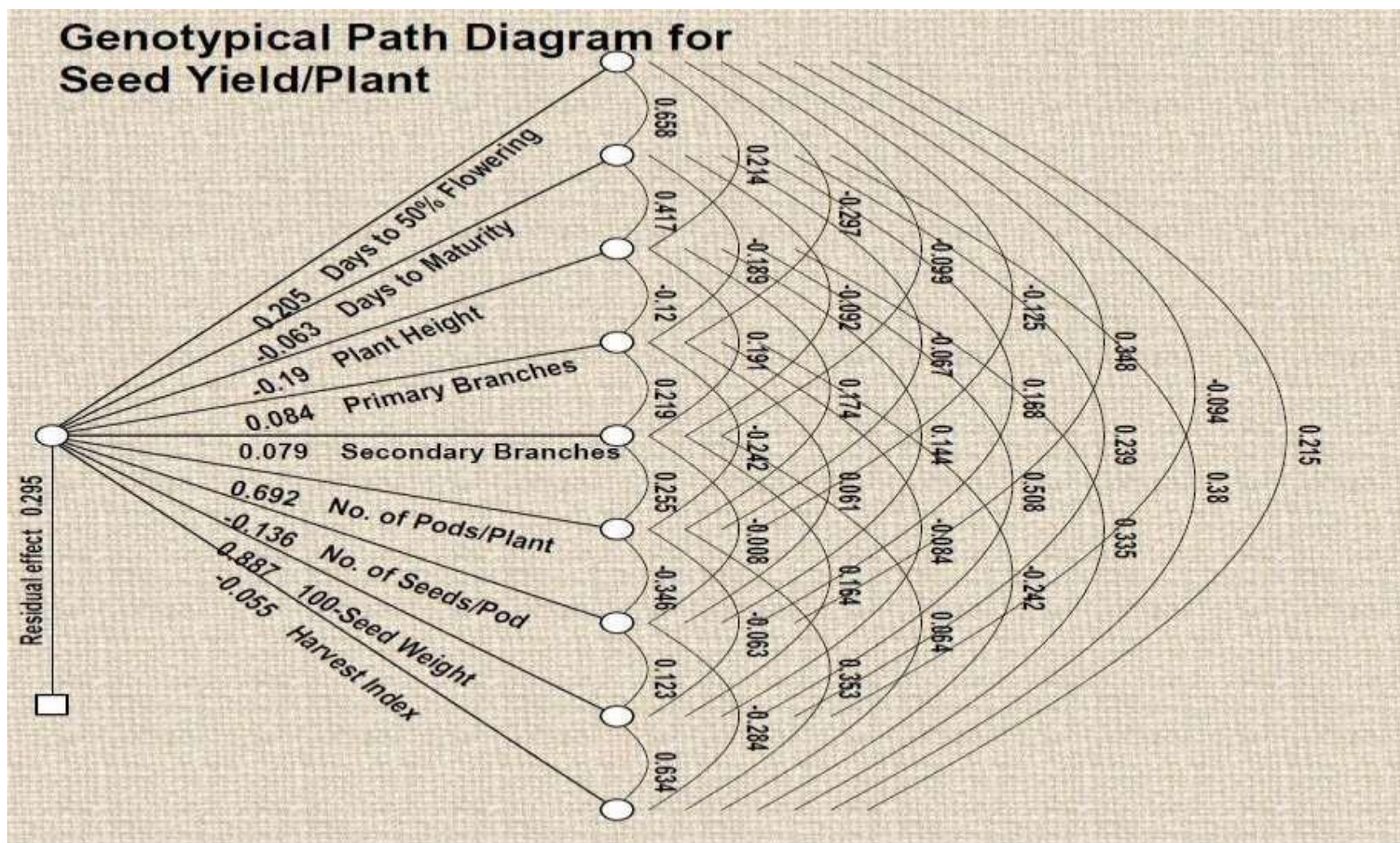


Fig. 4.4: Diagram showing the phenotypic path correlation of yield and its component characters of chickpea.

4.6 DISCUSSION

An attempt has been made in the current study entitled “**Genetic Diversity, Correlation and Path Analysis Studies in Chickpea (*Cicer arietinum* L.)**” to know the magnitude of genetic variability and interrelationship among yield attributing characters responsible for yield and genetic diversity among the chickpea genotypes.

Genetic advancement in any crop species is an important and ongoing process to face future problems. The strengths of available germplasm must be evaluated to discover possible genotypes that may be used for evolving desirable varieties to fulfill future demands, ultimately leading to the country's food and nutritional security. The success of any breeding programme is highly dependent on knowledge of the genetic diversity present in a given crop species for the characteristics under advancement. Yield is a complex character that is dependent on several quantitatively inherited component characters. As a result, before beginning any breeding programme, it is essential to have complete knowledge of the diversity present in the available genetic material, as well as the extent of association existing between yield and yield components. The diversity of parents is essential to a successful hybridization programme (Murthy and Arunachalam, 1966) because crosses between parents with the maximum genetic divergence are more likely to create desirable recombinants in the progenies. However, selecting the most suitable and genetically divergent parents is a challenging task for the plant breeder unless he is provided with the essential knowledge on the genetic variability and genetic diversity present in the available germplasm.

In the current study, 41 genotypes of chickpea were evaluated for study of genetic diversity, correlation and path analysis and also the associations between component characters and to estimate direct and indirect effect of the component characters on seed yield.

The biometrical techniques applied for the analysis of the data to know the salient findings of research work and the result obtained in relation to various aspects has been discussed in the light of literature under the following headings:

4.6.1 Mean performance

On the basis of mean performance for days to 50% flowering genotype ICC 16348 found early and for days to maturity the genotype ICC 14872 observed early maturing. The plant height is also important parameter which affects yield

performance of a species and is observed highest in genotype AKG 1702. ICC BG 73-1 showed maximum number of primary branches and highest number of secondary branches observed in ICC G-26. Highest number of pods per plant was observed in genotype ICC B-26. Genotypes AKG 1809 showed highest number of seeds per pod. Genotype ICC 8111-1 showed highest 100 seed weight and genotype ICC NO 114 showed highest harvest index. Highest seed yield per plant found in genotype ICC 813.

4.6.2 Genetic parameters

4.6.2.1 Variability

Knowledge of the nature and degree of genetic variability in a population is extremely valuable for planning an efficient breeding programme to improve the genotypes' yield potential. The coefficient of variation determines the amount of variability present for the various characters. The extent of heritable variation, however, cannot be assessed only by the genotypic coefficient of variation. The heritable estimates, together with genotypic coefficients of variation (GCV), would provide a better understanding of the amount of genetic advance to be expected by phenotypic selection (Burton, 1952). Hybridization, mutation, and other approaches to generate variability are used in modern breeding activities. This will help in identifying donors that excel in one or a few yield contributing traits and such genotypes can be efficiently used in combination breeding to improve yield. The genetic gain in conjunction with heritability estimates should form the criteria for selection based on phenotypic performance (Johansson *et al.* 1955).

The estimates of the phenotypic coefficient of variation (PCV) for all characters in the current study were higher than the estimates of the genotypic coefficient of variation (GCV), which might be related to the interaction of genotypes with the environment.

4.6.2.2 Range of variability

A wide range of variability was observed for all the characters except number of seeds per pod. The characters number of pods per plant, plant height, days to maturity, 100 seed weight, days to 50 % flowering and harvest index exhibited highest range of variability. The characters seed yield per plant and secondary branches per plant showed considerable amount of variability. Such variability present for quantitative traits in the present study could profitably be utilized for crop improvement in chickpea. The variability was lowest for number of seeds per pod. Similar results were obtained by Jeena *et al.* (2005), Dwevedi and Gaibriyal (2009), Borate *et al.* (2010), Sharma *et al.* (2010) and Thakur *et al.* (2018).

Estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for all of the characters studied varied slightly. The magnitude of PCV was higher than GCV for all characters, indicating that the apparent variation is not only due to genotypes but also due to the environment. Selection for such characteristics might sometimes be misleading. The estimates of genotypic as well as phenotypic coefficient of variation in the present study were highest for seed yield per plant followed by number of pods per plant, number of secondary branches per plant, 100 seed weight, plant height and number of secondary branches per plant. Number of seeds per pod, number of primary branches per plant and harvest index showed a medium genotypic and phenotypic coefficient of variation. For days to 50% flowering and days to maturity both the genotypic and phenotypic coefficient of variation was lowest. Earlier workers, Gumber *et al.* (2002) reported the highest values of phenotypic coefficient of variation (PCV) for seed yield per plant. Dwevedi and Gaibriyal (2009) reported the highest values of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for the trait 100 seed weight and number of pods per plant. Borate *et al.* (2010) reported values of phenotypic and genotypic variance were highest for number of pods per plant. Jadhav *et al.* (2012) reported similar values for the genotypic coefficient of variation and phenotypic coefficient of variation for 100 seed weight, harvest index, seed yield per plant. Kumar *et al.* (2012) reported high estimates of genotypic coefficient of variation and phenotypic coefficient of variation for 100 seed weight, seed yield per plant and plant height. Aarif *et al.* (2014) reported that 100 seed weight had the highest magnitude of the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). Chopdar *et al.* (2016) reported the highest values of genotypic coefficient of variation (GCV) for seed yield per plant. Alka dev *et al.* (2017) reported a low phenotypic coefficient of variation and genotypic coefficient of variation for days to 50 % flowering. Thakur *et al.* (2018) reported significant differences among all characters like number of pods per plant, number of primary branches per plant, 100 seed weight and harvest index.

4.6.2.3 Heritability and Genetic advance

The genotypic coefficient of variation (GCV) alone cannot determine the proportion of total heritable variation. The heritability estimates, on the other hand, are a better indicator of the heritable portion of the variation. The broad sense heritability includes the contribution of additive gene effects, allelic interaction due to

dominance, and allelic interaction due to epistasis. Burton (1952) proposed that the genetic coefficient of variation (GCV) and heritability estimates, when combined, provide a more accurate estimate of the amount of genetic advance (GA) expected through selection. Johnson *et al.* (1955) estimated that in a selection programme, heritability values and estimates combined provide a better idea of the genetic advance expected through selection. The magnitude and nature of genotypic and non-genotypic variation in the many characters determine the progress of any breeding programme because most economic characters (*e.g.*, yield) are complex in inheritance and are strongly influenced by various environmental conditions or factors. The study of heritability and genetic advance is extremely valuable in estimating the scope for improvement by selection. The heritability magnitude ensures the reliability with which the genotype may be identified based on its phenotype appearance.

In the present investigation, the range of broad sense heritability was from (51.60%) in harvest index to (96.10%) in plant height. Maximum heritability was observed for plant height (96.10%) followed by 100 seed weight (95.60%), days to maturity (92.00%), seed yield per plant (88.40%), number of pods per plant (84.80%), days to 50 % flowering (84.70%), number of primary branches per plant (83.90%), number of secondary branches per plant (79.80%) and number of seeds per pod (75.50%). The broad sense heritability is referred to the genetic portion of the phenotypic variability. As these characters having maximum broad sense heritability, there is a scope for selection for these character. Zeeshan *et al.* (2012) found high heritability for 100 seed weight and plant height.

The highest genetic advance was noticed for the character highest estimate in case of number of pods per plant (36.09%) and (46.25%) followed by plant height (21.40%) and (27.43%), seed yield per plant (13.73%) and (17.59%), 100 seed weight (10.90%) and (13.97%), days to maturity (10.60%) and (13.59%), days to 50 % flowering (7.46%) and (9.56%), harvest index (4.33%) and (5.55%), number of secondary branches per plant (3.59%) and (4.61%), number of primary branches per plant (0.68%) and (0.87%) and number of seeds per pod (0.31%) and (0.39%) at 5% and 1% level of significance respectively. This is indicating that these traits are under the control of additive gene action and potential possibilities exist for the improvement of these characters through simple selection. These findings are supported by similar noting of Kumar *et al.*, (2002) for number of pods per plant. Akhtar *et al.* (2011) for number of pods per plant and 100 seed weight, Jadhav *et al.*

(2012) for 100 seed weight, Padmawati *et al.* (2013) for number of primary branches per plant, Gul *et al.* (2013) for number of pods per plant, Suyog *et al.* (2018) seed yield per plant.

In the present investigation, heritability for number of seeds per pod and number of primary branches per plant were not associated with high genetic advance, indicating that these characters are controlled by non-additive gene action *i.e.* dominance deviation or epistasis, hence there is limited scope for further improvement through selection for these characters.

The characters viz. seed yield per plant, number of pods per plant, 100 seed weight and plant height showed a high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). High heritability was found in plant height, 100 seed weight, days to maturity and seed yield per plant where high genetic advance as per cent of mean was found in seed yield per plant followed by 100 seed weight, plant height, number of pods per plant and number of secondary branches per plant.

Thus considering the estimates of genetic parameters like the genotypic coefficient of variation, heritability and genetic advance as per cent of mean, it can be pointed out that, the characters like seed yield per plant, 100 seed weight, number of pods per plant, days to maturity, number of secondary branches per plant, number of primary branches per plant, days to 50% flowering, number of seeds per pod and harvest index are the most important in characters chickpea improvement.

4.6.3 Genetic divergence

Heritable improvement is based on genetic divergence caused by genetic factors. Plant breeders have always been fascinated by a wide range of crop plant diversity that might serve as raw material for any breeding programme. As a result, detailed knowledge about genetic divergence is essential for an effective breeding programme. Higher heterotic effects are known to be produced by genetically diverse parents, resulting in desirable recombinants in breeding material. Multivariate analysis, as proven by Mahalanobis (1936) D² statistics, is a quantitative measure of genetic variability among a set of genotypes. As a result, genetic divergence analysis was used to attempt to find suitable lines among forty one genotypes of chickpea.

4.6.3.1 Diversity

The estimates of D² values ranged from (49.00) to (1217.31) which indicate the presence of adequate diversity among genotypes studied. Sivakumar and Muthiah

(2000), Kumar *et al.* (2002), Jeena *et al.* (2005), Sandhu *et al.* (2006), Dwevedi and Gaibriyal (2009), Gaikwad *et al.* (2012), Ambilwade *et al.* (2018) and Ponnuru Akhil *et al.* (2019) also reported wide genetic diversity in chickpea germplasm.

4.6.3.2 Cluster formation

The goal of cluster formation and evaluating intra and inter cluster divergence is to provide the basis for a hybridization programme. The theoretical premise underlying such grouping is that genotypes in the same cluster are less varied from each other than those in separate clusters and will not provide the required heterotic response and segregants in further generations.

As a result, the breeding programme should be designed such that the parents are chosen from different clusters with greater genetic diversity in the genotypes. Crosses involving parents with extreme divergence have also been shown to decrease heterosis (Moll *et al.*, 1965). As a result, while selecting parents based on genetic diversity, their performance and cluster mean for the characters should also be taken into consideration in the crop improvement programme.

In the present investigation, forty one genotypes were grouped into twelve clusters. Cluster I was with the highest number of genotypes (23) followed by cluster IV (09), clusters II (01), cluster V (01), cluster VI (01), cluster VII (01), cluster VIII (01), cluster IX (01), cluster X (01), cluster XI (01) and cluster XII (01) genotype respectively. Nimbalkar and Harer (2001) reported ten solitary clusters.

The inter cluster distance (D) ranged from (7.00) to (34.89). The maximum inter cluster distance (D=34.89) was observed between cluster VI and cluster XII followed by cluster VIII and XII (D=32.71), cluster VI and cluster X (D=31.02), cluster V and cluster VI (D=30.33) and cluster V and VII (D=29.30). The minimum inter cluster distance (D=7.00) was between clusters III and VII. At inter cluster level, clusters VI and XII had the highest value which was followed by clusters VIII and XII. The cluster means for different characters showed considerable differences among the clusters for all the characters.

The cluster mean for days to 50 per cent flowering varied from (41.00) cluster VI to (54.00 days) cluster V. The cluster mean for days to maturity ranged from (94.00) cluster IX to (113.50 days) cluster V. The cluster mean for plant height ranged between (35.16) cluster IV to (73.55 cm) cluster X. The cluster mean for the number of primary branches per plant ranged between (2.00) cluster III to (3.10) cluster VII

and cluster XII. The cluster mean for secondary branches per plant ranged between (7.00) cluster VI to (14.30) cluster XII.

The cluster mean for number of pods per plant was maximum in cluster II (120.30) and it was minimum in cluster VII (44.50). The cluster mean for number of seeds per pod was maximum in cluster IX and X (1.30) and it was minimum in cluster VI and VIII (1.00). The cluster mean for 100 seed weight was minimum in cluster VI (13.20 g) and it was the maximum in cluster XII (36.00 g). The cluster mean for harvest index was maximum in cluster III (44.91%) and minimum in the case of cluster VI (32.61%). The cluster mean for seed yield per plant ranged between (13.40 g) cluster VI to (41.25 g) cluster IX.

It was found that the characters viz., seed yield per plant, plant height and 100 seed weight were the major contributors towards divergence. The performance of genotypes and the characters with the maximum contribution towards divergence should be considered for the improvement of chickpea.

The maximum contribution towards divergence was observed by Renuka *et al.* (2018) in pods per plant, harvest index and 100 seed weight. Dwevedi and Gaibriyal (2009) observed that the highest contribution was exhibited by harvest index, 100 seed weight and number of pods per plant. Singh *et al.* (2012) reported maximum contribution by days to 50% flowering. Devendrappa *et al.* (2011) reported by days to maturity.

Reddy *et al.* (2021) found that maximum contribution towards the total divergence was of the no of secondary branches per plant (35%), no of pods per plant (14.5%), seed yield per plant(10%), harvest index(9%), plant height(6.53%) which contributed to 75% of the total divergence followed by no of seeds per plant (6%), days to maturity (5%), seed index(3.2%), days to 50% pod setting(3%), biological yield per plant. Soumyashree *et al.* (2021) reported the highest contribution for the genetic divergence was found to by number of pods per plant seed yield per plant.

Tengse *et al.* (2021) reported the percentage contribution of the ten characters investigated to overall divergence is Seed yield per plant (22.03 percent) was found to be the most important factor in divergence. It was followed by 100 seed weight (19.49%), number of pods per plant (17.85%), harvest index (9.72%), number of seeds per pod (7.97%), plant height (6.84%), number of secondary branches per plant (6.33%), number of primary branches per plant (3.95%), days to maturity (3.62%), and days to 50% flowering (3.62%).

4.6.4 Character association

4.6.4.1 Correlation studies

Correlated characters are of interest for two main reasons: first, because of the genetic cause of correlation through linkage and pleiotropic action of genes, and second because of the change brought about by selections. It is essential to understand how the improvement of one character causes simultaneous changes in other characters, as well as natural selection (Falconer, 1960).

In the current study, the genotypic correlation coefficients were greater than the phenotypic correlation coefficients, showing that, while there is an intrinsic association between the characters analysed, the environment has little influence in determining these associations (Johanson *et al.* 1955).

The characters viz. number of pods per plant, 100 seed weight, harvest index, number of secondary branches per plant and plant height recorded a highly positive significant correlation with seed yield at both genotypic and phenotypic level. In other words, an increase in the magnitude of these characters would lead to an increase in the magnitude of grain yield.

Earlier studies too have indicated such a positive significant correlation for number of pods per plant by Guler *et al.* (2001). Arshad *et al.* (2004) found that seed yield had a positive and significant correlation with number of pods per plant, plant height, and 100 seed weight. Vaghela *et al.* (2009) found that seed yield per plant has a significant and positive correlation with number of pods per plant, number of primary branches per plant, harvest index, and 100 seed weight at genotypic as well as phenotypic levels. Gohil and Patel (2010) reported that 100 seed weight, harvest index, number of pods per plant and number of seeds per pod has a positive significant relationship with seed yield per plant. Yucel and Anlarsel (2010) found significant and positive relationships between seed yield and harvest index. Akhtar *et al.* (2011) observed that seed yield per plant had a significant and positive correlation with 100 seed weight, number of pods per plant and plant height. Babbar *et al.* (2012) reported that seed yield per plant showed a highly significant and positive correlation with number of seeds per pod, number of pods per plant, plant height and 100 seed weight. Bhanu *et al.* (2017) found a positive significant relationship between seed yield, and number of pods per plant, number of secondary branches.

Shedge *et al.* (2019) found a positive significant relationship between harvest index, number of pods per plant, number of secondary branches per plant, number of

primary branches per plant and number of seeds per pod. Shara *et al.* (2019) observed that seed yield per plant had a significant and positive correlation with number of secondary branches, 100 seed weight, number of pods per plant. Shanmugam *et al.* (2019) reported that seed yield per plant showed a highly significant positive correlation with number of seeds per pod, number of secondary branches per plant, 100 seed weight and harvest index.

Tengse *et al.* (2021) found Seed yield per plant had significant positive correlation with harvest index ($p=0.5044$; $g=0.6752$), 100 seed weight ($p=0.3738$; $g=0.4779$), number of pods per plant ($p=0.2999$; $g=0.4321$) and number of secondary branches per plant ($p=0.2629$; $g=0.3401$) at both phenotypic and genotypic level and days to 50% flowering ($g=0.2081$) at genotypic level. While significant negative correlation with number of primary branches per plant ($p=-0.2216$; $g=-0.3462$) at both phenotypic and genotypic level.

From the foregoing discussion on character associations, it is evident that characters viz., number of pods per plant, 100 seed weight, harvest index, number of secondary branches per plant and plant height displayed a positive correlation with seed yield per plant at both genotypic and phenotypic levels. Hence, these characters could be given due emphasis in formulating selection criteria for the improvement of seed yield in chickpea.

4.6.5 Path coefficient analysis

Path coefficient analysis is basically a standardized partial regression coefficient that divides correlation into direct and indirect effects. The total correlation coefficient between yield and its component characters might be misleading at times since it can overestimate or underestimate its association with other characters. Because many characters affect a given trait, direct selection based on correlated coefficient must be split into direct and indirect effects using path coefficient analysis in these cases. Thus, when the correlation and path coefficient are being used together, they can provide a deeper understanding of the cause and effect relationship between different pairs of characters. As a guideline for interpretation of path analysis results, the following key points may be kept in view as suggested by Singh and Chaudhary (1977).

If the correlation coefficient between a causal factor and its impact is almost equal to its direct effect, then correlation describes the true relationship and direct

selection through this trait will be effective. If the correlation coefficient is negative and the direct effect is also negative, we must abandon the character selection.

The characters viz., 100 seed weight, number of pods per plant, number of secondary branches per plant, days to 50% flowering, harvest index and number of primary branches per plant on seed yield in decreasing order of magnitude revealing that these were major yield contributing traits in chickpea.

Similar results were reported by Talebi *et al.* (2007) for number of seeds per pod, number of pods per plant and harvest index. Thakur and Sirohi (2009) reported the highest positive direct effect of harvest index and number of pods per plant on grain yield. Harvest index showed a positive direct effect on seed yield as reported by Ozveren and Anlarsal (2010), Yucel and Anlarsel (2010) and Chopdar *et al.* (2016). Number of pods per plant had also a direct effect on grain yield as reported by Gaikwad and Monpara (2011). Zali *et al.* (2011) recorded number of secondary branches per plant height has a positive direct effect on grain yield. Kumar *et al.* (2012) reported the highest positive direct effect of number of pods per plant on seed yield. Jeevani *et al.* (2013) and Muhammad *et al.* (2013) reported a positive direct effect of number of pods per plant, harvest index on seed yield. Hasan and Deb (2014) and Parhe *et al.* (2014) reported number of secondary branches per plant, 100 seed weight, number of pods per plant and had a positive direct effect on grain yield. Harvest index showed a positive direct effect on seed yield studied by Sohaib *et al.* (2016). Alka Dev *et al.* (2017) reported number of pods per plant and harvest index had a positive direct effect on seed yield. Similarly, Thakur *et al.* (2018) showed harvest index and number of pods per plant had a positive direct effect on seed yield per plant.

Manoj Kumar *et al.* (2018) days to flowering and total pod number exhibited high positive direct effects on seed yield. Shara *et al.* (2019) showed number of branches per plant, number of seeds per pod, harvest index and number of pods per plant had a positive direct effect on seed yield per plant. Mansa *et al.* (2019) Character association analysis revealed that number of secondary branches per plant, number of pods per plant, and harvest index showed a highly significant and positive correlation with seed yield per plant.

From the above discussion, it is evident that 100 seed weight, number of pods per plant, number of secondary branches per plant, days to 50% flowering and harvest index showed a positive direct effect on seed yield.

CHAPTER – V
SUMMARY AND CONCLUSIONS

CHAPTER – V

SUMMARY AND CONCLUSION

The current study, “**Genetic Diversity, Correlation and Path Analysis Studies in Chickpea (*Cicer arietinum* L.)**” was carried out during the *Rabi* 2021-22 to study the nature and magnitude of genetic variability present in all genotypes for quantitative characters in chickpea, as well as grouping genotypes into various clusters.

Forty one chickpea genotypes were examined in RBD (randomized block design) with 2 replications. 10 characters were studied viz., days to 50 per cent flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight (g), harvest index (%) and seed yield per plant (g).

The treatment differences in ANOVA were found statistically significant for most of the characters. The magnitude of the genotypic and phenotypic coefficients of variation also revealed that the experimental materials had a good amount of variability. In the present study, high estimates of the genotypic and phenotypic coefficient of variation were observed for seed yield per plant followed by number of pods per plant, 100 seed weight, plant height and number of secondary branches per plant.

5.1 Variability and genetic parameters

The highest broad sense heritability was observed for plant height followed by 100 seed weight, days to maturity, seed yield per plant, number of pods per plant, days to 50 % flowering, number of primary branches per plant, number of secondary branches per plant, number of seeds per pod and harvest index. The highest genetic advance as per cent of mean was noticed for the character number of pods per plant followed by plant height, seed yield per plant, 100 seed weight, days to maturity, days to 50% flowering, harvest index, number of secondary branches per plant, number of primary branches per plant and number of seeds per pod.

5.2 Genetic divergence

The D^2 values showed adequate genetic diversity among the genotypes studied. Based on D^2 values all the genotypes were grouped into twelve clusters with the varying

number of genotypes in the clusters. The clustering pattern of these genotypes does not follow the geographical distribution. The maximum genetic distance (D) of 34.89 was found between the clusters VI and XII.

5.2.1 Cluster formation

The goal of cluster formation and assessing inter and intra cluster divergence is to select best parents to be chosen for hybridization programmes. Crossing between genotypes from the same cluster would not result in the desired improvement in any character; therefore, the parents chosen for crossing should be from different clusters. The more the genetic diversity in the genotypes the greater the divergence between two clusters. Crosses involving parents with a high degree of divergence have also been reported to decrease in heterosis. As a result, while selecting parents based on genetic diversity, their performance and cluster mean for the characters must also be taken into consideration while selecting the parents. In the current study, the intra cluster distance (D^2) and the cluster means for the ten characters studied are presented in Table 4.5 and Table 4.7 respectively.

The intra cluster distance (D^2) ranges from 68.72 to 90.06. The inter cluster distance (D^2) ranges from 49.00 to 1217.31. The maximum inter cluster distance ($D^2 = 1217.31$) was observed between cluster VI and cluster XII followed by cluster XII and VIII ($D^2 = 1069.94$), cluster VI and cluster X ($D^2 = 962.24$), cluster V and cluster VI ($D^2 = 919.90$) and cluster V and VIII ($D^2 = 860.24$). The minimum inter cluster distance ($D^2 = 49.00$) was between clusters III and VII.

The cluster mean for days to 50 per cent flowering varied from 41.00 (cluster VI) to 54.00 days (cluster V). The cluster mean for days to maturity ranged from 94.00 (cluster IX) to 113.50 days (cluster V). The cluster mean for plant height ranged between 35.16 (cluster IV) to 73.55 cm (cluster X). The cluster mean for the number of primary branches per plant ranged between 2.00 (cluster III) to 3.10 (cluster VII and XII). The cluster mean for secondary branches per plant ranged between 7.00 (cluster VI) to 14.30 (cluster XII).

The cluster mean for number of pods per plant was maximum in cluster II (120.30) and it was minimum in cluster VII (45.50). The cluster mean for number of seeds per pod was maximum in cluster IX and X (1.30) and it was minimum in cluster VI

and VIII (1.00). The cluster mean for 100 seed weight was minimum in cluster VI (13.20 g) and it was the maximum in cluster XII (36.00 g). The cluster mean for harvest index was maximum in cluster III (44.91%) and minimum in the case of cluster VI (32.61%). The cluster mean for seed yield per plant ranged between 13.40 g (cluster VI) to 41.52 g (cluster XI).

5.3 Correlation

From correlation studies were conducted at both the genotypic and phenotypic levels to determine the direction and magnitude of association between characters. It indicates that a strong inherent association between various characters studied and genotypic expression of correlation was influenced by the environmental condition comparatively less. The characters viz. number of pods per plant, 100 seed weight, harvest index, number of secondary branches per plant and plant height recorded a highly positive significant correlation with seed yield at both genotypic and phenotypic level. This indicates the simultaneous improvement of these characters through selection.

5.4 Path coefficient analysis

From path coefficient analysis it is indicated that the characters viz., 100 seed weight, number of pods per plant, number of secondary branches per plant, days to 50% flowering, harvest index and number of primary branches per plant on seed yield in decreasing order of magnitude revealing that these were major yield contributing traits in chickpea. Hence, the selection of genotypes based on these characters as a selection criterion would help improve the seed yield potential of chickpea.

5.5 CONCLUSION

Based on finding generated from the present investigation, the following conclusions can be drawn, which may be considered for improvement in chickpea crop in future breeding programmes.

The wide range of genetic variability observed for the majority of the characters, as evidenced by significant genotype variances, suggests that it could be useful in the isolation of better germplasm lines. The phenotypic coefficients of variation (PCV) were slightly higher than the genotypic coefficients of variation (GCV), indicating that the

environment plays a role in governing these traits. Similarly, the magnitude of GCV and PCV was observed high for the characters viz., seed yield per plant followed by number of pods per plant, 100 seed weight, plant height, number of secondary branches per plant and number of primary branches per plant. It indicates that the selection of desired germplasm for these traits may be worthwhile for improving seed yield in the future breeding programme.

The characters viz., seed yield per plant showed high GCV and PCV, moderate heritability and high genetic advance as per cent of mean. Number of pods showed high GCV and PCV, moderate heritability and high genetic advance as per cent of mean. 100 seed weight showed moderate GCV and PCV, high heritability and moderate genetic advance as per cent of mean.

LITERATURE CITED

LITERATURE CITED

- Aarif, M., Rastogi, N.K., Johnson, P.L. & Chandrakar, P.K. (2014). Genetic analysis of seed yield and its attributing traits in *Kabuli* chickpea (*Cicer arietinum* L.). *J. Food Leg.* 27(1), 24-27.
- Abhishek Kumar, G., Suresh Babu and Roopa Lavanya, G. (2012). Character association and path analysis in early segregating population in chickpea (*Cicer arietinum* L.). *Legume Res.*, 35(4):337-340.
- Akhtar, L. H., Parvez, Muhammad A. & Muhammad, N. (2011). Genetic divergence and inter-relation studies in chickpea (*Cicer arietinum* L.). *Pak. J. Agri. Sci.* 48(1), 35-39.
- Alka, Dev. (2017). Genetic variability studies in *Desi* chickpea (*Cicer arietinum* L.) genotypes. *IJCM App. Sci.* 6(4), 20-25.
- Allard, R.W. (1961). Relationship between genetic diversity and consistent performance in different environments. *Crop Sci.* 1(2), 127-133.
- Ali. Q., Tahir, M. H. N., Sadqat, H. A., Aeshad, S., Ashan, M., Farooq, J., Waseem, M. and Iqbal, A. (2011). Genetic variability and correlation for quantitative traits in chickpea (*Cicer arietinum* L.). *J. Bacteriol Res.*, 3(1): 6-9.
- Ambilwade, B., Magar, A.S., Gadade, S.B. & Suresh, B.G. (2018). Genetic Diversity studies in chickpea (*Cicer arietinum* L.) germplasm. *Int. J. Curr. Microbiol. App. Sci.* 7(9), 2757-2763.
- Anonymous, (2018-19) Annual report of research work on pulses 2018-2019, IIPR Kanpur.
- Anonymous, (2019-20) Annual report of research work on pulses 2019-2020, IIPR Kanpur.
- Arora, P. P., Jeena, A. S. and Upreti, M. C. (2003). Path analysis for yield improvement in chickpea. *Agrc. Sci. Digest*, 23 (2): 116-118.
- Arshad, M., Bakhsh, A. & Ghafoor, A. (2004). Path coefficient analysis in chickpea under rainfed condition. *Pak. J. Bot.* 36, 75-81.
- Astereki, H., Sharifi, P. and Pouresmael, M. (2017). Correlation and path analysis for grain yield and yield components in chickpea (*Cicer arietinum* L.). *Genetika*, 49 (1): 273 - 284

- Aswathi, P. V., Ganesamurthy, K. & Jayamani, P. (2019). Genetic variability for morphological and biometrical traits in chickpea (*Cicer arietinum* L.). *Electronic Journal of Plant Breeding*. 10(2), 699-705.
- Babbar, A., Prakash, V., Tiwari, P. & Iquebal, M.A. (2012). Genetic variability for chickpea (*Cicer arietinum* L.) under late sown season. *Legume Res.* 35(1), 1-7.
- Bala, I., Kalia, R. and Kumar, B. 2015a. Exploitable genetic variability and determination of selection criteria using path coefficient analysis in chickpea. *Bangladesh Journal Botany*. **44 (1)**: 139-142.
- Bhanu, A.N., Singh, M.N., Tharu, R. & Saroj, S.K. (2017). Genetic variability, correlation and path coefficient analysis for quantitative traits in chickpea enotypes. *Indian J. Agric. Res.* 51(5), 425-430.
- Bohare, Tinkeshwari V., Kulwal, Pawan L., Chahande, Rahul V., Bedis, Madhukar R., Mhase, Laxmsan B. & Shinde, Swati D. (2020). Genetic diversity analysis in chickpea (*Cicer arietinum* L.) genotypes. *Journal of Pharmacognosy and Phytochemistry*. 9(2), 899-903.
- Borate, V.V., Dalvi, V.V. & Jahav, B.B. (2010). Estimates of genetic variability and heritability. *J. Maharashtra Agric. Univ.* 35(1), 47-49.
- Burton, G.W. (1952). Quantitative inheritance in pearl millet (*P.glaucum* L.). *Agron. J.* 501- 503.
- Chahande, Rahul V., Kulwal, Pawan L. and Mhase, Laxman B. (2020). Genetic diversity analysis in chickpea (*Cicer arietinum* L.) genotypes grown under drought stress condition. *Journal of Pharmacognosy and Phytochemistry*. 9(4), 3307-3310.
- Chief statistician commissionerate of agriculture report, Pune 2020-21.
- Chowdhury, M.A., Vandenberg B. & Warkentin T. (2002). Cultivar identification and genetic relationship among selected breeding lines and cultivars in chickpea (*Cicer arietinum* L.). *Euphytica*. 127, 317-325.
- Chopdar, D.K., Baudhbharti., Sharma, P.P., Dubey, R.B., Bragendra. & Meena, B.L. (2016). Studies on genetic variability, character association and path analysis for yield and its contributing traits in chickpea (*Cicer arietinum* L.). *Agril. Res. Communication Centre J. Legume res.* 40(5), 824-829.

- Cochran, W.G. & Cox, G.M. (1957). Experimental design. John Wiley and Sons N.Y., London. 82-90 and 403-412.
- Damber, A.D., Deshmukh, R.B. and Naval, P.K. 1984. Analysis of genetic variability in chickpea. *Journal of Maharashtra Agricultural University*. 9(3): 350.
- Dasgupta, T.; Islam, O.; Gayen, P. and Sarkar, K.K. 1987. Genetic divergence in Chickpea. *Experimental Genetics*. 3(1-2): 15-21.
- Dawane, J.K., Jahagirdar, J.E. & Shedje, P.J. (2020). Correlation Studies and Path Coefficient Analysis in Chickpea (*Cicer arietinum* L.). *Int.J.Curr.Microbiol. App. Sci*. 9(10), 1266-1272.
- Deshmukh, R.B. And Patil, J.V. 1997. Genetic divergence in Chickpea. *Aladras Agricultural Journal*. 84(11/12): 664-666.
- Devendrappa, J., Viswanatha, K.P., Mallikarjun, B.P., Ambalika, D.S. & Gavisiddappa, Choudki V.M. (2011). Assessment of genetic diversity in chickpea (*Cicer arietinum* L.) *Am.-Eu. J. Sustain Agric*. 2(3), 205-211.
- Dewey, D.R. & Lu, K.H. (1959). A correlation and path coefficient analysis of a component of Wheat grass seed production. *Agron. J*. 51, 515-518.
- Dhuria, N. and Babbar, A. 2017. Estimation of genetic variability and interrelationships of quantitative traits for improvement of kabuli chickpea (*Cicer arietinum* L.). *Journal of Food Legumes*, 30(1): 25-29
- Directorate of economics and statistics report, 2020-2021.
- Dubey and Srivastava, S. B. L. (2007). Analysis of genetic diversion for yield determinants in chickpea (*Cicer arietinum* L.). *Plant archives*. 7(1):153-155.
- Dwevedi, K.K. & Gaibriyal, L. M. (2009). Assessment of genetic diversity of cultivated Chickpea. *Asian J. of Agricultural Sciences*. 1(1), 7-8.
- Falconer, D.S. (1960). Correlated character, introduction to quantitative genetics, 312, published by Longman Group Ltd., London.
- Fisher R. A., (1918) The correlation between relatives on the supposition of mendelian inheritance. *Trans. R. Soc. Edinb*. 53: 399-433.
- Fisher, R.A & Yates. F. (1943). Statistical table for Biological Agricultural and Medical Research (2nd ed.). Oliver and Boyd Ltd. London.

- Gaikwad, A.R., Desai, N.C., Langhi, A.M. & Jadhav, S.D. (2012). Studies on genetic variability in chickpea (*Cicer arietinum* L.). *EM Int.* 17(3), 585-558.
- Gaikwad, S.R. & Monpara, B.A. (2011). Genetic variation in F₂ populations and their potential in the improvement of seed yield in chickpea (*Cicer arietinum* L.). *J. Agric. Res. Technol.* 36(3), 527- 530.
- Galton, F. (1889). Co-relations and their measurement, chiefly from anthropometric data. *Proc. Roy. Soc. London*, 45, 135–145.
- Gaur, R. S., Tiwari, A. and Mishra, S. P. 2014. Correlation and path coefficient analysis for seed yield and its components in chickpea (*Cicer arietinum* L.). *Trends in Biosciences*, 7(1): 54-57
- Gediya, L., Patel, D.A., Parmar, D.J., Patel, R. & Rahevar, R. (2018). Assessment of genetic diversity of chickpea genotypes using D2 statistics. *IJCS.* 6(4), 3177-3181.
- Gohil, D.P. & Patel, J.D. (2010). Character association and path analysis in chickpea (*Cicerarietinum* L.) under conserved soil moisture. *Legume Res.* 33(4), 283-286.
- Gul, R., Khan, H., Bibi, M., Ain, Q.U. & Imran, B. (2013). Genetic analysis and interrelationship of yield attributing traits in chickpea (*Cicer arietinum* L.). *J. Anim. & Pl. Sci.* 23(2), 521-526.
- Guler, M., Adak, M.S. & Ulukah, H. (2001). Determining relationship among yield and some yield components using path coefficient analysis in Chickpea. *European J. Agron.* 14(2), 161-166.
- Gumber, R.K., Singh, S., Rathore, P. & Singh, K. (2002). Selection indices and character association in Chickpea. *Indian J. Pulses Res.* 13(2), 56-58.
- Hasan, M.T. & Deb A.C. (2014). Estimates of direct and indirect effects between yield and yield Components and selection indices in chickpea (*Cicer arietinum* L.). *Tropical Res. an Int. J.* 1(2), 65-72.
- Hanson, W.D., Robinson, H.F. & Comstock, R.E. (1956). Biometrical studies of yield in segregating population Korean Lespandeza. *Agron. J.* 48, 268-272.

- Jadhav, R.S., Mohir, M.N. & Ghodke M.K. (2012). Genetic variability in chickpea. *Bioinfolet*. 9(2), 199-201.
- Jakhar, D.S., Kamble, M.S., Singh, A. & Kumar, S. (2016). Performance of chickpea (*Cicer arietinum* L.) genotypes in the Kolhapur region. *International Journal of Agriculture, Environment and Biotechnology Citation, IJAEB*. 9(2), 283-289.
- Janghel, D.K., Krishan Kumar, R., Sunil., & Chhabra, A.K. (2019). Genetic Diversity Analysis, Characterization and Evaluation of Elite Chickpea (*Cicer arietinum* L.) Genotypes. *Int. J. Curr. Microbiol. App. Sci*. 9(01), 199-209.
- Jeena, A.S. & Arora, P.P. (2002). Mahalanobis D2 technique in chickpea. *Agricultural Science Digest*. 22(3), 209-210.
- Jeena, A.S., Arora P.P. & Upreti, M.E. (2005). Divergence analysis in Chickpea. *Legumes res*. 28(2), 152-154.
- Jivani, J.V., Mehta., Vaddoria, M.A. & Ravallata. (2013). Correlation and path coefficient analysis in chickpea (*Cicer arietinum* L.). *Elec. J. of Plant Breeding*. 4(2), 1167-1170.
- Johnson, H.W., Robinson, H.F. & Comstock, R.E. (1955). Genotypic and phenotypic correlation in soybean and their implications in selection. *Agron. J.* 47, 477-482.
- Jukanti, A.K., Gaur, P.M., Gowda, C.L. & Chibbar, R.N. (2012). Nutritional quality and health benefits of chickpea (*Cicer arietinum* L.). *British J. of Nutrition*. 108, s11-s26.
- Kashyap, O.P. & Rastogi, N.K. (2003). Genetic divergence in chickpea. *Indian J. Plant Genet. Resources*. 16(1), 1-3.
- Khan, R.F. & Khan, H. (2011). Dissection of genetic variability and heritability estimates of Chickpea germplasm for various morphological markers and quantitative traits. *Saehad J. Agric*. 27(1), 67- 72.
- Kobraee, S., Shamsi, K., Rasekhi, B. and Kobraee, S. 2010. Investigation of correlation analysis and relationships between grain yield and other quantitative traits in chickpea (*Cicer arietinum* L.). *African Journal of Biotechnology* Vol. 9(16): 2342-2348.
- Kumar, A., Babu, G. U. & Lavnya, G. R. (2012). Character association and path analysis in early segregating population in chickpea. *Legume Res*. 35(4), 337-340.

- Kumar, S., Jeena, A.S. & Arora, P.P. (2002). Genetic variability and its importance in chickpea (*Cicer arietinum* L.). *Agric. Sci. Digest*. 22(3), 215-216.
- Li, C.C. (1954). Population Genetics. The University of Chicago Press, Chicago and London. pp. 28-41.
- Mahalanobis, P.C. (1928). A statistical study at Chinese head measurement. *J. of Asiatic Soc.* 25, 301- 377.
- Mahalanobis, P.C. (1936). On the generalized distance in statistics. *Proc. Nat. Ins. Sci. India*. 2, 49-55.
- Manasa, B., Shanthi Priya, M., Jayalakshmi, J., & Umamaheswari, P. (2019). Character association and path coefficient analysis in extra large and large seeded *Kabuli* chickpea (*Cicer arietinum* L.). *Ind. J. Pure App. Biosci.* 7(5), 166-171.
- Manoj Kumar., Anshuman, Singh. & Devi, S. Rhods. (2018). Correlation, path analysis and genetic variability, of yield, and yield components in chickpea (*Cicer arietinum* L.). *International Journal of Fauna and Biological Studies*. 5(3), 131-135.
- Moll, R.H., Lonnquist, R.H., Veler, J. Fortune. & Johnson, E.C. (1965). The relationship of heterosis and genetic divergence in maize. *Genetics*. 52, 139-144.
- Muhammad, A., Bakhsh, A. & Ghafoor, A. (2004). Path coefficient analysis in chickpea. *Pak. J. Bot.* 36(1), 75-81.
- Muhammad, A.M., Muhammad, M.B. & Muhammad, Saleem. (2013). Estimation of genetic variability and path analysis of grain yield and its components in chickpea (*Cicer arietinum* L.). *Int. J. Scientific and Engineering Research* 4. ISSN 2229-5518.
- Murty, B.R. & Arunachalam, V. (1966). The nature and divergence in relation to breeding system in some crop plants. *Indian J. Genet.* 26, 188-198.
- Nadiya, A. Al-Saady., Saleem, K. Nadaf., Ali, H. Al-Lawati. & Saleh, A. Al-Hinai. (2019). Genetic diversity of indigenous chickpea (*Cicer arietinum* L.). Germplasm Collection. *Global Advanced Research Journal of Agricultural Science*. (ISSN: 2315-5094). 8(4), 166-174.
- Narendra, Kumar. (1997). Genetic diversity among chickpea accessions. *Indian J. Genet.* 57(1), 87-90.

- Nimbalkar, R.D. & Harer, P.N. (2001). Genetic diversity in chickpea. *J. Mah. Agric. Univ.* 26(1), 106- 107.
- Noor, F., Ashraf, M. & Gafoor, A. (2003). Path analysis and relationship among quantitative traits in chickpea. *Pakistan J. of biological Science.* 6(6), 551-555.
- Ozveren, Y.D. & Anlarsal, A.E. (2010). Determination of selection criteria with path coefficient analysis in chickpea breeding. *Bulg. J. Agric. Sci.* 16, 42-48.
- Padmavati, P.V., Murthy, S.S., Rao, V.S. & Lal Ahamad, M. (2013). Correlation and path coefficient analysis in Kabuli chickpea (*Cicer arietinum* L.). *Int. J. Appl. Biol. Pharma. Tech.* 4(3), 107-110.
- Panse, V.G. & Sukhatme, P.V. (1967). Statistical methods of genotypic and phenotypic variability in groundnut. *J. Maharashtra Agric. Univ.* 12(3), 319-321.
- Parhe, S.D., Harer, P.N. & Nagawade, D.R. (2014). Investigation of genetic divergence in chickpea (*Cicer arietinum* L.) genotypes. *The Bioscan an Int. Quarterly J. of Life Sci.* 9(2), 879-882.
- Ponnuru, Akhil., Lal, G.M. & Munagala, Sai Kiran. (2019). Genetic diversity studies in chickpea (*Cicer arietinum* L.) germplasm. *Journal of Pharmacognosy and Phytochemistry.* 8(4), 2549-2552.
- Pooran Chand and Singh, F. 1995. Genetic divergence in chickpea. *Agricultural Science Digest Karnal.* 15(3):104-106.
- Rao, C.R. (1952). Advanced statistical methods in biometrical research. John Wiley and Sons. Inc., New York. 351-364.
- Rao, S.K. and Singh, R.K. 1994. Genetic diversity and elite chickpea genotypes. *Agricultural Science Digest Karnal.* 14(3/4) :153-155.
- Reddy J.M., Gabrial M. Lal, Velugoti Priyanka Reddy, Subhadra Pattanayak, V. Rohith Guptha, C. Kalyan Sagar and P. Venkata Bala Brahmanjaneyulu. (2021). Studies on Geneticdiversity in *Desi* Chickpea (*Cicer arietinum* L.) using D2 Statistics. *International Journal of Plant & Soil Science* 33(17): 100-104.
- Renukadevi, P. & Subbalakshmi, B. (2006). Correlations and path coefficients analysis in chickpea. *Legume Res.* 29(3), 201-211.

- Renuka, Shivwanshi. & Anita, Babbar. (2018). Genetic divergence analysis in chickpea germplasm. *Legume Res. - An International Journal*. (42), 715-718.
- Robinson, H.F. (1966). Quantitative genetics in relation to breeding on centennial of Mendelism. *Indian J. Genet.* 26(A), 171-187.
- Saleem, M., Shahzad, K., Javid, M., and Rauf, S. A. 2002. Heritability estimates for grain yield and quality characters in chickpea (*Cicer arietinum* L.). *Int. J. Agric. Biol.*, 4: 275-276.
- Sandhu, J.S., Singh, P. & Singh, A. (2006). Genetic divergence in chickpea in different environments. *Tropical science*. 46, 23-30.
- Searle, S. R. 1961. Phenotypic, genotypic and environmental correlations. *Biometrics*. 17(3): 474- 480.
- Shanmugam, Mohan. & Kalaimagal, Thiagarajan. (2019). Genetic variability, correlation and path coefficient analysis in chickpea (*Cicer arietinum* L.) for yield and its component traits. *Int. J. Curr. Microbiol. App. Sci.* 8(05), 1801-1808.
- Shara, J. Hama. (2019). Correlation and path coefficient analysis for seed yield and yield components in chickpea under rainfed condition. *Journal of Kerbala for Agricultural Sciences*. Vol (6), No. (1).
- Sharma, L.K. & Saini, D.P. (2010). Variability and association studies for seed yield and yield components in chickpea (*Cicer arietinum* L.). *Res. J. Agric. Sci.* 1(3), 209-211.
- Shedge, P.J., Patil, D.K., & Gite, V.K. (2019). (a) Study on genetic divergence in Desi chickpea (*Cicer arietinum* L.). *Int. J. Curr. Microbiol. App. Sci.* 8(07), xx-xx.
- Shedge, P.J., Patil D.K., & Misal, M.R. (2019). (b) Assessment of genetic variability in chickpea (*Cicer arietinum* L.). *Int. J. Curr. Microbiol. App. Sci.* 8(07), xx-xx.
- Shaikh, A. B., D. K. Patil, Deepak A. Kharad, Prashant B. Kardile and Yogesh Pawar 2020. Phenotypic and Genotypic Path Coefficient Analysis Studies in Chickpea (*Cicer arietinum* L.). *Int.J.Curr.Microbiol.App.Sci.* 9(10):3947-3956
- Shaikh, A. B., D. K. Patil, Yogesh Pawar, Deepak A. Kharad and Prashant B. Kardile 2020. Estimation of Phenotypic and Genotypical (Above Digonal) Correlation

Coefficients in Yield and its Component Characters in Chickpea (*Cicer arietinum* L.). *Int.J.Curr.Microbiol.App.Sci.* 9(10):3957-3967

- Singh, M., Singh, A. & Rhods, D.S. (2018). Correlation, path analysis and genetic variability of yield and yield components in chickpea (*Cicer arietinum* L.). *International Journal of Fauna and Biological Studies*. 5(3), 131-135.
- Singh, K.P. and Sareen, P.K. 1993. Genetic divergence in chickpea. *International Journal of Tropical Agriculture*. 11(1):57-62.
- Singh, R.K. & Chaudhary, B.D. (1977). Biometrical methods in quantitative genetic analysis. Kalyani publishers, New Delhi. 215-218.
- Singh, Rupinder Pal., Singh, Inderjit., Singh, Sarvjeet. & Sandhu, J.S. (2012). Assessment of genetic diversity among interspecific derivatives in chickpea. *J. of Food Legumes*. 25(2), 150-152.
- Sivakumar, S. & Muthiah, A.R. (2000). Genetic divergence in chickpea germplasm. *Madras Agric. J.* 87(1-3), 48-50.
- Snedcor, G.W. & Cochran, W.G. (1967). Statistical methods. 6th Oxford and IBH Publ. Co. Calcutta, 172.
- Sohaib, S.M., Ahsan, M., Mehmood, Z., Abdullah, M., Shakoore, A. & Ahmad, Irfan M. (2016). Genetic variability and interrelationship of various agronomic traits using correlation and path analysis in chickpea (*Cicer arietinum* L.). *Academia J. of Agril. I Res.* 4(2), 082-085.
- Soumyashree R., M. D. Patil And I. S. Katageri, (2021) Genetic diversity for seed and productivity traits in chickpea (*Cicer arietinum* L.). *J. Farm Sci.*, 34(2): (134-137).
- Suyog, D. Warkad., Gabrial, M. Lal., Nikhil, A. & Suryawanshi. (2018). Study on genetic diversity in chickpea (*Cicer arietinum* l.) germplasm. *IJABR*. 8(3), 347-35.
- Talebi, R., Faydz, F. & Jelodar, A. (2007). Correlation and path coefficient analysis of yield and yield components of chickpea under dryland condition in the west of Iran. *Asian J. of Plant Sci.* 6(7), 1151-1154.

- Tamvar, Mayuriben R., Patel, Sunayan R., Patil, Sunil S., Naik, Arpan J. & Patel, Harshad N. (2019). Diversity study through D2 analysis in chickpea. *The Pharma Innovation Journal*. 8(9), 140-143.
- Tengse SM, Sarode SB, Shinde AV and Deshmukh SS. (2021). Assessment of genetic divergence in chickpea [*Cicer arietinum* L.]. *The Pharma Innovation Journal* 2022; 11(1): 1061-1065.
- Tengse SM, Sarode SB, Shinde AV and Deshmukh SS. (2021). Assessment of correlation and path analysis in chickpea [*Cicer arietinum* L.]. *The Pharma Innovation Journal* 2022; 11(1): 184-188.
- Thakur, N.R., Toprope, V.N. & Phanindra K.S. (2018). Genetic diversity analysis in chickpea (*Cicer arietinum* L.). *Int. J. Curr. Microbiol. App. Sci.* Special issue- 6, 904-91.
- Thakur, S. & Sirohi, A. (2009). Correlation and path analysis in chickpea under different seasons. *Legume Res.* 32(1), 1-6.
- Upadhyaya, H.D., Dwivedi., Gowda, C.L. & Singh, S. (2007). Identification of diverse germplasm lines for agronomic traits in a chickpea (*Cicer arietinum* L.). Core collection for use in crop improvement. *Field Crop Res.* 100, 320-326.
- Vaghela, M.D., Poshia, V.K., Savaliya, V.K., Davada, B.K. & Mungra, K.D. (2009). Studies on character association and path analysis for seed yield and its components in chickpea (*Cicer arietinum* L.). *Legume Res.* 32(4), 245-249.
- Vijaykumar, C.H.M., Salimath, P.M., Giud, J.V. and Parameshwarappa, R. 1991. The nature of genetic divergence in chickpea. *Journal of Maharashtra Agricultural University*. **16**(2) :176-178.
- Wilks, S.S. (1932). Certain generalization in the analysis of variance. *Biometrics*. 24, 471-494.
- Wright, S. (1921). Correlation and causation. *J. Agric. Re.* 20, 557-565.
- Yadav, P., Tripathi, D. K., Khan, K. K. and Yadav, A. K. (2015). Determination of genetic variation and heritability estimates for morphological and yield traits in chickpea (*Cicer arietinum*) under late sown conditions. *Indian Journal of Agricultural Sciences*, 85(7): 877–882.

- Yucel, D.O. & Analarsal, A.E. (2010). Determination of selection criteria with path coefficient analysis in chickpea (*Cicer arietinum* L.) breeding. *Bulgarian J. Agric. Sci.* 16(1), 42-48.
- Yucel, D. O., Anlarsal, A. E., Yucel, C. 2006. Genetic variability, correlation and path analysis of yield and yield contributing characters in chickpea (*Cicer arietinum* L.). *Turk J. Agric For* 30: 183-188.
- Zali, H., Farshadfarb, E. & Sabaghpour, S.H. (2011). Genetic variability and interrelationships among agronomic traits in chickpea (*Cicer arietinum* L.) genotypes. *Crop Breed. J.* 1(2), 127-132.
- Zena, A. S., Arora, P. P. and Upreti, M. C. 2008. Path coefficient analysis for enhancing the yield of chickpea, *Bhartiy Krishi Anusandhan Patrika*, Vol.:23, No. 3-4.
- Zeeshan, M., W. Arshad, S. Ali, M. Owais, M. Zulkiffal & M. Hussain. (2012). Genetic divergence and character association in chickpea (*Cicer arietinum* L.) under rainfed conditions. *Wudpecker J. Agric. Res.* 2(1), 028-032.

CRRICULAM VITAE

CURRICULAM VITAE

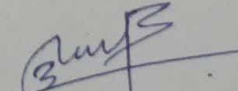
Name of the student : Gadkar Utkarsh Ganesh
Date of Birth : 28/08/1998
Nationality : Indian
Department : Genetics and Plant Breeding
Permanent Address : At. Post. Tugaon Tq. Osmanabad Dist. Osmanabad
Mobile No. : 7057118087
Email id : gadkarutkarsh@gmail.com
Title of Thesis : "Genetic Diversity, Correlation and Path Analysis Studies in Chickpea (*Cicer arietinum* L.)"

Academic Qualification:

Courses / degree	Name of the Institute / college	University / Board	Year of Passing	Percentage % / CGPA	Class / grade
SSC	Bhai Uddhavrao Patil High School, Tugaon, Tq. Osmanabad Dist. Osmanabad	Latur Board	2014	87.20	F.C.W. D.
HSC	Dr. Chandrabhanu Sonwane jr. college, Ukkadgaon, Tq. Barshi Dist. Solapur	Pune Board	2016	75.54	First
B.Sc. (Agriculture)	College of Agriculture, Badnapur, Dist. Jalna	V. N. M .K. V. Parbhani	2020	82.10	First

Date: 30/11/2022

Place: Badnapur


 Gadkar U.G.