GENETIC VARIABILITY AND STABILITY ANALYSIS FOR YIELD AND ITS CONTRIBUTING TRAITS IN CHICKPEA (*Cicer arietinum* L.)

THESIS

Submitted to
Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola
in partial fulfilment of the requirements
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By

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Enrolment Number –KK/908 **2019**

DECLARATION OF STUDENT

I hereby declare that the experimental work and its interpretation of the thesis entitled **"GENETIC VARIABILITY AND STABILITY ANALYSIS FOR YIELD AND ITS CONTRIBUTING TRAITS IN CHICKPEA (*Cicer arietinum* L.)''** or part thereof has neither been submitted for any other degree or diploma of any University, nor the data have been derived from any thesis / publication of any University or scientific organization. The source of materials used and all assistance received during the course of investigation have been duly acknowledged.

Place: Akola (**BANKAR SACHIN GOVINDRAO)**

Date: / / 2019 Enrolment No. KK-908

CERTIFICATE

This is to certify that thesis entitled **"GENETIC VARIABILITY AND STABILITY ANALYSIS FOR YIELD AND ITS CONTRIBUTING TRAITS IN CHICKPEA (*Cicer arietinum* L.)''** submitted in partial fulfilment of the requirement for the degree of **Master of Science in Agriculture (Agricultural Botany)"** of Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola is a record of bonafide research work carried out by **Bankar Sachin Govindrao** under my guidance and supervision.

The subject of the thesis has been approved by the Student's Advisory Committee.

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(C) List of Abbreviations

%	-	Per cent
/	-	Per
C.D.	-	Critical Difference
C.V	-	Critical Variance
GCV	-	Genotypic Coefficient of Variation
PCV	-	Phenotypic coefficient of variation
EGA	-	Expected Genetic advance
Cm	-	Centimetre
d.f.	-	Degree of freedom
Deptt.	-	Department
Dr. PDKV	-	Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola
e.g.	-	Example gratia (for example)
et al.	-	Et alia (and others)
etc.	-	Etcetra
Fig.	-	Figure
g	-	Gram
ha	-	Hectare
i.e.	-	That is
M.Sc.	-	Master of Science
FAO	-	Food and Agricultural Organization
SE	-	Standard error
SE(d)	-	Standard error of difference
Viz.	-	Videlicet (namely)
J	-	Journal
σ2	-	Variance
No.	-	Number

(D) THESIS ABSTRACT

a)	**Title of the thesis**	:	**GENETIC VARIABILITY AND STABILITY ANALYSIS FOR YIELD AND ITS CONTRIBUTING TRAITS IN CHICKPEA (*Cicer arietinum* L.)**
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ABSTRACT

The present investigation entitled "**Genetic variability and stability analysis for yield and its contributing traits in chickpea (*Cicer arietinum* L.)''** was undertaken with view to estimate extent of genetic variability among the chickpea genotypes and estimate stability for yield and its components. Twenty genotypes were sown on three different environments (Akola, Buldana, Nagpur) in a Randomized Block Design, with three replications for measuring stability of genotypes for different characters. The data was subjected to statistical analysis as per Eberhart and Russell (1966) model. The ANOVA reveled highly significant difference among the all genotypes for all the characters studied indicating the presence of substantial amount of genetic variability. The character number of pods per plant showed medium GCV (14.88%) accompanying with medium broad sense heritability (47.70%) and higher expected genetic advance (21.17%) values indicating thereby amount of variation in aforesaid character. The higher magnitude of PCV as compared to GCV in respect of characters, number of pods per plant, seed yield per plant, indicated the greater effect of environment on these characters. The high heritability estimate was showed in protein content (89%) followed by medium heritability (40-60%) for the characters 100 seed weight (49.90%), number of pods per plant (47.70%) and number of seeds per pod (47%). This indicated that these characters are may be governed by non-additive component of variation which is non fixable, heterosis breeding can be fruitfully exploited in improving these characters. The character seed yield per plant and number of secondary branches per plant showed medium GCV (12.24 and 10.73) accompanying with medium heritability (37.30 and 37.40) and medium expected genetic advance (15.41 and 13.53). The character days to maturity showed low GCV (1.63%) accompanying with low heritability (20%) and low expected genetic advance (1.51%).

In general, genotypic variances were found significant for, days to 50% flowering, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight, seed yield per plant and protein content, except days to maturity when tested against G X E interaction. Environmental variance was significant for all the studied characters except days to 50% flowering, protein content. Genotype x environmental interactions was non-significant for all the traits. Linear

components of G X E interaction was found significant for the characters viz., days to 50% flowering and 100 seed weight (g) whereas pooled deviation (nonlinear component) was found significant for the traits viz., days to maturity, number of secondary branches per plant, number of pods per plant, number of seeds per pod, seed yield per plant. Environment (linear) effects were also significant for all the studied characters except protein content.

The most of genotypes showing wider adaptability for different characters studied viz., AKG-1303, AKG-1401, Phule G-0405 and BDNG-797 recorded average stability for days to 50 % flowering. The genotypes AKG-1303, AKG-1401, BDNG 2015-9, Phule G-0819-43, Phule G-15109, Phule Vikram and JAKI-9218 recorded average stability for plant height. The genotypes viz., AKG-1401, AKG-1506, BCP-60, Phule G-0819-43, Phule G-0405, AKRG 1701 and AKRG 1702 recorded average stability for maturity. The genotypes viz., BCP-60, Phule G-15109, AKRG 1701, BDNG-797, Vijay, Phule Vikram, PDKV Kanchan and JAKI-9218 recorded average stability for primary branches per plant. The genotypes viz., AKG-1504, Phule G-15109, BDNG-797, Vijay, PDKV Kanchan and JAKI-9218 recorded average stability for secondary branches per plant.

The genotype viz., AKG-1401, Phule G-13107, AKRG-1702, BDNG-797 and JAKI-9218 recorded average stability for number of pods per plant. The genotypes, Phule G-0405, AKRG 1701, Digvijay and Phule Vikram recorded average stability for seeds per pod. The genotypes AKG-1401, AKG-1506, BDNG 2015-9, BCP-60, Phule G-13107, Phule G-15109, AKRG 1702, and JAKI-9218 recorded average stability for 100 Seed weight. The genotypes AKG-1401, AKG-1506, BCP-60, Phule G-15109, AKRG 1701, AKRG 1702, PDKV Kanchan and JAKI-9218 recorded average stability for seed yield per plant. The genotypes AKG-1506, BDNG 2015-6, Phule G-15109, Phule G-0405, AKRG 1702, BDNG-797, Vijay, Digvijay and PDKV Kanchan recorded their average stability for protein content (%).

The above average stability was observed for the genotypes Phule G-0405 for plant height, genotype BDNG 2015-6 for 100 seed weight, genotype AKG-1303 for the character protein content (%). The below average stability was observed for the genotype Phule G-13107 for number of primary branches per plant, genotype BDNG 2015-9 for seed yield per plant.

CHAPTER I

INTRODUCTION

1.1 Background Information

Chickpea (*Cicer arietinum* L.) is the third most important food legume in the world. It is grown in more than 45 countries in the world. India is the largest producer and rank first in area and production, sharing 75% of total world production. Pulses constitute an important component in Indian agricultural economy and nutrition since centuries. The pulse crops are also called as grain legumes and have been valued as nutritious and protein rich food, fodder and feed. They have a pivotal role in agriculture, on account of the ability to fix atmospheric nitrogen by symbiotic association with microbes and it helpful to the enrichment of soil substantially. The deep penetrating root system enables the pulse crop to utilize the limited available moisture more efficiently and maintain the soil structure for sustainable productivity over years. The farmers have therefore chosen the pulse crop under highly diversified condition in India. Pigeon pea, horsegram and mothbean are example of *kharif legumes*, whereas chickpea, lathyrus, lentil is the *rabi* legumes known for ability to withstand under moisture stress condition.

Chickpea (*Cicer arietinum* L.) is one of the premier pulse crop of Indian subcontinent. India is the largest chickpea producer as well as consumer in the world. Chickpea is cultivated in diverse agro-climatic conditions in India and grown under both rainfed and irrigated conditions. Majority of the area is under rainfed farming and is one of the cause of low productivity in the country. Chickpea remarkably predominates among other pulse crops in terms of both area and production. The year 2017-18 marked significant increase in area under chickpea. In world it is grown on 14.54 million ha area with total annual production of chickpea is 14.78 million tonnes and average productivity of 968 kg/ha during 2017-18 (FAO Stat. 2017-18). In India it is grown on 10.56 million ha area with total annual production of chickpea is 11.23 million tonnes and average productivity of 1063 kg/ha during 2017-18. In Maharashtra it is grown on 20.00 lakh ha area with total production of 17.61 lakh tonnes and average productivity of 1018 kg/ha during 2017-18 (DAC, GOI, New Delhi). Further, in Vidharbha region of the Maharashtra, it is grown on 6.30 lakh ha area with total production of 5.51 lakh tonnes and average productivity of 810 kg/ha during 2016-17 (Anonymous, 2016-17).

Chickpea (*Cicer arietinum* L.) is a self-pollinated crop belonging to the Leguminaceae family of the Tribe Cicereae. Chickpea is the only cultivated species under the genus '*Cicer*' and has 2n = 2x = 16 chromosomes with relatively small genome size of 738.09 Mbp (Varshney *et al.* 2013). The chickpea also known as Bengal gram, *chana* and in Marathi it also called as *Harbhara*. The plant grows between 20-50 cm height and has smaller feathery leaves on either side of the stem. It has pink or white flowers with blue, violet or pink veins. Chickpea need a subtropical or tropical climate with more than 400 mm of annual rain.

There are two main kinds of chickpea, Desi and Kabuli. Desi, which has small, darker seeds and a rough seed coat, cultivated mostly in Indian subcontinents, Ethiopia, Mexico and Iran. Desi (meaning country or local) is also called as Bengal gram or *Chola*. Desi chickpeas have markedly higher fiber content than Kabulis and hence a very low glycemic index which may make them suitable for people with blood sugar problems. Kabuli, which has white or milky white colour, larger seeds and smoother seed coat, mainly grown in southern Europe, Northern Africa, Afghanistan, Pakistan, Turkey and India. Kabuli (meaning from Kabul) is also called as *Safed Chana*.

Most of the pulse crops add about 0.5 to 1.5 tonnes of organic matter through falling of leaves during maturity and also fix, on an average, 61-225 Kg nitrogen per hectare. The nitrogen fixing ability of pigeonpea is the highest 225 Kg/ha followed by chickpea 103 Kg/ha, lentil 101 kg/ha, peas 65 Kg/ha and mungbean 61 Kg/ha (Elkan, 1992).

Chickpea provides high quality protein to the people. People in the developed countries consider it as a health food. The chickpea is a good source of protein (24.6%), carbohydrate (64.6%) and vitamins (Abu-Salem and Abou, 2011). It also provides calcium, magnesium, potassium, phosphorus, iron, zink and manganese (Ibrikci *et al.,* 2003). This food legume has diversified uses, and presently as many as 140 countries are importing chickpea (Gaur *et al.,* 2012). It is mostly used in the form of '*Dal*'. About 75 per cent of the total production is consumed as '*Dal*' in India.

Besides high protein content, pulses are also rich source of certain essential amino acids, which are lacking in cereals. On the other hand, some of the sulphur containing essential a mino acids, which lack in the pulses, are abundantly present in the cereals. Therefore, when we get adequate quantity of mixed food (cereals and pulses together) in our diet, the calories as well as protein requirements are fully met. By virtue of these characteristics, pulses have attained much importance in recent years because of emphasis on improvement in diet to combat malnutrition in developing countries.

The per capita availability of the pulses has declined from 64 g/capita/day (1951-56) to about 34 g/capita/day (1998-99) as against the FAO/WHO's recommendation of 80 g/capita/day (Asthana and Chaturvedi, 1999). If we take into account the total protein nutrition derived from other protein sources such as food grains, milk and its products, egg, fish meat etc., 55g/capita/day requirement of pulses may be the realistic target. It is estimated that country's population will touch nearly 1350 million by 2020 AD and country would then need a minimum of 30.3 million tonnes of pulses (Asthana and Chauturvedi, 1999). Also as per Indian Council of Medical Research (ICMR) per day per capita requirement of pulses, cereals and oilseed is 80g, 435g and 125g, respectively. However, at present hardly 43.7% requirement of pulses is fulfilled.

Mature chickpeas can be cooked and eaten cold in salad. Cooked in stews, ground into flour called gram flour (also known as chickpea flour and *besan* and used primarily in Indian cuisine). Chickpeas are used to make curries and one of the most popular vegetarian foods in India, Pakistan, Bangladesh and the UK. Green leaves/twigs of a chickpea are used in preparing a nutritious vegetable in the countries of South Asia. These are also used as high protein fodder mixed with cereal leaves.

Chickpea stover is fed to the cattle/goats as nutri-rich supplement to their major cereal fodder in the lean season.

1.2 Importance of study

Crop variety developed should show stable performance under different environments, especially in India where wide range of environment is prevailing. It is a need to develop genotype with high degree of adaptability levels over a wide range of ecogeographical conditions for successful exploitation of its inherent potential. A variety is said to be stable which can adjust its phenotypic and genotypic status in response to changing environment.

Genotype x environment interaction is supposed to be one of the genetic parameter responsible for phenotypic stability and adaptation. There are many investigations done in the past and continued till today with a view to identify a stable and adaptable genotype for different yield contributing characters.

Genetic Variability is one of the most important characteristics and distinctive feature of any population. A plant population with higher variability provides greater opportunity for improvement. Hence, it is essential to study and utilize the existing variability in population, variance is the amount of variation present among the member of the population. Genetic variation for traits is important in breeding programms and for selecting desirable genotypes.

The major chickpea crop area is grown under rainfed condition in Maharashtra, where sowing is carried under residual soil moisture. Under such situation suitable sowing period is last week of September to first week of October for obtaining better yield from rainfed crop. For optimum sown irrigated crop suitable date is 20th October to 10th November. However, some farmers use to sow crop in the month of December or even later. In this situation, it is very important that, the genotype should perform very well or it should show stable performance during these sowing periods. Hence, there is enough scope to improve the productivity of this crop by developing stable, high yielding, disease and pest resistance, drought tolerant varieties suitable for different environments.

1.3 Objective of study

Therefore, the present investigation on "Genetic variability and stability analysis for yield and its contributing traits in chickpea (*Cicer arietinum* L.)" was undertaken with the following objectives:

1. To estimate extent of genetic variability among the chickpea genotypes.
2. To estimate stability for yield and its components.

1.4 Hypothesis

The genetic variability study is helpful to estimate the suitable parameter of variation such as heritability estimates and expected genetic advance for the individual characters. Variability is therefore the key factors, which determine the amount of progress expected from selection.

Stability of cultivar refers to its consistency in performance across environments and is affected by the presence of G X E interaction. In the presence of significant G X E interaction, the stability parameters are estimated to determine the superiority of individual genotype across the range of environments. A specified genotype does not exhibit the same phenotypic expression under different environments and different genotype responds differently to a specified environment. Stability is the ability of a certain variety to maintain stable yield under changing environmental conditions and assessed through several stability parameters. Among them, regression coefficient (bi) and deviation from regression (S^2di) proposed by Eberhart and Russell (1966) have extensively been used in multi-environment trials. Therefore, present investigation carried out for identification stable genotypes of chickpea.

1.5 Scope and limitations of the study

Genetic variability is the basic requirement for any selection. Unless and until there is large amount of variability present in the population, the breeder has little scope for selection. Genetic association play significant role to study inter-relationship among the characters.

Stability analysis is an important tool for plant breeders in predicting response of various genotypes over changing environments. Thus a proper understanding of the magnitude and nature of G X E interactions and stability of the complex traits like yield and yield components in chickpea would be of great help. However, estimation of mean performance and environmental index is not independent and there is a combined estimation of sum of squares for environments and interactions, which lead to the limitation of the present study.

The yield is very complex character and depends upon a numerous genetical factors interacting with environment. The environment has a bearing on the most of the characters which are quantitatively inherited and hence, selection made in field is not reliable. The present study was suggested with scope for identification of stable varieties under different environment is essential for chickpea improvement programme.

CHAPTER II

REVIEW OF LITERATURE

The literature on genetic variability and stability analysis of seed yield and other contributing characters of chickpea *(Cicer arietinum* L.) have been reviewed and presented under different subheadings.

2.1. Genetic variability

2.1.1. Analysis of variance

2.1.2. Coefficients of variation

2.1.3. Heritability

2.1.4. Genetic advance

2.2. Stability analysis

2.1. Genetic variability

2.1.1. Analysis of variance

Analysis of variance is a collection of statistical model and associated estimation procedure use to analyse differences among group means in a sample and it is useful for comparing group means for statistical significance, and It is a parametric statistical technique use to compare datasets. This technique was invented by R. A. Fisher and is thus often refer to as Fisher's ANOVA.

Astereki *et al.* (2015) evaluated twenty-five chickpea genotypes and analysed variances for genotypic differences, and were found significant for seed yield, number of days to flowering, days to maturity, flowering period, canopy height, number of pods per plant, biological yield and harvest index.

Srivastava *et al.* (2017) reported that analysis of variance revealed significant differences among the genotypes for all the characters studied.

Arora *et al. (*2018) in the analysis of variance with respect to yield and its contributing characters of chickpea clearly indicated that the mean sum of square due to genotype were highly significant for all the studied character viz., days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seed per pod,100-seed weight (g), seed yield per plant.

Barad *et al.* (2018) studied fifty diverse *Kabuli* chickpea genotypes sown under timely and late sowing conditions. Analysis of variance revealed significant differences among the genotypes for all the characters viz., 100-seed weight, seed yield per plant, days to 50% flowering, days to maturity, reproductive phase duration, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seed per pod,100-seed weight (g).

Kishor *et al*. (2018) evaluated forty chickpea genotypes and the analysis of variance revealed highly significant differences among genotypes for all the characters viz., days to 50% flowering, days to maturity, 100-seed weight, plant height, number of seeds per plant, lower branch height, number of pod per plant, biological yield per plant, seed yield per plant, number of primary branches per plant and harvest index.

Singh *et al.* (2018) in variability studies observed highly significant difference among genotypes for all the characters indicating the presence of adequate amount of genetic variability among the genotypes. days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod,100-seed weight (g), biological yield per plant (g), harvest index (%) and seed yield per plant.

Thakur *et al.* (2018) reported that analysis of variation shown highly significant differences among the genotypes for all the character studied viz., days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seed per pod,100-seed weight (g), in hundred genotypes of chickpea.

2.1.2. Coefficients of variation

Genetic variability is a measure of the tendency of individual genotypes in a population to vary from one another. The variability of a trait describes how much that trait tends to vary in response to environmental and genetic influences. genetic variability in a population is important for biodiversity, because without variability, it becomes difficult for a population to adapt environmental changes. Hence variability is the most key aspect of any research for a breeder, amount of which determining the extent of sources of selection.

Various parameter of genetic variability are mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad sense habitability and genetic advance. The idea of partitioning of variance was given by Fisher (1950), further many workers also suggested various technique for estimation of components of variation.

Sharma *et al.* (1990) recorded high genotypic coefficient of variation for number of pods per plant, seed yield per plant, 100-seed weight and number of branches per plant in chickpea.

Tripathi and Arora (1991) observed high phenotypic coefficient of variation for biological yield and seed yield per plant in chickpea.

Mishra *et al.* (1994) studied genetic parameters in thirty-two genotypes of chickpea and reported high range and coefficient of variation for number of pods per plant, plant height, seed yield per plant and number of branches per plant.

Rao *et al.* (1994) evaluated sixteen bold seeded chickpea genotypes for developmental traits and reported maximum variability for seed yield followed by harvest index and biological yield.

Chand (1999) studied genetic divergence among forty-nine genotypes of chickpea was estimated for seven quantitative traits. The genotypes were grouped into eight clusters.

Nimbalkar (2000) observed in chickpea that genotypic and phenotypic coefficients of variability were highest for 100-seed weight and lowest for days to maturity.

Arora and Jeena (2001) evaluated forty genotypes of chickpea for genotypic and phenotypic coefficient of variation for eighteen quantitative characters and found the highest genetic coefficient of variation in 100-seed weight, followed by primary branches per plant and seeds per plant.

Jeena and Arora (2001) evaluated ninety-six chickpea genotypes and found high genotypic and phenotypic coefficient of variation for 100-seed weight.

Kumar *et al.* (2001) evaluated twenty-six genotypes for genotypic and phenotypic coefficient of variation for twelve quantitative characters, in which pods per plant exhibited the highest amount of genetic variability, followed by secondary branches per plant, seed yield per plant, 100-seed weight primary branches per plant and number of seeds per plant.

Ali *et al.* (2002) recorded maximum genetic coefficient of variation for secondary branches per plant, total weight of a plant, pods per plant and seed yield per plant which reflects that these traits response to selection.

Altnbas (2002) tested newly developed eight *kabuli* chickpea (*Cicer arietinum*) lines (1-8) and two cultivars (Ispanyol and Men-92) in Turkey, during 1997-98, 1998-99 and 1999-2000, to study the genotypic variability.

Parshuram *et al.* (2003) studied sixteen chickpea cultivars and observed that phenotypic coefficient of variation ranged from 4.01% for days to maturity to 58.62% for number of seeds per plant. The genotypic coefficient of variation was low for all characters except plant height and number of leaves per plant indicating low environmental impact for both characters.

Ajinder *et al.* (2004) studied genetic variability, heritability and genetic advance for grain yield and its components in thirty genotypes of *desi* chickpea under normal and late sown conditions. The results showed that 100-seed weight had comparable phenotypic and genotypic coefficients of variation under both sowing conditions.

Usmani *et al.* (2005) evaluated thirty genotypes and recorded high phenotypic coefficient of variation for pod bearing length, seed yield per plant, plant height, harvest index (%) and number of pods per plant showed high genotypic coefficient of variation.

Durga *et al.* (2007) studied genetic variability on yield and yield components of chickpea and revealed maximum genotypic coefficient of variation for branches per plant, followed by pods per plant and seed yield.

Thakur and Sirohi (2008) evaluated genetic variability, heritability, genetic advance for yield and nine other economic traits in chickpea. The study revealed considerable genetic variability among the genotypes for all the traits. Genotypic and phenotypic coefficients of variation were more or less similar for all the characters. phenotypic and genotypic coefficients of variation were high for seed yield per plant, biological yield per plant, pods per plant and 100-seed weight.

Vaghela *et al.* (2008) evaluated fifty genotypes of *Kabuli* chickpea (*Cicer arietinum* L.) and estimated high genotypic coefficient of variation for seed yield per plant and number of pods per plant.

Bhavani *et al*. (2009) evaluated twenty-seven genetically diverse genotypes of chickpea and noticed higher estimates of genotypic coefficient of variation(GCV) and phenotypic coefficient of variation(PCV) for seed yield per plant, number of primary branches per plant, number of seeds per pod, number of pods per plant, 100-seed weight and harvest index.

Tomar and Singh (2009) evaluated forty-five genotypes of chickpea and observed maximum genotypic and phenotypic coefficient of variation were found maximum for number of seeds per plant.

Alwani *et al.* (2010) evaluated the differences between genotypic (GCV) and phenotypic (PCV) coefficient of variability were very small. The results recommended to selection line M-20 that was the desirable line for both seed yield per plant (33g to 40g) and protein content (22.17% to 24.72%) as compared to other lines.

Sreelakshmi *et al.* (2010) studied genetic variability on yield and yield components of chickpea and found high genotypic and phenotypic coefficient of variation for seed yield, number of pods per plant and number of fruiting branches per plant, indicated additive gene action for these traits.

Akhtar *et al.* (2011) estimated high phenotypic coefficient of variation for days to flowering, days to maturity, plant height and seed yield than genotypic coefficient of variations, which means that the expression of these traits is more influenced by environmental effects. It was, suggested that the grain yield could be improved by using the 100-seed weight and number of pods per plant as selection criterion in chickpea.

Babbar *et al.* (2012) evaluated forty-four promising lines of chickpea under late sown condition. The maximum genotypic coefficient of variation was noticed for total number of seeds per plant and total number of pods per plant.

Shweta *et al.* (2013) observed phenotypic and genotypic coefficients of variation were found maximum for seed yield per plant followed by pods per plant and seeds per pod whereas minimum for days to maturity.

Kuldeep *et al.* (2014) evaluated hundred advance breeding lines of chickpea under heat stress condition and found high estimates of genotypic and phenotypic coefficient for seed yield per plant followed by 100-seed weight, harvest index, number of effective pods per plant, total number of pods per plant and number of secondary branches.

Parhe *et al*. (2014) evaluated fifty-one genotypes of chickpea. Seed yield per plant had maximum phenotypic and genotypic coefficient of variation followed by 100-seed weight.

Desai *et al.* (2015) observed highest genotypic coefficient of variation for 100-seed weight followed by number of pods per plant, seed yield per plant and number of seeds per pod.

Dhuria and Babbar (2015) observed high genotypic coefficient of variation and phenotypic coefficient of variation for height of first fruiting node, number of effective pods per plant, number of seeds per plant and seed yield per plant.

Alka Dev *et al.* (2017) observed harvest index recorded maximum phenotypic range of variation followed by 100-seed weight, number of pods per plant, plant height and number of nodules per plant. The high to moderate genotypic coefficient of variation and phenotypic coefficient of variation was observed for harvest index, plant height, 100-seed weight and number of seeds per pods, seed yield per plant, number of secondary branches per plant and number of primary branches per plant.

Astereki *et al.* (2015) evaluated phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for seed yield, days to flowering, flowering period, canopy height, number of pods per plant, biological yield and harvest index.

Tiwari *et al.* (2017) evaluated thirty diverse genotypes of chickpea and observed the higher genotypic and phenotypic coefficient of variation were recorded for days to first flowering, number of branches per plant, plant height, days to maturity, number of pods per plant, 100seed weight, seed yield per plant.

Arora *et al.* (2018) studied fifty genotypes of *kabuli* chickpea. Maximum variability was recorded for number of pods per plant and minimum for number of days to maturity. There was close agreement between genotypic coefficient of variation and phenotypic coefficient of variation for number of days to flowering, days to maturity and 100-seed weight.

Kishor *et al*. (2018) recorded high phenotypic and genotypic coefficient of variation for number of pods per plant followed by biological yield per plant, number of seeds per plant, seed yield per plant, number of primary branches par plant, 100-seed weight.

Babbar and Tiwari (2018) estimated coefficients of variation for different character in forty genotypes of chickpea and reported the biological yield showed the highest phenotypic and genotypic coefficient of variation (53.8% and 53.2%), followed by seed yield per plant (51.9% and 51.2%), effective pods per plant (44.6% to 43.6%) and total number of pods per plant (43.2% and 41.2%). Whereas, plant height (29.3% and 29.1%) had moderate phenotypic and genotypic coefficient of variation while, other traits viz. harvest index, 100-seed weight, days to maturity, days to flower initiation, days to 50% flowering, days to pod initiation and number of seeds per pod exhibited low phenotypic and genotypic coefficient of variation.

Barad *et al.* (2018) studied fifty diverse *Kabuli* chickpea genotypes and reported highest genotypic coefficient of variation and phenotypic coefficient of variation for both of the sowing condition for seed yield per plant, number of primary branches per plant and 100-seed weight. The high genotypic coefficient of variation indicated the presence of wide variation for the characters under study to allow selection for individual traits.

Johnson *et al.* (2018) recorded high values of phenotypic coefficients of variation for secondary branches per plant, pod per plant, hydration index, seed yield per plant, hydration capacity seed per plant, biological yield, number primary branches per plant, Swelling index in all three environments E1, E2 and E3.

Singh *et al.* (2018) observed highest genotypic coefficient of variation for seed yield per plant followed by harvest index, number of pods per plant, 100-seed weight and plant height.

Thakur *et al*. (2018) estimated coefficients of variation for different characters in hundred genotypes of chickpea and reported the high phenotypic coefficient of variation and genotypic coefficient of variation were observed for seed yield per plant followed by number of secondary branches per plant, 100-seed weight, number of seeds per plant, number of pods per plant and number of primary branches per plant, respectively indicating that these traits were main yield contributing characters.

2.1.3. Heritability

Heritability in broad sense is the ratio of genotypic variance to phenotypic variance or total variance. It is calculated from total genetic variance which is consists of additive, dominance and epistatic variances. It is good index of the transmission of characters from parents to their off spring.

Sharma *et al.* (1990) evaluated seventy genotypes of chickpea and reported high heritability for days to maturity, plant weight, 100-seed weight and number of branches per plant.

Nimbalkar (2000) observed highest heritability was highest for 100-seed weight and lowest for plant spread.

Jeena and Arora (2001) recorded high heritability for 100-seed weight, followed by primary branches per plant and seeds per plant.

Arshad *et al.* (2003) studied twenty-four genotypes of chickpea and recorded high heritability with low genetic advance of day to 50% flowering, days to maturity and 100-seed weight. High heritability of secondary branches and biological yield coupled with high genetic advance revealed that additive gene effects are important in determining character. Grain yield had positive and significant with plant height, pod per plant, 100-seed weight and biological yield.

Patel *et al.* (2004) evaluated twenty-four chickpea genotypes each of desi, *kabuli* and gulabi types. High heritability coupled with high genetic advance as percentage of mean was found for biological yield per plant in desi chickpea; seed yield per plant, harvest index, biological yield per plant in *kabuli* chickpea. While, number of seeds per plant, seed yield per plant and 50% podding in gulabi chickpea.

Mohammad *et al.* (2005) evaluated eighteen elite genotypes of chickpea and two cultivars for yield and its components in an experiment. High heritability estimates were obtained for 100-seed weight

(97.7%), plant height (96.9%), seed yield (90.9%), total weight (89.8%), pods per plant (88%), seeds per pod (87.1%) and seeds per plant (86.2%).

Saleem *et al.* (2005) studied eighteen elite genotypes and observed high heritability for pods per plant, seeds per plant, 100-seed weight and total weight of plant.

Usmani *et al.* (2005) evaluated thirty genotypes and recorded high heritability for yield contributing traits viz., pod bearing length, seed yield per plant, plant height and harvest index.

Durga *et al.* (2007) noticed high heritability in chickpea for days to 50% flowering and test weight, indicating that improvement is possible through direct selection in respect of these traits.

Sidramappa *et al.* (2008) recorded high heritability for pods per plant, seed yield per plant, seed weight, days to 50% flowering, days to pod initiation and plant height.

Thakur and Sirohi (2008) reported the high heritability coupled with high expected genetic advance for seed yield per plant, biological yield per plant, 100-seed weight, pods per plant and plant height revealed the preponderance of additive gene effects in the expression of these traits.

Vaghela *et al.* (2008) recorded that heritability was higher for all the traits except plant height in chickpea.

Dwevedi and Gaibriyal (2009) evaluate twenty-five genotypes of chickpea and recorded moderate to high degree of heritability.

Tomar and Singh (2009) recorded high heritability in broad sense for all the traits except days to maturity.

Alwani *et al.* (2010) evaluated seven local lines of chickpea and recorded that heritability for protein content varied from (0.83) to (0.93) indicat the presence of a considerable proportion of total variability due to genetic causes.

Akhtar *et al.* (2011) studied twenty advance genotypes of chickpea and recorded that greatest heritability for 100-seed weight and number of pods per plant compared to other characters.

Farshadfar and Sabaghpour (2011) observed that heritability greater for days to maturity to 50% flowering, plant height, number of primary branches and number of secondary branches.

Khan et al. (2011) recorded high heritability for days to 50% flowering followed by biological yield per plant, plant height, 100-seed weight, grain yield per plant and days to maturity.

Khan et al., (2011) estimates high heritability for days to 50% flowering followed by biological yield per plant, plant height, 100-seed weight, grain yield per plant and days to maturity.

Shweta *et al.* (2013) observed that high heritability with high genetic advance as percent of mean for secondary branches per plant, seed yield per plant, 100-seed weight, pods per plant and plant height.

Parhe *et al*. (2014) observed that high magnitude of heritability was recorded for 100-seed weight. High heritability coupled with high genetic advance was observed for number of pod per plant, 100-seed weight, days to 50% flowering and plant height.

Johansan *et al*. (2015) reported high heritability coupled with high genetic advance in characters *viz.,* 100-seed weight, seed volume, hydration capacity seed per plant, hydration index and swelling index in E1, E2, E3 and E4 and pods per plant in E1 and E2. Biological yield per plant in E2, E3 and E4 and primary branches per plant in E2 and E3 and plant height in E3, which indicates that the heritability is due to additive gene action and the selection based on these character may be effective.

Astereki *et al.* (2015) stated that heritability of canopy height, days to flowering and days to maturity was greater than the heritability of the other traits.

Srivastava *et al.* (2017) reported number of pods per plant followed by days to maturity and seed-index exhibited high estimates of heritability (bs) as well as genetic advance.

Tiwari *et al.* (2017) recorded high heritability estimates were found for plant height, 100-seed weight and days to first flowering. Moderate heritability was found for number of pods per plant, number of seeds per pod, days to 80% maturity and low heritability for number of branches per plant, seed yield per plant, plant height. High heritability estimates coupled with high genetic advance were observed for 100-seed weight and days to first flowering.

Arora *et al.* (2018) evaluated fifty genotypes of *kabuli* chickpea and reported highest heritability for 100-seed weight followed by seed yield per plant and number of pods per plant indicated that these characters can be used as the genetic parameters for the improvement and selection of high yielding genotypes in *kabuli* chickpea.

Babbar and Tiwari (2018) evaluated forty genotype and reported high heritability in days of maturity, followed by plant height, days to pod initiation, days to 50% flowering, biological yield, days to flower initiation, seed yield per plant, effective pods per plant, total number of pods per plant, harvest index, 100-seed weight and number of seeds per pod in pooled analysis. Characters showing high heritability coupled with high genetic advance as percentage of mean were biological yield per plant, seed yield per plant and total number of pod per plant in all the three environments and pooled analysis.

Barad *et al.* (2018) observed maximum heritability for 100-seed weight, number of secondary branches per plant, number of primary branches per plant, days to 50% flowering, number of seeds per pod, days to maturity, plant height, number of pods per plant, seed yield per plant and reproductive phase duration.

Johnson *et al.* (2018) observed high heritability estimates coupled with high genetic advance for the characters viz; plant height, number of primary branches per plant, number of secondary branches per plant, pods per plant, biological yield per plant,100-seed weight, seed yield per plant, seed volume, hydration capacity seed per plant, hydration index and swelling index all three environmentsE1, E2 and E3 indicated the role of additive genetic variance in the expression of these characters. Rest of the characters were having moderate to low heritability coupled in high to low genetic advance as percentage of mean indicated the role of non-additive genetic component in their expression.

Kishor *et al*. (2018) estimated high heritability for number of seeds per plant followed by number of pods per plant, 100-seed weight, biological yield per plant, days to 50% flowering, plant height, lower branch height, days to maturity, seed yield per plant, number of primary branches per plant while it was low for harvest index and number of seeds per pod.

Singh *et al.* (2018) studied one hundred five chickpea cultivars and observed high heritability estimates for 100-seed weight, plant height, days to maturity, number of pods per plant, biological yield per plant, harvest index, seed yield per plant and days to 50 per cent flowering.

Thakur *et al.* (2018) estimated heritability for different character in hundred genotypes of chickpea and reported that broad sense heritability was high (>70%) for number of seed per plant followed by days to 50% flowering, test weight, number of pods per plant, plant height, number of secondary branches per plant and seed yield per plant. Remaining trait like harvest index showed low estimates of heritability.

2.1.4. Genetic advance

The improvement in mean genotypic value of selected plants over the parental population is known as genetic advance. It is the measure of genetic gain under selection. Success of genetic advance under selection depends on three main factors i.e. Genetic variability, Heritability and Selection intensity.

Patil and Phadnis (1977) studied eighty one lines of chickpea and reported the highest genetic advance for number of pods per plant and 100-seed weight.

Nimbalkar (2000) recorded highest genetic advance for 100-seed weight and lowest for days to maturity.

Pratap *et al*. (2004) evaluated thirty-eight genetically diverse early maturing chickpea genotypes in four different environments, revealed that seed yield, 100-seed weight and biological yield showed high genetic advance.

Dwevedi and Gaibriyal (2009) recorded high genetic advance was observed for number of pods per pant, harvest index and biological yield.

Tomar and Singh (2009) recorded genetic advance as per cent mean was maximum for seeds per plant.

Vaghela *et al.* (2009) evaluated fifty genotypes of *Kabuli* chickpea (*Cicer arietinum* L.) and found that high genetic advance expressed as a percentage of mean was exhibited by seed yield per plant and number of pods per plant.

Alwani *et al.* (2010) evaluated seven local lines of chickpea and recorded high genetic advance (GA) (51.5 to 62.7) % was achieved for seeds yield per plant. The environmental variance (σ^2e) was very low for days to maturity and protein content.

Srivastava *et al.* (2017) reported seed-index and number of pods per plant exhibited high estimates of genetic advance expressed as percent of mean.

Tiwari *et al.* (2017) observed high estimates of expected genetic advance for 100-seed weight, number of pods per plant, days to fîrst flowering and number of seeds per pod and low for seed yield per plant, number of branches per plant, plant height and days to maturity.

Arora *et al.* (2018) studied fifty genotypes of *Kabuli* chickpea and reported high genetic advance expressed as percentage of mean was observed for number of pods per plant, 100-seed weight and seed yield per plant.

Babbar and Tiwari (2018) evaluated forty genotype and reported that high heritability coupled with high genetic advance as percentage of mean were biological yield per plant, seed yield per plant and total number of pod per plant in all the three environments and pooled analysis.

Barad *et al.* (2018) reported maximum genetic advance as per cent of mean under both sowing conditions for number of primary branches per plant, 100-seed weight, seed yield per plant, number of secondary branches per plant, number of pods per plant, plant height, reproductive phase duration and days to 50 per cent flowering.

Kishor *et al*. (2018) reported that genetic advance as per cent of mean was found highest for number of pods per plant followed by biological yield per plant, number of seeds per plant, seed yield per plant, number of primary branches per plant, 100-seed weight; moderate for lower branch height, plant height, days to 50% flowering; while low for day to maturity, harvest index, number of seeds per pod.

Singh *et al.* (2018) studied 105 chickpea cultivars and observed that high heritability coupled with high genetic advance for 100-seed weight, number of pods per plant, harvest index, seed yield per plant and plant height would be helpful for indirect selection in improvement of seed yield and expected genetic advance as percent of mean was high for seed yield per plant, harvest index, 100-seed weight, number of pods per plant and biological yield per plant.

Thakur *et al.* (2018) estimated the genetic advance as per cent of mean was higher for 100 seeds weight (61.18), number of secondary branches (60.31) followed by seed yield per plant (58.71), number of seeds per pod (56.62) and number of pods per plant (49.30) indicating that direct selection for these traits would be effective for the improvement.

2.1 Concept of stability

A specified genotype does not exhibit the same phenotypic expression under different environments and different genotype responds differently to a specified environment. Stability of cultivar refers to its consistency in performance across environments and is affected by the presence of G X E interaction. In the presence of significant G X E interaction, the stability parameters are estimated to determine the superiority of individual genotype across the range of environments.

G X E interaction in chickpea is the differential response of genotype in a different environmental condition such interaction complicate testing and selection of chickpea genotype breeding program and result in reduce overall genetic DNA in chickpea in general, a genotype is consider stable when its performance across environment does not deviate from the average performance of a group of standard genotypes several method have been propose genotype environment interaction and phenotypic stability. Genotype environment interaction from analysis of variance is partition into heterogeneity of regression coefficient (bi) and the sum of deviation (s^2di) from regressions. Finlay and Wilkinson (1963) defined a genotype with regression coefficient equal to zero (bi=0) as stable, while Eberhart and Russel (1966) define genotype with di=1 to be stable. Most of biometricians consider di as stability parameter rather than bi (Eberhart and Russel,1966). According to the joint regression model, a stable genotype is one with a high mean yield, bi=1 and di=0 (Eberthart and Russell, 1966).

Their for, it is essential to find out phenotypically chickpea genotype for yield, which could perform more or less uniformly under different environmental conditions. As seed yield is complex character and largely depends upon its contributing characters. To breed a stable variety knowledge on the extent of genotype x environment interaction for seed yield and its contributing characters is essential. (shivani and shreelashmi)

Eberhart and Russell (1966) gave the second model of stability of genotype(s) and expressed the phenotypic stability of each variety by two parameters, the slope of the line and the sum of squares of deviations from regression. They define a stable variety as one with unit regression (bi=1) and least deviation from linearity ($S^2di=0$).

Perkins and Jinks (1968) used regression coefficient and the deviation from regression, as the parameters of stability, but regression of genotype x environment interaction obtained on environmental index. Genotype x environment interactions which commonly occur in plant material are of considerable importance in developing improved varieties. Hence in recent years much emphasis has been laid on nature of G X E interactions.

Mehra and Ramanujam (1979) studied stability of forty-six chickpea genotypes in nine environments, at three locations. G x E interaction was found to be highly significant for all characters except seeds per pod. Major portion of G X E interaction was linear and thus predictable; however non-linear interaction was also considerable. The association between adaptability parameters of yield and its component brought out the fact that main component of yield stability was stability of pods number per plant. Two populations from crosses NP-58 x 1707 and NP-1102 x 1713 were found to possess specific adaptability for good environments.

Bahl *et al.* (1980) tested a set of eight chickpea cultivars at eleven locations in peninsular India. The genotypes PG-2, BEG-482 and the check Annigeri were unstable while cultivar, BDN 9-3 was found to possess general adaptability for the peninsular zone.

Mehra *et al.* (1980) studied nature and magnitude of G X E interaction in eleven varieties of chickpea for yield in northern India at sixteen locations. The mean square due to varieties was significant for yield, seed size and plant height. The analysis of stability for yield and three components revealed that BG- 209, Pant-114 and Pant-115 genotypes with wide adaptability.

Singh and Mehra (1980) evaluated twenty genotypes grown at six locations for three yield components and reported that, the genotype x environment interaction was significant for all traits except seeds per pod. The genotypes G-130, T3, Pant 104 and C-468 were stable for pods per plant. The genotype NP53 recorded the highest 100-seed weight but was unstable for seed size.

Singh and Singh (1980) studied stability of component characters in relation with stability of yield. They analysed how the component characters interact. The relationship among predictable behaviour of G X E interaction of component traits and yield revealed that the linear response of yield was positively and significantly associated only with linear response of tillers per plant, whereas yield per spike was positively associated with number of grains per spike and test weight. The evaluation of G X E interaction gives an idea of stability of the population under study.

Jain *et al.* (1984) studied thirty-two chickpea genotypes for yield stability at three locations in Pantnagar district. They observed the existence of high G X E interaction for all characters. Inspite of non-significance of linear component of G X E interactions, few genotypes exhibited bi > 1 or bi < 1 for seed yield per plant, seeds per pod and harvest Index. Accordingly, the genotype showing wide adaptability and specific adaptation were identified, K-4 was found suitable for better management conditions. Pant G-110 showed promise for moderate input management and Kaka, NEC 240 and Pink-2 appeared worthwhile for poor environmental conditions.

Sharma and Maloo (1989) evaluated twenty-one diverse varieties of chickpea for their phenotypic stability in three environments. Genotype x environment interaction component was significant for number of primary branches and grain yield per plant. Linear component was of higher magnitude and significant for all the characters except number of primary branches and days to 50% flowering. The high yielding genotype IC-7840 possessed stability for number of primary branches, while RSG-40 expressed wide adaptability under optimum environments for grain yield per plant.

Bouslama *et al.* (1990) studied yield stability for sixteen genotypes grown at two locations over three consecutive seasons. Linear and non-linear components were found significant for all the traits and non-linear component was higher in magnitude. ILC-6, ILC-191, ILC- 194, ILC-202, ILC-3279 were considered most adaptable.

Baisakh and Nayak (1991) evaluated seventeen genotypes of chickpea to study the stability parameters for yield and maturity with three replications at Bhubaneswar. They reported significant differences for G, E and G X E interaction for grain yield. Linear and non-linear components were predominant in G X E interaction in maturity, whereas non-linear component in yield, secondary branches and days to 50% flowering. ICCC-6 was the most stable genotype for yield and maturity.

Singh *et al.* (1991) studied a set of thirty-nine genotypes of chickpea (*Cicer arietinum* L.) for stability. The September sowing gave the highest average yield (X = 9.91 g) followed by the mid-October sowing (X = 9.36 g). The November sowing gave the poorest yield (X = 6.28 g). The yield performance of genotypes in relation to sowing dates has been discussed and the optimum sowing time suggested was from last week of September to mid-October. G x E interaction was significant for all the characters studied. The linear component of G X E interaction was significant for primary branches per plant and pods per plant. Whereas, the non-linear component was significant for secondary branches per plant, seeds per pod and seed yield per plant. The genotype BGM-418 was found suitable for early or mid-October sowing. The performance of RSG-2 genotype was little influenced by different sowing dates.

Deshmukh *et al.* (1998) measured stability of eight promising genotypes for yield potential under five different environments. The linear component of G X E interaction was significantly higher in magnitude as compared to non-linear components. Pooled analysis revealed significant differences among G, E and G X E interaction for yield. Genotype Vijay showed high stability in yield across the locations followed by PG-82207 and PG- 87227.

Mhase *et al.* (1998) studied stability of sixteen promising chickpea genotypes under rainfed condition in western Maharashtra at five locations. They observed significant interaction between genotypes and environment for grain yield. Linear component of G X E interaction found significant for yield and yield contributing characters and of higher magnitude than nonlinear component. Vijay was found to be most stable genotype, while Chafa and JAKI- 9532 were unstable under rainfed condition. Phule G- 92028, JAKI-9507, ICCV-1 and JAKI-9523 showed above average stability (bi <1 and non-significant S^2di) thus suitable for poor environment. While Vishal and AKG-46 exhibited below average stability (bi > 1 and non-significant S^2di) suitable for favourable environment.

Sood *et al.* (2000) assessed stability of thirty-two genetically diverse chickpea genotypes at Himachal Pradesh under four environments. They observed significant G X E interaction for all the traits under study. Eight genotypes were found promising and stable for seed yield/plant. HPG- 72 having significantly higher yield than the check C-235 was however, suitable for favourable environment only. Among the genotypes HPG-33 was observed to be highly promising and stable for yield and other three important yield components.

Sirohi *et al.* (2001) evaluated twenty-five promising genotypes of chickpea in subtropical zone of the Himachal Pradesh. Both linear and non-linear components of G X E interaction was significant for all the traits and non-linear components was of higher magnitude. Significant differences were observed due to genotype, environments and genotypes x environment interaction for all the traits. Five genotypes viz., HPG-25, HPG-17, HPG-28, HPG-14, HPG-34 was sorted out for high seed yield along with stability for yield and other yield contributing traits on the basis of bi = 1 and S^2di = 0.

Rao and Rao (2004) studied thirty promising genotypes of chickpea for stability parameters. Significant differences were observed due to genotypes, environments and genotype x environment (Linear) interaction for all the traits. However, G x E (non-linear) was found to be non-significant for plant height, harvest index, yield per plant and 100 seed weight. Five genotypes viz., PG-95311, ICCV- 42, ICCV-95334, Pusa390 and Pusa-362 were sorted out stable for yield and other yield contributing traits on the basis of bi = 1 and $S^2di=0$.

Prakash (2005) tested a set of twenty two chickpea genotypes to identify high yielding stable genotype for harsh and erratic environment of Rajasthan. Both linear and non-linear components of G X E interactions were significant for all the traits except primary, secondary branches per plant and grain yield. The chickpea genotypes GNG-1451, GNG-1485 and GNG- 1486 were found stable.

Singh and Sandhu (2006) studied a set of ninety genotypes of chickpea for Genotype × Environment interaction for grain yield and its components over three environments created by different sowing dates. Genotypes and environment were found significantly diverse. The G×E interaction were highly significant for all the characters, except seeds per pod and harvest index.

Malhotra *et al.* (2007) showed that genotype X environment (G x E) interaction plays a significant role in the relative expression of different cultivars in different environment. This study examined the extent and nature of G X E interaction on the yield of chickpea and identified genotypes that can produce high yield in both season. Sixteen sets of genotypes were evaluated at lattice designs at two contrasting locations in Syria and Lebanon in both spring and winter. The dual season lines identified were FLIP98-121C, FLIP97-49C, FLIP97-50C and FLIP97-21C for Syria; FLIP98-90C, FLIP99-37C, FLIP97-56C and FLIP97-131C for Lebanon. They suggested that these genotypes be evaluated in multi-location trials with larger plots to identify the most desirable promising lines suitable for dual season planting.

Bakhsh *et al.* (2008) stated that Genotype X environment interaction (G X E) is a major constraint to identify single superior genotype for a number of variable environments. In order to quantify G X E interaction effect on grain yield in chickpea, 16 chickpea genotypes were studied for grain yield at six locations for two years, using randomized complete block design. The parametric approach and stability parameters indicated that genotypes viz., BRC-1, BRC-220 and BRC-224 were relatively stable in different environments.

Segherloo *et al.* (2008) identified genotypes that have high yield and stable performance across the different locations. The seventeen genotypes were tested at six different research stations for two years in Iran. They identified FLIP94-123C was most stable genotype.

Gupta and Sharma (2009) evaluated fifty-two chickpea genotypes of advance breeding lines of AICRP centres were sown at three different soil temperatures i.e. 24.5^0C, 21.5^0C and 18.5^0C in randomized block design with two replications to know the stability in Phenological, yield and yield attributes over different environments in chickpea. In pooled analysis the mean square due to genotypes, environments and G X E interaction were highly significant for all the traits except G X E interaction of biological yield per plant. Six genotypes viz., GNG-1407, IPC-99-47, GL-99016, BG-2002, BG-2003 and H-98-58 were above average yielder and showed their suitability for favourable environmental condition.

Alwani *et al.* (2010) evaluated seven local lines of chickpea, these lines were grown during two seasons at two different locations. Genotype-environment interaction and genetic parameters were studied for seed yield per plant (g), days to maturity and protein content. The results showed that effect of location (L) and season (E) was highly significant ($P < 0.01$) while the interaction among Locations, Seasons and Genotypes (L X E X G) was not significant ($P > 0.05$).

Asuman *et al*. (2010) identified the stable genotype from nineteen chickpea cultivars grown in arid and semi-arid conditions at three locations for two years 2005-06. Experiment conducted in RBD with three replications. Yield parameter and stability parameter calculated according to Finlay - Wilkinson and Ketata statistical methods. Results showed the Menemen 92 (4) and Izmir 92 (6) were the highest yielding and stable cultivars at three locations during the study period in terms of plant height, pod height and grain yield.

Chaudhary and Haque (2010) evaluated forty-two lines of chickpea including two checks grown during winter season (*rabi*) for three years in twelve environments for stability parameter at Chhota nagpur region. Pooled analysis or variance revealed that, the mean sum of square due to genotypes and environment for primary branches per plant, secondary branches per plant and grain yield per plant (g) found highly significant.

Duzdemir (2011) studied the influence of genotype x environment interactions on phenological characteristics of chickpea. The G X E interactions highly significant for flowering period and vegetation period. Stability analysis was carried out for all characteristics according to Finlay-Wilkinson and Eberhart-Russel models. Stable genotypes for each characteristic were found for two parameters.

Farshadfar *et al*. (2011) studied the effect of genotype (G) and genotype X environment interaction (GE) on grain yield of seventeen chickpea genotypes (*Cicer arietinum* L.) in five different research stations of Iran. Yield data were analyzed using the GGE biplot method. E (environment explained 86.44% of the total (G + E + GE) variation, whereas G and GEI captured 2.48% and 11.08%, respectively. The first two principal components (PC1 and PC2) were used to create a 2-dimensional GGE biplot and explained 56% and 24% of GGE sum of squares (SS), respectively. Collective analysis of the biplots suggests three chickpea mega-environments in Iran. The first mega-environment contained locations: Kermanshah and Gorgan with genotypes G4 and G17. Genotypes G13 and G14 gave the high performance in location Ilam and genotypes G15 gave the high performance in locations Lorestsn and Gachsaran. Genotypes G4, G7, G15 and G17 had the highest mean yield and genotypes G8 and G9 had the poorest mean yield. Also genotypes G1, G4, G7, G10 and G17 were highly stable. On the other hand, Gorgan was the best representative of the overall locations and the most powerful to discriminate genotypes.

Rao (2011) studied twenty-one advanced breeding lines selected from All India Coordinated trials and one local popular variety

“Annigeri’ over three years to identify high yielding stable genotypes. Genotype, environment and G X E interaction variance found to be significant. Genotypic variance over environments was significant for grain yield, pods per plant and 100-seed weight. Both linear and nonlinear components were found to be important for the traits studied. Significant non-linear component for grain yield indicated the predictability of the trait. Of all the genotypes C-506 and C-527 were found to be stable.

Adeel *et al.* (2012) conducted experiment on fifteen genotypes of chickpea for stability of different yield parameters under three diverse environments (Bhakkar, Chakwal and Rawalpindi) in the Punjab province of Pakistan and results showed that genotypes 01067, 3CC-113 and AZC-06 showed stable performance for days to flowering and number of pods per plant. The genotypes CMC211-5 and 3CC-116 depicted stable performance for days to flowering and grain yield per plant. The genotypes Bittal-98 was stable for number of pods per plant and grain yield per plant. The genotype CH24100 was stable for days to flowering and 100 grain weight. The genotype Dasht with the highest grain yield per plant was found stable for 100 grain weight.

Chaudhary *et al.* (2012) studied fifty genetically diverse genotypes for G X E interaction and stability parameters in ten quantitative characters. The linear component of genotype x environment (G x E) interaction was significant for plant height, biological yield and seed yield. The non-linear component of genotype x environment (G x E) interaction was non-significant for all the traits when tested against pooled error.

Parameshwarappa *et al*. (2012) evaluated chickpea germplasm lines representing minicore collection obtained from ICRISAT, Hyderabad (A.P) for assessing genetic variability under three environments. Considerably high variability was observed for most of the productivity related traits in E3 (irrigated 2005-06). Over all the environments, genotype ICC 6279 was found to be early flowering. For seed yield per plant, ICC 13124 was the only top yielder in all the three environments. The genotype ICC 13124 was found promising for earliness, large seed size and high yield per plant in all the environments suggesting that this accession is best suited for both rainfed and irrigated condition during the rabi season.

Shafi *et al.* (2012) evaluated fifteen genotypes for stability of different yield parameters under three diverse environments (Bhakkar, Chakwal and Rawalpindi) in the Punjab province of Pakistan. Varience due to genotypes, environments, genotype x environment and environment (linear) was highly significant for days to flowering, plant height, number of pods per plant, 100 grain weight and grain yield per plant across the environments. By using Eberhart and Russel method of stability analysis genetic differences among diverse cultivars were calculated. The results showed that different genotypes depict significant genotype x environment (linear) response under contrasting conditions. Eight genotypes viz.,01067, 3CC-113, AZC-06, CMC-211-5,3CC-116, Bittal-98, CH-24100 and Dasht were found stable for yield and other yield contributing traits.

Wani *et al*. (2012) evaluated that extent of biological damage in M1 and M2 generations along with genetic variability for yield and yield contributing traits in M3 and M4 generations of chickpea following mutagenesis with EMS and SA. The breeding behavior of the mutants was studied through M1-M4 generations. All the mutagenic treatments brought about dose dependent diminution in seed germination, pollen fertility and seedling growth in M1 and M2 generations. The reduction was more prominent in M1 than in M2 generation, indicating that some sort of recovery mechanism must be operating in the superseding period. A significant increase in mean values for pod bearing branches per plant, pods per plant, 100-seed weight (g) and total plant yield (g) was noticed in both M3 and M4 generations. Moreover, the magnitude of genotypic coefficient of variation, heritability and genetic advance for yield and its contributing components were recorded to be higher in the mutagenized population. Increase in mean values in conjunction with an augment in genetic variability advocate further possibilities of selecting more promising lines with high yield and genetic potential. The mutants isolated can be utilized in future as suitable genetic source material in breeding, genetic and functional genomics research.

Chaturvedi *et al.* (2013) evaluated eighteen elite breeding lines and three released cultivars of chickpea (*Cicer arietinum* L.) and found that pooled analysis of variance revealed that the mean sum of squares for all traits studied were found highly significant (except days to maturity) indicating presence of high amount of variability among the genotypes and environments. Above average stability showed by genotypes IPC 2006-103, IPC 2007–28 and DCP 923 indicated the adaptability of these genotypes to specifically unfavorable environments. As per Eberhart and Russell (1966) model on the basis of mean grain yield, regression coefficient and deviation from regression, genotype IPC 2007–69 was found most suitable for favourable environments, and DCP 92-3 and IPC 2006-112 were specifically adapted to poor environments.

Elham *et al.* (2014) studied that phenotypic stability of yield and yield components of chickpea genotypes an experiment was conducted using a randomized completely block design (RCBD) with three replications under rainfed and irrigated conditions. Combined analysis of variance over stress and non-stress conditions resulted in highly significant differences in the interaction of genotypes X environments. Biplot analysis separated stability indices Ri2 and Pi in single groups (G1) and (G3) respectively. bi, CVi, and grain yield were classified as group 2 (G2), while Sdi2 and Wi2 were clustered as group 1 (G1). As within group variance is minimum, therefore G1 and G2 stability indicators are similar in classifying the genotypes according to their stability under different environmental conditions. Consequently, only one of these parameters would be sufficient to select the stable genotypes in a breeding program. The stability parameters of G2 are desirable for simultaneous selection of yield and yield stability, accordingly based on G2 group of stability parameters (bi, CVi, and grain yield) genotypes 11, 13 and 20 were discriminated as the most stable genotypes with high grain yield. Path analysis over environments revealed that relative contribution of number of seed per pod (NSPO) in the phenotypic stability of grain yield (GY) is higher than hundred seed weight (HSW) (V3) and number of pod per plant (NPPL) (V1). Environmental components of genotype × environment interaction exhibited that absolute value of r1 and r3 in all environments was higher than r2 indicating that sensitivity of NPPL and HSW to the environmental variation was higher than NSPL. Therefore, high grain yield and stability of chickpea genotypes were because of higher genotypic component V2 (NSPO) and lower environmental components r2 (NSPP).

Tesfamichael *et al*. (2014) studied genetic variation and heritability of selected agronomic traits among chickpea genotypes. Replicated field experiments were conducted for sixty genotypes during the long and short rain seasons of 2013 at Kabete and Juja using alpha lattice design. Data were collected for days to 50 % flowering, plant height, days to 75 % maturity, pods per plant, yield per ha and 100-seed weight and analysed using SAS 2013. Genotypes and genotype by environment interactions showed highly significant ($p < 0.0001$) variations for all studied traits. Genotypes were classified as early (< 50 days), moderate (50 – 55 days), late (55 – 60 days) and very late (> 60 days) in flowering. Fifteen genotypes were early (< 115 days) and 14 were late (> 120 days) in maturity. Genotypes took longer in flowering and maturity during the long rains in comparison with short rains in both sites. Genotypes further varied with respect to yield traits and categorized as low, moderate and high. The highest yield per ha was recorded by ICC 9636 while ICC 9002 recorded the lowest. Broad sense heritability was high for most traits except days to 75 % maturity during long rains and pods plant -1 in long rain Kabete. Characters with high broad sense heritability would be used as selection criterion for better yield. Promising, early flowering and maturing genotypes with reasonable yield traits from this study can be exploited for genetic improvement of chickpea.

Balapure *et al.* (2015) used AMMI analysis of variance for seed yield clearly indicated that the mean sum of square for genotypes was significant, suggesting broad range of diversity among genotypes. The environmental variances was highly significant for all the characters. G x E mean sum of square was significant for seed yield which indicates that the performance of genotypes was differential over the environments. The proportion of sum of square for G X E for seed yield kg/plot was 26.04 %.

Three genotypes viz., Phule G-07102, Phule G-09103 and Digvijay exhibited stable performance over all environment (non-interacting) for seed yield kg/plot. The environments E3 (sowing date 1/11/2011), E4 (sowing date 16/11/2011) and E5 (sowing date 1/12/2011) had good conditions for most of the genotypes while at the same time, the PCA score for these three environments were nearly zero indicating all genotypes produced fairly stable seed yield.

Homayoun *et al*. (2015) evaluated that forty *Kabuli* type chickpea genotypes were assessed for seed yield in four stations over three successive years (2010-2013) at west highlands of Iran. Combined analysis of variance for seed yield revealed significant differences between genotypes, locations, and interaction between these two sources. The mean seed yield of genotypes averaged over environments showed that V4 and V2 had the highest (1163.58 kg ha-1) and the lowest seed yield (759.07 kg ha-1), respectively. Significant G X E interaction implied that chickpea genotypes had various responses to different environments and, the stability analysis could be performed. To investigate G X E interaction and identify the best performing stable genotypes, several stability parameters were employed. According to Wricke's ecovalance, stability variance, plaisted method, and genotypic stability V5, V8 and V3 were the most stable genotypes. Based on CV, regression coefficient and MS(GE), V1 and V5 found to be stable and adapted to diverse environments, and the other genotypes distributed among stability statistics. Based on the AMMI biplot, twelve test environments divided into two mega environments. These mega environments included very cold districts like Maragheh and similar areas, and relatively softened regions of Kurdistan and similar environments. For these two mega environments, V6 and V4 showed more adaptability, respectively. In conclusion, the two genotypes, V4 (FLIP 00-39C) and V6 (FLIP 99-26C) could be recommended as new cultivars to chickpea farmers for autumn sowing in west areas of Iran.

Johansan *et al*. (2015) observed that the genotype JG 11 was stable for primary branches per plant overall environments. GCP 101 was stable for biological yield per plant. Vaibhav, Indira Chana-1 and JGK 1 were stable for 100-seed weight. JG 14, Indira Chana-1, JG 74 and GCP 101 were stable for seed yield per plant and JG 14 and JG 74 were stable for harvest index over all the environments.

Mohamed *et al.* (2015) evaluated eight chickpea cultivars for genetic variability, yield stability and contribution of yield attributes to seed yield. Most of the traits recorded highly significant difference ($P \leq 0.01$) due to cultivars, seasons and their interaction.

Shivani and Sreelakshmi (2015) studied analysis of variance for seed yield and its components traits revealed that genotypes differed significantly for all the characters except days to 50 %flowering, number of primary branches per plant and seed yield (kg / ha) variance due to nonlinear components of environment was significant for days to 50% flowering, primary branches per plant and test weight indicating the role of unpredictable portion of environment influencing this trait. the genotypes ICC 11574 followed by ICC 5034 and ICCV 09104 had below average stability and were specifically adaptable to favourable environment. The genotypes ICCV 86105, ICCV 09118, ICC 5360 and ICCV 08311 were adapted to favourable environment (bi>1), higher mean and significant deviation, while the genotypes ICCV 09314, ICCV 86111, ICCV 0938, ICC 5583 were adapted to poor environment.

Bhardwaj *et al.* (2016) evaluated varieties of chickpea of Chhattisgarh state across fifteen varied environments. Data were subjected to genotype x environment interaction (GEI) and yield stability analysis to determine the suitable varieties for varied environments. GGE bi-plot analysis depicted the adaptation pattern of genotypes at varied environments and discrimination ability of environments. Thus, varieties JG-16 and JG-14 highly unstable whereas JG-63 were highly stable, followed by JG-11 and Vaibhav.

Hasan and Deb (2017) studied stability analysis of yield and yield components in chickpea (*Cicer arietinum* L.) carried out experiment to estimate genotype X environment interaction and the stability parameters. The analysis of variance showed that the genotypes and year were significantly different for most of the character. The results of joint regression analysis exhibited that the mean square due to genotypes were significant for all studied traits.

Sharma and Johnson (2017) Genotype x environment interaction and stability analysis for yield traits in chickpea (*Cicer arietinum* L.) carried out investigation during *Rabi* 2016-17 at five different locations in Chhattisgarh to determine the stability for days to 50% flowering, days to maturity, plant height, pods per plant, 100-seed weight (g) and seed yield(kg/ha).

Babbar and Tiwari (2018) studied stability parameters such as Mean (X), regression coefficient (βi) and deviation from regression (s2di) were estimated for all the twelve characters of each genotype. Partitioning of analysis of variance displayed highly significant results for genotype, environment linear and pooled deviations, Env. + Var X Env. and var. X Env. Linear. In the stability analysis genotypes found highly significant for all the character except total number of pods per plant and effective pods per plant. In genotype x environment interaction days to maturity, plant height, number of seeds per pod and biological yield were found significant. The variation due to environment (linear) was found significant for all the character. The distribution of genotypes has been presented in Table 2. The component G X E (linear) was significant for plant height, days to maturity and biological yield, suggesting that major portion of G X E interaction was attributed to linear component in respect to these traits, although non-linear component (pooled deviation) was highly significant for all character except harvest index.

Kizilgeci (2018) studied nineteen chickpea genotypes were examined for stability assessment in different environments in Turkey. The analysis of variance showed that the genotypes and locations were significantly differed in the majority of the studied characters. The regression coefficient, deviations of the regression coefficients, coefficient of variation, ecovalence and stability variance were calculated for chickpea genotypes. The stability parameters were varied by the planting dates and environments in which the chickpea genotypes were grown. Among the studied chickpea genotypes, genotype ‘FLIP98-143C’ was considered as high grain yield and low b value and produced the minimum deviation regarding the regression, genotypic variance, coefficient of variation, ecovalence and stability variance. Therefore, the genotype ‘FLIP98-143C’ may be used as a stable and high yielding variety in the future and also it may be used in future breeding programs to develop good varieties.

CHAPTER III

MATERIALS AND METHODS

The investigation on "Genetic Variability and Stability Analysis for Yield and Its Contributing Traits in Chickpea (*Cicer arietinum* L.)" was carried out during *rabi* 2017-18 under Pulses Research Unit, Dr. PDKV Akola, Agriculture Research Station, Buldana. College of Agriculture Nagpur. The details of the material used, methods adopted and statistical procedures followed are described below.

3.1. Experiment material

The material used for the present study consisted of fourteen newly developed genotypes and six released varieties chickpea. These chickpea varieties and genotypes evaluated in three different locations (Akola, Buldana & Nagpur),

Table 3.1. List of Chickpea genotypes with their source

Sr. No.	Genotypes	Source
1	AKG-1303	Dr. PDKV, Akola
2	AKG-1401	Dr. PDKV, Akola
3	AKG-1506	Dr. PDKV, Akola
4	AKG-1504	Dr. PDKV, Akola
5	BDNG-2015-9	VNMKV, Parbhani
6	BDNG-2015-6	VNMKV, Parbhani
7	BDNG-2016-1	VNMKV, Parbhani
8	BCP-60	MPKV, Rahuri
9	PHULE G-13107	MPKV, Rahuri
10	PHULE G-0819-43	MPKV, Rahuri
11	PHULE G-15109	MPKV, Rahuri

12	PHULE G-0405	MPKV, Rahuri
13	AKRG-1701	Dr. PDKV, Akola
14	AKRG-1702	Dr. PDKV, Akola
15	BDNG-797	VNMKV, Parbhani
16	VIJAY	MPKV, Rahuri
17	DIGVIJAY	MPKV, Rahuri
18	PHULE VIKRAM	MPKV, Rahuri
19	PDKV- KANCHAN	Dr. PDKV, Akola
20	JAKI-9218	Dr. PDKV, Akola

3.2 Experimental method

3.2.1 Experimental design

These twenty genotypes were evaluated in a Randomized Block Design with three replications for each location were grown during *Rabi* of 2017-18. Data were recorded on five randomly selected plants from each row. The gross plot size was 4.0 x 1.2 m. Each row consisted of 4 m length and row to row and plant to plant distance was kept 30 cm and 10 cm, respectively. A basal dose of 25: 50: 30 NPK kg/ha was applied at the time of sowing.

Field operations viz., gap filling, thinning and inter culturing were carried out as and when required so that the field was kept free from weeds. Recommended plant protection measures were adopted for control for pests and diseases.

Seed material of these genotypes was obtained from the Seed Research Unit, Dr. PDKV, Akola

3.2.2 Details of experiment.

1.	**Design**	**: Randomized Block Design (RBD)**
2.	**Replications**	**: 3**
3.	**Number of genotypes**	**: 20**
4.	**Spacing**	**: 30 x 10 cm**
5.	**No. of rows**	**: 4**
6.	**Row length**	**: 4 m**
7.	**Gross plot**	**: 4 x 1.2 m^2.**
8.	**Net plot**	**: 3.8 x 1.2 m^2.**
9.	**Fertilizer dose**	**: 25:50:30 NPK kg/ha.**
10.	**Dates of sowing**	**: 1. Akola: 07-11-2017**
		2. Buldana: 01-11-2017
		3. Nagpur: 22-11-2017
11.	**Locations**	**: Three location in different environment.**
		E1: Pulses Research Unit, Dr. PDKV Akola.
		E2: Agriculture Research Station, Buldana.
		E3: College of Agriculture, Nagpur.

3.2.3 Cultural practices

The standard package of practices were followed to raise a good crop.

3.2.4 Observations recorded

Randomly selected five competitive plants in each genotype of each replication were used for recording the observations and averages were worked out.

A. On plot basis

1 Days to 50% flowering

The number of days required from sowing to the day on which 50 % of the plants from the plots showed flower opening were recorded.

2 Days to maturity

The Number of days required from the date of sowing to complete maturity of the crop were recorded.

B. On plant basis

3 Plant height (cm)

The height of the plant was measured from five randomly selected plants from each replication of each genotype in centimeters (cm) from soil level to the tip of the plant canopy at maturity.

4 Number of primary branches per plant

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

5 Number of secondary branches per plant

Fruiting branches arising from primary branches were recorded at the time of harvest.

6 Number of pods per plant

At harvest, total number of pods per plant, were counted from five randomly selected plants per each genotype in each replication.

7 Number of seeds per pod

The number of seeds in each of 10 pods of selected five plants was recorded and average was worked out as number of seeds per pods on each plant.

8 100 seeds weight (g)

In each replication of the genotype 100 seeds were counted at random and weighed separately on precision electronic balance and mean 100 seed weight was recorded.

9 Seed yield per plant (g)

The seed obtained from five randomly selected plants was weighed separately on precision electronic balance and the mean seed yield was calculated and recorded as grain yield per plant.

10 Protein content (%)

The nitrogen percentage of grain chickpea was estimated by Kjeldahl method. The protein content was calculated by multiplying the nitrogen % with factor 6.25.

3.3 Statistical analysis

The data was collected on randomly selected five plants per replication in each plot for each character. The collected data was subjected for testing the genotypic differences (Fisher, 1950).

3.3.1 Analysis of variance

The model for experimental design used in randomized block design can be expressed as follows.

$$Yij = \mu + bi + tj + eij$$

Where,

Yij = Performance of j^{th} genotype in i^{th} block

M = General mean

Bi = True effect of i^{th} block

tj = True effect of j^{th} treatment

eij = Random errors which are supposed be identically and independently distributed with normal distribution having mean zero and variance σ^2e.

ANOVA for Randomized Block Design

Sources of variation	D.F	S.S	M.S.S. expected
Replications (Block)	(r-1)	SSr	M_1 (σ^2e +$g\sigma^2$r)
Treatments (Genotypes)	(g-1)	SSg	M_2(σ^2e +r $\sigma^2 g$)
Error	(r-1) (g-1)	SSe	M_3(σ^2e)S
Total	(rg-1)	SSt	

1. Genotypic variance ($\sigma 2g$) $= \dfrac{M2 - M3}{r}$

2. Phenotypic variance ($\sigma 2p$) $= \dfrac{M2 - M3}{r} + M3$

3. Environmental variance ($\sigma^2 e$) = M3

Where, r = number of replications

g = number of genotypes

M1= mean square due to replication

M2= mean square due to genotypes

M3= mean square due to error

3.3.2 Genetic parameters

The genetic parameters, such as mean, range, genotypic coefficients of variation (GCV), phenotypic coefficients of variation, heritability and genetic advance for different characters were work out for all the genotypes under study as per the standard procedures.

1. Mean

The mean was calculated by conventional method as follows:

$$Xi = \sum_{i=1}^{n} \frac{Xi}{n}$$

Where, $\sum Xi$= Sum of all observations

n = number of observations

2. Range

Range is the difference between the least and the greatest terms of a series of observation and thus provides the information about the variability present in the genotypes

3. Phenotypic coefficient of variation (PCV)

$$\sigma^2 p = \sigma^2 g + \sigma^2 e$$

$PCV = \frac{\sigma p}{\bar{X}} \times 100$ where $\sigma p = \sqrt{\sigma^2 p}$

4. Genotypic Coefficient of Variation (GCV)

$$GCV = \frac{\sigma g}{\bar{X}} x100 \quad \text{where } \sigma g = \sqrt{\sigma^2 p}$$

Where,

$\sigma^2 p$ = Phenotypic variance

σp = Phenotypic standard deviation

σ^2g = Genotypic variance

σg = Genotypic standard déviation

σ^2e = Environnent variance

$\bar{X}$ = General Mean

5. Heritability (Broad Sense)

It is the ratio of genotypic variance to the phenotypic variance. Heritability for the present study was calculated in broad sense by adopting the formula suggested by Hanson *et al*. (1956).

$$h^2 \text{ (bs) \%} = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where,

h^2 (bs) = heritability in broad sense,

σ^2g = Genotypic variance,

σ^2p = Phenotypic variance

6. Genetic advance

Improvement in the mean genotypic value of selected plants over the parental population is known as genetic advance. Expected genetic advance (GA) was calculated by the method of Johnson *et al*. (1955).

$$G\ A = K.\ \sigma p\ \ h^2(bs)$$

Where,

GA =Genetic advance

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

h^2 =Heritability of the character

σp =Phenotypic standard deviation

7. Genetic advance as percentage of mean

It was calculated by the following formula

$$\text{GA as percentage of mean} = \frac{\text{Genetic advance}}{\text{General mean}} \times 100$$

GA was categorized as

GA% of mean	0-10%	- Low
GA% of mean	10-20%	- Moderate
GA% of mean	20% and above	- High

3.4 Stability analysis

Stability analysis was performed as per Eberhart and Russell (1966), have further modified the above technique and proposed one more stability parameters, namely deviation from regression. The phenotypic stability is based on regression analysis. The environment and genotype x environment interactions were partitioned into three components *viz.*, environment (linear), genotype x environment (linear) and deviation from regression (pooled deviation over the genotypes). The following genetic model defining these parameters was used for the present analysis of stability performance.

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

Where,

Y_{ij} = variety mean of the i^{th} genotype in the j^{th} environment.

μ_i = mean of the i^{th} genotype over all environment.

β_i = regression coefficient that measure the response of i^{th}

genotype in the j^{th} environment.

δ_{ij} = deviation from regression i^{th} genotype in the j^{th} environment.

I_j = environmental index obtained as the mean of all the genotypes in the j^{th} environment minus the grand mean. First the mean of each genotype will be calculated for all the characters in different environments then arranged on the two-way table for the estimation of stability parameters.

1. Environmental Index (I_j)

$$I_j = \frac{\sum_i Y_{ij}}{g} - \frac{\sum_i \sum_j Y_{ij}}{ge}$$

Where,

I_j = Environmental index.

$\sum_i Y_{ij}$ = Summation of all the genotypes for j^{th} environment.

g = number of genotypes**.**

$\sum_i I \sum_j Y_{ij}$ = Summation of the genotypes over the entire environment.

ge = number of genotypes x number of environments.

The environment index (I_j) is equal to the d_i (additive genetic contribution to i^{th} genotype) of (Perkins and Jinks, 1968).

2. Regression co-efficient

The first satiability parameter is a regression co-efficient. The regression co-efficient of the varietal mean on environmental index will be estimate for each genotypes in the experiment of follows.

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

Where,

$\sum_j Y_{ij} I_j$ = S.P. of the i^{th} genotype x environment index in j^{th} environment.

$\sum_j I_j^2$ = S.S. for environmental index.

The appropriate analysis of variances is presented in a tabulated form. With this model the sum of square, due to environment and genotype x environment are partitioned into environment (linear), genotype x environment (linear) and deviation from the regressions model.

3. Deviation from regression

The performance of all genotype can be predicated by using estimate of parameters.

$$(y_{ij} = x_i + b_i I_j)$$

Where,

x_i is the estimate of the μ_i

The deviation ($S_{ij} = Y_{ij} = Y_{ij}$) are squared and summed to provide an estimate of another stability parameter ($S^2 d_i$)

$$S^2 d_i = \frac{\sum_j \delta_{ij}^2}{(e-2)} - \frac{S_e^{\ 2}}{r}$$

The estimate of deviations from regression ($S^2 d_i$) suggests the degree of reliance that should be put to linear regression in interpretation of the data. If these values are significantly deviating from zero, the expected phenotype cannot be predicted satisfactorily. When, deviations ($S^2 d_i$) are not significant the conclusion may be drawn by the joint consideration of mean, yield and regression coefficient (b_i) values (Finlay and Wilkinson, 1963 and Eberhart and Russell, 1966) as below:

Regression Coefficient	Stability	Mean	Remarks
$\hat{b} = 1$	Average	High	Well adopted to all environments
$\hat{b} = 1$	Average	Low	Poorly adopted to all environments
$\hat{b} \rangle 1$	Below average	High	Specially adapted to favorable environments
$\hat{b} \langle 1$	Above average	High	Specially adapted to unfavorable environments

Analysis of Variance for stability parameters

Square of Variation	d.f.	S.S.	M.S.S
Total	(ge-1)	$\sum_i \sum_j Y_{ij}^2 - CF$	
Genotype (G)	(g-1)	$1/e \sum_j Y_i^2 - CF$	MSS1
Environment + G X E Interaction	g (e-1)	$\sum_i \sum_j Y_{ij}^2 - \sum_j Y_i^2 / e$	
Environment (linear)	1	$1/g \left(\sum_j Y_{ij} I_j \right)^2 / \sum_j I_j^2 = SSenvironments$	
Gx Envs (linear)	(g-1)	$\sum_i \left[\left(\sum_j Y_{ij} I_j \right)^2 / \sum_j I_j^2 \right] - SSenvironments_{Linear}$	MSS2
Pooled deviation	g (e -2)	$\sum_i \left[\left(\sum_j Y_{ij}^2 - Y_i^2 / e \right) \right] - \left[\frac{\left(\sum_j Y_{ij} I_j \right)^2}{\sum_j I_j^2} \right] = \sum_i \sum_j \partial_{ij}^2$	MSS3
Genotype 1	(e -2)	$\left(\sum_j Y_{ij}^2 - Y_i^2 / e \right) - b_i \sum_j Y_{ij} I_j = \sum_j \partial_{gj}^2$	
Genotype 2	(e -2)		
Genotype i	(e -2)		
Genotype g	(e -2)		
Pooled error	e (r-1) (g-1)	-	-

Where,

r = number of replications.

g = number of genotypes.

e = number environments.

S^2/er = estimate of the pooled error of the variance of a genotype linear at the j^{th} environment & jS_{ij} = [jy_{ij} –$y^2{}_i e$] – $(jy_{ij}\ I_j)^2$ / jI^2 j).

Environment linear and Genotype X Environment (Linear) will be calculated as per the formulae suggested by (Dabholkar, 1992).

Test of significance:

Stable genotype of one with b_i= 1.0 and S^2d_i = 0 the significant of the difference among genotypes means:

Ho: µ1= µ2....... µg can be formed approx. by the F test, F = MSS_1/ MSS_3, with homogenous deviation mean square since MSS_3 in the pooled deviation. If there are no difference among regression coefficient (β1=β2= ...... = βg), this F test will be approximately the same an F = MSS_1/ MSS_3 (genotype x environments) in the standard analysis of variance. If there are differences among genotypes in error response to a varying environmental Index, F value will be larger.

The hypothesis that there, are no genetic differences among the genotypes for their regression on the environmental index i.e. H_0 = (µ1=µ2=......= µg), can also be tested approximately F test, F= MSS_2/ MSS_3.

Thus all the linear variance was tested against pooled deviation mean square (MSS_3). An approximate tested of the deviation from regression for each genotype can be obtained,

$$F = \left[\left(\sum_j \delta_{ij}^2 \right) \Big/ (s-2) \right] \Big/ pooled\ error$$

The test of significance carried for the stability parameters e.g. for phenotypic index & regression coefficient are as follows.

$$S.E. = \sqrt{\frac{error\ M.S.}{r.e}}$$

$$F = \frac{I_j - \mu}{(S.E.)}$$

Thus, C.D. for I_j is equal to S.E. X t_{table} at 0.05 percent and error d.f.

The hypothesis that any regression coefficient does not differ from units can also be tested by the approximate ‘t’ test. The S.E. and ‘t’ for regression coefficient will be calculated as follows:

$$S.E._{(b)} = \sqrt{\frac{M.S.\text{ due to pooled deviation}}{\sum_{j} I_j^2}}$$

t = (b-1) / S.E. (b) Thus, C.D. for b-1 is equal to S.E.(b) X t_{table} at 0.05 percent and error d.f.

CHAPTER IV

RESULTS AND DISCUSSION

The results of the present investigation on "Genetic variability and stability analysis for yield and its contributing traits in chickpea (*Cicer arietinum* L.)" was carried out during *Rabi* 2017-18 growing season at three locations, i.e. Pulses Research Unit, Dr. PDKV, Akola (E1), Agriculture Research Station, Buldana (E2) and College of Agriculture Nagpur (E3). The experimental result of investigation has been given under following headings.

4.1 Analysis of variance for three locations

4.2 Mean performance of various characters at three locations

4.3 Genetic variability studies

4.4 Pooled analysis of variance for stability across environments

4.5 Estimates of environmental indices

4.6 Stability parameters

4.1 Analysis of variance for different locations

The analysis of variance was carried out for all the characters across the three locations (Akola, Buldana and Nagpur) under study is presented in Table 4.1. The ANOVA revealed highly significant differences among the all genotypes for all the characters across the three locations (Akola, Buldana and Nagpur) viz. days to 50% flowering, plant height (cm), days to maturity, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, 100 seeds weight (g), seed yield per plant (g) and protein content. This indicated that, the genotypes under study exhibited sufficient variability in terms of meeting the requirement of the present experimentation.

Table 4.1: Analysis of variance for various characters of chickpea for three environments (Akola, Buldana and Nagpur)

Source of Variations	D.F.	Days to 50 % Flowering	Plant Height (cm)	Days to maturity	Number of primary branches per plant	Number of secondary branches per plant
Environment 1 (Akola)						
Replications	2	17.55	30.17	18.31	0.21	3.60
Genotypes	19	16.31**	35.04**	26.78**	0.41**	9.71**
Error	38	6.72	13.59	6.38	0.10	1.17
Environment 2 (Buldana)						
Replications	2	5.06	70.22	15.26	0.04	1.80
Genotypes	19	17.92**	74.48**	35.84**	0.37**	5.53**
Error	38	7.32	21.85	7.24	0.10	0.59
Environment 3 (Nagpur)						
Replications	2	7.81	67.93	23.81	0.04	1.98
Genotypes	19	19.20**	89.06**	19.86**	0.23**	3.68**
Error	38	7.90	26.20	7.97	0.05	0.74

***Significant at 5%, **Significant at 1%**

Table 4.1: Continued……

Source of Variations	D.F.	Number of pods per plant	Number of seeds per pod	100 seeds weight (g)	Seed yield per plant (g)	Protein content (%)
Environment 1 (Akola)						
Replications	2	29.64	0.006	0.37	0.57	0.33
Genotypes	19	299.49**	0.03**	8.97**	13.03**	4.18**
Error	38	15.81	0.008	2.43	1.39	0.21
Environment 2 (Buldana)						
Replications	2	29.15	0.011	0.90	3.68	0.47
Genotypes	19	439.15**	0.04**	14.92**	21.54**	5.65**
Error	38	16.09	0.008	2.07	1.62	0.19
Environment 3 (Nagpur)						
Replications	2	42.65	0.017.	1.31	10.64	0.50
Genotypes	19	182.04**	0.078**	18.57**	12.96**	5.43**
Error	38	20.54	0.010	1.98	3.45	0.18

***Significant at 5%, **Significant at 1**

4.2 Mean performance of various characters at three locations

The data collected on different characters in each of the twenty genotypes of chickpea were analysed location wise to find out the performance of each genotype across three locations. The mean values for each location and for means overall three locations for different traits are presented in Table 4.2.

1. Days to 50 % flowering

In E1 the genotype BDNG 2015-9 (48.00 days) was earliest to flower followed by the genotype PDKV Kanchan (50.00 days). In E2 the genotype PDKV Kanchan (47.00 days) was found significantly earliest to flower followed by the genotype AKG-1303 (49.33 days). In E3 the genotype BDNG 2015-6 (48.00 days) was found significantly earliest to flower followed by the genotype Phule G-0819-43 (50.67 days).

In overall locations, the significant difference was found among the genotypes of chickpea. In overall locations the genotype PDKV Kanchan was found significantly earliest to flower (50.00 days) followed by BDNG-797 (51.11days). Whereas, the genotype AKRG 1702 and Phule G-15109 were found late to flowering (57.00 & 57.33 days).

2. Plant height (cm)

In E1 the genotype AKG-1303 (47.04 cm) was recorded significantly highest plant height followed by Phule Vikram (45.00 cm). Whereas, the genotype Vijay (32.23 cm) was with lowest plant height followed by PDKV Kanchan (35.72cm).

In E2 the genotype Phule G-13107 (61.73 cm) was found significantly highest plant height followed by Phule Vikram (54.87 cm). Whereas, the genotype BDNG-797 (42.33 cm) was with lowest plant height followed by AKRG 1701 (42.73cm).

In E3 the genotype AKG-1303 (62.00 cm) was found significantly highest plant height followed by Phule G-13107 (60.80 cm), Whereas the genotype AKRG 1702 (43.00 cm) was with lowest plant height followed by AKG-1506 (45.93 cm).

Table 4.2a: Mean performance of chickpea genotypes over different environments

Sr. No	Genotypes	Days to 50 % Flowering (days)				Plant Height (cm)			
		E1	E2	E3	Mean	E1	E2	E3	Mean
1	AKG-1303	53.00	49.33	51.67	51.33	47.04	51.80	62.00	53.61
2	AKG-1401	51.33	54.00	53.00	52.78	39.58	44.60	55.93	46.70
3	AKG-1506	53.00	53.33	56.33	54.22	40.59	43.87	45.93	43.46
4	AKG-1504	52.00	50.33	55.67	52.67	36.99	48.07	46.53	43.86
5	BDNG 2015-9	48.33	51.67	56.00	52.00	41.00	49.60	57.47	49.36
6	BDNG 2015-6	52.67	54.00	48.00	51.56	40.67	44.53	46.73	43.98
7	BDNG 2016-1	55.00	54.67	53.67	54.44	39.33	43.00	54.67	45.67
8	BCP-60	53.00	55.00	51.00	53.00	36.00	43.27	52.33	43.87
9	Phule G-13107	55.00	52.00	51.00	52.67	39.27	61.73	60.80	53.93
10	Phule G-0819-43	51.33	53.33	50.67	51.78	42.00	53.00	56.00	50.33
11	Phule G-15109	57.00	56.67	58.33	57.33	40.00	49.53	59.13	49.56
12	Phule G-0405	53.00	51.67	52.00	52.22	43.00	48.40	52.80	48.07
13	AKRG 1701	50.67	51.00	53.00	51.56	38.01	42.73	46.67	42.47
14	AKRG 1702	58.00	56.33	56.67	57.00	37.65	43.87	43.00	41.51
15	BDNG-797	50.00	51.67	51.67	51.11	36.53	42.33	49.33	42.73
16	Vijay	54.33	56.00	55.67	55.33	32.23	47.27	53.67	44.39
17	Digvijay	52.33	52.33	55.33	53.33	36.90	44.27	57.13	46.10
18	Phule Vikram	52.00	50.67	54.33	52.33	45.00	54.87	58.67	52.84
19	PDKV Kanchan	50.00	47.00	53.00	50.00	35.72	44.47	49.93	43.37
20	JAKI-9218	52.00	52.33	53.33	52.56	41.60	45.00	53.67	46.76
	Means	**52.7**	**52.66**	**53.51**	**52.96**	**39.45**	**47.31**	**53.12**	**46.63**
	SE (m)±	2.11	2.21	2.29	0.95	3.01	3.81	4.18	1.62
	CD $_{0.05}$	4.28	4.47	4.64	2.66	6.09	7.72	8.46	4.53
	CD $_{0.01}$	5.74	5.99	6.22	3.52	8.16	10.35	11.33	5.98

***Significant at 5%, **Significant at 1%**

In over all three environments indicated that the genotypes Phule G-13107 (53.93 cm) was the tallest among all genotypes followed by and at par viz. AKG 1303 (53.61 cm) and Phule Vikram (52.84 cm), Whereas the genotypes AKRG 1702 (41.51 cm) were found significantly dwarf.

3. Days to maturity

In E1 the genotype AKRG 1702 was found earliest (94.00 days). Whereas, BDNG 2015-6 (104.0 days) and Digvijay (104.0 days) were late in maturity. The maturity was ranged between 94 to 104 days.

In E2 the genotype Digvijay (92.00 days) and AKG-1401 (93.00 days) was found significantly earliest. Whereas, JAKI-9218 (105.0 days) and BDNG-797 (104.0 days) were late in maturity.

In E3 the genotype AKG-1506 was found significantly earliest (103.7 days) followed by the genotypes AKRG 1702 (106.0 days). Whereas, Vijay (115.0 days) and BDNG-797 (114.0 days) were late in maturity.

In overall locations the genotype AKRG 1702 was found earliest (98.8 days) followed by the genotype AKG-1401 (100.1 days), Phule G-0819-43 (100.1 days) and Phule G-0405(100.1 days).

4. Number of primary branches per plant

In E1 the genotype AKRG 1702 (4.1) and JAKI-9218 (4.1), in E2 the genotype PDKV Kanchan (3.6) and JAKI-9218 (3.4), in E3 the genotype PDKV Kanchan (3.5), Vijay (3.3) and JAKI-9218 (3.2) produced maximum number of primary branches per plant.

In overall locations the genotype JAKI-9218 (3.6), PDKV Kanchan (3.6) was found significantly maximum number of primary branches per plant followed by the genotype Vijay (3.5) and Phule G-15109 (3.4). Highest number of primary branches were recorded in E1 (Akola) followed by E2 (Buldana) and E3 (Nagpur).

Table 4.2b: Mean performance of chickpea genotypes over different environments.

Sr. No	Genotypes	Days to maturity (days)				No. of primary branches per plant			
		E1	E2	E3	Mean	E1	E2	E3	Mean
1	AKG-1303	103.7	97.3	107.0	102.7	3.5	2.7	2.5	2.9
2	AKG-1401	99.3	93.0	108.0	100.1	3.2	2.4	2.7	2.8
3	AKG-1506	101.0	97.3	103.7	100.7	3.3	2.9	2.4	2.9
4	AKG-1504	99.0	101.0	110.3	103.4	3.3	3.1	2.6	3.0
5	BDNG 2015-9	102.7	95.7	110.0	102.8	3.1	2.8	3.1	3.0
6	BDNG 2015-6	104.0	101.0	110.0	105.0	2.6	2.9	2.6	2.7
7	BDNG 2016-1	98.0	103.3	108.0	103.1	3.1	2.2	2.7	2.7
8	BCP-60	99.0	98.0	110.0	102.3	3.6	2.9	2.9	3.1
9	Phule G-13107	101.0	99.0	107.7	102.6	3.5	3.0	2.9	3.1
10	Phule G-0819-43	96.0	96.3	108.0	100.1	3.8	3.2	2.9	3.3
11	Phule G-15109	96.0	100.3	110.3	102.2	3.7	3.3	3.0	3.4
12	Phule G-0405	97.0	95.3	108.0	100.1	3.7	2.5	2.8	3.0
13	AKRG 1701	98.7	96.0	107.3	100.7	4.1	2.8	3.0	3.3
14	AKRG 1702	94.0	96.3	106.0	98.8	3.9	2.7	2.5	3.1
15	BDNG-797	98.7	104.0	114.0	105.6	3.7	3.3	2.8	3.3
16	Vijay	103.0	99.0	115.0	105.7	3.9	3.3	3.3	3.5
17	Digvijay	104.0	92.0	107.0	101.0	3.3	3.2	2.8	3.1
18	Phule Vikram	103.3	100.3	109.3	104.3	3.3	3.1	2.9	3.1
19	PDKV Kanchan	101.7	100.0	107.0	102.9	3.6	3.6	3.5	3.6
20	JAKI-9218	102.3	105.0	107.7	105.0	4.1	3.4	3.2	3.6
	Means	**100.11**	**98.51**	**108.71**	**102.45**	**3.51**	**2.97**	**2.84**	**3.11**
	SE (m)±	2.06	2.19	2.30	1.11	0.27	0.26	0.19	0.11
	CD $_{0.05}$	4.17	4.45	4.66	3.11	0.54	0.53	0.39	0.32
	CD $_{0.01}$	5.59	5.96	6.25	4.11	0.73	0.72	0.52	0.42

***Significant at 5%, **Significant at 1%**

5. Number of secondary branches per plant

In E1 the genotype Phule G-15109 produced highest number of secondary branches per plant (11.8), followed by the genotype JAKI-9218 (11.4) and AKRG 1701 (11.3). In E2 the genotype Phule G-15109 produced highest number of secondary branches (10.2), followed by the genotype AKRG 1701 (9.0) and Vijay (8.7). In E3 the genotype Vijay produced highest number of secondary branches per plant (14.3). followed by the genotype AKRG 1701 (12.8) and BCP-60 (12.7).

In overall locations the genotype Phule G-15109 was found significantly maximum number of secondary branches (11.4) followed by the genotype Vijay (11.1) and AKRG 1701 (11.0). Highest number of secondary branches were recorded in E3 (Nagpur) followed by E1 (Akola) and E2 (Buldana)

Table 4.2c: Mean performance of chickpea genotypes over different environments.

Sr. No	Genotypes	No. of secondary branches per plant				No. of pods per plant			
		E1	E2	E3	Mean	E1	E2	E3	Mean
1	AKG-1303	7.6	4.7	10.5	7.6	55.67	31.07	52.40	46.38
2	AKG-1401	9.1	5.7	11.8	8.8	48.00	42.80	66.87	52.56
3	AKG-1506	9.0	8.5	9.6	9.0	59.13	51.60	49.67	53.47
4	AKG-1504	9.8	8.1	10.7	9.5	41.67	37.20	58.73	45.87
5	BDNG 2015-9	7.7	7.9	11.7	9.1	40.00	37.07	61.47	46.18
6	BDNG 2015-6	4.7	6.1	11.3	7.4	24.40	23.93	39.27	29.20
7	BDNG 2016-1	8.9	5.5	10.9	8.5	40.67	25.27	55.13	40.36
8	BCP-60	7.9	6.2	12.7	8.9	39.60	43.27	58.73	47.20
9	Phule G-13107	10.2	6.5	11.5	9.4	50.20	46.60	55.13	50.64
10	Phule G-0819-43	8.9	7.1	11.4	9.1	36.87	44.07	64.20	48.38
11	Phule G-15109	11.8	10.2	12.2	11.4	48.93	76.60	68.00	64.51
12	Phule G-0405	8.7	7.0	10.3	8.7	49.60	39.07	56.60	48.42
13	AKRG 1701	11.3	9.0	12.8	11.0	68.80	58.73	75.07	67.53
14	AKRG 1702	10.6	6.5	10.3	9.1	44.87	42.80	70.00	52.56
15	BDNG-797	11.0	8.3	12.1	10.5	47.53	42.93	60.13	50.20
16	Vijay	10.3	8.7	14.3	11.1	46.07	33.67	58.47	46.07
17	Digvijay	7.3	8.1	11.9	9.1	33.00	50.27	64.00	49.09
18	Phule Vikram	6.5	7.9	9.9	8.1	33.33	51.07	61.73	48.71
19	PDKV Kanchan	9.1	7.2	11.7	9.3	44.17	57.27	61.27	54.23
20	JAKI-9218	11.4	7.9	11.1	10.1	54.13	39.27	55.73	49.71
	Means	**9.09**	**7.35**	**11.44**	**9.30**	**45.33**	**43.73**	**59.63**	**49.56**
	SE (m)±	0.88	0.62	0.70	0.43	3.25	3.28	3.70	2.57
	CD $_{0.05}$	1.78	1.27	1.43	1.20	6.57	6.63	7.50	7.19
	CD $_{0.01}$	2.39	1.70	1.91	1.59	8.81	8.88	10.05	9.49

***Significant at 5%, **Significant at 1%**

6. Number of pods per plant

In E1 the genotype AKRG 1701 (68.80) was found significantly highest number of pods per plant followed by and at par viz., AKG-1506 (59.13), AKG-1303 (55.67) and Jaki-9218 (54.13),

In E2 the genotype Phule G-15109 (76.60) was found significantly highest number of pods per plant followed by AKRG 1701 (58.73), PDKV Kanchan (57.27) and Phule Vikram (51.07).

In E3 the genotype AKRG 1701 (75.07) was found significantly highest number of pods per plant followed by. AKRG 1702 (70.00) and Phule G-15109 (68.00).

In overall locations the genotype AKRG 1701 was found significantly highest number of pods per plant (67.53) followed by the genotype Phule G-15109 (64.51). For pods per plant E3 (Nagpur) was superior (59.63) followed by E1 (Akola) (45.33), E2 (Buldana) (43.73).

7. Number of seeds per pod

In E1 the genotype Phule Vikram (1.4), in E2 the genotype AKRG 1701 (1.5) and in E3 the genotype BDNG 2015-6 (1.6) produced significantly highest number of seeds per pod.

The genotype AKRG 1701 (1.5) produced significantly highest number of seeds per pod followed by BDNG 2015-6 (1.35), Phule G-0405 (1.36), Digvijay (1.38) and Phule Vikram (1.4) in over all the three environments. For seeds per pod the environment E3 (Nagpur) (1.29) was superior followed by E2 (Buldana) (1.27), E1 (Akola) (1.17).

8. 100 seed weight (g)

In E1 the genotype BCP-60 (26 g) and Phule G-15109 (26 g) recorded highest 100 seed weight followed by Phule G-13107 (25.67 g), BDNG 2015-6 (25 g), and AKRG 1701 (25 g). In E2 the genotype AKG-1401 (26.67 g) was found significantly highest 100 seed weight followed by BDNG 2015-6 (26.57 g). In E3 BCP-60 (26.67 g) was found significantly highest 100 seed weight followed by and at par viz., BDNG 2015-6 (26 g) and AKG-1401 (25.33 g).

In overall location the genotype BDNG 2015-6 (25.86 g) had shown promising for 100 seed weight and equally followed by AKG-1401 (25.78 g) and BCP 60 (25.78 g). On the mean performance basis over three environments maximum 100 seed weight was recorded in E1 (Akola) (23.51).

Table 4.2d: Mean performance of chickpea genotypes over different environments

Sr. No	Genotypes	Number of seeds per pod				100 seeds weight (g)			
		E1	**E2**	**E3**	**Mean**	**E1**	**E2**	**E3**	**Mean**
1	AKG-1303	1.3	1.4	1.3	1.3	23.17	22.67	18.67	21.50
2	AKG-1401	1.1	1.3	1.2	1.2	25.33	26.67	25.33	25.78
3	AKG-1506	1.2	1.3	1.1	1.2	23.00	24.00	21.67	22.89
4	AKG-1504	1.0	1.1	1.3	1.1	23.33	21.80	22.33	22.49
5	BDNG 2015-9	1.2	1.2	1.4	1.3	23.67	25.00	24.00	24.22
6	BDNG 2015-6	1.2	1.3	1.6	1.4	25.00	26.57	26.00	25.86
7	BDNG 2016-1	1.1	1.2	1.2	1.2	23.67	22.33	21.33	22.44
8	BCP-60	1.2	1.4	1.3	1.3	26.00	24.67	26.67	25.78
9	Phule G-13107	1.1	1.2	1.3	1.2	25.67	25.27	23.00	24.64
10	Phule G-0819-43	1.1	1.3	1.1	1.2	22.67	21.00	19.00	20.89
11	Phule G-15109	1.2	1.2	1.3	1.2	26.00	24.00	22.67	24.22
12	Phule G-0405	1.3	1.3	1.5	1.4	22.33	21.47	19.00	20.93
13	AKRG 1701	1.3	1.5	1.5	1.5	23.00	21.20	24.33	22.84
14	AKRG 1702	1.2	1.1	1.3	1.2	25.00	24.00	21.00	23.33
15	BDNG-797	1.0	1.1	1.0	1.0	21.67	22.27	19.33	21.09
16	Vijay	1.0	1.1	1.2	1.1	23.33	20.20	18.33	20.62
17	Digvijay	1.2	1.4	1.5	1.4	23.33	22.00	20.33	21.89
18	Phule Vikram	1.4	1.3	1.5	1.4	19.33	19.87	21.00	20.07
19	PDKV Kanchan	1.1	1.2	1.1	1.2	20.67	18.67	23.33	20.89
20	JAKI-9218	1.2	1.1	1.3	1.2	24.00	25.00	23.00	24.00
	Means	**1.17**	**1.27**	**1.29**	**1.24**	**23.51**	**22.93**	**22.02**	**22.82**
	SE (m)±	0.07	0.07	0.08	0.04	1.27	1.18	1.15	0.59
	$CD_{0.05}$	0.15	0.15	0.17	0.10	2.58	2.38	2.33	1.64
	$CD_{0.01}$	0.20	0.20	0.23	0.14	3.45	3.19	3.12	2.16

***Significant at 5%, **Significant at 1%**

9. Seed yield per plant (g)

In E1 the genotype JAKI-9218 was found significantly highest yield per plant (14.07 g) followed by the genotypes AKG-1506 (14.00 g) and AKRG 1701 (14.00 g). In E2 the genotype AKG-1506 was recorded significantly higher yield per plant (16.17 g) followed by the genotypes AKRG 1701 (16.13 g) and AKRG 1702 (14.30 g). In E3 the genotype AKRG 1701 recorded maximum yield per plant (18.67 g) followed by the genotypes AKRG 1702 (18.33 g), Digvijay (18.00 g).

Table 4.2e: Mean performance of chickpea genotypes over different environments.

Sr. No	Genotypes	Seed yield per plant (g)				Protein content (%)			
		E1	**E2**	**E3**	**Mean**	**E1**	**E2**	**E3**	**Mean**
1	AKG-1303	13.07	8.10	12.10	11.09	20.37	20.13	20.59	20.36
2	AKG-1401	12.10	10.80	17.00	13.30	18.40	18.33	18.54	18.42
3	AKG-1506	14.00	16.17	15.20	15.12	19.43	19.27	19.37	19.36
4	AKG-1504	9.97	9.03	15.13	11.38	17.23	17.73	17.37	17.44
5	BDNG 2015-9	11.33	11.50	18.00	13.61	18.43	17.97	17.17	17.86
6	BDNG 2015-6	7.07	7.70	15.00	9.92	19.50	19.37	19.21	19.36
7	BDNG 2016-1	10.93	7.33	12.00	10.09	18.47	18.13	18.21	18.27
8	BCP-60	11.60	12.53	15.83	13.32	18.57	18.53	18.33	18.48
9	Phule G-13107	13.13	12.33	12.20	12.56	17.60	17.60	17.47	17.56
10	Phule G-0819-43	9.00	12.93	14.00	11.98	17.31	17.26	17.23	17.27
11	Phule G-15109	13.33	14.00	16.90	14.74	19.52	19.20	19.23	19.32
12	Phule G-0405	12.20	9.03	15.13	12.12	20.47	20.73	20.63	20.61
13	AKRG 1701	14.00	16.13	18.67	16.27	18.47	18.60	18.40	18.49
14	AKRG 1702	12.13	14.30	18.33	14.92	19.47	19.60	19.27	19.44
15	BDNG-797	12.00	10.40	14.23	12.21	20.17	20.37	20.14	20.22
16	Vijay	11.03	12.60	14.13	12.59	20.63	20.28	20.57	20.49
17	Digvijay	8.20	14.00	18.00	13.40	21.33	22.47	21.37	21.73
18	Phule Vikram	8.20	12.87	13.00	11.36	20.60	21.47	21.18	21.08
19	PDKV Kanchan	13.20	14.07	16.20	14.49	19.90	20.12	20.43	20.15
20	JAKI-9218	14.07	14.17	15.07	14.43	18.47	18.40	18.60	18.49
	Means	**11.53**	**12.00**	**15.31**	**12.94**	**19.22**	**19.28**	**19.17**	**19.22**
	SE (m)±	0.96	1.04	1.52	0.68	0.38	0.36	0.35	0.15
	CD $_{0.05}$	1.95	2.11	3.07	1.91	0.76	0.72	0.70	0.42
	CD $_{0.01}$	2.62	2.83	4.12	2.52	1.02	0.97	0.94	0.55

***Significant at 5%, **Significant at 1%**

In overall locations the genotype AKRG 1701 was found significantly highest yield per plant (16.27 g) followed by the genotype AKG-1506 (15.12 g) and AKRG 1702 (14.92 g). Whereas, the genotype was BDNG 2015-6 recorded lowest yield per plant (9.92 g). Highest yield per plant were recorded in E3 (Nagpur) (15.31 g) followed by E2 (Buldana) (12.00 g) and E1 (Akola) (11.53 g).

10. Protein content (%)

In E1 the genotype Digvijay (21.33%), in E2 the genotype Digvijay (22.47%) and in E3 the genotype Digvijay (21.37%) recorded highest protein content.

In overall locations the genotype Digvijay recorded highest protein content (21.73%) followed by the genotype Phule Vikram (21.08%), Phule G-0405 (20.61%). For protein content E2 (Buldana) was superior (19.28%) followed by E1 (Akola) (19.22%), E3 (19.17%).

4.3 Genetic variability studies

The values of Range, Mean, Genotypic coefficient of variation, Phenotypic coefficient of variation, Heritability in broad sense and Expected Genetic Advance per cent over mean for various characters are presented in Table 4.3.

4.3.1 Genotypic Coefficient of Variation (%).

It is revealed from Table 4.3 that genotypic coefficient of variation (GCV) ranged from 1.63 (days to maturity) to 14.88 % (number of pods per plant) for different character under study. The moderate GCV were recorded for number of pods per plant (14.88%) followed by seed yield per plant (12.24%), number of secondary branches per plant (10.73%), whereas lowest GCV were recorded by number of seeds per pod (8.49%), number of primary branches per plant (7.76%), 100 seed weight (7.68%), plant height (7.47%), protein content (6.63%), days to 50% flowering (3.07%) and days to maturity (1.63%).

4.2.2 Phenotypic Coefficient of Variation (%)

The phenotypic coefficient of variation (Table 4.3) ranged from 3.65% (days to maturity) to 21.54 % (number of pods per plant) for various characters under study. The high PCV were recorded for the number of pods per plant (21.54%) followed by seed yield per plant

(20.03%). The moderate PCV were recorded for number of secondary branches per plant (17.55%), number of primary branches per plant (13.45%), plant height (12.83%), number of seeds per pod (12.37%), 100 seed weight (10.88%), whereas lowest PCV were recorded by protein content (7.03%), days to 50% flowering (6.21%) and days to maturity (3.65%).

4.2.3 Heritability estimates in broad sense (%)

Broad sense heritability results presented in Table 4.3 revealed that heritability estimates ranged from 20.00% (days to maturity) to 89.00% (protein content) for various characters under study. High heritability estimate in broad sense was observed for protein content (89.00%). The medium heritability estimate in broad sense were observed for the characters viz. 100 seed weight (49.90%), number of pods per plant (47.70%), number of seeds per pod (47.00%). The low heritability estimate in broad sense recorded by the characters viz. number of secondary branches per plant (37.40%), seed yield per plant (37.30%), plant height (33.90%), number of primary branches per plant (33.30%), days to 50% flowering (24.40%) and days to maturity (20.00%).

4.3.4 Expected genetic advance (%)

Expected genetic advance percent over mean was estimated for different characters and result presented in Table 4.3. Data revealed that expected genetic advance percent over mean was in the range of 1.51% (days to maturity) to 21.17% (number of pods per plant) for different characters. The highest genetic advance percent over mean was observed for the character number of pods per plant (21.17%). The medium genetic advance percent over mean was observed for the characters seed yield per plant (15.41%), number of secondary branches per plant (13.53%), protein content (12.89%), number of seeds per pod (11.99%),100 seed weight (11.18%), The low genetic advance percent over mean was recorded for the character’s number of primary branches per plant (9.22%), plant height (8.96%), days to 50% flowering (3.12%) and days to maturity (1.51%).

Table 4.3 Estimate of coefficient of variation (PCV and GCV), heritability and genetic advance for ten quantitative characters in chickpea

Sr.No.	Character	Range	Mean	GCV(%)	PCV(%)	Heritability(%) (bs)	GA	EGA as % of mean
1	Days to 50% flowering	50.00-57.33	52.96	3.07	6.21	24.40	1.65	3.12
2	Plant height (cm)	41.51-53.93	46.63	7.47	12.83	33.90	4.18	8.96
3	Days to maturity	98.78-105.67	102.45	1.63	3.65	20.00	1.54	1.51
4	Number of primary branches per plant	2.67-3.56	3.11	7.76	13.45	33.30	0.29	9.22
5	Number of secondary branches per plant	7.40-11.40	9.30	10.73	17.55	37.40	1.26	13.53
6	Number of pods per plant	29.20-67.53	49.56	14.88	21.54	47.70	10.49	21.17
7	Number of seeds per pod	1.03-1.47	1.24	8.49	12.37	47.00	0.15	11.99
8	100 seed weight (g)	20.07-25.86	22.82	7.68	10.88	49.90	2.55	11.18
9	Seed yield per plant (g)	9.92-16.27	12.94	12.24	20.03	37.30	1.99	15.41
10	Protein content (%)	17.27-21.73	19.22	6.63	7.03	89.00	2.48	12.89

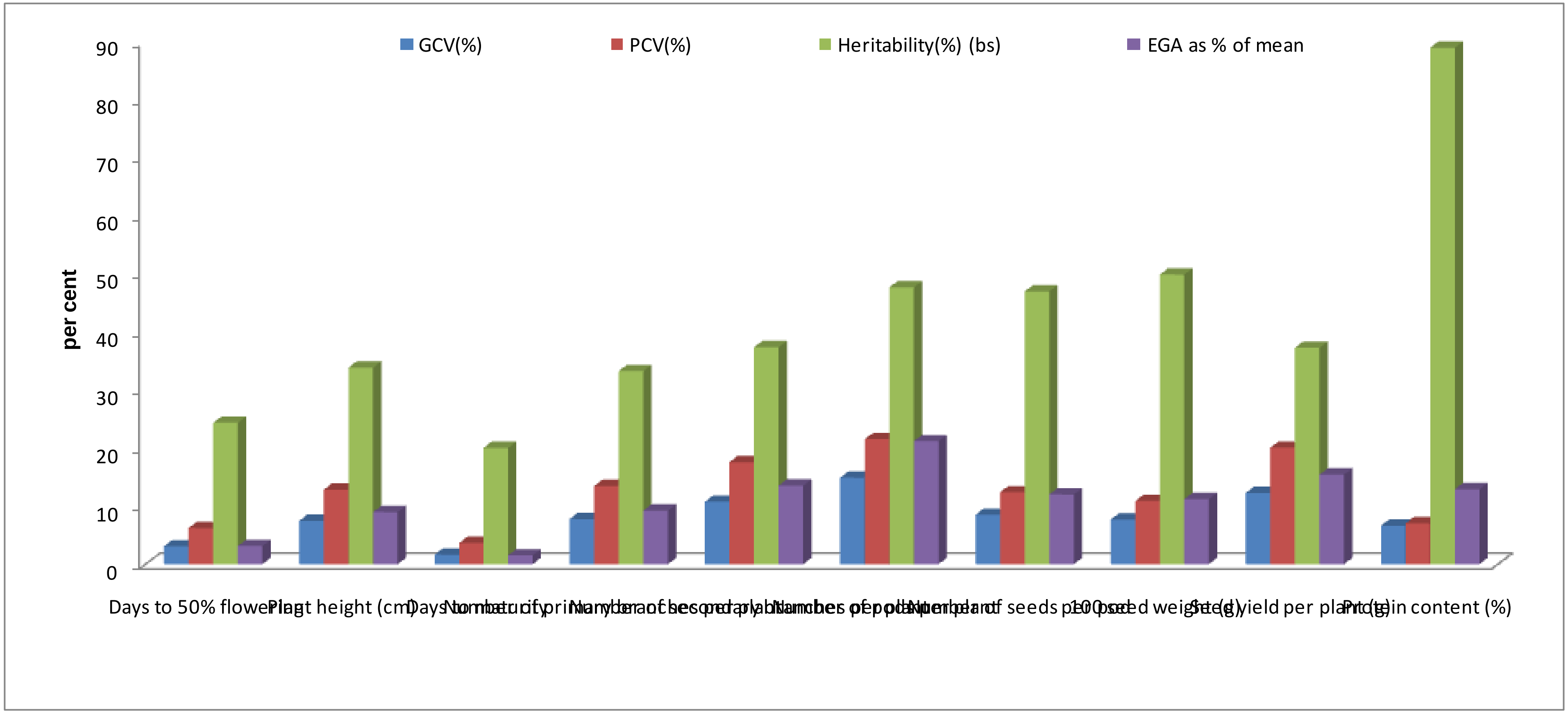

Fig. 1 Estimate of coefficient of variation (PCV and GCV), heritability and genetic advance for ten quantitative characters in chickpea

4.4 Pooled analysis of variance for stability across environments

The analysis of variance representing the mean sum of square due to different sources of variation as per Eberhart and Russell (1966) for the 10 characters is presented in Table 4.4.

Pooled analysis of variance over three different environment showed that, environmental variance was significant for all the studied characters except days to 50% flowering, protein content, when tested against G X E interaction, pooled deviation and pooled error. Genotypic variances were found significant for the characters viz., days to 50% flowering, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight, seed yield per plant and protein content, except days to maturity when tested against G X E interaction.

The G X E interactions were non-significant for all the traits when tested against pooled deviation and pooled error. The variance due to environments+ (genotype x environments) was significant for all the studied characters except days to 50% flowering, number of pods per plant, number of seeds per pod, protein content.

Pooled deviation effects were significant for the traits viz., days to maturity, number of secondary branches per plant, number of pods per plant, number of seeds per pod, seed yield per plant, when tested against pooled error. Partitioning of G X E interaction showed that, G x E (linear) effect were significant for the characters viz., days to 50% flowering and 100 seed weight. Environment (linear) effects were also significant for all the studied characters except protein content (%), when tested against pooled deviation and pooled error.

Table 4.4: Pooled analysis of variance for stability over the three environments for twenty chickpea genotypes

Sr.No	Source of Variations	G	E	GXE	E + (G x E)	E (Linear)	G x E (linear)	Pooled deviation	Pooled error
	DF	19	2	38	40	1	19	20	114
1	Days to 50% flowering	10.64**	4.64	3.59	3.64	9.27*	5.22*	1.85	2.44
2	Plant height (cm)	44.28**	940.46**	10.96	57.43**	1880.93**	12.70	8.75	6.85
3	Days to maturity	12.12	601.87**	7.69	37.40**	1203.73**	5.32	9.56**	2.40
4	Number of primary branches per plant	0.21**	2.55**	0.07	0.19**	5.10**	0.08	0.05	0.03
5	Number of secondary branches per plant	3.54**	84.21**	1.38	5.52**	168.42**	1.11	1.57**	0.28
6	Number of pods per plant	183.02**	1533.11**	61.94	135.50	3066.23**	40.46	79.25**	5.83
7	Number of seeds per pod	0.04**	0.08**	0.01	0.01	0.16**	0.005	0.01**	0.003
8	100 seed weight (g)	10.25**	11.32**	1.96	2.42*	22.63**	2.73*	1.12	0.72
9	Seed yield per plant (g)	8.94**	84.78**	3.46	7.52*	169.56**	3.38	3.35**	0.72
10	Protein content (%)	4.94**	0.06	0.07	0.07	0.13	0.07	0.07	0.06

***Significant at 5%, **Significant at 1%**

4.5 Estimates of environmental indices

Estimates of environmental indices (Ij) are presented in Table 4.5, which revealed that environment E1 (Akola) was favorable for characters i.e. number of primary branches per plant and 100 seed weight.

Table 4.5. Estimation of environment index (Ij) under different environments

Sr. No	Genotypes	Environmental index (Ij)		
		E1	E2	E3
1	Days to 50% flowering	-0.26	-0.29	0.56
2	Plant height (cm)	-7.17	0.68	6.49
3	Days to maturity	-2.33	-3.93	6.27
4	Number of primary branches per plant	0.41	-0.14	-0.27
5	Number of secondary branches per plant	-0.21	-1.94	2.15
6	Number of pods per plant	-4.23	-5.84	10.07
7	Number of seeds per pod	-0.07	0.02	0.05
8	100 seed weight (g)	0.69	0.11	-0.80
9	Seed yield per plant (g)	-1.42	-0.95	2.36
10	Protein content (%)	-0.004	0.059	-0.055

Environment E2 (Buldana) was favorable for characters viz., plant height, number of seeds per pod, 100 seed weight, protein content.

Environment E3 (Nagpur) was favorable for characters viz., days to 50% flowering, plant height, days to maturity, number of secondary branches per plant, number of pods per plant, number of seeds per pod, seed yield per plant

4.6 Stability Parameters for individual characters

An ideal genotype is defined as the one possessing high mean performance, with regression coefficient around unity (b_i=1) and deviation from regression (S^2d_i) close to zero. The linear regression is regarded as the measure of linear response of a particular genotype to the changing environment. If the regression coefficient (b_i) is greater than unity, the genotype is said to be highly sensitive to environmental fluctuations but adapted to high yielding environments. If the regression coefficient (b_i) is equal to unity, it indicates the average sensitivity to environmental fluctuations and adaptable to all environments. If the regression coefficient (b_i) is less than unity, it indicates less sensitivity to environmental changes and if this is accomplished by a high mean value, then the genotype is said to be better adapted for poor conditions. In the present study stability parameters such as mean ($\bar{x}$), regression coefficient (b_i) and deviation from regression (S^2d_i), as suggested by Eberhart and Russell (1966) were considered to explain and discuss the stability of different genotypes for various characters under consideration.

The three stability parameters *viz*., mean, regression coefficient (b_i) and mean square deviation from regression line (S^2d_i) were estimated for all the ten characters and the results obtained are presented character wise in the Tables 4.6

1. Days to 50 % flowering (No.)

The days to 50 % flowering ranged from 50.00 days (PDKV Kanchan) to 57.33 days (Phule G-15109) with a population mean of 52.96 days over three environments. Thirteen genotypes viz., AKG-1303 (51.33 days), AKG-1401 (52.78 days), AKG-1504 (52.67 days), BDNG 2015-9 (52.00 days), BDNG 2015-6 (51.56 days), Phule G-13107 (52.67 days), Phule G-0819-43 (51.78 days), Phule G-0405 (52.22 days), AKRG 1701 (51.56 days), BDNG-797 (51.11 days), Phule Vikram (52.33 days), JAKI-9218 (52.56 days), PDKV Kanchan (50.00 days) had mean values lower than the population mean, which is desirable for earliness.

The genotypes viz., AKG-1303 (51.33 days), AKG-1401 (52.78 days), Phule G-0405 (52.22 days) and BDNG-797 (51.11 days), had low mean values than population mean (52.96 days) with non-significant regression coefficient (bi= 0.73, 0.30, -0.35 and 0.94 respectively) with non-significant deviation from regression (S^2di= 4.15, 1.10, -1.58, and -1.04 respectively) indicating their average stability for this trait i.e. of earliness genotypes perform better under all environments, in respect which is desirable.

Table 4.6a Estimates of stability parameters for days to 50 % flowering and Plant Height (cm)

Sr. No	Genotypes	Days to 50% Flowering (days)			Plant Height (cm)		
		$\bar{x}$	b_i	S^2d_i	$\bar{x}$	b_i	S^2d_i
1	AKG-1303	51.33	0.73	4.15	53.61	1.07	2.31
2	AKG-1401	52.78	0.30	1.10	46.70	1.17	5.25
3	AKG-1506	54.22	3.78	-2.38	43.46	0.39*	-7.42
4	AKG-1504	52.67	5.45	-1.38	43.86	0.74	13.24
5	BDNG 2015-9	52.00	7.07	3.89	49.36	1.20	-6.95
6	BDNG 2015-6	51.56	-6.44	-1.86	43.98	0.45*	-7.35
7	BDNG 2016-1	54.44	-1.39	-2.42	45.67	1.09	10.09
8	BCP-60	53.00	-3.67	-0.72	43.87	1.18	-4.47
9	Phule G-13107	52.67	-2.89	2.31	53.93	1.65	59.92**
10	Phule G-0819-43	51.78	-2.07	-0.62	50.33	1.05	-1.67
11	Phule G-15109	57.33	1.81	-2.45	49.56	1.39	-6.03
12	Phule G-0405	52.22	-0.35	-1.58	48.07	0.72*	-7.41
13	AKRG 1701	51.56	2.59	-2.40	42.47	0.63*	-7.40
14	AKRG 1702	57.00	-0.54	-1.07	41.51	0.41	-0.92
15	BDNG-797	51.11	0.94	-1.04	42.73	0.93	-5.84
16	Vijay	55.33	0.54	-1.07	44.39	1.59	-2.57
17	Digvijay	53.33	3.60*	-2.48	46.10	1.45	4.58
18	Phule Vikram	52.33	3.64	-1.75	52.84	1.02	-4.77
19	PDKV Kanchan	50.00	5.50	1.48	43.37	1.04	-7.22
20	JAKI-9218	52.56	1.39	-1.42	46.76	0.86	0.83
	Mean	52.96			46.63		

***Significant at 5%, **Significant at 1%**

$\bar{x}$: - Mean Performance over 3 environments.

b_i – Regression coefficient

S^2d_i – Deviation from regression

2. Plant height (cm)

Plant height ranged from 41.51 cm (AKRG 1702) to 53.93 cm (Phule G-13107) with a population mean of 46.63 cm over three environments. Nine genotypes viz., AKG-1303 (53.61 cm), AKG-1401 (46.70 cm), BDNG 2015-9 (49.36 cm), Phule G-13107 (53.93 cm), Phule G-0819-43 (50.33 cm), Phule G-15109 (49.56 cm), Phule G-0405 (48.07 cm), Phule Vikram (52.84 cm), JAKI-9218 (46.76 cm), had mean values higher than the population mean, which is desirable for plant height.

The genotypes AKG-1303, AKG-1401, BDNG 2015-9, Phule G-0819-43, Phule G-15109 Phule Vikram and JAKI-9218 had non-significant values for regression coefficient (bi=1.07, 1.17, 1.20, 1.05, 1.39, 1.02, and 0.86, respectively) close to unity, with non-significant deviation from regression (S^2di=2.31, 5.25, -6.95, -1.67, -6.03, -4.77, 0.83, respectively) indicating their average stability for this trait i.e. genotypes perform better under all environments.

The genotypes Phule G-0405 had significant values for regression coefficient (bi=0.72) less than unity, with non-significant deviation from regression (S^2di= -7.41) indicating above average stability i.e. suitable for favorable environment. The genotype Phule G-13107 had significant values of S^2di indicating their unpredictability for this trait.

3. Days to maturity (No.)

The days to maturity ranged from 98.78 days (AKRG 1702) to 105.67 days (Vijay) with population mean of 102.5 days. Nine genotypes viz., AKG-1401 (100.1 days), AKG-1506 (100.7 days), BCP-60 (102.3 days), Phule G-0819-43 (100.1 days), Phule G-15109 (102.2 days), Phule G-0405 (100.1 days), AKRG 1701 (100.7 days), AKRG 1702 (98.78 days) and Digvijay (101.0 days) had low mean values than population mean (102.5 days) which is desirable for earliness.

The genotypes viz., AKG-1401, AKG-1506, BCP-60, Phule G-0819-43, Phule G-0405, AKRG 1701 and AKRG 1702 recorded lower mean performances (100.1, 100.7, 102.3, 100.1, 100.1, 100.7, and 98.78 respectively) and non-significant regression coefficient greater than unity (bi=1.32, 0.52, 1.21, 1.23, 1.25, 1.08, and 1.10, respectively) with non-significant deviation from regression (S^2di= 6.5, 1.5, -2.2, 0.1, -2.5, -2.1, and 5.9 respectively) indicating their general adaptability for this trait i.e. these genotypes perform better under all environment. The genotypes had significant values of S^2di AKG-1303, BDNG 2015-9, BDNG 2016-1, Phule G-15109, BDNG-797 and Digvijay indicate that we cannot predict the performance of these genotypes

4. Primary branches per plant

The number of primary branches per plant ranges from 2.67 (BDNG 2016-1) to 3.56 (JAKI-9218 and PDKV Kanchan) with a population mean (3.11). The genotype viz., BCP-60 (3.13), Phule G-13107 (3.11), Phule G-15109 (3.36), AKRG 1701 (3.29), BDNG-797 (3.27), Vijay (3.53), Phule Vikram (3.11), JAKI-9218 (3.56), and PDKV Kanchan (3.56) exhibited superior mean than population mean (3.11).

The genotypes viz., BCP-60, Phule G-15109, AKRG 1701, BDNG-797, Vijay, Phule Vikram ,PDKV Kanchan and JAKI-9218 had superior mean (3.13, 3.36, 3.29, 3.27, 3.53, 3.11,3.56 and 1.12 respectively) than population mean (3.11), non-significant regression coefficient (bi= 1.10, 0.98, 1.81, 1.23, 0.96, 0.60, 0.14 and 0.03 respectively) close to unity with non-significant deviation from regression (S^2di = -0.01, -0.01, 0.06, 0.02, -0.02, -0.01, and -0.02, respectively) indicating their average stability i.e., suitable for all environments.

Genotype Phule G-13107 has high mean (3.11) and regression coefficient (bi=1.34) significantly greater than unity with non-significant deviation from regression (S^2di = -0.03) is indicating below average stability i.e. suitable for favorable environment.

5. Secondary branches per plant

The number of secondary branches per plant ranged from 7.40 (BDNG 2015-6) to 11.40 (Phule G-15109) with a population mean (9.30). The genotypes viz., AKG-1504 (9.53), Phule G-13107(9.38), Phule G-15109 (11.40), AKRG 1701 (11.03), BDNG-797 (10.49), Vijay (11.11), PDKV Kanchan (9.33) and JAKI-9218 (10.13), exhibited superior mean than population mean (9.30).

Table 4.6b. Estimates of stability parameters for days to maturity and primary branches per plant

Sr. No	Genotypes	Days to maturity			Number of primary branches per plant		
		$\bar{x}$	b_i	S^2d_i	$\bar{x}$	b_i	S^2d_i
1	AKG-1303	102.7	0.76	10.8*	2.87	1.48*	-0.03
2	AKG-1401	100.1	1.32	6.5	2.76	1.00	0.05
3	AKG-1506	100.7	0.52	1.5	2.89	1.19	0.05
4	AKG-1504	103.4	1.05	4.3	3.02	0.87	0.06
5	BDNG 2015-9	102.8	1.22	10.4*	2.98	0.15	0.01
6	BDNG 2015-6	105.0	0.82	-1.1	2.71	-0.18	0.04
7	BDNG 2016-1	103.1	0.69	18.6**	2.67	1.00	0.15*
8	BCP-60	102.3	1.21	-2.2	3.13	1.10	-0.01
9	Phule G-13107	102.6	0.83	-2.4	3.11	1.34**	-0.03
10	Phule G-0819-43	100.1	1.23	0.1	3.29	1.30	-0.02
11	Phule G-15109	102.2	1.21	17.5**	3.36	0.98	-0.01
12	Phule G-0405	100.1	1.25	-2.5	3.00	1.53	0.08
13	AKRG 1701	100.7	1.08	-2.1	3.29	1.81	0.06
14	AKRG 1702	98.8	1.10	5.9	3.07	2.12	-0.03
15	BDNG-797	105.6	1.25	24.8**	3.27	1.23	0.02
16	Vijay	105.7	1.51	-1.3	3.53	0.96	-0.02
17	Digvijay	101.0	1.10	51.0**	3.09	0.52	0.03
18	Phule Vikram	104.3	0.82	-1.1	3.11	0.60	-0.01
19	PDKV Kanchan	102.9	0.66	-2.4	3.56	0.14	-0.02
20	JAKI-9218	105.0	0.38	1.9	3.56	1.12	0.03
	Mean	102.5			3.11		

***Significant at 5%, **Significant at 1%**

The genotypes viz., AKG-1504, Phule G-15109, BDNG-797, Vijay, PDKV Kanchan and JAKI-9218 had higher mean (9.53, 11.40, 10.49, 11.11, 9.33 and 10.13 respectively), then population mean (9.30) non-significant regression coefficient (bi= 0.61, 0.47, 0.90, 1.39,1.11 and 1.09 respectively) close to unity and non-significant deviation from regression (S^2di= -0.08, 0.07, 0.43, 0.16, -0.30 and 0.09 respectively) values indicating their average stability for this trait.

The genotypes viz., BDNG 2015-9, BDNG 2015-6, Phule G-13107, AKRG 1701, Digvijay, Phule Vikram, and JAKI-9218, exhibited significant deviation from regression (S^2di= 1.87, 8.30, 1.41, 0.06, 3.76 and 3.04, respectively) indicating their unpredictability for the given character.

6. Number of Pods per plant (no.)

The number of pods per plant ranged from 29.20 (BDNG 2015-9) to 67.53 (AKRG 1701) with population mean of 49.56. The genotypes viz., AKG-1401 (52.56), AKG-1506 (53.47) Phule G-13107 (50.64), Phule G-15109 (64.51), AKRG 1701 (67.53), AKRG 1702 (52.56), BDNG-797, (50.20), JAKI-9218 (49.71), and PDKV Kanchan (54.23) exhibited superior mean than population mean (49.56).

Table 4.6c. Estimates of stability parameters for number of secondary branches per plant and number of pods per plant

Sr. No	Genotypes	Number of secondary branches per plant			Number of pods per plant		
		$\bar{x}$	b_i	S^2d_i	$\bar{x}$	b_i	S^2d_i
1	AKG-1303	7.58	1.41	-0.16	46.38	0.72	270.97**
2	AKG-1401	8.84	1.48	0.11	52.56	1.44	-1.88
3	AKG-1506	9.04	0.26**	-0.31	53.47	-0.33	26.74*
4	AKG-1504	9.53	0.61	-0.08	45.87	1.29	-3.21
5	BDNG 2015-9	9.07	0.97	1.87**	46.18	1.52*	-5.98
6	BDNG 2015-6	7.40	1.36	8.30**	29.20	0.99	-5.46
7	BDNG 2016-1	8.47	1.29	0.51	40.36	1.54	78.25**
8	BCP-60	8.91	1.61	0.46	47.20	1.12	8.92
9	Phule G-13107	9.38	1.18	1.41*	50.64	0.46	-1.98
10	Phule G-0819-43	9.13	1.06	-0.31	48.38	1.52	40.76**
11	Phule G-15109	11.40	0.47	0.07	64.51	0.20	388.82**
12	Phule G-0405	8.69	0.81	-0.24	48.42	0.86	36.13**
13	AKRG 1701	11.03	0.92	0.06**	67.53	0.79	32.86*
14	AKRG 1702	9.13	0.89	3.80	52.56	1.20	-5.85
15	BDNG-797	10.49	0.90	0.43	50.20	1.00	-1.59
16	Vijay	11.11	1.39	0.16	46.07	1.29	47.76**
17	Digvijay	9.11	0.99	3.76**	49.09	1.38	185.22**
18	Phule Vikram	8.13	0.54	3.04**	48.71	1.19	188.45**
19	PDKV Kanchan	9.33	1.11	-0.30	54.23	0.62	94.17**
20	JAKI-9218	10.13	1.09	0.09	49.71	1.32	-2.1
	Mean	9.30			49.56		

***Significant at 5%, **Significant at 1%**

Genotype viz., AKG-1401, Phule G-13107, AKRG 1702, BDNG-797 and JAKI-9218 had higher mean values (52.56, 50.64, 52.56, 50.20 and 49.71 respectively) and non-significant regression coefficient values (bi= 1.44, 0.46, 1.20, 1.00 and 1.32 respectively) close to unity and non-significant deviation from regression (S^2di= -1.88, -1.98, -5.89, -1.59 and -2.1 respectively) indicating its average stability for this trait.

The genotypes viz., AKG-1303, AKG-1506, BDNG 2016-1, Phule G-0819-43, Phule G-15109, Phule G-0405, AKRG 1701, Vijay, Digvijay, Phule Vikram, and PDKV Kanchan has significant value of S^2di indicating their unpredictability for the given character.

7. Seeds per pods (no.)

The number of seeds per plant ranged from 1.03 (BDNG-797) to 1.47 (AKRG 1701) with population mean of 1.24. The genotype, Phule G-0405, AKRG 1701, Digvijay and Phule Vikram had higher mean performances (1.37, 1.47, 1.38 and 1.40, respectively) than population mean (1.24) and non-significant regression coefficient values (bi= 1.11, 1.80, 2.46 and 0.21, respectively) close to unity and non-significant deviation from regression (S^2di= 0.00,0.00, 0.00, and 0.01 respectively) indicating its average stability for this trait.

Genotypes viz., AKG-1303, AKG-1506, BDNG 2015-9, BDNG 2015-6, BCP-60, Phule G-0819-43, exhibited significant values of (S^2di= 0.01, 0.03, 0.01, 0.03, 0.01, 0.04, respectively) indicating their unpredictability for the given character.

8. 100 Seed weight (g)

100 seed weight of genotypes ranged from 20.07 g (Vijay) to 25.86 (Phule G-12110) with the population mean of 22.82 g. The genotypes AKG-1401, AKG-1506, BDNG 2015-9, BCP-60, Phule G-13107, Phule G-15109, AKRG 1702, and JAKI-9218 had superior mean (25.78, 22.89, 24.22, 25.78, 24.64, 24.22, 23.33, and 24.00, respectively) than population mean (22.82 g.) and non-significant regression coefficient (bi=0.13, 1.04, -0.10, -0.61, 1.85, 2.16, 2.74 and 0.81, respectively) close to unity and non-significant deviation from regression (S^2di= 0.47, 0.81, 0.25,

0.96, 0.44, -0.37, -0.50, and 0.56, respectively) indicating their average stability i.e. suitable for all environmental conditions.

The genotypes viz., AKRG 1701 and PDKV Kanchan had significant deviation from regression (S^2di) values indicating their unpredictability for given character.

Genotype BDNG 2015-6 has high mean (25.86) and regression coefficient (bi=-0.55) significantly less than unity with non-significant deviation from regression (S^2di= 0.21) is indicating above average stability i.e. suitable for favorable environment.

Table 4.6d. Estimates of stability parameters for number of seeds per pod and 100 seeds weight

Sr. No	Genotypes	Number of seeds per pod			100 seeds weight		
		$\bar{x}$	b_i	S^2d_i	$\bar{x}$	b_i	S^2d_i
1	AKG-1303	1.34	-0.11	0.01*	21.50	3.14	0.31
2	AKG-1401	1.18	0.89	0.00	25.78	0.13	0.47
3	AKG-1506	1.20	0.08	0.03**	22.89	1.04	0.81
4	AKG-1504	1.13	2.01	0.00	22.49	0.56	0.16
5	BDNG 2015-9	1.28	1.82	0.01*	24.22	-0.10	0.25
6	BDNG 2015-6	1.36	2.13	0.03**	25.86	-0.55**	0.21
7	BDNG 2016-1	1.18	1.00	0.00	22.44	1.52	-0.58
8	BCP-60	1.28	1.29	0.01*	25.78	-0.61	0.96
9	Phule G-13107	1.21	1.61	0.00	24.64	1.85	-0.44
10	Phule G-0819-43	1.16	0.78	0.04**	20.89	2.43	-0.66
11	Phule G-15109	1.23	1.11	0.00	24.22	2.16	-0.37
12	Phule G-0405	1.37	1.11	0.00	20.93	2.28	-0.58
13	AKRG 1701	1.47	1.80	0.00	22.84	-1.12	2.81*
14	AKRG 1702	1.20	0.21	0.01	23.33	2.74	-0.50
15	BDNG-797	1.03	0.40	0.00	21.09	1.71	0.78
16	Vijay	1.11	1.10	0.00	20.62	3.23	0.24
17	Digvijay	1.38	2.46	0.00	21.89	1.99	-0.68
18	Phule Vikram	1.40	0.21	0.01	20.07	-1.13*	-0.69
19	PDKV Kanchan	1.16	0.19	0.00	20.89	-2.09	5.32**
20	JAKI-9218	1.21	0.09	0.01	24.00	0.81	0.56
	Mean	1.24			22.82		

***Significant at 5%, **Significant at 1%**

9. Seed yield per plant (g)

The seed yield per plant ranged from 9.92 g (BDNG 2015-6) to 16.27g (AKRG 1701) with the population mean of 12.94 g. The genotypes viz., AKG-1303, BDNG 2016-1, Phule G-0819-43, Phule G-0405, Digvijay and Phule Vikram had significant deviation from regression (S^2di) values indicating their unpredictability for given character.

Genotypes AKG-1401, AKG-1506, BCP-60, Phule G-15109, AKRG 1701, AKRG 1702, PDKV Kanchan and JAKI-9218 had high mean performance (13.30 g, 15.12 g, 13.32 g, 14.74 g, 16.27 g, 14.92 g, 14.49 g and 14.43 g respectively) with non-significant regression coefficient (bi= 1.51, 0.09, 1.08, 0.92, 1.06, 1.19, 0.74 and 1.03 respectively) and non-significant deviation from regression (S^2di= 1.28, 1.52, -0.67,-0.74, 0.58, 0.32, -0.63 and 0.47 respectively) indicating their average stability for this character.

Genotype BDNG 2015-9 had high mean, with regression coefficient significantly greater than unity (bi) and non-significant deviation from regression (S^2di) indicating below average stability i.e. suitable for favorable environment.

10. Protein content (%)

The protein content ranged from 17.27% (Phule G-0819-43) to 21.73% (Digvijay) with the population mean of 19.22%. Genotypes AKG-1506, BDNG 2015-6, Phule G-15109, Phule G-0405, AKRG 1702, BDNG-797, Vijay, Digvijay and PDKV Kanchan had high mean performance (19.36, 19.36, 19.32, 20.61, 19.44, 20.22, 20.49, 21.73 and 20.15, respectively) with non-significant regression coefficient (bi= -0.95, 1.28, -0.47, 1.01, 2.91, 2.04, -2.61, 10.02 and -2.56, respectively) and non-significant deviation from regression (S^2di = -0.06, -0.04, -0.01, -0.04, -0.07, -0.07, -0.05, 0.12 and 0.03 respectively) indicating their average stability for this character.

The genotypes viz., BDNG 2015-9 and Phule Vikram had significant deviation from regression (S^2di) values indicating their unpredictability for given character.

Genotype AKG-1303 had high mean (20.36%) than population mean (19.22%) with regression coefficient significantly less than unity (bi = -3.99) and non-significant deviation from regression (S^2di = -0.07) indicating above average stability i.e. suitable for favorable environment.

Table 4.6e. Estimates of stability parameters for seed yield per plant and protein content (%)

Sr. No	Genotypes	Seed yield per plant			Protein content (%)		
		$\bar{x}$	b_i	S^2d_i	$\bar{x}$	b_i	S^2d_i
1	AKG-1303	11.09	0.28	12.41**	20.36	-3.99*	-0.07
2	AKG-1401	13.30	1.51	1.28	18.42	-1.80	-0.07
3	AKG-1506	15.12	0.09	1.52	19.36	-0.95	-0.06
4	AKG-1504	11.38	1.54	0.63	17.44	3.41	-0.01
5	BDNG 2015-9	13.61	1.84**	-0.52	17.86	6.53	0.48**
6	BDNG 2015-6	9.92	2.14	-0.70	19.36	1.28	-0.04
7	BDNG 2016-1	10.09	0.70	7.05**	18.27	-0.88	-0.01
8	BCP-60	13.32	1.08	-0.67	18.48	1.68	-0.06
9	Phule G-13107	12.56	-0.17	-0.50	17.56	1.13	-0.07
10	Phule G-0819-43	11.98	0.95	5.38**	17.27	0.23	-0.07
11	Phule G-15109	14.74	0.92	-0.74	19.32	-0.47	-0.01
12	Phule G-0405	12.12	1.17	6.26**	20.61	1.01	-0.04
13	AKRG 1701	16.27	1.06	0.58	18.49	1.78	-0.07
14	AKRG 1702	14.92	1.49	0.32	19.44	2.91	-0.07
15	BDNG-797	12.21	0.80	1.21	20.22	2.04	-0.07
16	Vijay	12.59	0.69	0.01	20.49	-2.61	-0.05
17	Digvijay	13.40	2.08	10.99**	21.73	10.02	0.12
18	Phule Vikram	11.36	0.82	8.52**	21.08	2.97	0.26*
19	PDKV Kanchan	14.49	0.74	-0.63	20.15	-2.56	-0.03
20	JAKI-9218	14.43	1.03	0.47	18.49	-1.74	-0.07
	Mean	12.94			19.22		

***Significant at 5%, **Significant at 1%**

4.7 DISCUSSION

In any crop improvement programme existence of sufficient amount of genetic variability is a prerequisite for success of any breeding programme. It is therefore necessary to assess the extent of variability existing in the population. Variability can be assessed by estimating genetic parameters like Phenotypic coefficient of variation, Genotypic coefficient variation, Heritability as well as Expected genetic advance percent over mean. The genetic variability estimated in terms of genotypic coefficient variation and phenotypic coefficient of variation is not sufficient for the estimation of heritable variation. The heritable variation can be estimated with the greater degree of accuracy, when heritability studied along with genetic advance. The heritability values in broad sense are also helpful in selection on the basis of phenotypic performance of the quantitative characters. However, heritability estimates alone are not of any use in predicting the results of selection unless it is accompanied by genetic advance.

4.7.1 Analysis of Variance

The main objective of the present investigation was to study the variability present in twenty genotypes of chickpea. The estimates of mean sum of square due to genotypes were highly significant for all the characters (Table 4.1), indicating the presence of genetic variability in the existing material. Comparable results were reported by Srivastava et al. (2017), Arora *et al*. (2018), Barad *et al.* (2018), Kishor *et al.* (2018), Singh *et al*. (2018), Thakur *et al.* (2018) in chickpea.

4.7.2 Genetic variability

In the present findings phenotypic coefficient of variation were observed to be higher than the corresponding genotypic coefficient of variation for all the characters studied, however, the differences were narrow which implied their relative resistance to environmental variation. It also described that genetic factors were predominantly responsible for expression of those attributes and selection could be made effectively on the basis of phenotypic performance. Comparable results were reported by

Jeena and Arora (2001), Thakur and Sirohi (2008), Bhavani *et al*. (2009), Sreelakshmi *et al.* (2010), Shweta *et al.* (2013), Parhe *et al*. (2014), Babbar and Tiwari (2018), Thakur *et al.* (2018) in chickpea.

i. Phenotypic coefficient of variations

The high PCV were recorded for the number of pods per plant (21.54%) followed by seed yield per plant (20.03%). The moderate PCV were recorded for number of secondary branches per plant (17.55%), number of primary branches per plant (13.45%), plant height (12.83%), number of seeds per pod (12.37%), 100 seed weight (10.88%), whereas lowest PCV were recorded by protein content (7.03%), days to 50% flowering (6.21%) and days to maturity (3.65%). Comparable results were reported by Tripathi and Arora (1991), Usmani *et al.* (2005), Akhtar *et al.* (2011), Astereki *et al.* (2015), Babbar and Tiwari (2018), Johnson *et al.* (2018), Thakur *et al.* (2018) in chickpea.

ii. Genotypic Coefficient of Variation (%).

The moderate GCV were recorded for number of pods per plant (14.88%) followed by seed yield per plant (12.24%), number of secondary branches per plant (10.73%), whereas lowest GCV were recorded by number of seeds per pod (8.49%), number of primary branches per plant (7.76%), 100 seed weight (7.68%), plant height (7.47%), protein content (6.63%), days to 50% flowering (3.07%) and days to maturity (1.63%). Comparable results were reported by Durga *et al.* (2007), Vaghela *et al.* (2008), Babbar *et al.* (2012), Desai *et al.* (2015), Babbar and Tiwari (2018), Johnson *et al.* (2018), Singh *et al.* (2018), Thakur *et al.* (2018) in chickpea.

iii. Heritability estimates in broad sense (%)

Heritability which denotes the proportion of genetically controlled variability expressed by a programme for a particular character or a set of character is very important biometrical tool for guiding plant breeders for adoption of appropriate breeding procedures. High heritability in broad sense is helpful in identifying appropriate character for selection and enables the breeder to select superior genotypes on the basis of phenotypic expression of quantitative characters. The estimated values of heritability in broad sense were classified as very high (above 90%), high (75-90%), medium (50-75%) and low (less than 50%).

High heritability estimate in broad sense was observed for protein content (89.00%). The medium heritability estimate in broad sense were observed for the characters viz. 100 seed weight (49.90%), number of pods per plant (47.70%), number of seeds per pod (47.00%). The low heritability estimate in broad sense recorded by the characters viz. number of secondary branches per plant (37.40%), seed yield per plant (37.30%), plant height (33.90%), number of primary branches per plant (33.30%), days to 50% flowering (24.40%) and days to maturity (20.00%). Comparable results were reported by Nimbalkar (2000), Tiwari *et al.* (2017), Barad *et al.* (2018), Johnson *et al.* (2018), Singh *et al.* (2018). Thakur *et al.* (2018) in chickpea.

iv. Expected genetic advance (%)

The highest genetic advance percent over mean was observed for the character number of pods per plant (21.17%). The medium genetic advance percent over mean was observed for the characters seed yield per plant (15.41%), number of secondary branches per plant (13.53%), protein content (12.89%), number of seeds per pod (11.99%),100 seed weight (11.18%), The low genetic advance percent over mean was recorded for the character’s number of primary branches per plant (9.22%), plant height (8.96%), days to 50% flowering (3.12%) and days to maturity (1.51%). Comparable results were reported by Nimbalkar (2000), Vaghela *et al.* (2009), Srivastava *et al.* (2017), Tiwari *et al.* (2017), Babbar and Tiwari (2018), Barad *et al.* (2018), Singh *et al.* (2018), Thakur *et al.* (2018) in chickpea.

The genotypes performing well under different environments are necessary to have optimum yield level when sown at different environments. Therefore, in this investigation studies on the performance of different genotypes at three environments were taken and the results have been discussed in this chapter under appropriate sub-headings.

4.7.3 Response of genotypes to three different environments

It is revealed that, the mean number of days required for 50 per cent flowering and physiological maturity were greatly influenced by different environments. The genotype PDKV Kanchan recorded lower number of days for 50 %flowering i.e., 50.00 days. Lowest numbers of days to 50 % flowering were recorded by environment E2 (Buldana). The environment E2 was earliest for maturity followed by environment E1. Among all genotypes, AKRG 1702 (98.8 days) was earliest to maturity over the three environments followed by AKG-1401 (100.1 days). Present study revealed that under environment E2, all the varieties took less number of days to flower and less number of days to maturity. This was due to early sowing which resulted into early flowering and early maturity.

It is seen from the mean data presented for plant height that, the highest mean plant height was recorded in environment E3 (Nagpur). In over all three environments indicated that the genotypes Phule G-13107 (53.93 cm) was the tallest among all genotypes followed by and at par viz. AKG 1303 (53.61 cm) and Phule Vikram (52.84 cm). In overall locations the genotype JAKI-9218 (3.6), PDKV Kanchan (3.6) was found significantly maximum number of primary branches per plant followed by the genotype Vijay (3.5) and Phule G-15109 (3.4). Number of primary and secondary branches played important role in determining seed yield in chickpea. Maximum number of primary branches were recorded in environment E1 (Akola) (3.51) followed by environment E2 (Buldana) (2.97) and E3 (Nagpur) (2.84). In overall locations the genotype Phule G-15109 was found significantly maximum number of secondary branches (11.4) followed by the genotype Vijay (11.1) and AKRG 1701 (11.0). Highest number of secondary branches were recorded in E3 (Nagpur) followed by E1 (Akola) and E2 (Buldana)

The pods per plant is an important yield component, reported to be significantly positively correlated with seed yield per plant and is affected by different environment. In overall locations the genotype AKRG 1701 was found significantly highest number of pods per plant (67.53) followed by the genotype Phule G-15109 (64.51). For pods per plant E3

(Nagpur) was superior (59.63) followed by E1 (Akola) (45.33), E2 (Buldana) (43.73). The genotype AKRG 1701 (1.5) produced significantly highest number of seeds per pod followed by BDNG 2015-6 (1.35), Phule G-0405 (1.36), Digvijay (1.38) and Phule Vikram (1.4) in over all the three environments. For seeds per pod the environment E3 (Nagpur) (1.29) was superior followed by E2 (Buldana) (1.27), E1 (Akola) (1.17). In overall location the genotype BDNG 2015-6 (25.86 g) had shown promising for 100 seed weight and equally followed by AKG-1401 (25.78 g) and BCP 60 (25.78 g). On the mean performance basis over three environments maximum 100 seed weight was recorded in E1 (Akola) (23.51 g).

From the results, it is observed that the seed yield per plant was affected due to different environments. In overall locations the genotype AKRG 1701 was found significantly highest yield per plant (16.27 g) followed by the genotype AKG-1506 (15.12 g) and AKRG 1702 (14.92 g). Whereas, the genotype was BDNG 2015-6 recorded lowest yield per plant (9.92 g). The maximum seed yield was recorded in E3 (Nagpur) environment and decreased drastically for E2 (Buldana) and E1 (Akola) environments. In overall locations the genotype Digvijay recorded highest protein content (21.73%) followed by the genotype Phule Vikram (21.08%), Phule G-0405 (20.61%). For protein content environment E2 (Buldana) was superior (19.28%) followed by E1 (Akola) and E3 (Nagpur).

4.7.4 Genotype x environment interaction studies

Productivity of the population is the function of its adaptability. Significant achievement in crop production may be possible by breeding varieties for their stability for yield and yield components. Plant breeding is said to be the management of genetic variability. Plant breeders look for greater variability in crop plants for evolving strains which give maximum yield over the environments and show consistent performance. There is no direct measurement for genetic variability. However, the same can be inferred from the phenotype, which is a linear function of genotypes, environment and their interaction. Phenotype usually gets changed when a genotype is grown over varying environments. It has been shown that, interactions are widely present irrespective of nature of material. This sets limits to the expected progress. The interactions of genetic and non-genetic factors on phenotypic expression is called genotype x environment (G x E) interaction which is widely present and substantially contributes to the non-realization of expected gain from selection (Comstock and Moll, 1963).

Stable genotypes are particularly of great importance in the country like India, where the crops are grown as a risk under varied environmental conditions. G x E interaction certainly plays an important role in the evaluation and execution of breeding programmes. Allard and Bradshaw (1964) have critically reviewed this phenomenon and brought out its implications in applied plant breeding. Thus, G x E interaction is important in the expression of quantitative characters, which are controlled by polygenic systems and largely influenced by environmental fluctuations.

The process of identification of stable genotype is difficult because of G x E interaction. Although the plant breeders have observed genetic differences for adaptability, they have been unable to fully exploit these differences in breeding stable genotypes. This has been largely due to the problem of defining and measuring phenotypic stability. Various attempt was made to characterize the behaviours of genotypes in response to varying environments. Statistically approach of Finlay and Wilkinson (1963) has proved considerably useful to measure the phenotypic stability in the performance of genotype. They considered linear regression slope (bi) as a measure of stability. This regression analysis proposed by Finlay and Wilkinson (1963) was improved upon by Eberhart and Russell (1966). They introduced one more parameter, deviation from regression (S^2di) which accounts for unpredictable irregularities in the response of genotypes to varying environments.

Various methods have been proposed for statistical analysis of G X E interaction from time to time. Growing a set of genotypes under a large number of environments and combined analysis is useful in assessing the G X E interaction and comparing different types of populations, but it did not go any further towards dynamic interpretation of the stability of individual genotypes. The most widely used approach in this respect is the regression technique in which G X E interaction component of variability partitioned into its linear and non-linear portions for assessing the stability of genotypes over a range of environments. This is known as joint regression analysis. Many workers have contributed to the development of this approach, notable amongst them are, Finlay and Wilkinson (1963), Eberhart and Russell (1966), Freeman and Perkins (1971).

The information on the relative stability of the genotypes for different yield components is essential. The results obtained on different stability parameters estimated for the different characters separately with a view to identify suitable conditions. They are discussed in brief below. In the present investigation twenty genotypes of chickpea were studied through genotype x environment interaction and stability analysis. The material was sown on three different locations viz., Akola, Buldana, Nagpur and stability of genotypes assessed by following Eberhart and Russell (1966) model.

4.7.5 Pooled Analysis of variance

The pooled analysis of variance for phenotypic stability as per Eberhart and Russel (1966) indicated that mean differences due to genotypes were statistically significant for the characters, days to 50% flowering, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight, seed yield per plant and protein content, except days to maturity when tested against G X E interaction. (Table 4.4).

The G X E interactions were non-significant for all the traits when tested against pooled deviation and pooled error. Partitioning of G X E interaction showed that, G x E (linear) effect were significant for the characters viz., days to 50% flowering and 100 seed weight. Environment (linear) effects were also significant for all the studied characters except protein content, when tested against pooled deviation and pooled error. The significance of pooled deviation (non-linear) effects for the characters viz., days to maturity, number of secondary branches per plant, number of pods per plant, number of seeds per pod, seed yield per plant, confirmed the presence of G X E interaction for various traits.

Prakash (2005) also observed significant linear and non-linear components of G X E interactions for all the traits except primary and secondary branches and seed yield. Deshmukh *et al.* (1998), Sirohi *et al.* (2001), Rao and Rao (2004), Rao (2011) observed significant differences among genotype, environment and G X E interaction for all the studied characters in chickpea.

4.7.6 Stability parameters for individual characters

Finlay and Wilkinson (1963) considered linear regression slope (bi) and emphasized the need of both 'bi' and deviation from regression 'S^2di' as measure of stability. Further Eberhart and Russell (1966) showed the need of both regression coefficient (linear) (bi) and deviation from regression (S^2di) (non-linear) in evaluating genotypes for phenotypic stability by measuring G X E interactions.

These points are considered for deciding stability of genotypes i.e. the genotypes with at least mean performance statistically greater than population mean (also with in population mean + S.E.) and S^2di low or non-significant and (1) 'bi' approaching to unity or not significantly deviating from unity are regarded with general adaptability or average stability. (2) 'bi' significantly greater than unity is considered as better adaptable to rich or favourable environment (below average stability). (3) 'bi' significantly less than unity and or having lower magnitude than unity is considered as better adaptable to poor or unfavourable environment (above average stability). The genotypes with significant S^2di components are considered as highly unpredictable. In some cases, relative 'bi' Eberhart and Russell (1966) method was preferred because of its explicit nature.

The estimates of environmental indices for 10 characters (Table 4.5) under the present study showed that environment E1 (Akola) was favourable for the characters like number of primary branches per plant and 100 seed weight. Environment E2 (Buldana) was favorable for characters viz., plant height, number of seeds per pod, 100 seed weight and protein content. Environment E3 (Nagpur) was favorable for characters viz., days to 50% flowering, plant height, days to maturity, number of secondary branches per plant, number of pods per plant, number of seeds per pod, seed yield per plant.

In general environment E3 (Nagpur)) was most favorable for yield and yield contributing characters.

The stability parameters estimated for different traits are presented in Table 4.6 which helped to identify genotypes with general and specific adaptability. Yield is the end product depends on holding certain morphological and physiological attributes and allowing others to vary, resulting in predictable G X E interaction for ultimate character the yield. The study of stability in yield components in this respect therefore, is of great importance. The results of the present investigation carried in this direction are discussed below.

1 Days to 50 % flowering

For this trait, the genotype AKG-1303, AKG-1401, Phule G-0405 and BDNG-797 recorded lower mean, non-significant regression coefficient (bi) close to unity, with non-significant deviation from regression (S^2di) exhibited average stability for this trait.

The linear and non-linear components of G X E interaction were found to be significant. Similar results were reported by Sharma and Maloo (1989), Baisakh and Nayak (1991), Rao and Rao (2004), Prakash (2005), in their stability studies in chickpea. Babbar and Tiwari (2018).

2. Plant height (cm)

The genotypes AKG-1303, AKG-1401, BDNG 2015-9, Phule G-0819-43, Phule G-15109 Phule Vikram and JAKI-9218 recorded higher mean, non-significant for regression coefficient (bi) close to unity, with non-significant deviation from regression (S^2di) indicating their average stability for this trait i.e. genotypes perform better under all environments.

The genotypes Phule G-0405 had significant values for regression coefficient (bi) less than unity, with non-significant deviation from regression (S^2di) indicating above average stability i.e. suitable for favorable environment. Similar results were reported by Sharma and Maloo

(1989), Prakash (2005), Chaudhary *et al.* (2012), Balapure *et al.* (2015), Shivani and Sreelakshmi (2015), Babbar and Tiwari (2018)

3. Days to maturity

The genotypes viz., AKG-1401, AKG-1506, BCP-60, Phule G-0819-43, Phule G-0405, AKRG 1701 and AKRG 1702 recorded lower mean performances, non-significant regression coefficient (bi) greater than unity and non-significant deviation from regression (S^2di) indicating their general adaptability for this trait i.e. these genotypes perform better under all environment.

The linear and non-linear component of G X E interaction were significant. Singh and Kumar (1993), Baisakh and Nayak (1991), Popalghat *et al.* (1998), Prakash (2005), Balapure *et al.* (2015), Shivani and Sreelakshmi (2015), Babbar and Tiwari (2018) were also observed non-significant regression coefficient (bi) and non-significant deviation from regression (S^2di) for days to maturity in chickpea.

4. Primary branches per plant

The genotypes viz., BCP-60, Phule G-15109, AKRG 1701, BDNG-797, Vijay, Phule Vikram, and PDKV Kanchan had non-significant regression coefficient (bi) close to unity with high population mean and non-significant deviation from regression (S^2di) indicating their average stability i.e., suitable for all environments.

Genotype Phule G-13107 had significant regression coefficient (bi) greater than unity and non-significant deviation from regression (S^2di) is indicating below average stability i.e. suitable for favorable environment.

Similar results were reported for primary branches per plant in chickpea by Sirohi *et al.* (2001), Singh and Sandhu (2006), Gupta and Sharma (2009), Chaudhary and Haque (2010), Balapure *et al.* (2015), Babbar and Tiwari (2018).

5. Secondary branches per plant

The genotypes viz., AKG-1504, Phule G-15109, BDNG-797, Vijay, and PDKV Kanchan had higher mean, non-significant regression coefficient (bi) close to unity and non-significant deviation from regression (S^2di) values indicating their average stability for this trait.

Similar results were reported by Sirohi *et al.* (2001), Sharma and Maloo (1989), Singh *et al.* (1991), Singh and Sandhu (2006), Gupta and Sharma (2009), Balapure *et al.* (2015), Babbar and Tiwari (2018)

6. Number of Pods per plant (no.)

The genotype viz., AKG-1401, Phule G-13107, AKRG 1702, BDNG-797 and JAKI-9218, had higher mean, non-significant regression coefficient values (bi) close to unity and non-significant deviation from regression (S^2di) indicating its average stability for this trait.

Mehra and Ramanujan (1979), Singh *et al.* (1991), Rao and Rao (2004), Malhotra *et al*. (2007), Chaudhary and Haque (2010), Shivani and Sreelakshmi (2015). reported similar results in chickpea.

7. Seeds per pod (no.)

The genotype, Phule G-0405, AKRG 1701, Digvijay and Phule Vikram had higher mean performances, non-significant regression coefficient (bi) close to unity and non-significant deviation from regression (S^2di) indicating its average stability for this trait. Comparable results were reported by Mehra *et al.* (1980), Singh and Mehra (1980), Deshmukh *et al.* (1998), Sood *et a*l. (2000), Prakash (2005) Babbar and Tiwari (2018) in their stability studies with chickpea.

8. 100 Seed weight (g)

The genotypes AKG-1401, AKG-1506, BDNG 2015-9, BDNG 2015-6, BCP-60, Phule G-13107, Phule G-15109, AKRG 1702, and JAKI-9218 had superior mean, non-significant regression coefficient (bi) close to unity and non-significant deviation from regression (S^2di) indicating their average stability i.e. suitable for all environmental conditions.

Genotype BDNG 2015-6 had significant regression coefficient (bi) less than unity and non-significant deviation from regression (S^2di) is indicating above average stability i.e. suitable for favorable environment. Similar results were reported by Sirohi *et al.* (2001), Prakash (2005), Singh and Sandhu (2006), Gupta and Sharma (2009), Rao *et al.* (2011), Babbar and Tiwari (2018),

9. Seed yield per plant (g)

Genotypes AKG-1401, AKG-1506, BCP-60, Phule G-15109, AKRG 1701, AKRG 1702 and PDKV Kanchan had high mean performance, non-significant regression coefficient (bi) and non-significant deviation from regression (S^2di) indicating their average stability for this character.

Genotype BDNG 2015-9 had high mean, with regression coefficient significantly greater than unity (bi) and non-significant deviation from regression (S^2di) indicating below average stability i.e. suitable for favorable environment.

Similar results were obtained by Mehra and Ramanujan (1979), Singh *et al*. (1991), Rao and Rao (2004), Malhotra *et al*. (2007), Chaudhary and Haque (2010), Chaudhary *et al.* (2012), Rao *et al.* (2011), Shivani and Sreelakshmi (2015), Balapure *et al.* (2015) Babbar and Tiwari (2018) in chickpea.

10. Protein content (%)

Genotypes AKG-1506, BDNG 2015-6, Phule G-15109, Phule G-0405, AKRG 1702, BDNG-797, Vijay, Digvijay and PDKV Kanchan had high mean performance, non-significant regression coefficient (bi) and non-significant deviation from regression (S^2di) indicating their average stability for this character.

Genotype AKG-1303 had high mean, with regression coefficient significantly less than unity (bi) and non-significant deviation from regression (S^2di) indicating above average stability i.e. suitable for favorable environment. Similar results were reported by Alwani *et al.* (2010).

Table 4.7. Nature of stability of chickpea genotypes under different environments

Sr. No.	Character	Genotypes showing stability		
		Average stability (suitable for all environments)	Above average stability (bi<1) (suitable for poor environment)	Below average stability (bi>1) (suitable for rich environment)
1	Days to 50% flowering	AKG-1303, AKG-1401, Phule G-0405 and BDNG-797		
2	Plant height (cm)	AKG-1303, AKG-1401, BDNG 2015-9, Phule G-0819-43, Phule G-15109 Phule Vikram and JAKI-9218	Phule G-0405	
3	Days to maturity	AKG-1401, AKG-1506, BCP-60, Phule G-0819-43, Phule G-0405, AKRG 1701 and AKRG 1702.		
4	Number of primary branches per plant	., BCP-60, Phule G-15109, AKRG 1701, BDNG-797, Vijay, Phule Vikram, PDKV Kanchan and JAKI-9218.		Phule G-13107
5	Number of secondary branches per plant	AKG-1504, Phule G-15109, BDNG-797, Vijay, and PDKV Kanchan.		
6	Number of pods per plant	AKG-1401, Phule G-13107, AKRG 1702, BDNG-797 and JAKI-9218.		
7	Number of seeds per pod	Phule G-0405, AKRG 1701, Digvijay and Phule Vikram.		
8	100 seed weight (g)	AKG-1401, AKG-1506, BDNG 2015-9, BCP-60, Phule G-13107, Phule G-15109, AKRG 1702, and JAKI-9218.	BDNG 2015-6	
9	Seed yield per plant (g)	AKG-1401, AKG-1506, BCP-60, Phule G-15109, AKRG 1701, AKRG 1702 PDKV Kanchan, and JAKI-9218.		BDNG 2015-9
10	Protein content(%)	AKG-1506, BDNG 2015-6, Phule G-15109, Phule G-0405, AKRG 1702, BDNG-797, Vijay, Digvijay and PDKV Kanchan.	AKG-1303	

CHAPTER V

SUMMARY AND CONCLUSIONS

The present study entitled "Genetic Variability and Stability Analysis for Yield and Its Contributing Traits in Chickpea (*Cicer arietinum* L.)" was carried out at Pulses Research Unit, Dr. PDKV Akola, Agriculture Research Station, Buldana and College of Agriculture, Nagpur with the objectives of determining the suitable genotypes for different environments. The field experiment was conducted and evaluated twenty genotypes of chickpea under three different locations viz., E1 (Akola), E2 (Buldana), and E3 (Nagpur) during the year 2017-18 in a Randomized Block Design with three replications.

The data from each of these three environments was collected on days to 50 % flowering, days to maturity (days), plant height (cm), number of primary branches per plant (No.), number of secondary branches per plant (No.), number of pods per plant (No.), number of seeds per pod (No.), 100 seed weight (g), seed yield per plant (g) and protein content (%). Stability analysis was done following the approach given by Eberhart and Russel (1966).

5.1 Response of genotypes to three different environments

The ANOVA revealed highly significant differences among the all genotypes for all the characters studied indicating the presence of sufficient amount of genetic variability among the newly developed genotypes of chickpea.

Mean performance of different genotypes over three environments indicated that the genotypes PDKV Kanchan was the earliest for days to 50 % flowering (50 days) followed by BDNG-797 (51.11 days), whereas the genotypes AKRG 1702 (98.8 days) and AKG 1401 (100.10 days) were the earliest in maturity. In over all three environments indicated that the genotypes Phule G-13107 (53.93 cm) was the tallest among all genotypes followed by and at par viz. AKG 1303 (53.61 cm) and Phule Vikram (52.84 cm).

In overall locations the genotype JAKI-9218 (3.6), PDKV Kanchan (3.6) were found significantly maximum number of primary branches per plant followed by the genotype Vijay (3.5) and Phule G-15109 (3.4). While the genotype Phule G-15109 exhibited maximum number of secondary branches (11.4) followed by the genotype Vijay (11.1) and AKRG 1701 (11.0). In overall locations the genotype AKRG 1701 recorded significantly highest number of pods per plant (67.53) followed by the genotype Phule G-15109 (64.51). The genotype AKRG 1701 (1.5) produced significantly highest number of seeds per pod followed by BDNG 2015-6 (1.35), Phule G-0405 (1.36), Digvijay (1.38) and Phule Vikram (1.4) in over all the three environments.

In overall locations the genotype AKRG 1701 recorded significantly highest yield per plant (16.27 g) followed by the genotype AKG-1506 (15.12 g) and AKRG 1702 (14.92 g). The highest yield per plant was recorded at E3 (Nagpur) environment (15.31 g) followed by E2 (Buldana) (12.00 g) and E1 (Akola) (11.53 g).

In overall locations the genotype BDNG 2015-6 (25.86 g) was promising for 100 seed weight and equally followed by AKG-1401 (25.78 g) and BCP 60 (25.78 g). The genotypes Digvijay (21.73%) and Phule Vikram (21.08%) were observed promising for protein content (%) among the all genotypes.

5.2 Coefficient of variances, heritability, Expected genetic advance:

The character number of pods per plant showed medium GCV (14.88%) accompanying with medium heritability (47.70%) and higher expected genetic advance (21.17%) values indicating thereby amount of variation in aforesaid character.

The higher magnitude of PCV as compared to GCV in respect of characters, number of pods per plant, seed yield per plant, indicated the greater effect of environment on these characters.

The high heritability estimate was showed in protein content (89%) followed by medium heritability (40-60%) for the characters 100 seed weight (49.90%), number of pods per plant (47.70%) and number of seeds per pod (47%). This indicated that these characters are may be governed by non-additive component of variation which is non fixable, heterosis breeding can be fruitfully exploited in improving these characters.

The character seed yield per plant and number of secondary branches per plant showed medium GCV (12.24% and 10.73%) accompanying with medium heritability (37.30% and 37.40%) and medium expected genetic advance (15.41 and 13.53). The character days to maturity showed low GCV (1.63%) accompanying with low heritability (20%) and low expected genetic advance (1.51%).

5.3 Pooled analysis of variance

Pooled analysis of variance showed significant genotypic variances for, days to 50% flowering, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight, seed yield per plant and protein content, except days to maturity when tested against G X E interaction. Environmental variance was significant for all the studied characters except days to 50% flowering and protein content.

Linear components of G X E interaction was found significant for the characters viz., days to 50% flowering and 100 seed weight when tested against pooled deviation and pooled error whereas pooled deviation (nonlinear component) was found significant for the traits viz., days to maturity, number of secondary branches per plant, number of pods per plant, number of seeds per pod, seed yield per plant. Environment (linear) effects were also significant for all the studied characters except protein content. The G X E interactions were non-significant for all the traits.

5.4 Estimation of environmental index

An environments E3 (Nagpur) was found to be most favorable for seed yield and its contributing characters except number of primary branches per plant, 100 seed weight and protein content.

5.5 G x E interaction and stability parameters

Genotype x environmental interactions was non-significant for all the traits. Non-linear component of G X E interactions was highly significant for the character's viz. days to 50% flowering and 100 seed weight.

The most of genotypes showing wider adaptability for different characters studied viz., AKG-1303, AKG-1401, Phule G-0405 and BDNG-797 recorded average stability for days to 50 % flowering. The genotypes AKG-1303, AKG-1401, BDNG 2015-9, Phule G-0819-43, Phule G-15109, Phule Vikram and JAKI-9218 recorded average stability for plant height. The genotypes viz., AKG-1401, AKG-1506, BCP-60, Phule G-0819-43, Phule G-0405, AKRG 1701 and AKRG 1702 recorded average stability for maturity. The genotypes viz., BCP-60, Phule G-15109, AKRG 1701, BDNG-797, Vijay, Phule Vikram, PDKV Kanchan and JAKI-9218 recorded average stability for primary branches per plant. The genotypes viz., AKG-1504, Phule G-15109, BDNG-797, Vijay, PDKV Kanchan and JAKI-9218 recorded average stability for secondary branches per plant. The genotype viz., AKG-1401, Phule G-13107, AKRG-1702, BDNG-797 and JAKI-9218 recorded average stability for number of pods per plant.

The genotypes, Phule G-0405, AKRG 1701, Digvijay and Phule Vikram recorded average stability for seeds per pod. The genotypes AKG-1401, AKG-1506, BDNG 2015-9, BCP-60, Phule G-13107, Phule G-15109, AKRG 1702, and JAKI-9218 recorded average stability for 100 Seed weight. The genotypes AKG-1401, AKG-1506, BCP-60, Phule G-15109, AKRG 1701, AKRG 1702, PDKV Kanchan and JAKI-9218 recorded average stability for seed yield per plant. The genotypes AKG-1506, BDNG 2015-6, Phule G-15109, Phule G-0405, AKRG 1702, BDNG-797, Vijay, Digvijay and PDKV Kanchan recorded their average stability for protein content (%).

The above average stability was observed for the genotypes Phule G-0405 for plant height, genotype BDNG 2015-6 for 100 seed weight, genotype AKG-1303 for the character protein content (%).

The below average stability was observed for the genotype Phule G-13107 for number of primary branches per plant, genotype BDNG 2015-9 for seed yield per plant.

5.6 Conclusions

I. This experimental study revealed sufficient amount of genetic variability among the genotypes of chickpea under study.

II. The character number of pods per plant recorded moderate GCV (14.88%) accompanying with medium heritability (47.70%) and higher expected genetic advance (21.17%).

III. The high heritability estimate was showed in protein content (89%) followed by medium heritability (40-60%) for the characters 100 seed weight (49.90%), number of pods per plant (47.70%) and number of seeds per pod (47%).

IV. The environments E3 (Nagpur) was found to be most favorable for seed yield and its contributing characters.

V. Non-linear component of G X E interactions was highly significant for the character’s days to 50% flowering and 100 seed weight.

VI. Genotypes AKRG-1701, AKG-1506 and AKRG-1702 recorded high seed yield and showed average stability for yield and most of the yield contributing characters, hence adaptable to all three types of environments. These genotypes may be useful in chickpea breeding programme to develop stable varieties.

VII. Genotype Phule G-13107 and BDNG 2015-9 showed below average stability for most of the yield contributing characters hence further may be used for rich or favorable environment.

VIII. Genotype Phule G-0405, BDNG 2015-6 and AKG-1303 showed above average stability for most of the yield contributing characters hence further may be used for poor or unfavorable environment.

CHAPTER VI

IMPLICATIONS

On the basis of results obtained through investigation in chickpea (*Cicer arietinum* L.) which was undertaken with a view to detect “Genetic variability and stability analysis for yield and its contributing traits in chickpea (*Cicer arietinum* L.)” and to identify genotypes suitable for different predictable environments, the studied work might be suggested for further utilization in breeding programme.

Genotypes AKRG-1701, AKG-1506 and AKRG-1702 recorded high seed yield and showed average stability for yield and most of the yield contributing characters, hence adaptable to all three types of environments. These genotypes may be useful in chickpea breeding programme to develops stable varieties.

The genotype BDNG 2015-9 showed below average stability for seed yield/ plant hence may be used further for favorable environment.

The genotype Phule G-0405 showed above average stability for plant height, BDNG 2015-6 for 100 seed weight and AKG-1303 for protein content hence these may be used for unfavorable environments.

CHAPTER VII

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