Identification of Chickpea (C*icer arietinum* L.) genotypes promising for mechanical harvesting

M. Sc. (Ag.) Thesis

by

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DEPARTMENT OF GENETICS AND PLANT BREEDING
COLLEGE OF AGRICULTURE
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Identification of Chickpea (C*icer arietinum* L.) genotypes promising for mechanical harvesting

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CERTIFICATE - I

This is to certify that the thesis entitled **"Identification of Chickpea (*Cicer arietinum L.*) genotypes promising for mechanical harvesting"** submitted in partial fulfillment of the requirement for the degree of **Master of Science in Agriculture** of the Indira Gandhi Krishi Vishwavidyalaya, Raipur, (C.G.) is a record of the bonafide research work carried out by **Himakara Datta Mandalapu** under our guidance and supervision. The subject of the thesis has been approved by the Student's Advisory Committee and the Director of Instructions.

No part of the thesis has been submitted for any other degree or diploma (certificate, award etc.) or has been published/published part has been fully acknowledged. All the assistance and help received during the course of the investigations have been duly acknowledged by him.

Ritu Nair Saxena.

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COLLEGE OF AGRICULTURE
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Signature of Major Advisor
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(Himkara Datta Mandalapu)

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LIST OF NOTATIONS/ SYMBOLS

%	Percentage
∑	Summation
cm	Centimeter
DF	Degree of freedom
et al.	And co-worker/ and others
Fig.	Figure
g	Gram
h^2bs	Heritability broad sense
ha	Hectare
i.e.	That is
kg	Kilogram
m^2	Square meter
mm	Milli metre
^oC	Degree Celsius
S. No.	Serial number
Viz.	Namely
Mt	million ton
Km/hr	Kilometer per hour
RF	Rainfall
MSS	Mean sum of square
MST	Treatment means sum of square
MSE	Error means sum of square

LIST OF ABBREVIATIONS

ANOVA	Analysis of Variance
BY	Biological Yield
DTF	Days to 50% Flowering
DTM	Days to Maturity
DUS	Distinct Uniform Stable
GA	Genetic Advance
GAM	Genetic Advance as Percentage of Mean
GCV	Genotypic Coefficient of Variation
HOFP	Height of 1st Pod from Ground Level
HI	Harvest Index
HSW	Hundred seed weight
MSS	Mean Sum of Squares
NPB	Number of Primary Branches
NPP	Number of Pods Per Plant
NSB	Number of Secondary Branches
NSP	Number of Seeds per Pod
PCV	Phenotypic Coefficient of Variation
PH	Plant Height
PLYG	Plot Yield in grams
UPGMA	Un-weighted Pair Group Method with Arithmetic Mean

THESIS ABSTRACT

a)Title of the Thesis:	Identification of Chickpea (*Cicer arietinum* L.) genotypes promising for mechanical harvesting
b) Full name of the student:	Himakara Datta Mandalapu
c) Major Subject	Genetics and Plant Breeding
d) Name and Address of the Major Advisor:	Dr. Ritu R. Saxena Principal Scientist, Department of Genetics and Plant Breeding, College of Agriculture, IGKV, Raipur
e) Degree to be Awarded:	M.Sc. (Agriculture)

M.H. Datta

Signature of the Student

Ritu

Signature of Major Advisor

Date: 1-07-2021

Signature of Head of the Department

ABSTRACT

The experiment entitled "Identification of Chickpea (*Cicer arietinum* L.) genotypes promising for mechanical harvesting" was conducted using thirty six desi chickpea genotypes. Observations on quantitative and morphological traits had been noted on five plants which were chosen from every plot and replications at different growth stages. Analysis of variance on thirteen characters showed significant values in MSS values for eleven traits. Two traits viz., number of primary branches and number of seeds per pod did not show any significant variations. The presence of significant levels of

variation implies the presence of variability in the observed characters. This variability can be tapped into and be used in further development of the genotypes

The magnitudes of PCV observed were higher than the magnitudes for GCV. This indicated the impact of role of environment over the genotypic effect, finally influencing the phenotypic effect. Biological yield, number of pods per plant, number of secondary branches, plot yield and hundred seed weight were the traits which showed high PCV coupled with high GCV. Four characters, namely, height of first pod, no. of primary branches, harvest index, and no. of seeds per pod possessed high values of PCV along with moderate to low values of GCV.

High values for both heritability and genetic advance can be seen in characters such as heightof first pod (cm), plant height, and hundred seed weight. Plot yield showed high GAM with moderate heritability. Hundred seed weight was the only trait presenting high values of PCV, GCV along with high heritability and high GAM.

A positive significant relationship was observed between plot yield and harvest index and 100 seed weight whereas, negative relation was observed for traits such as days to maturity, number of secondary branches, and days to 50% flowering with plot yield. Hundred seed weight demonstrated positive association with height of first pod followed by plant height, biological yield and harvest index.

Path analysis with plot yield as dependent variable, showed positive direct effects by biological yield and harvest index at phenotypic level and at genotypic level, biological yield, harvest index, number of secondary branches, plant height showed a very high direct effect on plot yield. Plant height reported very positive direct effect on height of first pod (as dependent trait) at phenotypic level whereas, at genotypic level, hundred seed weight and no. of secondary branches showed very positive direct effect on HOFP.

Cluster analysis through Un-weighted Pair- Group Method with Arithmetic averages (UPGMA) using Euclidean distances divided the 36 genotypes under study into seven clusters. Cluster I that is comprised of 14 genotypes showed the highest value for intra cluster distance and the least by clusters V and VII with an inter-cluster distance of 0.000 as they contain only one genotype in each of them

Around 17 genotypes out of studied 36 genotypes showed a first pod height more than 30 cm. These genotypes exhibited suitable first pod height amenable for machine harvesting.

Based on seed coat colour, out of the 36 observed genotypes, 30 genotypes had brown coloured seed coat, 5 genotypes had dark brown coloured seed coat and one genotype had green coloured seed coat.

Six genotypes namely JG 24, IG 2020-15, RLBGMH-4, PBC 574, GJG 1916, and Phule G 191616 recorded both high first pod height and plot yield (g). Thus, we can infer that these six genotypes are suitable and promising as parents for further improvement or for developing into a cultivar.

थीसिस सार

a) थीसिस का शीर्षक:	चना में यांत्रिक कटाई के लिए जीनोटाइप की पहचान (सिसर एरीटिनम एल.)
b) छात्र का पूरा नाम:	हिमकारा दत्ता मंडलपु
c) प्रमुख विषय :	आनुवंशिकी और पादप प्रजनन
d) प्रमुख सलाहकार का नाम और पता:	डॉ. रितु आर. सक्सेना प्रमुख वैज्ञानिक, आनुवंशिकी एवं पादप प्रजनन विभाग, कृषि महाविद्यालय, आईजीकेवी, रायपुर,
e) प्रदान की जाने वाली उपाधि:	एम. एससी. (कृषि)

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प्रमुख सलाहकार के हस्ताक्षर

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विभागाध्यक्ष के हस्ताक्षर

सार

चना में यांत्रिक कटाई के लिए जीनोटाइप की पहचान (सिसर एरीटिनम एल.) शीर्षक के प्रयोग में छत्तीस देसी चना जीनोटाइप का उपयोग किया गया। पांच पौधों पर मात्रात्मक और रूपात्मक लक्षणों पर अवलोकन किया गया था, जिन्हें प्रत्येक भूखंड से चुना गया था और विभिन्न विकास चरणों में प्रतिकृतियां थीं। तेरह वर्णों पर विचरण के विश्लेषण ने ग्यारह वर्णों के लिए वर्गों के माध्य योग में महत्वपूर्ण मान दिखाए। दो लक्षणों जैसे प्राथमिक शाखाओं की संख्या और प्रति फली में बीजों की संख्या में कोई महत्वपूर्ण अंतर नहीं दिखा। भिन्नता के महत्वपूर्ण स्तरों की उपस्थिति का तात्पर्य प्रेक्षित वर्णों में परिवर्तनशीलता की उपस्थिति से है। इस परिवर्तनशीलता का दोहन किया जा सकता है और जीनोटाइप के आगे के विकास में उपयोग किया जा सकता है।

पीसीवी के परिमाण जीसीवी के परिमाण से अधिक थे। इसने जीनोटाइपिक प्रभाव पर पर्यावरण की भूमिका के प्रभाव का संकेत दिया और अंत में फेनोटाइपिक प्रभाव को प्रभावित किया। जैविक उपज, प्रति पौधा फलियों की संख्या द्वितीयक शाखाओं की संख्या, भूखंड की उपज और सौ बीज भार ऐसे लक्षण थे जो उच्च जीसीवी के साथ उच्च पीसीवी दिखाते थे। चार लक्षण, पहली फली की ऊंचाई, प्राथमिक शाखाओं की संख्या, प्रति फली में बीजों की संख्या और फसल सूचकांक में पीसीवी के उच्च मूल्यों के साथ & साथ जीसीवी के मध्यम से निम्न मान थे।

पहली फली की ऊंचाई, पौधे की ऊंचाई और सौ बीज वजन जैसे लक्षणों में आनुवंशिकता और आनुवंशिक प्रगति दोनों के लिए उच्च मूल्यों को देखा जा सकता है। प्लॉट यील्ड ने मध्यम आनुवंशिकता के साथ उच्च मान दिखाया। सौ बीज भार ही एकमात्र थी जो पीसीवी और जीसीवी के उच्च मूल्यों को उच्च आनुवंशिकता और उच्च जीएएम के साथ प्रस्तुत करती थी।

प्लॉट की उपज हार्वेस्ट इंडेक्स और सौ बीज वजन के बीच एक सकारात्मक महत्वपूर्ण संबंध देखा गया, जबकि, फूलों के दिनों, परिपक्वता के दिनों और प्लॉट उपज के साथ माध्यमिक शाखाओं की संख्या के लिए नकारात्मक संबंध देखा गया। सौ बीज के वजन ने पहली फली की ऊंचाई के बाद पौधे की ऊंचाई, जैविक उपज और फसल सूचकांक के साथ सकारात्मक संबंध दिखाया।

फेनोटाइपिक स्तर पर, आश्रित चर के रूप में प्लॉट की उपज प्लॉट की उपज पर उच्च सकारात्मक प्रत्यक्ष प्रभाव दर्ज किया, इसके बाद जैविक उपज और फसल सूचकांक द्वारा प्लॉट की उपज पर मध्यम प्रत्यक्ष प्रभाव और जीनोटाइपिक स्तर पर, जैविक उपज, फसल सूचकांक, माध्यमिक शाखाओं की संख्या , पौधे की ऊंचाई ने भूखंड की उपज पर उच्च से बहुत अधिक प्रत्यक्ष प्रभाव दिखाया। पौधे की ऊंचाई ने फेनोटाइपिक स्तर पर पहली फली की ऊंचाई (आश्रित विशेषता के रूप में) पर बहुत सकारात्मक प्रत्यक्ष प्रभाव दिखाया, जबकि जीनोटाइपिक स्तर पर, सौ बीज वजन और माध्यमिक शाखाओं की संख्या ने एचओएफपी पर बहुत सकारात्मक प्रत्यक्ष प्रभाव दिखाया।

यूक्लिडियन दूरियों का उपयोग करते हुए अंकगणित औसत (यूपीजीएमए) के साथ गैर-भारित जोड़ी समूह विधि के माध्यम से क्लस्टर विश्लेषण ने अध्ययन के तहत 36 जीनोटाइप को सात समूहों में विभाजित किया। क्लस्टर I के भीतर अधिकतम इंट्रा क्लस्टर दूरी पाई गई, जिसमें 14 जीनोटाइप और क्लस्टर V और VII शामिल हैं, जिनकी इंटर-क्लस्टर दूरी 0.000 है क्योंकि उनमें से प्रत्येक में केवल एक जीनोटाइप है।

अध्ययन किए गए 36 जीनोटाइप में से लगभग 17 जीनोटाइप ने 30 सेमी से अधिक की पहली पॉड ऊंचाई दिखाई। इन जीनोटाइप्स ने मशीन कटाई के लिए उपयुक्त पहली पॉड ऊंचाई प्रदर्शित की।

बीज कोट रंग के आधार पर, देखे गए 36जीनोटाइप में से 30 जीनोटाइप में भूरे रंग का बीज कोट था, 5 जीनोटाइप में गहरे भूरे रंग का बीज कोट था और एक जीनोटाइप में हरे रंग का बीज कोट था।

छह जीनोटाइप नामत: JG 24, IG 2020-15, RLBGMH-4, PBC 574, GJG 1916, और Phule G 191616 ने उच्च प्रथम पॉड ऊंचाई और प्लॉट उपज (g) दोनों दर्ज किए। इस प्रकार, हम अनुमान लगा सकते हैं कि ये छह जीनोटाइप माता-पिता के रूप में और सुधार के लिए या एक कल्टीवेटर के रूप में विकसित होने के लिए उपयुक्त और आशाजनक हैं।

CHAPTER-I
INTRODUCTION

Chickpea (*Cicer arietinum L.*) is a winter annual crop belonging to the family Leguminosae. It has a diploid chromosome number of 2x=2n=16 and a genome size of approximately 738-Mb (Varshney *et al*., 2013). It is an annual herb which doesn't grow more than 1.0 m in height and has an indeterminate growth habit. The plants can be classified into semi erect, erect, semi spreading, spreading and prostrate based on the angle formed by the branches with respect to the ground. The leaves are compound imparipinnate with serrated margins and are oval or elliptical in shape. The root system is a tap root system and is characterized by the presence of root nodules, which corroborates the symbiotic relation with the symbiotic Rhizobium bacteria (*Mesorhizobium ciceri*). The inflorescence is an axillary raceme with a single flower but occurrence of two or three flowers also has been reported in rare instances. The flower is papilionaceous type with 5 petals and diadelphous arrangement (9 stamens fused and one free stamen) and a globose stigma (Sajja *et al*., 2017). Chickpea is a highly self-pollinated crop.

Studies conducted by Ladizinsky showed that its center of origin to be near South East Turkey that was present in the fertile crescent where crops like wheat, peas, and barley were domesticated (Ladizinsky & Adler, 1976). Further, geographic analyses established S.E turkey as the primary center of domestication and India and Ethiopia as the secondary centers (Sokolkova *et al*., 2020). The dispersion of the crop from south east Turkey ensued its development into two different crop types, namely Kabuli (*var. Macrosperma*) and Desi (*var. Microsperma*) types (Lucas & Fuller, 2014). Archeological findings near the sites of Indus Valley civilization establish the cultivation of chickpea in Pakistan approximately from 2500 BCE, with further spread into the Indian subcontinent by ca. 2000 – 1500 BCE (Fuller & Harvey, 2006). The Indian vernacular name of the large seeded type of chickpea (*Kabuli* chana) indicates its arrival into India just 200 years ago via Afghanistan due to the similarity of the name to that of the Afghanistan's capital city Kabul (van der Maesen, 1987).

Chickpea is known by many names such as *Bengal gram* which is of Anglo-Indian origin name, *Garbanzo* in English and Spanish, *Chana* in Hindi which is derived from *Chennuka* in Sanskrit. In southern India, it goes by the name of *kadalai* in Tamil and Malayalam, *Senagalu* in Telugu, *kadale* in Kannada. In the other parts of the world it has different vernacular names in different parts of the country such as *hamoos pea* in Arabic, *nakhut* in Turkey, *kikkererwten* in Dutch, *ceci* in Italian, *poischiche* in French, *Kichererbse* in German, *cizrna* in Czech.

There are 9 annuals and 34 perennials in the genus *Cicer*. The infra-generic classification has pigeonholed the genus *Cicer* into four sections, namely *Monocicer, Chamaecicer, Polycicer, Acanthocicer* based on the lifespan, morphology and geographical distribution (van der Maesen, 1987). The section *monocicer* consists of eight species which are annuals and consists of the cultivated species *C.arietinum* and seven wild species which include *C. reticulatum, C. yamashitae, C. cuneatum, C. bijugum, C. pinnatifidum, C. judaicum and, C. echinospermum.* This genus is of high importance for the improvement of chickpea (Rizvi & Sarker, 2020).

The Gene pool concept and its pertinence in crop development was given by Harlan and De Wet in 1971 (Harlan & de Wet, 1971). The gene pool is catalogued into primary, secondary, and tertiary gene pools. The primary gene pool comprises of the cultivars and landraces of *C. arietinum*. While the secondary gene pool, consists of two wild species *C. reticulatum* which produces fertile hybrid when crossed with *C. arietinum* and *C. echinospermum*. The tertiary gene pool contains the remaining annual and perennial species. This gene pool serves as a potential source for improvement in chickpea, such as *C. pinnatifidum* for drought resistance (Bhattarai & Fettig, 2005), *C. bijugum, C. judaicum* and *C. pinnatifidum* for ascochyta blight resistance (Pande *et al*., 2006) and *C. judaicum* for resistance in botrytis gray mold (Pande *et al*., 2006).

Chickpea has well found its place in global as well as Indian cuisine. Chickpea is used to make curries and its flour is used to prepare snacks in Indian cuisine. Hummus is a preparation of ground chickpea paste which serves as a dip or sauce and is predominantly found in the cuisine of the Middle East. Chickpea

flour is substituted for wheat for baking purposes to make breads, cookies, biscuits etc. Apart from these, chickpeas are also consumed raw or in boiled forms as a healthy snack.

Chickpea has nutritional content and well ensured it to be a part of the dietary needs. Chickpea has a protein content of 22.76% which makes it one of the major source for the former, 9.94% of crude fiber and 46.81% of non-fibrous carbohydrates on dry matter basis (Sis, *et al*., 2007). It is rich in aspartic acid, glutamic acid and arginine while, the sulphur containing amino acids are limiting (Jukanti *et al*., 2012). It is also rich in vitamins such as B9 (Folic acid), B2 (Riboflavin), B6 (Pyridoxine) and tocopherol (Vitamin E), inositol and minerals such as iron and phosphorus (Jukanti *et al*., 2012).

With such sound nutritional profile, chickpea consumption offer many health benefits. Chickpea has a low glycemic index which is an indicator of how much the blood sugar levels are increased due to the consumption of specific food. Chickpea's GI is around 28 ± 9 which makes it low GI food and, hence, they can be included in the diet for diabetic patients. Including chickpeas in diet also helps in controlling blood pressure, cholesterol, and also for weight loss (Jukanti *et al*., 2012). Consumption of chickpea also reduces the risk of cancer. Studies conducted show that butyrate, a short chained fatty acid produced from chickpea diet in adults has shown to reduce the occurrence of colorectal cancer (Fernando *et al*., 2010). Similarly other compounds such as β-sitosterol, a phytosterolin chickpea reduced carcinogen induced colonic tumors (Deschner *et al*., 1982).

Since, chickpea forms such an important part of the diet; there is a large demand for chickpea in India among other countries. In the year 2019, about 13 million hectares was under chickpea cultivation all around the world. This produced around 11.8 million tons for consumption. Of the 13 million hectares cultivated around the world, about 11.9 million hectares of chickpea cultivation was done in Asia which accounts to approximately 92% of the total area under chickpea cultivation. In India, the total area under chickpea cultivation was around 9.5 million hectares and with a production about 9.9 million tons with productivity of 1041 kg/ha (*Source*: FAOSTAT, 2019). An overlook on the import and export

data of chickpea shows us that India as an exporter of chickpeas stand in 8th position with a trade volume of 62,082 MT and a trade value of 62 million USD. Russia is the highest exporter of chickpeas with a trade volume of 305,424 MT with a value of 135 million USD. India stands 2nd in total chickpea imports from other countries next to Pakistan with an import volume of 371,883 MT which values about 203.6 million USD (*Source:* UN COMTRADE database). In India, Madhya Pradesh accounts for the majority of the chickpea area and production with 35.90 lakh hectares and 49.95 lakh tons respectively followed by Maharashtra. In Chhattisgarh, chickpea was grown in about 2.93 lakh ha which constitutes about 2.77% of the total area cultivated for chickpea. The state produced about 2.23 lakh tons of chickpea which amounts to about 1.82% of the total production (*Source*: Success report 2018-19, Farmer portal).

With the ever increasing production costs and migration of work force from agricultural sectors to other sectors, mechanization of maximum practices possible is the need of the hour. World bank data shows us about 62.56% of workforce was employed in agricultural sector in 1991 which has plummeted down to 41.49% in 2020. Out of the existing workforce, women constitute 53.6% of the total workforce (*Source:* World Bank data, 2020). Conventionally the plants are harvested by pulling out of the ground by hand and are then threshed mechanically. But this practice has its own constraints such as the unavailability of labourers during the harvesting period due to high demand and the nitrogen fixing nodules are lost while pulling out plant that leads to loss of N-fixing bacteria in the soil (Golpira *et al.*, 2013). A comparative economic analysis between machine harvested and threshed chickpea farms and manually harvested and mechanically threshed farms in Maharashtra and Madhya Pradesh showed a net returns of Rs 989 and Rs 1168, respectively (Shilpa *et al*., 2017). Schemes implemented by the government of India like, Submission on Agricultural mechanization (SMAM) and the availability of custom hiring centres ensures the availability of machines or equipment for hiring along with the skilled operators (Mehta *et al*., 2019). All the aforementioned factors create an increased demand for development of machine harvestable varieties of chickpea for cultivation. The first machine harvestable chickpea variety NBeG 47 was developed by ANGRAU, Andhra Pradesh with the

collaboration of ICRISAT, Hyderabad in 2016 (*Source: ICRISAT*). Machine harvestable varieties should be taller and erect than, the present semi erect varieties as the present varieties incur heavy harvest losses during machine harvesting. A machine harvestable cultivar should be erect, about 30-40% taller than the existing varieties with optimum 1st pod height at 30 cm from the ground level to minimize the harvesting losses (Sahu *et al*., 2019).

Character association between yield and yield components plays a pivotal role in developing crop varieties with better yield through a well-orchestrated breeding program. The efficacy of a breeding program rests centrally on the direction and magnitude of the association between yield and yield components and also the relative importance of each factor involved in contributing to grain yield (Adesoji *et al*., 2015). Associating and studying how the traits related to mechanical harvesting such as plant height or 1st pod height effect the grain yield, gives us insights into how they can be used further for developing cultivars.

Genetic diversity is considered to be important for realizing heterotic response in F_1 and a broad spectrum of variability in segregating generation. The need of parental diversity in optimum magnitude to obtain superior genotypes to recover transgressive segregates has also been repeatedly emphasized by several researchers. Mahalanobis's D^2 Statistic is a very sensitive tool for measuring genetic divergence based on quantitative traits and is widely used by many geneticists and breeders for selecting divergent parents for hybridization aiming at yield improvement in chickpea. For the realization of heterotic response in F_1 and a large spectrum of heterogeneity in generation segregation, genetic diversity analysis is considered essential.

The present inquiry will be carried out bearing into account the aforementioned viewpoints, with the following objectives:

1. Phenotyping for machine harvestible, yield and yield related traits.
2. Character association and study of direct and indirect effects for pod height and yield related traits.
3. Genetic divergence analysis of yield attributing traits and traits related to mechanical harvesting.

CHAPTER-II

REVIEW OF LITERATURE

Literature authored by various scientists and researchers that is available for the research titled "**Identification of Chickpea (*Cicer arietinum* L.) genotypes promising for mechanical harvesting"** has been discussed below under the following headers:

2.1 Analysis of variance (ANOVA)

2.2 Phenotypic and Genotypic coefficients of variation

2.3 Heritability (broad-sense) (h^2_{bs})

2.4 Genetic advance as percentage of mean (GAM) (%)

2.5 Correlation coefficient analysis

2.6 Path analysis

2.7 Cluster analysis

2.1 Analysis of Variance (ANOVA):

Genetic diversity is important for plant survival in nature as well as crop improvement. Plant breeders are able to grow new and improved cultivars with desirable characteristics thanks to the diversity in plant genetic resources. Analysis of variance (ANOVA) identifies the presence of variation present in the study population and divides it into different components. It also provides the basis for test of significance. ANOVA identifies the variation present between groups and among groups. The variation within groups is solely due to environment and is categorized into environmental variance.

Malik *et al*., (2010) experimental results of ANOVA showed significant differences for biological yield, no. of pods/plant, harvest index, seed yield/plant, no. of secondary branches and 100 seed weight. A high genotypic variability was observed for harvest index, no. of pods/plant, biological yield/plant and seed yield.

Jadhav *et al.* (2012) noted that days to maturity demonstrated peak range of variability trailed by number of seeds per pod, number of pods per plant, days to 50% flowering, harvest index, seed yield per plant, 100 seed weight, plant height and number of secondary branches per plant.

Syed *et al*., (2012) did analysis for variability on 27 genotypes of chickpea found maximum variation in no. of pods/plant followed by no. of primary branches/plant and seed yield/plant.

Pandey *et al*., (2013) reported results through ANOVA revealed that genotypic differences were significant for all characters except days to flowering and no. of grains/pod.

Funga *et al.*, (2017) conducted a combined ANOVA analysis for 17 chickpea genotypes tested across eight environments for grain yield. The results showed a significant variation for genotypes (G), environments (E) and genotype X environment (G x E) interactions.

Biru *et al*., (2017) experimented on 16 chickpea lines and recorded that ANOVA estimates show significant differences for all characters except for seeds/pod and branches/plant.

Banik *et al*., (2018) estimates on components of variation showed that the magnitude of genotypic variances in no. of pods per plant was the highest followed by days to 50% flowering while the highest phenotypic variance was recorded by no. of pods/plants followed by plant height.

Kerketta *et al*., (2018) stated that mean sum of squares due to genotypes is significant in analysis of variance with pods/plant, biological yield and plant height showing higher phenotypic and genotypic variances.

Thakur *et al*., (2018) analysis for ANOVA showed highly significant differences for all the characters studied among the genotypes such asdays to 50% flowering, plant height, number of primary branches and secondary branches/plant, total pods/plant, total number of seeds/plant, 100 seed weight, seed yield/plant, and harvest index.

Gediya *et al*., (2019) reported highly significant differences for traits among genotypes under study implying the opportunity for selection. Wide range of phenotypic variance was revealed for no. of pods/plant, 100 seed weight, biological yield/plant, no. of branches/plant and seed yield/plant.

2.2 Phenotypic and Genotypic coefficients of variation:

The basic idea of the study of variation is its partitioning into components attributable to different causes. The relative magnitude of these components can determine the genetic property of a population. The estimation of components of variance helps us in the assessment of the relative importance of various determinants of the phenotype, in particular the role of heredity versus environment (Falconer & Mackay, 1996).Lack of or limited genetic variability is an essential factor for the limited progress achieved in increasing the productivity of grain legumes, including chickpea.

The range of mean cannot wholly reflect the overall variance in the material under study. As a result, PCV and GCV are determined. When these parameters have a high value, it implies more variability, and vice versa (Gangashetty *et al*., 2013). A marginal difference between PCV and GCV means that the climate has a lower impact on the studied traits.

Ramanappa *et al*., (2013) investigation on chickpea germplasm lines for quantitative characters showed that PCV and GCV for grain yield plant^{-1} and number of pods plant^{-1}are higher compared to other traits.

Sonwani *et al.* (2017) noticed high GCV and PCV for the traits *viz.*, no. of primary branches plant-1, no. of pods plant-1, and seed yield plant-1 after evaluating sixteen genotypes of chickpea.

Raju *et al*., (2017) showed that high estimates for PCV and GCV were recorded in100 pod weight, number of secondary branches per plant, seed yield per plant, number of seeds per pod, 100 seed weight and number of pods per plant.

Joshi *et al*., (2018) experimented on 252 lines of RIL population. Seed yield/plant, biological yield, 100 seed weight and harvest index noted a high GCV and PCV estimates.

Kishor *et al*., (2018) outcome of analysis on 40 genotypes of chickpea showed that GCV values were lower than PCV values for all the traits. The highest and least values for both PCV and GCV are recorded for pods/plant and days to maturity respectively.

Vishnu *et al*., (2018) analysis on chickpea cultivars under rain fed and irrigated conditions showed low PCV and GCV estimates for angle of primary

branch and moderate PCV and GCV for 1st pod height whereas plant height showed moderate PCV and low GCV in both the conditions.

Kerketta *et al.*, (2018) witnessed high GCV and PCV values for biological yield ensued by seed index and harvest index.

Aswathi *et al*., (2019)assessed genetic variability in 52 desi chickpea genotypes. High GCV and PCV was observed for single plant yield, 100 seed weight, no of secondary branches, no of pods/plant, and 1st pod height.

Kumar *et al*., (2019) observed both high PCV and GCV for pods/ plant, no. of pods/ plant.

Jayalakshmi *et al*., (2020) divulged that 1st pod height exhibited moderate PCV and GCV while the same parameters are low for angle of primary branch.

2.3 Heritability (broad-sense) (h^2_{bs}):

Heritability in broad sense denotes the proportion of overall variability attributed to genetic factors or the genotypic variation to total variance ratio. It is a good indicator of the transfer of traits from parents to offspring (Falconer, 1960).

Zali *et al*., (2010) determined the association between traits and their genetic parameters in 17 chickpea genotypes. Results showed that days to 50% maturity, plant height, days to 50% flowering, no. of seeds/plant, no. of primary and secondary branches/plant have high heritability value which indicated additive gene action on these traits.

Gul *et al*., (2013) analyzed 20 genotypes and found the highest estimates in seed yield/plant, primary branches, secondary branches, and 100 seed weight for broad-sense heritability.

Meena *et al.* (2014) evaluated 22 newly developed chickpea genotypes for various genetic parameters. High heritability in a broad sense has been observed for seed yield per plant (94.00), biological yield (94.10), and pods per plant (91.50).

Jain *et al*. (2014) detected high broad sense heritability teamed with genetic advance for plant height, 100-seed weight and seed yield plant^{-1}.

Tilahun *et al*. (2015) reported high heritability for seed per pod, 100 seed weight and pods per plant and high genetic advance revealed that additive gene

effects were important in determining these traits. Estimation of correlation coefficients showed that pods per plant, plant biomass, plant height, and harvest index and 100-grain weight were positively correlated with grain yield

Biru *et al*., (2017) reported value of more than 80% for broad sense heritability for 100 seed weight.

Ton *et al.* (2017) in their assay reckoned that no. of primary branches and secondary branches per plant, 100-seed weight and harvest index showed high heritability.

Banik *et al*. (2018) showed high values of broad sense heritability complemented by high genetic advance as per cent of mean for number of pods per plant, days to 50 per cent flowering, 100 seed weight, plant height demonstrating that these traits could be prominently reigned by additive gene action.

Aswathi *et al.,* (2019)analysis and results on variability studies showed high heritability coupled with GA as % of mean for single plant yield, 100 seed weight, no. of secondary branches, no. of pods/plant and 1st pod height.

Kumar *et al*., (2019) observed high heritability in seed index succeeded by harvest index, primary and secondary branches/plant.

2.4 Genetic advance as percentage of mean (GAM %)

The concept "genetic advance" refers to an increase in the mean genotypic value of selected plants over the base population.The efficacy of genetic advance by selection is determined by the three factors namely genetic variability, heritability and selection intensity (Allard, 1960).Genetic advance is often expressed as a percentage of the mean. A high value of Genetic advance means that the attribute under investigation is influenced by additive gene action, while a low value indicates non additive gene action.

Babbar *et al.,* (2012) reported days to 50% flowering, days to maturity, plant height, 100 seed weight and seed yield per plant were showing high heritability coupled with medium genetic advance as percentage of mean, whereas, number of seeds per plant and number of pods per plant showing medium heritability and high genetic advance as percentage of mean.

Ramanappa *et al.,* (2013) assessed 179 genotypes and revealed that high heritability in broad sense coupled with high genetic advance as per cent mean was recorded for grain yield per plant, number of pods per plant, 100 seed weight, days to 50% flowering and number of seeds per pod suggesting that these traits under the control of additive gene action and potential possibilities exist for the improvement of these traits through simple selection.

Pandey *et al*., (2013) stated that high GA as % of mean coupled with high heritability was observed for seeds/pod, days to flowering, pods/plant and plant height.

Babbar et al., (2015) found high GA as % of mean coupled with high heritability for 100 seed weight, no. of effective pods, seed yield/plant and biological yield.

Biru *et al.,* (2017) results show that traits such as 100 seed weight, no. of pods/plant, no. of seeds/pod and grain yield showed high heritability coalesced with high genetic advance as % of mean.

Kerketta e*t al*., (2018) discerned a high GA as % of mean in biological yield, seed yield/plant tailed by plant height.

Banik e*t al*., (2018) showed high GA as % of mean for no. of pods/plant, days to 50% flowering and plant height.

Arora *et al.,* (2018) conducted experiment on fifty genotypes of chickpea for assessment of genetic variability. Genetic advance as percent of mean was maximum for number of pods per plant. High heritability coupled with high genetic advance was observed in case of number of pods per plant.

Hagos *et al* (2018) assessed 12 chickpea genotypes and revealed that High heritability coupled with high expected genetic advance as percent of mean were estimated for number of secondary branches per plant, number of pods per plant and 100 seed.

Aswathi *et al.,* (2019) observed that genetic advance as % of mean was high for characters like single plant yield, 100 seed weight, no. of secondary branches, no of pods/plant, no. of seeds/plant, 1st pod height.

2.5 Correlation coefficient analysis

The degree to which two variables change in relation to each other is measured by correlation analysis (Franzese & Juliano, 2018). A positive correlation values suggest that two variables shift in the same direction, while negative correlations suggest that two variables change in a contrary direction It specifies the selection factor characteristics on which genetic yield improvement can be based by measuring the reciprocal interaction between different plant characteristics. Variation in other characteristics, due to pleiotropy or genetic linkage, also influences the inheritance of quantitative traits. As a result, knowledge of the relationship between yield and its characteristics gained by genotypic and phenotypic correlation estimation aids in assessing the amount of improvement that may be brought about in the characters.

Kobraee *et al*., (2010) correlation analysis showed that no. of seeds/plant, no. of pods/plant, plant height and biological yield has the highest positive correlation with grain yield.

Ojha *et al*. (2011) reported that positive and highly significant correlation between pods per plant and secondary branches per plant, biological yield per plant with days to 50% flowering, days to maturity, secondary branches per plant and pods per plant.

Gul *et al*., (2013) observed that no. of pods/plant has high significant positive association at both phenotypic and genotypic levels with no. of secondary branches and seed yield/plant, while no. of pods/plant has positive and significant relation with no. of primary branches/plant at phenotypic level.

Malik *et al*., (2014) evaluated 113 desi genotypes and the co-efficient of correlation analysis showed that seed yield/plant is positively associated with primary branches/plant and secondary branches/plant.

Johnson *et al.*, (2015) analyzed the correlation coefficients of yield attributing characters and found that seed yield/plant has a positive correlation with harvest index and biological yield.

Tesfamichael *et al.* (2015) the reported that positive and significant correlation of seed yield with biomass, pod filling period, pod per plant, number of primary and secondary branches per plant.

Salgotra (2016) reported that seed yield/plant were significantly and positively correlated with plant height, number of pods/plant, number of seeds/pod, 100 seed weight and negatively correlated with number of secondary branches and days to 50% flowering.

Kerketta *et al*., (2018) acknowledged that grain yield at genotypic and phenotypic level exhibited positive and significant correlation with biological yield.

Thakur *et al*., (2018) reported positive correlation of seed yield with 100 seed weight, harvest index, no. of pods/plant, and no. of secondary branches/plant. Significant negative correlation was noticed for 100 seed weight with harvest index, no. of pods/plant and seeds/plant.

Jayalakshmi *et al*., (2020) remarked that plant height and 1st pod height exhibited a strong positive association between each other and with shoot biomass.

2.6 Path analysis

Presence of variability in a population allows selection to evolve a range of suitable characters. The information on correlation of character, direct and indirect results contributed to yield by each character would be an additional advantage in supporting the selection process. Correlation and path analysis determine the degree to which yield and components are associated and also show the relative importance of their direct and indirect impacts, thus making their interaction with grain yield clear. Such a study may ultimately help the breeder develop its selection strategies to increase grain production.

Kayan *et al*., (2012) found that plant height and biological yield had the highest indirect positive effect on grain yield among other traits.

Kobraee *et al*., (2010) investigation on three cultivars showed that date of sowing has a positive effect on 1st pod height, plant height, no. of secondary branches, no. of pods/plant and other yield attributes beside the effect of cultivar.

Ali *et al*., (2012)reported that traits such as days to 50% days to flowering, plant height, secondary branches, and biomass/plant had direct and positive effect on grain yield whereas no. of primary branches/plant and no. of pods/plant has direct effects.

Petrova *et al*., (2016) analysis on nine traits in PCA revealed that seed per pod & 100 seed weight have strong negative direct effects, while others had positive direct effects at varying degrees. Thus such characters can be used as selection criterion for increasing yield.

Mehmood *et al*., (2016) discovered a positive correlation between seed yield and plant height, 100 seed weight, pods/plant, seeds/plant and seeds/plot at both phenotypic and genotypic levels.

Kumar *et al*., (2019)inferred that biological yield, plant height, harvest index, days to maturity have direct effects on yield and are the highest contributors for the same.

Babbar *et al*., (2015) analysis by path analysis for understanding factors influencing seed yield revealed that flower initiation, biological yield and number of secondary branches have high positive and direct effect on seed yield/plant while a negative direct effect is exhibited on the same characters by harvest index and flower initiation while plant height and number of primary branches had indirect positive effects on harvest index.

Kerketta *et al*., (2018) observed that biological yield had direct and high positive effect on seed yield/plant at both genotypic and phenotypic levels from which it can be surmised that the aforementioned character can be used as an effectual parameter for direct selection in yield improvement programs.

Erdemci *et al.* (2016) analysis by path coefficient analysis showed that the effects of no. of pods/plant and plant height on seed yield/plant is direct, positive and highest in magnitude compared to other traits. However, plant height and no. of primarybranches/plant exhibited highest indirect effect on seed yield/plant through no. of pods/plant.

Qurban *et al.,* (2010) conducted experiment using 23 genotypes of chickpea and concluded that 100- seed weight followed by pods per plant, number of primary branches per plant, secondary branches per plant, days taken to maturity and seeds per pod contributed maximum direct effect on grain yield. Moreover, number of days taken to flowering, plant height and biomass per plant had negative direct effect on grain yield.

2.7 Cluster analysis

Genetic diversity is important because it is the foundation for plant survival in nature and crop improvement. Using Mahalanobi's D^2 statistics,it is possible to identify the genetically divergent parents. D^2 assesses the degree of heterogeneity at the genotypic level as well as the comparative ratio of each component trait to overall divergence. It is a measure of a single observation's uniqueness based on differences between the observation's value and the mean values for all other instances over all independent variables. It is measured at inter-cluster and intra-cluster levels.

Kayan *et al*., (2012) cluster analysis has divided the characters into two clusters that are closely related to grain yield. Plant height, pods/plant, biological yield are grouped in the first cluster while harvest index and dry weed biomass were placed in the second cluster.

Jivani *et al*., (2013) analysis on the yield trait showed that seed yield/plant, biological yield/plant, harvest index, no. of pods/plant and 100 seed weight are highly responsive to selection. Seed yield/plant, 100 seed weight, and no. of pods/plant contributed more than 63% of total genetic divergence.

Zali *et al*., (2010) inferred that 96% of the yield variation is due to 100 seed weight and no. of pods/plant through regression analysis.

Sharifi *et al*., (2018) analysis by clustering method segregated the genotypes into two major groups and four clusters. Clusters I and IV have genotypes with high seed yield and harvest index, while cluster III is not suitable for yield attributing traits.

Johnson *et al*., (2015) experiment consisted of evaluation of 112 genotypes that included germplasm lines, improved varieties and advanced breeding lines. The genotypes were divided into eight clusters by cluster analysis. Cluster IV exhibited highest cluster mean for 100 seed weight while cluster I for plant height.

Babbar *et al*., (2015) grouped their 31 chickpea genotypes into 13 clusters with the aid of Mahalanobi's D^2 statistics. Cluster IX exhibited high cluster mean of 51.07 cm for plant height (cm), while cluster X showed a high mean of 22.93g for seed yield/plant.

Syed *et al*., (2012) analysis on 27 genotypes of chickpea *viz.* cluster analysis grouped them into 5 clusters. The largest cluster being cluster II with 11 genotypes followed by cluster III with 7 genotypes. The highest inter cluster distance was found between cluster I and cluster II with a value of 16.55 units.

Geethanjali *et al*. (2018) conducted an experiment to analyse the genetic diversity. The analysis resulted in genotypes being grouped into five clusters where, maximum diversity is contributed by 100-seed weight.

Mahmood *et al*., (2018) evaluated 15 genotypes and have grouped them into 3 clusters on the basis of similarity of characters by cluster analysis. Based on the distance between clusters, the dendrogram depicted that members of clusters I and III are the most diverse and cluster I exhibited higher values for plant height and 50% flowering while cluster II expressed higher values for days to 90% maturity and cluster III showed higher values for pods/plant, harvest index and seed yield.

Gaikwad *et al.* (2014) conducted an experiment on 40 chickpea genotypes and grouped them into eight clusters and best cluster for various traits was estimated using inter cluster distance. The whole analysis indicated that maximum divergence was contributed by characters, *viz.*, pods/plant, no. of secondary branches/plant, days to 50% flowering and 100-seed weight.

CHAPTER- III
MATERIALS AND METHODS

The present investigation entitled, **"Identification of Chickpea (*Cicer arietinum* L.) genotypes promising for mechanical harvesting"** was carried out during *rabi,* 2020-21. The procedures followed & materials used during the course of analysis are introduced under:

3.1 Experimental site:

The present research work was conducted at Research cum Instructional farm Department of Genetics and Plant Breeding, College of agriculture, Indira Gandhi Agricultural University, Raipur, Chhattisgarh, during the *rabi* season of 2020-21.

3.2 Climate and weather:

Chhattisgarh is situated between 17°14'N and 24°45'N latitudes and 79°16' E and 84°15' E longitudes. Raipur (C.G.) lies at 21°16'N latitude and 81°36' E longitude with an altitude of (289.60m) above mean sea level. The maximum monthly mean temperature was 39.6°C during March 2021 and minimum monthly mean temperature was 12.00°C during December 2020. The overall total rainfall during crop growing period was (16.00 mm) (Table 3.1). The data pertaining to total rainfall, monthly lower and highest temperatures, RH, evaporation and shining sunshine hours of total crop growing time have been presented in Fig.3.1.

Table 3.1: Average monthly meteorological data of Raipur from November 2020 to April 2021

Month	Max. T (°C)	Min. T (°C)	Total RF (mm)	RH I (%)	RH II (%)	VP I (mm)	VP II (mm)	WS (Kmph)	EP (mm)	SS (hrs)
Nov-20	30.80	15.90	0.40	85.00	33.00	13.00	10.90	3.00	102.80	7.80
Dec-20	29.30	12.00	0.00	87.00	31.00	10.10	9.00	2.00	93.20	5.40
Jan-21	30.20	13.90	4.60	81.00	31.00	10.50	9.40	2.50	99.90	4.00
Feb-21	31.00	12.90	2.40	79.00	27.00	9.80	8.50	2.70	114.20	7.60
Mar-21	36.21	18.75	7.60	64.87	21.70	11.71	9.10	3.69	184.10	7.12
Apr-21	39.60	22.80	1.00	53.00	19.00	13.10	10.00	4.80	238.50	7.20

3.3 Experimental Materials and Methods:

Thirty-sixgenotypes of chickpea were taken for this research (Table 3.2). The material was grown in the *Rabi* season of 2020-21.The chickpea seeds were sown in the field, in RCBD with 3 replications on 13th November, 2020. Each plot comprised of 4 rows of 4.0 m length in each replication. The row x row and plant x plant distance of 22.5 cm and10.0 cm and net plot area was 3.6 m^2. The seeds were pre-treated with Bavistin, Trichoderma, PSB, Rhizobium and PSB culture. Fertilizer dose @ of 20:40:20 kg per hectare (NPK) was applied.Two irrigations were given to the trial on 16-11-2020 and 28-12-2020. Random five plants are selected from each of the plot in each replication, were taken for collecting data on yield and yield attributing traits.

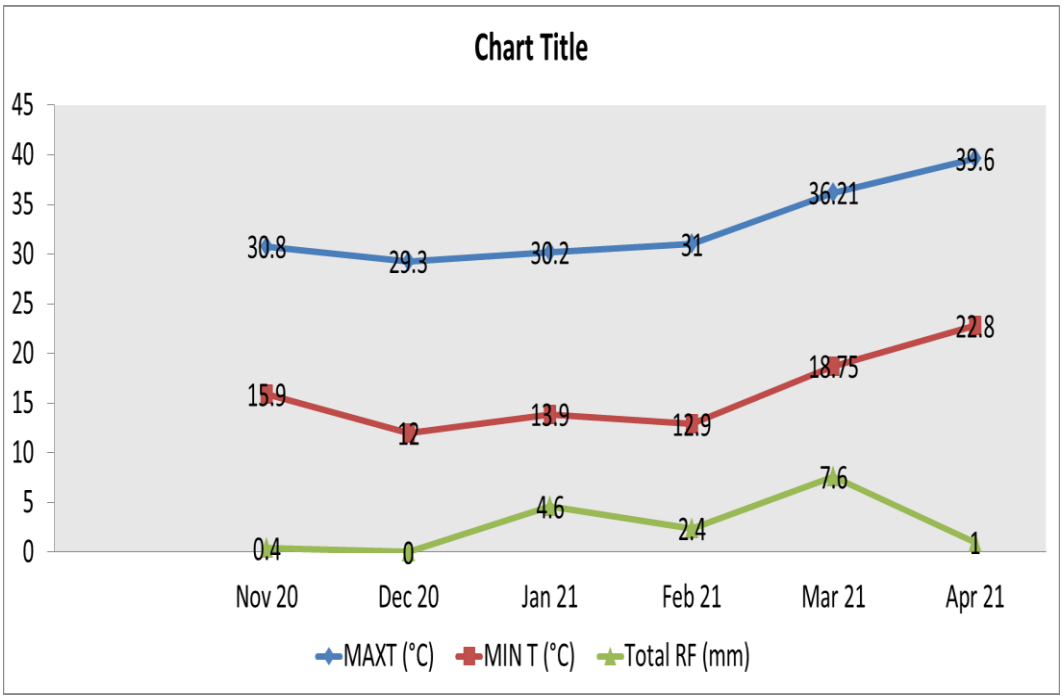


Fig 3.1: Meteorological data recorded during crop growth season (November, 2020 to April, 2021)



Fig 3.2: Irrigation of field



Fig 3.3a: Field view of experiment



Fig 3.3b: Field view of experiment



Fig 3.3c: Field view of experiment



Fig 3.3d: Field view of experiment

Table 3.2: List of chickpea genotypes

S. No	Accession No.	Entry name	S. No	Accession No.	
1	C-20452	RSGD-7714	19	C-20476	H 13-03
2	C-20453	PBC 582	20	C-20477	IPC 2017-141
3	C-20454	NBeG 1267	21	C-20478	ICCV 191608
4	C-20455	GL 15003	22	C-20480	Phule G 191616
5	C-20456	BG 3062	23	C-20483	Phule G 0405
6	C-20460	GJG 1913	24	C-20485	JG 24
7	C-20461	BG 4028	25	C-20486	RKGM 20-2
8	C-20462	IG 2020-15	26	C-20487	GL 117020
9	C-20463	PG 252	27	C-20488	IPCB 2015-132
10	C-20464	RKGM 20-1	28	C-20489	H 07-120
11	C-20465	IG 2020-16	29	C-20490	Phule Vikram
12	C-20466	RVSSG-97	30	C-20492	JG 2020-57
13	C-20467	Phule G 191618	31	C-20493	PBC 574
14	C-20468	RLBGMHG-3	32	C-20494	RVSSG-96
15	C-20469	ICCV 191612	33	C-20495	BG 4027
16	C-20470	RSGD-834	34	C-20496	IPC 2017-253
17	C-20471	JG 16	35	C-20497	RLBGMH-4
18	C-20475	PG 251	36	C-20498	GJG 1916

3.4 Observations recorded:

Twelve various yield and yield attributing traits were recorded and studied to fulfil the objectives and purpose of the study. Random five plants are selected from each of the plot and replications for collecting data of different traits at optimal plant growth period. For statistical analysis, average data from the sampled plants with respect to various traits are used.

Days to 50 % flowering (DTF):

Days to 50 % flowering were recorded when the plants attained 50 percent flowering with at least one open flower.

Days to maturity (DTM):

Days to maturity was recorded when the plants attained physiological maturity.

Height of the first pod (cm) (HOFP):

The height was estimated in centimetres (cm) from the surface of the crop to the first pod emergence.

Plant height (cm) (PH):

The plant height was estimatedin centimetres (cm) from the surface of the crop to the last tip of theplant.

Number of primary branches (NPB):

Total number of primary branches was recorded from randomly five plants and was averaged.

Number of secondary branches (NSB):

Total number of secondary branches was recorded from randomly five plants and was averaged.

Number of seeds per pod (NSP):

Total number of seeds per pod was counted in randomly five plants and was averaged.

Number of pods per plant (NPP):

Total number of pods per plant was counted in randomly five plants and was averaged.

100 grain weight (gm) (HSW):

Randomly 100 seed are taken from each of the entry and weighed in gram.

Biological yield per plant (g)(BY):

The crop was harvested and sun drying to 5 - 8 days and weight of each of the 5 plant except root was recorded in grams.

Harvest- index(%)(HI):

Harvest index was estimated as the ratio of grain yield to biological yield and the ratio of grain yield and biological yield are expressed in %.

Plot yield in grams (g) (PLYG):

The seed yield of each of the plot in each replication was recorded in grams after sun drying for five to eight days after harvesting.

3.5 Statistical analysis:

The data was notable in favour to divergent phenotypic and quantitative traits on the 13 yield and yield related characters of chickpea accessions were subjected to the statistical analysis.

3.5.1 Analysis of variance:

Firstly, mean values were worked out for all traits for each genotype. These mean data were utilized to calculate variability parameters *viz*. range, standard deviation, and coefficient of variation. ANOVA is calculated by using O.P.STAT software (Sheoran *et al.*, 1998).

Table 3.3 Skeleton of analysis of variance

Sourceof Variation	DF	SS	MSS	F Cal.
Replication	(r-1)	SSR	MSR	MSR/MSE
Genotypes	(g-1)	SSG	MSG	MSG/MSE
Error	(r-1)(g-1)	SSE	MSE	
Total	(rg-1)	SStotal		

3.5.2 Assessment of variability:

3.5.2.1 Range:

The minimum and maximum value of a trait tells its range, which is expressed as follows:

Range = maximum value – minimum value.

3.5.2.2 Mean($\bar{X}$):

Mean can be evaluated by sum of no. of observation by total no. of observation and the formula are follows as:

$$\bar{X} = \frac{\Sigma Xi}{N}$$

Where,
ΣX_i = sum of all the observation
N = total number of observation

3.5.2.3 Estimation of coefficient of variation (CV %):

The coefficient of variation for different traits was calculated by formula which is given by Burton and De Vane (1953). The category of magnitude of coefficient of variation was given as higher (greater than 20%), moderate (between 20% - 10%) and low (lower than 10%).

a) Phenotypic coefficient of variation (PCV%)

$$\text{PCV (\%)} = \frac{\sqrt{\sigma^2 p}}{\bar{x}} \text{ x } 100$$

b) Genotypic coefficient of variation (GCV%)

$$GCV\ (\%) = \frac{\sqrt{\sigma^2 g}}{\bar{x}} \times 100$$

3.5.2.4 Heritability (broad sense) (h^2_{bs} %):

Heritabilityis the ratio of variation due to difference between genotypic to the phenotypic variation for a character or a trait in a population. For the present study broad sense heritability was estimated and adopting the formula as suggested by Hanson *et al*., 1956.

The estimates of heritability broad sense were classified as low, moderate and high according to Johnson et al. (1955).

< 30 % – Low

31-60 % – Moderate

> 60 % – High

3.5.2.5 Genetic advance as percentage of mean (GA %):

Enhancement of mean phenotypic value of elected plants over the parental population is called as genetic advance. Expected genetic advance (GA) was estimated by method recommended by Johnson *et al.*, (1955). It is the ratio of genetic advance to the grand mean and is expressed in percent.

$$G\ A = K\ .h^2.\ p$$

Where,

GA = Genetic advance

K = Constant (Standardized selection differential) having the value of 2.06 at 5 percent level of selection intensity.

The genetic advance is interpreted as GA is greater than 20% = High; GA = 10 – 20 per cent = Moderate and GA less than 10 % Low.

3.5.3 Correlation coefficient analysis:

Estimate the correlative relationship between different traits through correlation coefficient analysis at phenotypic, genotypic and environment levels with the support of formula recommended by Miller *et al.* (1958).

3.5.4 Path analysis:

Path analysis was originally developed by Wright (1921) and first used for plant selection by Dewey and Lu (1959). It measures the direct and indirect contribution of independent variables on dependent variable. The results of path coefficient analysis are interpreted as per the following scale suggested by Lenka and Mishra (1973).

3.5.5Cluster analysis:

Cluster analysis is a multivariate method which aims to classify a sample of subjects (or objects) on the basis of a set of measured variables into a number of different groups such that similar subjects are placed in the same group. Cluster analysis has no mechanism for differentiating between relevant and irrelevant variables. Therefore, the choice of variables included in a cluster analysis must be underpinned by conceptual considerations. This is veryimportant because the clusters formed can be very dependent on the variables included. In the present study, Euclidian distance between genotypes was calculated from the standardized data matrix by Unweighted Pair Group Method using Arithmetic Averages (UPGMA) method and clustering was done by Agglomerative Hierarchical method using XLSTAT 2014 software.

CHAPTER – IV
RESULTS AND DISCUSSION

The analysis for the experiment titled **"Identification of Chickpea (*Cicer arietinum* L.) genotypes promising for mechanical harvesting"** was conducted on 36 genotypes. Observations were recorded on randomly tagged five plants from each genotype in each replication. The presence of genetic variability is confirmed through analysis of variance (ANOVA). Genetic variability present in the material was analyzed through various genetic variability estimates such as PCV, GCV, h^2bs, and GAM. Correlation studies provided the information on how the component variables affect the plot yield. Path analysis divides the correlation estimates into direct and indirect components, thus giving an idea on how the component traits affects the dependent trait. Cluster analysis grouped the genotypes into clusters based on their diversity. The results of the experiment are discussed below under the following headers:

4.1 Analysis of Variance

4.2 Genetic variability studies

4.3 Correlation analysis

4.4 Path coefficient analysis

4.5 Cluster analysis

4.6 Classification of genotypes based on height of first pod; plot yield and seed coat colour

4.1 Analysis of variance:

Analysis of variance on twelve characters showed significant values in mean sum of squares for eleven characters namely days to 50% flowering, days to maturity, height of first pod, plant height, number of secondary branches, number of pods per plant, biological yield, harvest index, hundred seed weight and plot yield. Two traits viz., numbers of primary branches and number of seeds per pod did not showed any significant variations. The presence of significant levels of variation implies the presence of variability in the observed characters. This variability can be tapped into and be used in further development of the genotypes. The ANOVA for all the twelve characters is encapsulated in table 4.1. Pandey *et al*., (2013) and Ramanappa *et al*., (2013) also reported non-significance for number of seeds per pod. Malik *et al*., (2014) reported low variability estimates for number primary branches and number of seeds per pod. Biru *et al*., (2017) reported non-significant estimates for number of seeds per pod and branches per plant.

Table 4.1: Analysis of variance of thirty six genotypes for twelve yield and yield attributing and machine harvestable traits during Rabi 2020-21

Source of variation	DF	DTF	DTM	HOFP	PH	NPB	NSB	NPP	NSP	BY	HI	HSW	PLYG
Treatment	35	135.13**	61.28**	87.93**	222.74**	0.42	20.22**	544.99**	0.16	139.38**	172.69**	125.17**	64388.25**
Replication	2	0.44	2.62	9.12	66.40	0.67	8.35	195.30	0.34	64.28	43.47	48.04	17523.95
Error	70	0.63	0.55	9.61	14.56	0.38	5.92	258.71	0.11	52.69	63.38	10.36	14405.05

*and ** Significant at 5% and 1% probability level, respectively

DTF = Days to 50% flowering; DTM = Days to maturity; HOFP = Height of 1stpod; PH = Plant height (cm); NPB = No. of primary branches; NSB = No. of secondary branches; NPP = No. of pods/plant; NSP = No. of seeds/pod; BY = Biological yield (g) (g); HI = Harvest index (%); HSW = Hundred seed weight (g); PLYG = Plot yield (g)

4.2 Genetic variability:

Genetic variability is said to exist in a population when, individual genetic traits in the said population have a proclivity to differ from each other. Any breeding effort must be built on this foundation. Estimating the said genetic diversity contained in a population may be done using a variety of approaches like range, genotypic and phenotypic coefficient of variations (GCV% and PCV%) and the probability of their transfer to the next generations through heritability analysis (h^2_{bs}) and GA%.

Genetic variability parameters were estimated for 12 quantitative traits *viz.,* days to 50% flowering, days to maturity, plant height (cm), height of first pod (cm), number of primarybranches, number of secondary branches, number of seeds per pod, number of pods per plant, biological yield(g), harvest index(%), hundred seed weight(g) and plot yield (g).

4.2.1 Mean and Range:

The mean and range values for the twelve quantitative characters are encapsulated in tables4.2a and 4.2b, respectively.

Days to 50% flowering: The range of days to 50% flowering varied from the least being 48 days and the highest being 73 days with a mean value of 62 days. Among the 36 genotypes studied, two genotypes namely IG 2020-15 and RVSSG-97 had flowered at 48 days while IPC 2017-253 took 73 days, which is the highest among the studied genotypes. The classification of genotypes based on their time taken for 50% flowering has been listed below in the table 4.3. None of the genotypes were extra early, while 11 genotypes are early. Majority of the genotypes i.e. 25 genotypes fell under the category of medium flowering i.e. 61-80 days. None of the genotypes flowered late in their flowering period.

Days to maturity: Days to maturity ranged from 94.6 days (IG 2020-15) to 111 days (PHULE VIKRAM) with an average of 104.52 days.

Height of 1st pod: The lowest and highest height noted for 1st pod height is 20.93 cm for JG 16 and 39 cm for IPC 2017-253, respectively with the mean being 29.41 cm.

Plant height (cm): The tallest genotype among the study material recorded 69.13 cm

Table 4.2a: Mean performance of thirty six genotypes for twelve yield and yield attributing and machine harvestable traits duringRabi 2020-21

S. No.	Entry	DTF	DTM	HOFP	PH	NPB	NSB	NSP	NPP	BY	HI	HSW	PLYG
1	RSGD-7714	58	96	21.80	42.47	2.40	8.20	1.40	33.07	14.53	49.43	16.00	646.33
2	PBC 582	63	97	27.60	50.27	2.73	11.73	1.33	44.73	19.40	52.89	25.67	718.00
3	NBeG 1267	62	98	21.93	41.80	2.20	10.13	1.00	37.73	14.33	59.04	23.33	555.00
4	GL 15003	55	107	26.40	47.80	1.87	8.13	1.00	29.53	10.00	43.52	14.00	394.00
5	BG 3062	65	105	27.00	58.07	2.60	10.67	1.00	67.67	30.00	47.81	22.00	489.67
6	GJG 1913	64	98	28.13	53.13	2.67	5.80	1.47	37.20	16.53	59.54	24.33	876.00
7	BG 4028	55	105	30.60	61.67	1.93	8.27	1.20	32.53	19.53	47.83	31.33	412.00
8	IG 2020-15	66	102	34.60	66.07	1.67	5.73	1.00	29.80	17.00	52.05	35.33	605.00
9	PG 252	65	110	30.07	54.40	1.93	8.93	1.67	30.07	16.00	42.20	20.67	479.67
10	RKGM 20-1	64	107	22.60	41.47	1.93	11.07	1.00	45.20	18.67	57.23	29.33	581.33
11	IG 2020-16	64	94	23.53	58.07	1.93	3.80	1.13	21.80	8.60	55.61	25.00	545.00
12	RVSSG-97	67	95	32.93	59.33	1.67	4.07	1.00	20.80	11.00	50.44	30.33	487.67
13	Phule G 191618	71	108	37.47	67.80	2.67	13.67	1.13	45.53	25.93	41.73	30.00	314.00
14	RLBGMHG-3	65	106	30.73	59.33	1.80	9.20	1.47	42.40	24.00	55.52	30.67	506.67
15	ICCV 191612	57	102	38.13	61.53	2.13	10.53	1.20	32.40	16.40	53.51	27.00	554.67
16	RSGD-834	59	101	23.53	42.40	2.53	7.73	1.33	33.47	11.13	53.45	18.67	628.67
17	JG 16	62	101	20.93	41.73	2.47	9.60	1.13	64.73	20.87	49.54	18.00	750.33
18	PG 251	70	109	25.64	55.27	2.80	13.51	1.00	51.20	16.93	25.88	10.67	59.33

DTF = Days to 50% flowering; DTM = Days to maturity; HOFP = Height of 1st pod; PH = Plant height (cm); NPB = No. of primary branches; NSB = No. of secondary branches; ; NPP = No. of pods/plant; NSP = No. of seeds/pod; BY = Biological yield (g); HI = Harvest index (%); HSW = Hundred seed weight (g); PLYG = Plot yield (g).

Table 4.2b: Mean performance of thirty six genotypes for twelve yield and yield attributing and machine harvestable traits duringRabi 2020-21

S. No.	Entry	DTF	DTM	HOFP	PH	NPB	NSB	NSP	NPP	BY	HI	HSW	PLYG
19	H 13-03	54	102	29.87	57.88	1.95	7.67	1.07	49.73	16.00	50.26	20.00	562.00
20	IPC 2017-141	51	106	33.73	59.20	1.67	5.47	1.27	26.87	12.07	40.21	22.67	499.67
21	ICCV 191608	61	104	34.93	68.20	2.13	9.60	1.20	52.53	28.00	49.70	33.33	517.67
22	Phule G 191616	64	108	31.87	62.80	3.20	15.20	1.07	64.00	26.20	49.74	22.67	587.67
23	Phule G 0405	68	109	22.60	46.33	2.33	13.27	1.00	46.87	18.07	55.82	21.67	507.33
24	JG 24	67	110	38.40	62.40	2.20	9.60	1.13	30.53	18.87	46.91	33.33	650.67
25	RKGM 20-2	64	104	26.13	49.60	1.87	9.27	1.13	25.53	11.53	53.51	25.67	646.33
26	GL 117020	64	102	32.93	58.20	2.73	6.53	1.47	36.20	16.40	57.88	28.00	562.00
27	IPCB 2015-132	68	108	33.47	58.53	1.93	7.47	1.27	27.67	8.67	41.52	13.67	454.33
28	H 07-120	67	109	32.00	56.80	2.40	9.87	1.00	27.60	8.87	32.41	11.00	475.00
29	Phule Vikram	61	111	27.00	55.00	2.20	9.80	1.13	50.87	20.73	48.09	23.00	496.33
30	JG 2020-57	65	102	22.27	42.07	2.13	8.33	1.00	28.67	8.27	49.09	16.00	605.00
31	PBC 574	61	104	31.93	59.73	2.20	8.87	1.00	27.60	19.67	50.60	24.00	719.33
32	RVSSG-96	72	102	25.40	45.27	1.93	8.07	1.53	28.60	8.53	47.08	13.33	418.67
33	BG 4027	61	106	24.00	59.93	1.87	11.87	1.27	71.80	34.93	42.40	23.67	357.33
34	IPC 2017-253	73	110	39.00	68.80	1.87	10.67	1.13	21.93	16.33	34.72	20.33	433.00
35	RLBGMH-4	66	109	34.87	69.13	2.20	10.47	1.33	35.93	28.73	37.93	29.67	633.00
36	GJG 1916	61	104	36.40	65.20	1.80	7.67	1.40	37.13	16.60	49.42	27.67	705.33

DTF = Days to 50% flowering; DTM = Days to maturity; HOFP = Height of 1st pod; PH = Plant height (cm); NPB = No. of primary branches; NSB = No. of secondary branches; NPP = No. of pods/plant; NSP = No. of seeds/pod; BY = Biological yield (g); HI = Harvest index (%); HSW = Hundred seed weight (g); PLYG =Plot yield (g).

Table 4.3: Grouping of genotypes based on time of flowering

	Class	EntryNo.	Genotypes	DTF
Time of flowering	**Early (40-60 days)**	11	IG 2020-16	48
		12	RVSSG-97	48
		20	IPC 2017-141	51
		8	IG 2020-15	53
		1	RSGD-7714	54
		6	GJG 1913	54
		19	H 13-03	54
		15	ICCV 191612	57
		2	PBC 582	58
		16	RSGD-834	59
		21	ICCV 191608	60
	Medium (61-80 days)	7	BG 4028	61
		29	Phule Vikram	61
		31	PBC 574	61
		33	BG 4027	61
		36	GJG 1916	62
		3	NBeG 1267	63
		17	JG 16	63
		5	BG 3062	64
		22	Phule G 191616	64
		26	RKGM 20-2	64
		10	GL 117020	65
		30	RKGM 20-1	65
		14	JG 2020-57	66
		35	RLBGMHG-3	66
		24	RLBGMH-4	67
		23	JG 24	68
		28	Phule G 0405	68
		27	H 07-120	69
		13	IPCB 2015-132	70
		9	Phule G 191618	71
		18	PG 252	71
		32	PG 251	71
		64	RVSSG-96	72
		34	GL 15003	73

(RLBGMH-4) while the shortest genotypes recorded a height 41.47 cm (RKGM 20-1) with a mean height of 55.80 cm.

Number of primary branches: The lowest value recorded for number of primary branches is 1.67 by IG 2020-15and IPC 2017-141while the highest being 3.20 by C-20480 with an average of 2.19.

Number of secondary branches: The lowest and highest values for secondary branches

are 3.80 (IG 2020-15) and 15.20 (PHULE G 191616) with a mean value of 9.26.

Number of seeds per pod: The mean numbers of seeds per pod are 1.16 while the range lies between 1.00 to 1.67 seedsper pod. Around 10 genotypes have the lowest value for seeds per pod while PG 252 recorded the highest value for number of seeds per pod.

Number of pods per plant: Lowest numbers of pods observed are for RVSSG-97 with 20.8 pods per plant while the highestnumber was observed for BG 4027 with 71.80 pods per plant with a mean value of 39.05 podsper plant.

Biological yield: The least biological yield observed is 8.27g for JG 2020-57 while the highest observed is 34.93g for BG 4027. Mean value for biological yield is 17.67 g.

Harvest Index: Harvest index ranged from a minimum of 25.88% for PG 251 to a highest of 59.54% for GJG 1913 with averaging at 48.16%.

Hundred seed weight: The hundred seed weight ranged from 10.67 g to 35.33 g with an average of 23.34 g. PG 251 had the least weight *i.e.* 10.67 g; while IG 2020-15 recorded the highest hundred seed weight i.e. 35.33 g.

Plot yield (g): The plot yield ranged from 59.33g to highest of 876.00g while averaging at 537.29g. Lowestplot yield (g) was recorded for PG 251 (59.33g) while the highest was recorded by GJG 1913(876.00g).

4.2.2 Phenotypic and genotypic coefficient of variation(%):

The division of variation into components attributed to various sources (genetic and environment) is the basic notion behind the study of variation. The relative quantity of these components can influence a population's genetic makeup. A number of analytical approaches for evaluating genetic variability have been provided by statistics. GCV and PCV are two of the most frequent procedures for determining the degree of heritable and non-heritable variation in the material under study.

According to Siva Subramanian and Madhavamenon (1973), genotypic and phenotypic coefficients of variation are classified as “Low (10%), moderate (10-20%), and large (> 20%)”. The PCV and GCV estimates for the characters under

study are provided in the table4.4.

The magnitudes of PCV were higher than the magnitudes of GCV. This indicated the impact of role of environment over the genotypic effect, finally influencing the phenotypic effect. The results are presented in table 4.4. the inference made from the study is that biological yield, number of pods per plant, number of secondary branches, plot yield and hundred seed weight were the traits which showed high PCV coupled with high GCV.

Four characters, namely, height of first pod, number of primary branches, number of seeds per pod and harvest index possessed high values of PCV along with moderate to low values of GCV. Days to maturity and days to flowering exhibited low PCV with low GCV.

From the above results it can be inferred that the values of phenotypic coefficient of variation (PCV) are higher than genotypic coefficient of variation (GCV) estimates and this was also concluded by Ramanappa *et al*., (2013) in their findings. From this one can infer that the variation is not only due to the genes but also due to the influence of environment on the character expression. High PCV values and low GCV values for number of primary branches and number of seeds per pod indicates that the variability present in these characters is due to the effects of environment. Similar findings by Aswathi *et al*., (2019), Babbar *et al.*, (2015), Basha *et al*., (2018), Parhe *et al*., (2014), Ramanappa *et al*., (2013), Vishnu *et al*., (2018) reached the same conclusion for respective characters.

Table 4.4: Descriptive statistics and genetic parameters of thirty-six genotypes for twelve yield and yield attributing and machine harvestable traits during Rabi 2020-21

Parameters	Mean	Min.	Max.	GCV (%)	PCV (%)	(h^2 bs) (%)	GAM (%)
DTF	62.50	48.00	73.33	7.20	9.31	59.78	11.46
DTM	104.52	94.67	111.33	4.31	4.36	97.34	8.75
HOFP	29.41	20.93	39.00	17.35	20.31	72.93	30.52
PH	55.80	41.47	69.13	14.90	16.38	82.71	27.92
NPB	2.19	1.67	3.20	4.40	29.08	2.29	1.37
NSB	9.26	3.80	15.20	23.31	35.85	42.29	31.23
NSP	1.16	1.00	1.67	10.49	30.47	11.85	7.44
NPP	39.05	20.80	71.80	25.29	48.46	27.23	27.18
BY	17.67	8.27	34.93	29.59	51.08	33.55	35.31
HI	48.16	25.88	59.54	12.52	20.74	36.45	15.57
HSW	23.34	10.67	35.33	26.66	30.07	78.63	48.70
PLYG	537.29	59.33	876.00	23.21	32.24	51.83	34.42

DTF = Days to 50% flowering; DTM = Days to maturity; HOFP = Height of 1st pod(cm); PH = Plant height (cm); NPB = No. of primary branches; NSB = No. of secondary branches; NPP = No. of pods/plant; NSP = No. of seeds/pod; BY = Biological yield (g); HI = Harvest index (%); HSW = Hundred seed weight (g); PLYG = Plot yield (g)

4.2.3 Heritability (h^2_{bs})% and Genetic Advance as percent of mean (GAM)%:

The degree of variation in a phenotypic trait in a population that is due to genetic variability between individuals in that population is estimated by heritability. It determines how much of a trait's variance may be attributable to hereditary causes rather than environmental influences. Broad sense heritability estimated from the ratio of total genetic variance to that of phenotypic variance. Genetic advance as percent of mean (GAM) estimates the increment in the mean genotypic value of the chosen plants over the parental population. Interpretationsbased on both the heritability estimates and GAM estimates would give a better insight on themode of gene action and the passing over of the character under study to the subsequent generations rather than the interpretations derived based on ether one of these estimate.

A high heritability value combined with a high GAM percent implies additive gene action, whereas a high heritability value combined with a low GAM percent implies non-additive gene action. Low heritability combined with low GAM percent values shows additive gene action, although low heritability values were caused by environmental influences. Low heritability and GAM values show non additive gene action and also the prevalence of environmental influence in the manifestation of the

character under study. The heritability and GAM values have been encapsulated in table 4.4.

Highest heritability estimate was shown by days to maturity, followed by plant height, hundred seed weight, and height of first pod. Moderate heritability was observed for characters like days to 50% flowering, and plot yield. Rest of the traits showed low heritability values.

High genetic advance as percent of mean (GAM) values were exhibited by hundred seed weight, biological yield, plot yield, number of secondary branches, height of first pod and plant height. Rest all other traits showed moderate to low magnitudes of GAM.

High values for both heritability and genetic advance can be seen in characters such as heightof first pod, plant height, and hundred seed weight. Plot yield showed high GAM with moderate heritability. This infers that the characters are governed by additive genes and the additive gene effects could most likely be the reason for high heritability. Selection for these characters in subsequent improvement programs could be effective.

Days to maturity showed high heritability coupled with low genetic advance values indicatingthe presence of non-additive gene action on this trait. High heritability was manifested by the environmental effects rather than the genotype.

Hundred seed weight was the only trait presenting high values of PCV, GCV coupled with high heritability and high GAM. Traits like biological yield, number of secondary branches, biological yield and plant yield showed moderate values for heritability while exhibiting high values of GAM along with high PCV and GCV indicates the additive gene effects of the trait and the effect of the environment on heritability.

Number of primary branches and number of seeds per pod exhibit low heritability and GAM which indicates that these characters were highly influenced by the environment and selectionfor these characters would be redundant.

Findings by Ramanappa *et al*., (2013) corroborate similar conclusions for h^2bs and GA% values for plant height, hundred seed weight, days to maturity and harvest index; Vishnu *et al*., (2018) for heritability estimates of height of first pod and plant height; Puri *et al*., (2013)for days to 50% flowering, days to maturity, harvest index and number of primary branches;Malik *et al*., (2010) for number of primary branches; Hagos *et al*., (2018) for number of primary branches; Biru *et al*., (2017) for branches

per plant.

4.3 Correlation studies

The degree of association between two variables, such as a complicated character and an associated trait, as well as the direction of change, is measured using correlation analysis. It proposes a strategy for selecting and improving specific associated trait in order to increase a complicated attribute like seed yield. Correlation studies aid in the comprehension of yield components and the effects of other characters on the same (Robinson *et al.,* 1951 and Johnson *et al.,* 1955).

Correlation is calculated at three levels: genotypic, phenotypic, and environmental, while the first two estimates indicates the magnitude of the underlying association. The phenotypic and genotypic correlations of different yield traits are provided in table 4.5. The relationship was studied and found that the genotypic correlation values were high in magnitude as compared to the phenotypic correlation values, indicating the less influence of environment.

A positive significant relationship was observed between plot yield and harvest index and hundred seed weight whereas, negative relation were seen for days to flowering, days to maturity and number of secondary branches with plot yield. The positive association between the two traits indicates that a hike in one of the trait will certainly increase the values for another trait. Likewise, a negative association tells that increase in one trait will lead to decrease in another trait.

Hundred seed weight showed positive association with height of first pod followed by plant height, biological yield and harvest index.

Number of seeds per pod showed positive and days to maturity and plant height recorded negative association with harvest index.

Biological yield recorded positive relation with days to maturity, plant height, and number of primary branches, number of secondary branches and number of pods per plant.

Number of pods per plant exhibited positive relationship with number of primary and secondary branches whereas, negative correlation was found with height of first pod.

Number of seeds per pod showed negative relations with primary branches; exhibited negative values with days to flowering, plant height, primary and secondary branches; Number of secondary branches had positive relations with days to maturity

and number of primary branches. Plant height recorded positive correlation with days to maturity and height of first pod; days to maturity had positive association with height of first pod and days to flowering.

From the above observations, we can infer that the improvement in plot yield could be brought about through selection for improvement in number of secondary branches,number of seeds per pod, harvest index, and hundred seed weight.

Equivalent findings were reported by Sharma *et al.,* (2019), Jha and Shil, (2015), Biabani *et al*.,(2011), Ali and Naveed, (2012), Kerketta *et al*., (2018), Yucel and Anlarsal, (2010), Babbar *et al*., (2015) for different traits studied.

4.4 Path analysis:

Path analysis gives information about how a component trait affects the dependant trait i.e. through direct effect and through other characters i.e. indirect effects. This shows whether the association with the dependant trait is due to the component trait's direct effect or by indirect effect *via* other component traits. Residual effect provides insight into other significant traits that are not explored in this study and their impacts on the dependent variable. The phenotypic and genotypic path analysis on various traits with plot yield and height of firstpod as dependant traits are discussed below in the tables

The results for the experiment are described based on their values as negligible (0 to 0.09), low (0.10 to 0.19), moderate (0.20 to 0.29), high (0.30 to 0.99) and very high (>1.00) as given by Lenka and Misra (1973).

The path analysis is done for two characters namely, plot yield and height of first pod as dependant traits individually at both genotypic and phenotypic levels.

4.4.1 Phenotypic direct and indirect effects on plot yield as dependant variable:

Phenotypic direct and indirect effects on plot yield as dependant variable are illustrated in table 4.6.

Direct positive effect on plot yield were recorded by biological yield and harvest index. However, these traits also reported positive significant correlation with yield. Rest of traits showed low direct effect.

Number of secondary branches and biological yield reported negative high indirect effect on plot yield. Number of pods per plant showed positive moderate indirect effect *via* biological yield on plot yield.

Table 4.5: Phenotypic and genotypic association among twelve traits in thirty six genotypes of chickpea

Traits		DTF	DTM	HOFP	PH	NPB	NSB	NSP	NPP	BY	HI	HSW	PLYG
DTF	**P**	**1.000**											
	G	**1.000**											
DTM	**P**	0.197*	**1.000**										
	G	0.263**	**1.000**										
HOFP	**P**	0.093NS	0.290**	**1.000**									
	G	0.154NS	0.358**	**1.000**									
PH	**P**	0.077NS	0.297**	0.813**	**1.000**								
	G	0.178NS	0.347**	0.896**	**1.000**								
NPB	**P**	0.180NS	-0.005NS	-0.131NS	-0.089NS	**1.000**							
	G	0.357**	0.116NS	-0.374**	-0.413**	**1.000**							
NSB	**P**	0.129NS	0.438**	-0.075NS	0.040NS	0.418**	**1.000**						
	G	0.412**	0.674**	0.004NS	0.018NS	1.670**	**1.000**						
NSP	**P**	-0.121NS	-0.101NS	0.091NS	0.025NS	-0.191*	-0.096NS	**1.000**					
	G	-0.054NS	-0.342**	0.077NS	-0.025NS	0.553**	-0.658**	**1.000**					
NPP	**P**	-0.108NS	0.143NS	-0.192*	0.027NS	0.341**	0.541**	0.108NS	**1.000**				
	G	-0.047NS	0.274**	-0.374**	-0.062NS	1.645**	0.704**	-0.576**	**1.000**				
BY	**P**	-0.049NS	0.237*	0.061NS	0.341**	0.283**	0.586**	0.087NS	0.799**	**1.000**			
	G	0.074NS	0.404**	0.270**	0.544**	0.479**	0.524**	0.003NS	0.708**	**1.000**			
HI	**P**	-0.121NS	-0.438**	-0.159NS	-0.253**	-0.039NS	-0.180NS	0.254**	0.127NS	-0.004NS	**1.000**		
	G	-0.404**	-0.762**	-0.418**	-0.435**	0.235*	-0.410**	0.364**	-0.161NS	-0.095NS	**1.000**		
HSW	**P**	-0.040NS	-0.098NS	0.405**	0.454**	-0.146NS	-0.067NS	0.180NS	0.106NS	0.383**	0.481**	**1.000**	
	G	-0.091NS	-0.111NS	0.484**	0.536**	-0.717**	-0.145NS	0.262**	-0.095NS	0.539**	0.426**	**1.000**	
PLYG	**P**	-0.189*	-0.366**	0.088NS	-0.067NS	-0.010NS	-0.290**	0.181NS	-0.057NS	-0.066NS	0.488**	0.268**	**1.000**
	G	-0.283**	-0.511**	-0.154NS	-0.277**	0.555**	-0.331**	0.512**	-0.174NS	-0.036NS	0.808**	0.303**	**1.000**

* and ** significant at 5% and 1% probability level; P = phenotypic and G = genotypic values

DTF = Days to 50% flowering; DTM = Days to maturity; HOFP = Height of 1st pod(cm); PH = Plant height (cm); NPB = No. of primary branches; NSB = No. of secondary branches; NPP = No. of pods/plant; NSP = No. of seeds/pod; BY = Biological yield (g); HI = Harvest index (%); HSW = Hundred seed weight (g); PLYG =Plot yield (g).

Table 4.6: Phenotypic direct and indirect effects of yield, yield attributing and machine harvestable traits on plot yield (g) as dependent trait

Traits	DTF	DTM	HOFP	PH	NPB	NSB	NSP	NPP	BY	HI	HSW	Phenotypic correlation with PLYG
DTF	**-0.109**	-0.029	0.003	0.001	0.024	-0.001	0.002	0.012	-0.013	-0.029	-0.007	**-0.189***
DTM	-0.022	**-0.144**	0.008	0.005	-0.001	-0.003	0.001	-0.016	0.064	-0.103	-0.017	**-0.366****
HOFP	-0.010	-0.042	**0.027**	0.012	-0.017	0.000	-0.001	0.022	0.017	-0.038	0.069	**0.088**
PH	-0.008	-0.043	0.022	**0.015**	-0.012	0.000	0.000	-0.003	0.092	-0.060	0.078	**-0.067**
NPB	-0.020	0.001	-0.004	-0.001	**0.133**	-0.002	0.003	-0.039	0.076	-0.009	-0.025	**-0.011**
NSB	-0.014	-0.063	-0.002	0.001	0.056	**-0.006**	0.001	-0.061	0.158	-0.043	-0.011	**-0.290****
NSP	0.013	0.015	0.002	0.000	-0.025	0.001	**-0.013**	-0.012	0.023	0.060	0.031	**0.181**
NPP	0.012	-0.021	-0.005	0.000	0.045	-0.003	-0.001	**-0.113**	0.215	0.030	0.018	**-0.057**
BY	0.005	-0.034	0.002	0.005	0.038	-0.003	-0.001	-0.090	**0.269**	-0.001	0.066	**-0.066**
HI	0.013	0.063	-0.004	-0.004	-0.005	0.001	-0.003	-0.014	-0.001	**0.236**	0.082	**0.488****
HSW	0.004	0.014	0.011	0.007	-0.019	0.000	-0.002	-0.012	0.103	0.114	**0.171**	**0.268****

Residual = 0.39536

Table 4.7: Genotypic direct and indirect effects of yield, yield attributing and machine harvestable traits on plot yield (g) as dependent trait

Traits	DTF	DTM	HOFP	PH	NPB	NSB	NSP	NPP	BY	HI	HSW	Genotypic correlation with PLYG
DTF	**-0.220**	-0.104	-0.010	0.118	-0.052	0.397	0.011	0.059	0.128	-0.667	0.134	**-0.283****
DTM	-0.058	**-0.397**	-0.023	0.231	-0.017	0.649	0.069	-0.345	0.695	-1.259	0.162	**-0.511****
HOFP	-0.034	-0.142	**-0.063**	0.596	0.055	0.004	-0.016	0.471	0.465	-0.690	-0.709	**-0.154**
PH	-0.039	-0.138	-0.057	**0.665**	0.060	0.017	0.005	0.078	0.936	-0.720	-0.784	**-0.277****
NPB	-0.079	-0.046	0.024	-0.275	**-0.146**	1.609	-0.112	-2.070	0.825	0.388	1.050	**0.555****
NSB	-0.091	-0.267	0.000	0.012	-0.244	**0.964**	0.133	-0.886	0.903	-0.678	0.213	**-0.331****
NSP	0.012	0.136	-0.005	-0.017	-0.081	-0.634	**-0.202**	0.725	0.005	0.602	-0.384	**0.512****
NPP	0.010	-0.109	0.024	-0.041	-0.241	0.679	0.116	**-1.259**	1.220	-0.267	0.138	**-0.174**
BY	-0.016	-0.160	-0.017	0.362	-0.070	0.505	-0.001	-0.892	**1.722**	-0.157	-0.789	**-0.036**
HI	0.089	0.302	0.027	-0.290	-0.034	-0.395	-0.074	0.203	-0.163	**1.653**	-0.624	**0.808****
HSW	0.020	0.044	-0.031	0.356	0.105	-0.140	-0.053	0.119	0.928	0.705	**-1.464**	**0.303****

Residual = -0.07230

Bold figures are direct effects and un-bold figures are indirect effects

DTF = Days to 50% flowering; DTM = Days to maturity; HOFP = Height of 1st pod(cm); PH = Plant height (cm); NPB = No. of primary branches; NSB = No. of secondary branches; NPP = No. of pods/plant; NSP = No. of seeds/pod; BY = Biological yield (g); HI = Harvest index (%); HSW = Hundred seed weight (g); PLYG = Plotyield (g).

4.4.2 Genotypic direct and indirect effects on plot yield as dependant variable:

The path analysis on plot yield (g) as dependant trait revealed the following genotypic directand indirect effects by the component characters on the dependant trait. Genotypic direct and indirect effects on plot yield as dependant variable are illustrated in table 4.7.

Biological yield, harvest index, number of secondary branches, and plant height showed high to very high direct effect on plot yield. However, the correlation estimates reported positive association of plot yield with harvest index whereas, negative correlation was seen between plot yield and plant height and number of secondary branches. Direct selection and improvement of these traits can achieve the improvement of the dependant trait. Number of pods per plant, hundred seed weight, days to flowering, days to maturity and number of seeds per pod exhibited very high to high negative indirect effect on plot yield. Hence election and improvement of indirect factors can also favour the improvement of the dependant variable.

Hundred seed weight showed very high positive indirect effect on plot yield *via* number of primary branches and negative indirect effect was seen *via* height of first pod (HOFP), plant height (PH), number of seeds per pod (NSP), biological yield (BY) and harvest index (HI). Furthermore, moderate to high indirect effect was achieved by number of secondary branches (NSB) through hundred seed weight (HSW) on plot yield.

Number of seeds per pod and hundred seed weight showed positive and days to maturity, days to flowering, height of first pod, plant height and number of secondary branches manifested negative indirect effect on plot yield *via* harvest index.

Biological yield recorded positive indirect effects on plot yield through hundred seed weight, number of primary and secondary branches, plant height, height of first pod and days to maturity.

Height of first pod, and number of seeds per pod recorded negative indirect effect on plot yield *via* number of pods per plant. Apart from this, number of primary branches, biological yield and number of secondary branches showed negative indirect effect *via* number of pods per plant.

Number of seeds per pod manifested positive indirect effect and plant height, number of primary branches, number of secondary branches, number of

pods per plant and biological yield showed positive indirect effect on plot yield.

Days to maturity, number of primary branches, number of pods per plant, biological yield showed positive but number of seeds per pod showed negative indirect effect on plot yield *via* number of secondary branches.

Positive correlation at phenotypic correlation level and negative correlation at genotypic correlation level and vice versa and positive direct effects in phenotypic path analysis and negative direct effects in genotypic path analysis and vice versa indicates the effects of the environment and genotype x environment interactions (G X E) to be reasons for the aforementioned changes.

4.4.3 Phenotypic direct and indirect effects on height of first pod as dependant variable:

The phenotypic path analysis of the characters under study with height of first pod as dependant variable produced the following results and these are tabulated in table 4.8.

Plant height reported very positive direct effect on height of first pod. The trait also bears positive correlation with height of first pod, thereby indicating that the selection of this trait will be rewarding for improvement of height of first pod. Further, moderate direct effect was achieved by hundred seed weight. A positive association was observed between height of first pod and hundred seed weight whereas, biological yield showed negative effect.

As far as indirect effects are concerned, hundred seed weight, days to maturity and biological yield reported indirect effect on height of first pod *via* plant height. Number of pods per plant showed negative indirect effect through biological yield. The results indicated that concurrent selection of indirect components for these traits ultimately leads to the improvement of the character under consideration.

4.4.4 Genotypic direct and indirect effects on height of first pod as dependant variable:

Genotypic path analysis of the component characters under study with height of first pod as the dependant variable generated the following results on direct and indirect effects of the component characters on the dependant variable. The results are tabulated under table 4.9.

At genotypic level, hundred seed weight and number of secondary branches showed very positive direct effect on height of first pod, however, hundred seed

weight also possessed positive correlation with the aforesaid trait. Plant height, number of seeds per pod and number of pods per plant recorded high direct effect on height of first pod. However, number of pods per plant recorded negative association with height of first pod.

Biological yield, harvest index recorded very high negative direct effect on height of first pod. Of these two traits, biological yield recorded positive and harvest index showed negative values of correlation with HOFP. Apart from this, days to flowering and days to maturity recorded high direct effect along with positive correlation with height of first pod.

Harvest index showed positive and number of secondary branches recorded negative indirect effect on height of first pod *via* days to maturity. Biological yield and hundred seed weight achieved positive indirect effect through plant height. Similarly, number of secondary branches and number of pods per plant showed positive indirect effect through number of primary branches.

Traits namely, number of primary branches, days to maturity, days to flowering, number of pods per plant and biological yield manifested positive indirect effect through number of secondary branches whereas, number of seeds per pod, harvest index and plot yield got negative indirect effect on HOFP through number of secondary branches.

Through biological yield, days to maturity, plant height, number of primary branches, number of secondary branches, number of pods per plant and hundred seed weight exhibited negative indirect effect whereas, was the only trait to record positive indirect effect on HOFP.

Days to flowering, days to maturity, plant height and number of secondary branches and, plot yield, hundred seed weight and number of seeds per pod exhibited positive as well as negative indirect effects on HOFP *via* harvest index.

The traits *viz.*, plant height, number of seeds per pod, biological yield, plot yield and number of primary branches recorded positive and negative indirect effects respectively through hundred seed weight.

Table 4.8: Phenotypic direct and indirect effects of yield, yield attributing and machine harvestable traits on height of first pod as dependant trait

Traits	DTF	DTM	PH	NPB	NSB	NSP	NPP	BY	HI	HSW	PLYG	Phenotypic corr. with HOFP
DTF	**-0.014**	0.028	0.062	0.015	0.015	-0.009	0.003	0.015	0.007	-0.010	-0.003	**0.093**
DTM	-0.003	**0.140**	0.239	0.000	0.052	-0.008	-0.004	-0.071	0.026	-0.024	-0.005	**0.290****
PH	-0.001	0.042	**0.804**	-0.007	0.005	0.002	-0.001	-0.102	0.015	0.112	-0.001	**0.813****
NPB	-0.003	-0.001	-0.072	**0.083**	0.050	-0.014	-0.010	-0.085	0.002	-0.036	0.000	**-0.131**
NSB	-0.002	0.061	0.032	0.035	**0.119**	-0.007	-0.016	-0.175	0.011	-0.016	-0.004	**-0.075**
NSP	0.002	-0.014	0.020	-0.016	-0.011	**0.075**	-0.003	-0.026	-0.015	0.045	0.003	**0.091**
NPP	0.002	0.020	0.022	0.028	0.064	0.008	**-0.029**	-0.239	-0.008	0.026	-0.001	**-0.192***
BY	0.001	0.033	0.274	0.023	0.070	0.007	-0.023	**-0.299**	0.000	0.094	-0.001	**0.061**
HI	0.002	-0.061	-0.204	-0.003	-0.021	0.019	-0.004	0.001	**-0.059**	0.119	0.007	**-0.159**
HSW	0.001	-0.014	0.365	-0.012	-0.008	0.014	-0.003	-0.114	-0.028	**0.247**	0.004	**0.405****
PLYG	0.003	-0.051	-0.054	-0.001	-0.034	0.014	0.002	0.020	-0.029	0.066	**0.014**	**0.088**

Residual = 0.204

Table 4.9: Genotypic direct and indirect effects on yield, yield attributing and machine harvestable traits on 1st pod height (cm) as dependant trait

Traits	DTF	DTM	PH	NPB	NSB	NSP	NPP	BY	HI	HSW	PLYG	Genotypic correlation with HOFP
DTF	**-0.716**	-0.201	0.114	0.090	0.570	-0.042	-0.028	-0.151	0.730	-0.218	0.066	**0.154**
DTM	-0.188	**-0.765**	0.222	0.029	0.932	-0.267	0.162	-0.823	1.377	-0.266	0.118	**0.358****
PH	-0.127	-0.265	**0.639**	-0.104	0.025	-0.020	-0.037	-1.108	0.787	1.282	0.064	**0.896****
NPB	-0.255	-0.089	-0.264	**0.253**	2.311	0.431	0.974	-0.977	-0.425	-1.717	-0.128	**-0.374****
NSB	-0.295	-0.515	0.011	0.422	**1.384**	-0.513	0.417	-1.069	0.742	-0.348	0.077	**0.004**
NSP	0.038	0.262	-0.016	0.140	-0.911	**0.780**	-0.341	-0.006	-0.659	0.628	-0.118	**0.077**
NPP	0.033	-0.209	-0.039	0.416	0.974	-0.450	**0.592**	-1.444	0.292	-0.226	0.040	**-0.374****
BY	-0.053	-0.309	0.347	0.121	0.725	0.002	0.419	**-2.038**	0.171	1.291	0.008	**0.270****
HI	0.289	0.582	-0.278	0.059	-0.567	0.284	-0.096	0.193	**-1.809**	1.021	-0.187	**-0.418****
HSW	0.065	0.085	0.342	-0.181	-0.201	0.205	-0.056	-1.099	-0.771	**2.394**	-0.070	**0.484****
PLYG	0.203	0.391	-0.177	0.140	-0.458	0.399	-0.103	0.073	-1.461	0.725	**-0.231**	**-0.154**

Residual = -0.263

Bold figures are direct effects and un-bold figures are indirect effects

DTF = Days to 50% flowering; DTM = Days to maturity; HOFP = Height of 1st pod; PH = Plant height (cm); NPB = No. of primary branches; NSB = No. of secondary branches; NPP = No. of pods/plant; NSP = No. of seeds/pod; BY = Biological yield (g); HI = Harvest index (%); HSW = Hundred seed weight (g); PLYG = Plot yield (g)

4.5 Cluster analysis:

Cluster analysis groups the genotypes based on their similarity into discrete groups called clusters. Each cluster has a group of genotypes that are similar. Different clusters are formed and the distance between them is based on the similarity between two clusters. Farther the distance between two clusters, more diverse they are. Different clusters and their components along with inter and intra cluster distances, cluster means and dendrogram are given in the tables.

4.5.1 Grouping of genotypes into different clusters:

Cluster analysis through Un-weighted Pair Group Method with Arithmetic averages (UPGMA) using Euclidean distances divided the 36 genotypes under study into seven clusters. Uneven distribution of the genotypes to different clusters took place with cluster I having highest genotypes (14 genotypes) followed by cluster IV (9 genotypes), clusters II and III (4 genotypes each), cluster VI (3 genotypes) and clusters V and VII having the least number of genotypes (1 each). This clustering pattern found evidence of genetic variability in the study population. The details of the clusters and their component genotypes are presented in the table 4.10 and Fig 4.1 and 4.2.

Table 4.10: Genotypes in each cluster

Clusters Number	No. of Genotypes	Genotypes
I	14	RSGD-7714, NBeG 1267, IG 2020-15, RKGM 20-1, IG 2020-16, ICCV 191612, RSGD-834, H 13-03, Phule G 191616, JG 24, RKGM 20-2, GL 117020, JG 2020-57, RLBGMH-4
II	4	PBC 582, JG 16, PBC 574, GJG 1916
III	4	GL 15003, IPCB 2015-132, RVSSG-96, IPC 2017-253
IV	9	BG 3062, PG 252, RVSSG-97, RLBGMHG-3, IPC 2017-141, ICCV 191608, Phule G 0405, H 07-120, Phule Vikram
V	1	GJG 1913
VI	3	BG 4028, Phule G 191618, BG 4027
VII	1	PG 251

4.5.2 Inter and intra cluster distances:

The maximum intra cluster distance was found within cluster I (43.266) that is comprised of 14 genotypes, followed by cluster II (31.158) with 4 genotypes, then cluster IV (30.361) consisting of 9 genotypes, followed by cluster III (27.044) with 4

genotypes, then comes cluster VI (25.764) with 3 genotypes and finally followed by clusters V and VII with an inter-cluster distance of 0.000 as they contain only one genotype in each of them.

Table 4.11: Inter and intra cluster distances

	I	II	III	IV	V	VI	VII
I	**43.26**	126.81	175.63	103.38	279.75	273.83	546.08
II		**31.15**	299.64	229.57	153.68	399.07	672.02
III			**27.04**	84.76	452.04	130.58	383.95
IV				**30.36**	382.75	170.88	442.88
V					**0.00**	551.86	825.02
VI						**25.76**	274.65
VII							**0.00**

Values in bold = Intra-cluster distance

The inter cluster distances are covered further in descending order depending on the inter cluster distances. The highest value for inter cluster distance was recorded for clusters V and VII (852.022), followed by clusters II and VII (672.028), clusters V and VI (551.867), clusters I and VII (546.087), clusters III and V (452.045), clusters IV and VII (442.887), clusters II and VI (399.074), clusters III and VII (383.956), clusters IV and V (382.752), clusters II and III (299.641), clusters I and V (279.758), clusters VI and VII (274.655), clusters I and VI (273.836), clusters II and IV (229.578), clusters I and III (175.637), clusters IV and VI (170.884), clusters II and V (153.681), clusters VI and III (130.586), clusters I andII (126.818), clusters I and IV (103.388), and clusters III and IV (84.764). The least inter cluster distance was noted between clusters III and IV indicating that these clusters are closely related and less available diversity between these two clusters while cluster V and VII, clusters II and VII noted the highest inter cluster distance indicating presence of ample genetic diversity amongst these clusters.

4.5.3 Cluster means:

Cluster means for each of the twelve component characters have been elucidated in the table 4.12. Cluster V (54 days) has the least mean for days to 50% flowering followed by cluster I (60 days) and cluster II (60 days) while cluster III (71 days) having the highest days for days to 50% flowering. The least mean for days to maturity was also recorded by cluster V (98 days) followed by cluster II (101 days) and cluster I (102.952 days) while cluster VII (109) having the highest cluster mean

value for days to maturity. Cluster III (31.067 cm) noted the highest mean for height of first pod followed by cluster VI (30.156 cm), cluster IV (30.111 cm) with least value being shown by cluster VII (25.644 cm).

Highest cluster mean for plant height was shown by cluster VI (63.489 cm) then cluster IV (57.407 cm), then cluster VII (55.267cm) while the minimum was exhibited by cluster V (53.133cm). Cluster VII (2.800), (13.511) showed highest cluster average for both number of primary branches and number of secondary branches respectively, while cluster V (2.667) and cluster VI (2.222) showed next to high values for number of primary branches and cluster VI (12.222) and cluster II (9.467) showed next to high values for number of secondary branches. Cluster III (1.900) and cluster V (5.800) recorded the least cluster means for number of primary branches and number of secondary branches respectively. Cluster VI (55.22) showed highest cluster mean for number of pods per plant with cluster VII (51.200) and cluster II (43.550) being next to highest values for the same while the least being exhibited by cluster III (26.933). Cluster V (1.467) exhibited highest cluster mean for number of seeds per pod and cluster VII (1.000) showed the minimum cluster means while cluster II (1.267) and cluster III (1.233) next to highest values for cluster means in number of seeds per pod. Cluster VI (29.044 g) exhibited highest cluster mean for biological yield followed by cluster II (19.133g), cluster IV (18.748g) while cluster III (10.883 g) showed lowest cluster mean for the same. The highest cluster mean for harvest index was exhibited by cluster V (59.539) followed by cluster I (51.831), cluster IV (46.910) while cluster VII (25.880) exhibited the least value for harvest index. Cluster mean for hundred seed weight was highest for cluster VI (27.778g) while least recorded for cluster VII (10.667g) and cluster I (25.000g) and cluster V (24.333g) showed next to highest values for seed weight. Cluster V (876.00g) exhibited the highest cluster mean for plot yield (g) followed by cluster II (723.g), cluster IV (495.519g) while cluster VII (59.333g) showed the least cluster mean for the aforementioned trait.

Fig 4.1: Dendrogram depicting the relationship of the genotypes under study.



Here, Observation = Entry

Fig 4.2: Dendrogram for relation between different clusters.

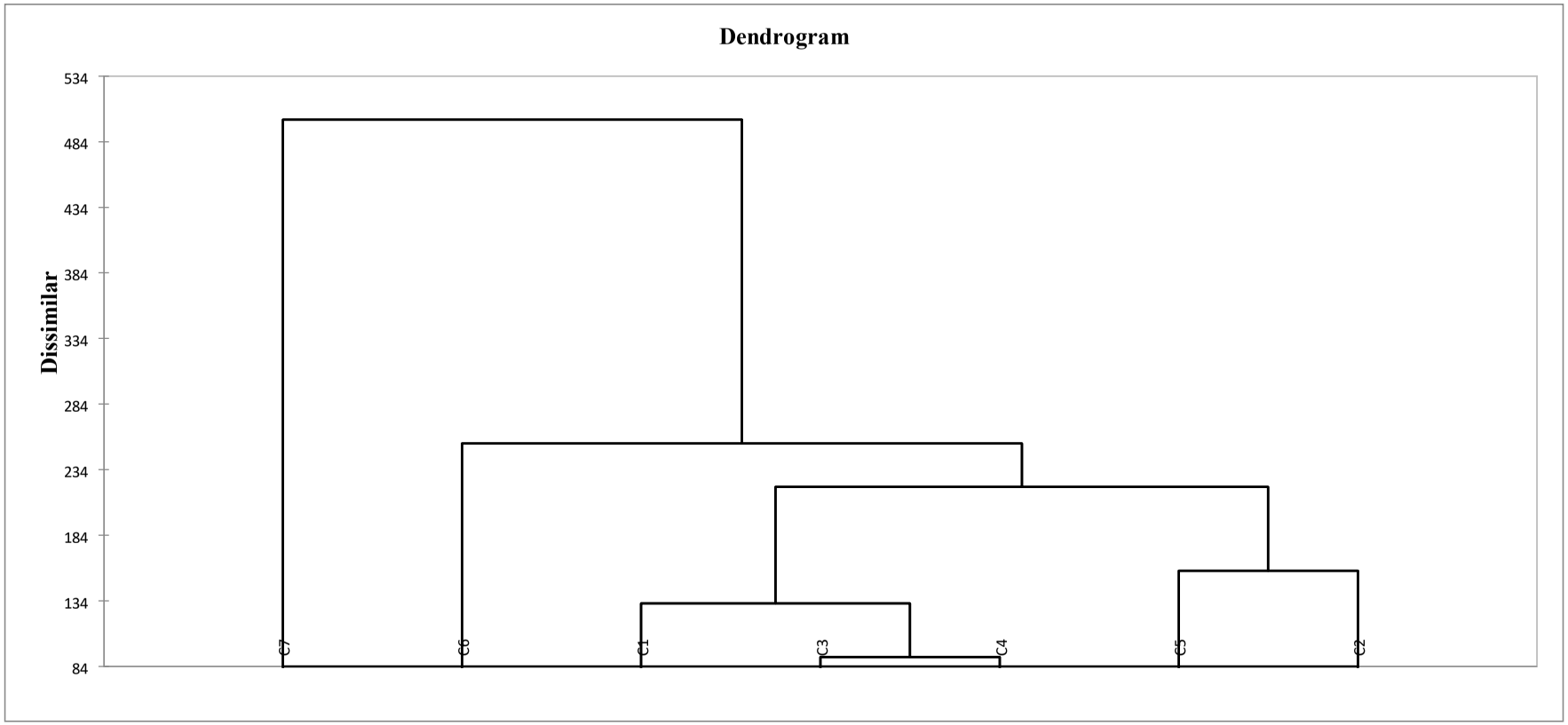


Table 4.12: Cluster means of twelve yield contributing traits

Cluster	DTF	DTM	HOFP	PH	NPB	NSB	NPP	NSP	BY	HI	HSW	PLYG
I	60.429	102.952	28.748	53.992	2.220	8.876	36.005	1.162	16.190	51.831	25.000	597.333
II	60.833	101.917	29.217	54.233	2.300	9.467	43.550	1.267	19.133	50.613	23.833	723.250
III	71.333	107.083	**31.067**	55.100	1.900	8.583	26.933	1.233	10.883	41.712	15.333	425.000
IV	61.926	106.333	30.111	57.407	2.081	8.985	40.630	1.193	18.748	46.910	23.926	495.519
V	**54.333**	**98.333**	28.133	53.133	2.667	5.800	37.200	**1.467**	16.533	**59.539**	24.333	**876.000**
VI	64.333	106.778	30.156	**63.489**	2.222	12.222	**55.222**	1.200	**29.044**	43.735	**27.778**	330.556
VII	70.667	109.667	25.644	55.267	**2.800**	**13.511**	51.200	1.000	16.933	25.880	10.667	59.333

DTF = Days to 50% flowering; DTM = Days to maturity; HOFP = Height of 1st pod; PH = Plant height (cm); NPB = No. of primary branches; NSB = No. of secondary branches; NPP = No. of pods/plant; NSP = No. of seeds/pod; BY = Biological yield (g); HI = Harvest index (%); HSW = Hundred seed weight (g); PLYG = Plot yield (g)



Brown **Dark Brown** **Green**

Fig 4.3 Pictorial presentation of different seed coat colours in chickpea genotypes

Cluster V exhibited high values for to 50% flowering, days to maturity, number of seeds per pod, harvest index and plot yield. Cluster VI exhibited highest cluster mean values for plant height, number of pods per plant, biological yield, and hundred seed weight.

Cluster III showed high values for of first pod while cluster VII showed high cluster means for number of primary branches and number of secondary branches.

For the improvement of yield, genotype GJG 1913 can be selected as it is the component of cluster V. In order to develop varieties amenable to mechanical harvesting, selection can be done from GL 15003, IPCB 2015-132, RVSSG-96, IPC 2017-253 that form cluster III.

4.6 Classification of genotypes:

4.6.1 Based on height of first pod:

Height of first pod helps in the development of chickpea cultivars suitable formechanical harvesting along with seed yield.

Chickpea cultivars with height of first pod (cm) above 30 cm are considered suitable for mechanical harvesting (Table 4.13). Around 17 genotypes out of studied 36 genotypes showed a first pod height more than 30 cm. IPC 2017-253 (39 cm) showed the highest first pod height followed by JG 24 (38.40 cm), ICCV 191612 (38.13 cm), Phule G 191618 (37.47 cm), GJG 1916 (36.40 cm), ICCV 191608 (34.93 cm), RLBGMH-4 (34.87 cm), IG 2020-15(34.60 cm), IPC 2017-141(33.73 cm), IPCB 2015-132 (33.47), RVSSG-97 (32.93 cm), GL 117020 (32.93 cm), H 07-120 (32.00 cm), PBC 574 (31.93 cm), Phule G 191616 (31.87 cm). These genotypes exhibited suitable first pod height amenable for machine harvesting.

Table 4.13: Ranking of genotypes based on their height of first pod

S. no.	Entry	HOFP (cm)	S. no.	Entry	HOFP (cm)
34	**IPC 2017-253**	**39.00**	7	BG 4028	29.00
24	**JG 24**	**38.40**	6	GJG 1913	28.13
15	**ICCV 191612**	**38.13**	2	PBC 582	27.60
13	**Phule G 191618**	**37.47**	5	BG 3062	27.00
36	**GJG 1916**	**36.40**	29	Phule Vikram	27.00
21	**ICCV 191608**	**34.93**	4	GL 15003	26.40
35	**RLBGMH-4**	**34.87**	25	RKGM 20-2	26.13
8	**IG 2020-15**	**34.60**	18	PG 251	25.64
20	**IPC 2017-141**	**33.73**	32	RVSSG-96	25.40
27	**IPCB 2015-132**	**33.47**	33	BG 4027	24.00
12	**RVSSG-97**	**32.93**	16	RSGD-834	23.53
26	**GL 117020**	**32.93**	11	IG 2020-16	23.53
28	**H 07-120**	**32.00**	10	RKGM 20-1	22.60
31	**PBC 574**	**31.93**	23	Phule G 0405	22.60
22	**Phule G 191616**	**31.87**	30	JG 2020-57	22.27
14	**RLBGMHG-3**	**30.73**	3	NBeG 1267	21.93
9	**PG 252**	**30.07**	1	RSGD-7714	21.80
19	H 13-03	29.87	17	JG 16	20.93

4.6.2 Based on seed coat colour: Out of the 36 observed genotypes, 30 genotypes had brown coloured seed coat, 5 genotypes had dark brown coloured seed coat and one genotype had green coloured seed coat (Table 4.14 and Fig. 4.3).

Table 4.14: Grouping of genotypes based on seed coat colour

Seed coat colour	Entry no.	Entry	Seed coat colour	Entry no.	Entry
Brown	2	PBC 582	**Brown**	21	ICCV 191608
	3	NBeG 1267		22	Phule G 191616
	4	GL 15003		23	Phule G 0405
	5	BG 3062		27	IPCB 2015-132
	6	GJG 1913		28	H 07-120
	7	BG 4028		29	Phule Vikram
	8	IG 2020-15		30	JG 2020-57
	9	PG 252		31	PBC 574
	10	RKGM 20-1		33	BG 4027
	11	IG 2020-16		34	IPC 2017-253
	13	Phule G 191618		35	RLBGMH-4
	14	RLBGMHG-3		36	GJG 1916
	15	ICCV 191612	**Dark Brown**	1	RSGD-7714
	16	RSGD-834		12	RVSSG-97
	17	JG 16		24	JG 24
	18	PG 251		25	RKGM 20-2
	19	H 13-03		26	GL 117020
	20	IPC 2017-141	**Green**	32	RVSSG-96

4.6.3 Genotypes with high first pod height and plot yield: In the table 4.15 given below comprises of genotypes with high first pod height and high plotyield among the observed 36 genotypes. Six genotypes namely JG 24, IG 2020-15, RLBGMH-4, PBC 574, GJG 1916, and Phule G 191616 recorded both high first pod height and plot yield. Thus, we can infer that these six genotypes are suitable and promising as parents for further improvement or for developing into a cultivar.

Table 4.15: Top fifteen genotypes with height of 1st pod more than 30 cm and high yield

S. NO.	Entry	HOFP	S. NO.	Entry	PLYG
34	IPC 2017-253	39.00	6	GJG 1913	876.00
24	**JG 24**	**38.40**	17	JG 16	750.33
15	ICCV 191612	38.13	**31**	**PBC 574**	**719.33**
13	Phule G 191618	37.47	2	PBC 582	718.00
36	**GJG 1916**	**36.40**	**36**	**GJG 1916**	**705.33**
21	ICCV 191608	34.93	**24**	**JG 24**	**650.67**
35	**RLBGMH-4**	**34.87**	1	RSGD-7714	646.33
8	**IG 2020-15**	**34.60**	25	RKGM 20-2	646.33
20	IPC 2017-141	33.73	**35**	**RLBGMH-4**	**633.00**
27	IPCB 2015-132	33.47	16	RSGD-834	628.67
12	RVSSG-97	32.93	**8**	**IG 2020-15**	**605.00**
26	GL 117020	32.93	30	JG 2020-57	605.00
28	H 07-120	32.00	**22**	**Phule G 191616**	**587.67**
31	**PBC 574**	**31.93**	10	RKGM 20-1	581.33
22	**Phule G 191616**	**31.87**	19	H 13-03	562.00

HOFP = Height of 1st pod (cm); PLYG = Plot yield (g)

CHAPTER -V
SUMMARY AND CONCLUSION

The primary focus of the current experiment titled "**Identification of Chickpea (Cicer arietinum L.) genotypes promising for mechanical harvesting**" is to identify genotypes that are both high yielding and amenable for machine harvesting. The research was carried out in the experimental field under the Department of Genetics and Plant Breeding, Research cum instructional farm, IGKV, Raipur, (C.G.) with 36 genotypes.

The investigation focused on 13 quantitative characters and one qualitative character *viz.,* Days to 50% flowering, Days to maturity, Height of first pod (cm), Plant height, Number of primary branches, Number of secondary branches, Number of seeds per pod, Number of pods per plant, Biological yield, Harvest index, Hundred seed weight, Plot yield (g) and Seed coat colour. The data obtained has be subjected to various statistical analyses such as genetic variability parameters, correlation Analysis, path coefficient analysis, and cluster analysis in order to find out how various characters interact with each other in order to obtain the required genotype that matches the requirements of our research problem. The outcomes of the aforementioned research are summarised in the following paragraphs.

- Analysis of variance on twelve characters showed significant values for MSS of eleven traits. Two traits *viz.*, "numbers of primary branches" and "number of seeds per pod" did not reveal any significant variations. The presence of significant levels of variation implies the presence of variability in the observed characters. This variability can be tapped into and be used in further development of the genotypes.
- Among the 36 genotypes studied, two genotypes namely IG 2020-15 and RVSSG-97 had flowered at 48 days while IPC 2017-253 took 73 days, which is the highest among the studied genotypes.
- The magnitudes of phenotypic co-efficient of variation were higher than the magnitudes of genotypic co-efficient of variation. This indicated the impact of role of environment over the genotypic effect, finally influencing the phenotypic effect. biological yield, no. of pods per plant, no. of secondary branches, plot yield, hundred seed weight

were the traits which showed high PCV coupled with high GCV. Four characters, namely, “height of first pod”, “number of primary branches”, “number of seeds per pod” and “harvest index” possessed high values of PCV along with moderate to low values of GCV.

- High values for both heritability and genetic advance was observed in characters such as height of first pod, plant height, and hundred seed weight. Plot yield showed high GAM with moderate heritability.
- Hundred seed weight was the only trait presenting high values of PCV, GCV coupled with a high heritability value and high GAM.
- Positive significant relationship was observed between plot yield and, harvest index and hundred seed weight whereas, negative relation were seen for days to flowering, days to maturity and no. of secondary branches with plot yield.
- 100 seed weight exhibited positive association with height of first pod followed by biological yield, plant height, and harvest index.
- Path analysis with plot yield as dependent variable, positive direct effect on plot yield were shown by biological yield and harvest index at phenotypic level and at genotypic level, biological yield, harvest index, number of secondary branches, and plant height showed high direct effect on plot yield.
- Plant height reported very positive direct effects on height of first pod (as dependent trait) at phenotypic level whereas, at genotypic level, hundred seed weight and number of secondary branches showed very positive direct effect on HOFP.
- Cluster analysis through Un-weighted Pair Group Method with Arithmetic averages (UPGMA) using Euclidean distances divided the 36 genotypes under study into seven clusters. The utmost intra cluster distance was found within cluster I (43.266) that is comprised of 14 genotypes and clusters V and VII with an inter-cluster distance of 0.000 as they contain only one genotype in each of them
- Around 17 genotypes out of studied 36 genotypes showed a first pod height more than 30 cm. These genotypes exhibited suitable first pod height amenable for machine harvesting.

- Based on seed coat colour, out of the 36 observed genotypes, 30 genotypes had brown coloured seed coat, 5 genotypes had dark brown coloured seed coat and one genotype had green coloured seed coat.
- Six genotypes namely C-20485, C-20498, RLBGMH-4, C-20462, C-20493, and C-20480 recorded both high first pod height and plot yield (g). Thus, we can infer that these six genotypes are suitable and promising as parents for further improvement or for developing into a cultivar

Conclusion:

The research study was taken into consideration with the aim to evaluate chickpea genotypes for high yield and machine harvestable character based on height of first node. From the results it can be concluded that the trait, height of first pod/node is of utmost importance as it tells the usage of combine harvester for harvesting of chickpea crop. In our study, there were six promising genotypes (JG 24, IG 2020-15, RLBGMH-4, PBC 574, GJG 1916, and Phule G 191616) which yield high along with hike in height of first pod.

Suggestions for future work

- For the creation of cultivars suitable for machine harvesting, an emphasis on plant height, height of first pod, and plot yield is critical.
- Hybridization or cultivar development programs using the above genotypes should be carried out to create promising machine harvestable cultivars.

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APPENDIX - A

Table - Meteorological data (Monthly): 2020-21

Month	MAXT (°C)	MIN T (°C)	Total RF (mm)	RH I (%)	RH II (%)	VP I (mm)	VP II (mm)	WS (kmph)	EP (mm)	SS (hr)
Nov-20	30.80	15.90	0.40	85.00	33.00	13.00	10.90	3.00	102.80	7.80
Dec-20	29.30	12.00	0.00	87.00	31.00	10.10	9.00	2.00	93.20	5.40
Jan-21	30.20	13.90	4.60	81.00	31.00	10.50	9.40	2.50	99.90	4.00
Feb-21	31.00	12.90	2.40	79.00	27.00	9.80	8.50	2.70	114.20	7.60
Mar-21	36.21	18.75	7.6	64.87	21.70	11.71	9.10	3.69	184.10	7.12
Apr-21	39.60	22.80	1.00	53.00	19.00	13.10	10.00	4.80	238.50	7.20

APPENDIX - B

Mean performance of thirty six genotypes for twelve yield, yield attributing and machine harvesting traits during Rabi 2020-21

S. No.	Entry	DTF	DTM	HOFP	PH	NP	NSB	NSP	NPP	BY	HI	HSW	PLYG
1	RSGD-7714	58	96	21.80	42.47	2.40	8.20	1.40	33.07	14.53	49.43	16.00	646.33
2	PBC 582	63	97	27.60	50.27	2.73	11.73	1.33	44.73	19.40	52.89	25.67	718.00
3	NBeG 1267	62	98	21.93	41.80	2.20	10.13	1.00	37.73	14.33	59.04	23.33	555.00
4	GL 15003	55	107	26.40	47.80	1.87	8.13	1.00	29.53	10.00	43.52	14.00	394.00
5	BG 3062	65	105	27.00	58.07	2.60	10.67	1.00	67.67	30.00	47.81	22.00	489.67
6	GJG 1913	64	98	28.13	53.13	2.67	5.80	1.47	37.20	16.53	59.54	24.33	876.00
7	BG 4028	55	105	30.60	61.67	1.93	8.27	1.20	32.53	19.53	47.83	31.33	412.00
8	IG 2020-15	66	102	34.60	66.07	1.67	5.73	1.00	29.80	17.00	52.05	35.33	605.00
9	PG 252	65	110	30.07	54.40	1.93	8.93	1.67	30.07	16.00	42.20	20.67	479.67
10	RKGM 20-1	64	107	22.60	41.47	1.93	11.07	1.00	45.20	18.67	57.23	29.33	581.33
11	IG 2020-16	64	94	23.53	58.07	1.93	3.80	1.13	21.80	8.60	55.61	25.00	545.00
12	RVSSG-97	67	95	32.93	59.33	1.67	4.07	1.00	20.80	11.00	50.44	30.33	487.67
13	Phule G	71	108	37.47	67.80	2.67	13.67	1.13	45.53	25.93	41.73	30.00	314.00
14	RLBGMHG-3	65	106	30.73	59.33	1.80	9.20	1.47	42.40	24.00	55.52	30.67	506.67
15	ICCV 191612	57	102	38.13	61.53	2.13	10.53	1.20	32.40	16.40	53.51	27.00	554.67
16	RSGD-834	59	101	23.53	42.40	2.53	7.73	1.33	33.47	11.13	53.45	18.67	628.67
17	JG 16	62	101	20.93	41.73	2.47	9.60	1.13	64.73	20.87	49.54	18.00	750.33
18	PG 251	70	109	25.64	55.27	2.80	13.51	1.00	51.20	16.93	25.88	10.67	59.33

DTF = Days to 50% flowering; DTM = Days to maturity; HOFP = Height of 1st pod; PH = Plant height (cm); NPB = No. of primary branches; NSB = No. of secondary branches; NPP = No. of pods/plant; NSP = No. of seeds/pod; BY = Biological yield (g); HI = Harvest index (%); HSW = Hundred seed weight (g); PLYG = Plot yield (g).

S. No.	Entry	DTF	DTM	HOFP	PH	NPB	NSB	NSP	NPP	BY	HI	HSW	PLYG
19	H 13-03	54	102	29.87	57.88	1.95	7.67	1.07	49.73	16.00	50.26	20.00	562.00
20	IPC 2017-141	51	106	33.73	59.20	1.67	5.47	1.27	26.87	12.07	40.21	22.67	499.67
21	ICCV 191608	61	104	34.93	68.20	2.13	9.60	1.20	52.53	28.00	49.70	33.33	517.67
22	Phule G 191616	64	108	31.87	62.80	3.20	15.20	1.07	64.00	26.20	49.74	22.67	587.67
23	Phule G 0405	68	109	22.60	46.33	2.33	13.27	1.00	46.87	18.07	55.82	21.67	507.33
24	JG 24	67	110	38.40	62.40	2.20	9.60	1.13	30.53	18.87	46.91	33.33	650.67
25	RKGM 20-2	64	104	26.13	49.60	1.87	9.27	1.13	25.53	11.53	53.51	25.67	646.33
26	GL 117020	64	102	32.93	58.20	2.73	6.53	1.47	36.20	16.40	57.88	28.00	562.00
27	IPCB 2015-132	68	108	33.47	58.53	1.93	7.47	1.27	27.67	8.67	41.52	13.67	454.33
28	H 07-120	67	109	32.00	56.80	2.40	9.87	1.00	27.60	8.87	32.41	11.00	475.00
29	Phule Vikram	61	111	27.00	55.00	2.20	9.80	1.13	50.87	20.73	48.09	23.00	496.33
30	JG 2020-57	65	102	22.27	42.07	2.13	8.33	1.00	28.67	8.27	49.09	16.00	605.00
31	PBC 574	61	104	31.93	59.73	2.20	8.87	1.00	27.60	19.67	50.60	24.00	719.33
32	RVSSG-96	72	102	25.40	45.27	1.93	8.07	1.53	28.60	8.53	47.08	13.33	418.67
33	BG 4027	61	106	24.00	59.93	1.87	11.87	1.27	71.80	34.93	42.40	23.67	357.33
34	IPC 2017-253	73	110	39.00	68.80	1.87	10.67	1.13	21.93	16.33	34.72	20.33	433.00
35	RLBGMH-4	66	109	34.87	69.13	2.20	10.47	1.33	35.93	28.73	37.93	29.67	633.00
36	GJG 1916	61	104	36.40	65.20	1.80	7.67	1.40	37.13	16.60	49.42	27.67	705.33

DTF = Days to 50% flowering; DTM = Days to maturity; HOFP = Height of 1st pod; PH = Plant height (cm); NPB = No. of primary branches; NSB = No. of secondary branches; NPP = No. of pods/plant; NSP = No. of seeds/pod; BY = Biological yield (g); HI = Harvest index (%); HSW = Hundred seed weight (g); PLYG = Plot yield (g).

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Higher Secondary	2014	Sri Chaitanya Educational Institutions (A.P)
B.Sc. (Agriculture)	2018	AC&RI, TNAU, Coimbatore (T.N)
M.Sc. (Agriculture)	Appearing	COA,IGKV Raipur(C.G.)

Professional Experience (if any):

RAWEP (Rural Agricultural Work Experience Program)

Member of any Professional Society (if any)

Awards/ Recognition -

Publications (if any): In numbers only

M.H. Datta

Signature