EFFECT OF PHENOLOGY ON GRAIN SIZE AND GRAIN YIELD IN KABULI CHICKPEA (*Cicer arietinum* L.)

By

PRITY SUNDARAM

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M/PBG/85/BAC/2012-13

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Place: Sabour

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Bihar Agricultural University, Sabour

Department of Plant Breeding and Genetics

Title of the thesis	**Effect of phenology on grain size and grain yield in kabuli chickpea (*Cicer arietinum* L.)**
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Abstract

Phenology (time to flowering, podding and maturity) plays an important role for adaptation of chickpea to short-season environment, as early phenology triggers early pod setting and finally early physiological maturity. In kabuli chickpea large-seeded varieties are gaining importance as they fetch high market price. Hence, the present investigation was undertaken to study the inheritance of phenology, seed size and seed yield and to study the association of phenology with seed size and seed yield in kabuli chickpea. The experiment comprising of five generations *viz.*, P_1, P_2, F_1, F_2 and F_3 of the four crosses namely, JGK 2 x ICC 16644 (C_1), KAK 2 x ICC 16644 (C_2), KRIPA x ICC 16644 (C_3) and ICC 17109 x ICC 16644 (C_4), was conducted in vertisol on 12th Nov 2013 at ICRISAT, in compact family block design with three replications and observations were taken on 11 characters. Significant differences among crosses as well as generations were found for all the traits except harvest index. Additive (d), dominance x dominance (l) and additive x additive (i) effects were important with duplicate type of epistasis for phenology. Additive effect (d), dominance effect (h) and additive x additive interaction (i) in C_1; additive effect (d) and dominance x dominance interaction (l) in C_2; only dominance gene effect (h) in C_3 and additive gene effect (d) in C_4 was important for seed yield per plant. Both the main effect *i.e.*, additive (d) and dominance (h) were important for 100-seed weight with the preponderance of additive gene action. For the cross C_2 and C_4 mainly additive gene effect (d) and additive x additive (i) interaction effect were important. Both the main effects and interaction effects were important with duplicate type epistasis for cross C_1 and C_3. Phenological traits showed non-significant association with seed yield per plant in all the segregating generations studied, except in F_3 generation of C_4 in which negative significant association was recorded. Phenology exhibited significant negative association with 100-seed weight in both the segregating generations of the cross C_1 and C_2 only. Result suggested that in certain genetic backgrounds it might be possible to breed early flowering cultivars with large seed size. The results also indicated that selection for early phenology may increase seed yield per plant but it depends on the genetic background of the parent used in the hybridization programme, however, generally it is difficult to improve both the yield as well as phenological traits simultaneously through selection.

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LIST OF ABBREVIATIONS

^0C	:	Degree Centigrade
^0E	:	Degree East
^0N	:	Degree North
%	:	Percent
ANOVA	:	Analysis of variance
C_1	:	JGK 2 × ICC 16644
C_2	:	KAK 2 × ICC 16644
C_3	:	KRIPA × ICC 16644
C_4	:	ICC 17109 × ICC 16644
cm	:	Centimeter
df	:	Degrees of freedom
F_1	:	First filial generation
F_2	:	Second filial generation
F_3	:	Third filial generation
g	:	Gram
GAM	:	Genetic advance as percent of mean
GCV	:	Genotypic Coefficient of variation
h^2_{bs}	:	Broad-sense heritability
ICRISAT	:	International Crop Research Institute for Semi-Arid Tropics
ha	:	Hectare
Hrs	:	Hours
P_1	:	Parent 1
P_2	:	Parent 2
PCV	:	Phenotypic coefficient of variation
S.Em (±)	:	Standard error of mean
Wt.	:	Weight

Chapter-I

INTRODUCTION

Demand for legume crops is increasing in many countries, particularly in arid and semi-arid regions. Grain legumes have various uses in farming systems, mainly as a good source of human and animal food and in the maintenance of soil fertility through N_2 fixation, especially in dry rainfed areas (Saxena, 1987, 1990).

Chickpea (*Cicer arietinum* L.), a self-pollinated and diploid (2n=2x=16) crop species with a genome size of 740 Mb belonging to the family Leguminosae and subfamily Papilionaceae, is the most important food legume crop of South Asia and the third most important food legume crop in the world after beans (*Phaseolus vulgaris* L.) and pea (*Pisum sativum* L.), in terms of annual production (FAOSTAT 2012). *Cicer arietinum* L. is the only cultivated species of the genus C*icer* which has 43 species (van der Maesen, 1987). Chickpea is a valuable source of dietary protein in many parts of the world for humans and in some cases, animal feed. The crop sown after chickpea is benefited by improved soil fertility (mainly through N_2 fixation by chickpea), particularly in the rainfed areas.

It is grown over an area of 12.34 million hectare with production of 11.62 million tons and productivity of 941 kg ha^{-1} (Food and Agriculture Organization 2012; accessed on 2014, June). India is the largest chickpea producing country accounting for 67% of the global chickpea production covering about 8.32 million ha area with annual production of 7.70 million tons grain. The present yield level is 925 kg ha^{-1}, which is far below the potential yield (5000 kg ha^{-1}) of the crop. The other major chickpea producing countries include Australia, Pakistan, Turkey, Myanmar, Ethiopia, Iran, Mexico, Canada and USA (Gaur *et al.*, 2012).

Bihar is a traditional state for chickpea cultivation covering an area of 61500 ha with production of 86200 tons and productivity of 1402 kg ha^{-1} (Directorate of Economics and Statistics, Govt. of Bihar 2012; accessed on 2014, June). As the soil health is an emerging and important issue for sustainable agriculture development, chickpea could be one of the reliable options for diversification of cropping system.

Moreover, about 11.7 million ha of rice area in India remains fallow during the winter season (Subbarao *et al.*, 2001). Hence, there is an ample scope of horizontal expansion of chickpea in rice fallows of Eastern U.P., Bihar, Jharkhand, West Bengal, Assam, Madhya Pradesh and Chhattisgarh covering more than 80% of total rice fallows in India.

Within cultivated chickpea, two distinct groups of cultivar are found; desi type and kabuli type. Desi type is characterized by pink flowers, angular shaped brown coloured small seeds which is adapted to South Asia and kabuli type is characterized by white flowers, owl's head shaped, beige coloured large seeds, predominates across West Asia and North Africa (WANA), America and Europe. Large-seeded kabuli types are gaining importance, as the market price of kabuli chickpea is up to twice that of desi chickpea (Upadhyaya *et al.,* 2006). Very large (>45 g 100-seed weight) kabuli chickpeas are being sold at about three times the price of desi chickpea and about two times the price of medium-seeded (~25 g 100-seed weight) kabuli chickpea in India (Gaur *et al.,* 2006). India pays huge amount of foreign exchange on import of extra large seeded kabuli chickpea from Turkey, Syria, Mexico, etc. Hence, the development of extra large seeded chickpea varieties will provide opportunities for farmers to grow these varieties in different states which will fetch maximum price in local market as well as save foreign exchange.

Export markets require uniform seed size, which may influence a range of processing properties including splitting, hydration and the quality of the final product, as it has for other food legumes (Poysa *et al*., 2002). Larger seed size coupled with other desirable traits *viz*., light colour commands price premiums in a market-dependant manner (Graham *et al.,* 2001). Seed weight was proposed as an accurate measure of chickpea seed size (Upadhyaya *et al.,* 2006). In chickpea, seed size, affects the seed yield (Vadivelu and Ramakrishnan 1983); it has also been considered as an important factor for subsequent plant growth parameters including germination, seedling vigour and seedling mass (Narayanan *et al.*, 1981; Dahiya *et al*., 1985).

Phenology (time to flowering, podding and maturity) plays critical role in adaptation of chickpea cultivars to different environments (Berger *et al.*, 2004). Early phenology is a key trait for adaptation of chickpea to short-season environments as it

helps the crop to escape from end-of-season stresses like drought, temperature extremities, and provides opportunity for growing chickpea in short windows of crop-season available (Gaur *et al.*, 2008). Early flowering triggers early pod setting and may enable these pods to reach physiological maturity in a timely manner (Or *et al.*, 1999).

Therefore, for an effort to breed early flowering, large seeded and high yielding genotypes it is important to have the knowledge, whether the flowering time affect seed size and yield or not. Better understanding of gene interactions that govern seed size along with the phenology of bold seeded kabuli chickpea is also essential to produce seed of particular size to meet the specific market demand through targeted breeding.

Large variations exist for seed size within and between chickpea types, with some desi types as large as kabuli types and some kabuli types as small as desi types (Kumar and Singh 1995), but majority of the varieties developed during the last few years are small-seeded to medium-seeded which do not meet the market preference for large and very large seed types (Upadhyaya *et al.*, 2011). Therefore, it is important to develop early maturing varieties with large seed size, but success in breeding depends upon the understanding the genetic bases of important traits. According to Kumar and Abbo (2001), lack of genetic knowledge is mainly responsible for the slow progress in chickpea breeding in general. The precise knowledge of magnitude and mode of gene action for traits helps in the choice of an effective breeding strategy to accelerate the pace of genetic improvement of large seeded kabuli chickpea.

Keeping in mind the above facts, the present investigation was carried out with the following objectives:

- To study the inheritance of time to flowering in kabuli chickpea.
- To study the inheritance of seed size in kabuli chickpea.
- To estimate the relative importance of additive and non-additive gene effects for flowering time, seed size (100-seed weight) and grain yield per plant.
- To study the relationship between phenology and seed size, and seed yield in kabuli chickpea.

Chapter-II

REVIEW OF LITERATURE

The present investigation concerned primarily to the study of genetics of time to first flower, seed size and seed yield in chickpea through generation mean analysis and the association analysis. The literature available relevant to this study in chickpea and other legumes are reviewed and presented briefly under the following headings.

2.1 Analysis of variance

2.2 Heritability and Genetic advance

2.3 Generation mean analysis

2.4 Correlation coefficient analysis

2.1 Analysis of variance

Plant population with higher variability provides greater opportunity to the improvement. Hence, it is essential to study and utilize the existing variability in the population. Johanson (1903) gave the basic idea of variability, while developing concept of pureline. Vavilov (1951) ascertained that greater the variability more the chances of obtaining desirable types and prove it to be the basic fundamental for improvement of crop plant through selection. Lush (1940) suggested the method of estimation of phenotypic, genotypic and environmental variances, which further permits estimation of phenotypic coefficients of variation (PCV), genotypic coefficients of variation (GCV) and environmental (ECV) (Burton, 1952). Works related to the coefficients of variation of different characters are reviews and presented here.

Vijayalakshmi *et al.* (2000) evaluated parental, F_2 and F_3 generations of two crosses (P 9623 x T 39-1 and RS 11 x T 39-1) in chickpea. They reported that crosses exhibited highly significant variation for plant height at maturity, number of pods per plant, number of seeds per plant, number of seeds per pod and 100-seed weight in the F_2 generation.

Ali *et al*. (2010) evaluated in 23 genotypes of chickpea for yield, components of variability and genetic advance. They observed that both genotypic coefficient of variation and phenotypic coefficient of variation were relatively greater for grain yield per plant and 100-seed weight, while for biomass per plant and number of pods per

plant both the coefficient of variation were moderate. For days to flower and days to maturity they reported low values of GCV and PCV.

Monpara and Dhameliya (2013) conducted an experiment for genetic analysis of five quantitative traits related to earliness and seed yield in eight crosses of chickpea. They recorded high amount of GCV for plant height at maturity while low to high estimates for days to flowering and days to maturity in different crosses. For grain yield per plant they reported moderate GCV. Earlier Singh *et al.* (1995), Yadav *et al.* (1999) and Arora and Jeena (2000) also reported moderate genotypic coefficient of variation for grain yield per plant in chickpea.

Shivkumar *et al*. (2013) studied the F_2 and F_3 progenies from a cross between ICC 13124 and WR 315 of chickpea and observed that phenotypic coefficient of variation was greater than the respective genotypic coefficient of variation for all the traits studied. Both GCV and PCV estimates were recorded to be the highest for grain yield per plant followed by number of seeds per plant. Similar results were obtained by Wanjari *et al.* (1996), Yaman *et al.*(1997) and Somyasharma and Singh (2001).

2.2 Heritability and Genetic advance

Arshad *et al.* (2004) studied variability, heritability, genetic advance and correlation coefficients for yield and its components in 24 advance lines of chickpea and they reported high broad-sense heritability with low genetic advance for days to flowering, days to maturity and 100 seed weight.

Anbessa *et al.* (2006) studied the inheritance of time to flowering in chickpea in a short-season temperate environment involving five generations of the three crosses. They reported that time of flowering exhibited high broad-sense heritability for days to flowering.

Bicer and Sakar (2008) studied the inheritance of some morphological traits in F_2 population obtained from a full 4 x 4 diallel cross in chickpea and reported high broad-sense heritability for grain yield per plant, days to first flower, plant height at maturity, number of pods per plant, number of seeds per plant and 100-seed weight.

Deb and Khaleque (2009) investigated three interline crosses of chickpea and proposed low value of the broad sense heritability for days to flowering while Ali *et al.* (2010) reported moderate value of the broad sense heritability for the trait.

Monpara and Dhameliya (2013) conduted an experiment for the genetic analysis of five quantitative traits related to earliness and seed yield in chickpea using eight F_2 segregating populations of eight different crosses. They reported moderate as well as high value of the broad sense heritability for days to first flowering in different F_2 generations of the six crosses of chickpea. They also reported high value of the broad-sense heritability along with moderate value of genetic advance as percent of mean for seed yield per plant in different F_2 generations of the six crosses of chickpea.

Shivkumar *et al*. (2013) studied the F_2 and F_3 progenies from a cross between ICC13124 and WR315 of chickpea and reported that grain yield per plant, plant height at maturity, number of pods per plant, number of seeds per plant, number of seeds per pod, and 100-seed weight exhibited high broad-sense heritability coupled with high genetic advance as percent of mean.

Singh and Rao (1991), Chavan *et al.* (1994), Jahagirdhar *et al*. (1994), Patil (1996), Jeena *et al*. (2005), Dubey and Srivastava (2007), Bicer and Sakar (2008), Baber *et al.* (2008), Sharma and Saini (2010), Ali *et al.* (2010), Karami and Talebi (2013), and Shivkumar *et al.* (2013) reported high broad sense heritability for grain yield in chickpea.

High estimates of genetic advance as percent of mean were noticed for 100 seed weight and seed yield per plant by Jahagirdar *et al.* (1994), Singh and Rao (1991) and Arora and Jeena (2000).

High estimates of broad-sense heritability coupled with high genetic advance as perent of mean for 100-seed weight in chickpea was recorded by Agarwal (1985), Sharma *et al.* (1990), Kumar *et al.* (1991), Jahagirdar *et al*. (1994), Rao *et al*. (1994), Patil (1996), Subaschandra *et al.* (2001) Burli *et al.* (2004), Arshad *et al.* (2004), Dubey and Srivastava (2007), Baber *et al.* (2008), Bicer and Sakar (2008), Sharma and Saini (2010), Ali *et al.* (2010), Hossain *et al.* (2010), Srinivasan *et al.* (2011), Karami and Talebi (2013), Sharma *et al.* (2013).

2.3 Generation mean analysis.

Time to first flower

Time of flowering plays an important role when the growing season is restricted by climatic factors like drought and high temperature. Losses in chickpea

production either due to biotic or abiotic stresses mostly occur during flowering and podding i.e. the later part of the cropping season (Kumar *el al*., 1996). Further, the duration of flowering period is also a major yield determinant because of the indeterminate growth habit in chickpea (Bonfil and Pinthus, 1995). Therefore, the development of short duration chickpea varieties that avoid end-of-the-season drought will increase the chickpea productivity. For which, genetic analysis of flowering time is very important.

Kidambi *et al.* (1988) studied three crosses *viz*., C_1, C_2 and C_3 of chickpea and concluded that days to first flower was governed by additive gene action in C_1 (WFWG III x T 20), it was controlled by duplicate type of epistasis in C_2 (T 88 x Bold seeded) and there was presence of linkage or higher order of interaction among additive gene actions in C_3 (NP-34 x P 1528-1-1).

Salimath and Bahl (1989) executed an experiment involving tall and dwarf type of chickpea varieties and they reported that additive and non-additive gene actions were important, the former being predominant for days to first flower and the later for days to maturity.

Parmar and Godawat (1990) reported additive gene actions for days to flowering in nine crosses and maturity times in eight out of ten crosses in peas involving seven parents. But in some crosses dupicate type of epistasis was also reported. Crosses 6587-1 x R-1038, 6587-1 x R-177 for flowering and Bonneville x A.F, A.F x R-839, 6587-1 x R-1038 for maturity were identified as promising ones.

Gumber and Sarvjeet (1996) studied the genetics of days to flowering in three crosses of chickpea in a subtropical long duration environment of Northern India and found that days to flowering was controlled by two duplicate genes and both the genes in homozygous recessive conditions caused early flowering.

Kumar and Rao (1996) selected a super early chickpea segregant, ICCV 96029, from the F_6 generation from a cross of two extra-early varieties, ICCV 2 and ICCV 93929. They found that ICCV 96029 flowered about a week earlier than either of the parents which indicated the oligogenic inheritance with complementary gene action with smaller effects between these two extra-early parents for days to first flower.

Jha *et al.* (1997) used line x tester analysis involving six lines and four testers to analyze the nature of gene action for some quantitative traits in chickpea. They reported that days to flowering was governed by additive gene action. Earlier, Singh *et al.* (1993) reported that days to flowering was predominantly under the control of additive genetic variance.

Sarode (1997) after his study on a diallel analysis in chickpea, concluded that non-additive gene action was more important than additive gene effect for the expression of days to first flower, whereas Venkateswarlu (1982) stressed the importance of additive gene action than non-additive gene action for flower initiation in *Pisum sativam* L. in F_1 and F_2 generations.

Kumar and van Rheenen (2000), identified a major recessive gene "*efl-1*" for early flowering, in a cross between the extra-early variety ICCV 2 and the medium-duration variety JG 62 at ICRISAT, Patancheru, which was responsible for about three weeks difference in flowering time between the two parents.

Girase and Deshmukh (2000) studied the genetic architecture of ten characters through generation mean analysis involving nine generations of each of the three crosses of chickpea. They observed that days to flowering was predominantly under control of dominance and dominance x dominance in the cross, Vijay x ICC 4958. In the cross, JG-62 x ICC-4958 either higher order of interaction or linkage or both played an important role whereas in the cross JG-62 x Vijay only additive x additive type of interactions were involved in the expression of this trait.

Craufurd *et al*. (2001) evaluated the parents, F_1, F_2 and BC_1 crosses made between two early (60 to 70days) and one late (160 to 170days) flowering pigeonpea genotypes. The genetic analysis of the segregation ratios, supported by Chi-square tests, indicated that in each of the crosses the duration from sowing to flowering was controlled by two genes assorting independently with predominance of additive quantitative effects.

Ishiyaku *et al.* (2005) studied the inheritance of time to first flower in cowpea by crossing a photoperiod-sensitive genotype (Kanannnado) to a photoperiod-insensitive variety (IT97D-941-1). They reported that additive effect and additive x

dominance interactions were the most important gene actions controlling the time of flowering.

Anbessa *et al.* (2006) studied the inheritance of time to flowering in chickpea in a short-season temperate environment involving five generations of the three crosses. They reported that time of flowering was controlled by two major genes along with other polygenes. According to them late flowering was dominant over early flowering for both the major genes with digenic interaction between them, mainly an additive x additive type.

Bhardwaj and Sandhu (2007) undertaken the generation mean analysis on six generations of two chickpea crosses to estimate the gene actions involved in inheritance of days to first flower. The observations on each of the crosses revealed that the dominance gene effect and dominance x dominance type of epistasis were higher in magnitude for days to flower initiation for the cross, GNG 469 x ICCV 93929, whereas in the cross PBG 5 x ICCV 93929, in addition to dominance gene effect, all the three types of interactions were also important.

Bicer and Sakar (2008) made 4 x 4 full-diallel cross set of chickpea (ILC 3279, Konya, Balikesir and Aknohut) to estimate the gene effects and genetic parameters of nine traits. They reported that additive and dominance effects were highly significant for days to flowering. Additive effects appeared several folds to that of the dominance, indicating the importance of the additive effects in the inheritance of days to flowering.

Srinivasan *et al.* (2011) crossed two chickpea land races, ICC 6263 (salt sensitive) and ICC 1431 (salt tolerant) to study the gene action involved in different traits under the saline and control conditions. The generation mean analysis in six populations revealed that for days to flowering, dominance effects were highly significant in the saline condition whereas, under the non-saline condition additive and additive x dominance interactions were playing important role.

Karami and Talebi (2013) from their study on a 5 x 5 half diallel cross in chickpea, opined that both additive and dominance genetic effects were significant for days to flowering.

Kumhar *et al.* (2013) estimated the gene effects for yield and yield components in chickpea in the five generations, of five crosses in chickpea, under irrigated and

rainfed conditions. They concluded that both main effects *i.e*., additive and dominance, were important for most of the characters including days to flowering in all the crosses under both the conditions. Additive x additive and dominance x dominance interactions were also significant in most of the crosses for days to flowering.

Importance of non-additive gene action for days to flowering was also reported by several workers like Pandey and Tiwary(1983), Sharma *et al.* (1990), Mishra (1991), Pundhir *et al.* (1991), Panchbhai *et al.*(1992) and Chavan *et al.(*1994), whereas Chandra (1968), Jivani and Yadavendra (1988), Uddin *et al*.(1990) and Jahagirdar *et al*. (1994) suggested additive gene action for the character.

Seed size and seed yield

Seed size has always been a trait of consumer preference (Singh, 1987) besides an important component of yield and adaptation (Singh and Paroda, 1986). Seed size is considered as an important factor for subsequent plant growth parameters including germination, seedling vigour and seedling mass (Narayanan *et al*. 1981; Dahiya *et al.* 1985). Vadivelu and Ramakrishnan (1983) also emphasized the effect of seed size on seed yield. Seed weight was proposed as an accurate measure of chickpea seed size (Upadhyaya *et al.* 2006). Therefore, to produce seed of a specific size, and to meet a specific market demand through targeted breeding, knowledge of the genetics that determine seed size is required. Indeed, a better understanding of the inheritance pattern and gene interactions involved in seed size is paramount to accelerate the genetic improvement of large seeded kabuli chickpea.

Screening of more than 16,000 accessions at ICRISAT has revealed a wide range of variation in seed size (40 to 630mg/seed) in the world chickpea germplasm collection (Upadhyaya, 2003). According to Athwal and Sandha (1967), Smithson *et al.* (1985) and Kumar and Singh (1995) small seed size was found dominant over large one. In contrast Niknejad *et al*. (1971) stated that large seed size was partially dominant over the small seed size and there was polygenic inheritance for the seed size.

Girase and Desmukh (2000) studied the genetics of yield and its components in chickpea by generation mean analysis involving nine generation of their crosses. They observed that grain yield per plant was predominantly under the control of dominance gene effect, while 100- seed weight was controlled by both additive and additive x

dominance gene effects in the cross C_1 (Vijay x ICC-4958). For cross C_2 (JG-62 x ICC-4958) and C_3 (JG-62 x Vijay) only additive gene effects were the major component in governing this character.

Hooda *et al*. (2000) studied parental, F_1, F_2 and F_3 generations of the crosses, Ms Prabhat (DT) x Manak and Ms Prabhat (DT) x H82 1 of pigeonpea. Estimation of gene effects using generation mean analysis revealed the importance of additive gene effect for 100-seed weight in both the crosses.

Khattak *et al.* (2004) used mean data of six basic generations and subjected to joint scaling test for two crosses in mung bean. In the presence of epistasis, a six parameter model was used to detect all types of gene actions. They recorded the duplicate type of non-allelic interactions for 1000-seed weight and complementary type of non-allelic interactions for seed yield per plant in both crosses.

Bhardwaj *et al*. (2005) using generation mean analysis in two crosses of cowpea reported that additive and dominance gene effects were highly significant for seed yield per plant and number of pods per plant. In both the crosses, additive gene effect for the number of pods per plant and seed yield per plant was greater than the dominance gene effect. They also recorded epistatic gene effects for all studied traits, except for seed yield per plant in both crosses.

Aher *et al*. (2006) applied generation mean analysis in three crosses of pigeonpea and observed that additive component in first cross, dominance component in second cross and both additive and dominance gene effects in third cross were significant for the number of seeds per plant.

Upadhyaya *et al.* (2006) studied parents, F_1, F_2, and backcross, along with reciprocal cross generations of a cross of chickpea between ICC11 255, a normal seed size parent (average 120mg/seed) and ICC 5002, a small seed size parent (average 50mg/seed). They concluded that the normal seed size was dominant over small seed size and in chickpea the seed size was controlled by two genes with dominance epistasis.

Bhardwaj and Sandhu (2007) studied six basic generations of two chickpea crosses and concluded that grain yield was under the control of additive gene effect in

cross, PBG 5 x ICC95929, while in cross, GNG 469 x ICC 93929 dominance gene effects as well as additive x additive effect were also important for governing this traits.

Deb and Khaleque (2009) reported that inheritance of seed yield per plant was governed by additive gene action in the three crosses of chickpea. They also reported non-allelic interaction and the presence of linkage for this trait.

Hossain *et al.* (2010) carried out an experiment on two RIL populations from intra-specific crosses of a kabuli-type (S95362; light cream colour) with two desi-types (Howzat and ICC3996; medium tan and dark tan colour, respectively). They concluded that seed size was governed by two major complementary genes, where small seed size was dominant over the large seed size. They also reported a close genetic relationship between seed size and seed weight.

Srinivasan *et al.* (2011) carried out generation mean analysis for the cross between salt sensitive and salt tolerance land races of chickpea in saline and normal condition. They reported that seed yield per plant was controlled by dominant gene effect under non-saline condition, whereas in saline condition it was controlled by additive gene effects. They also reported the importance of additive x additive and additive x dominance interactions in governing the 100-seed weight in both the conditions.

Upadhyaya *et al.* (2011) studied the inheritance of seed size in a cross involving two small-seeded kabuli cultivars, ICCV 2 and L 550. They reported that seed size in the two parents was controlled by two genes exhibiting additive effect with each parent having one pair of alleles with increasing effect at one locus in homozygous form.Similarly, Jivani and Yadavendra (1988), Sharma *et al*.(1990), Rao *et al*. (1994) and Mathur and Mathur (1996) from their studies, reported that additive gene action was very much important for 100-seed weight while Sandhu (1999) found that non-additive gene action was playing important role in governing the 100-seed weight.

Khodambashi *et al.* (2012) studied six basic generations to estimates heritability and gene action for grain yield and related traits in lentil. Generation mean analysis using both scaling and joint scaling tests indicated that additive, dominance and at least one of the epistatic effect (additive x additive, additive x dominance and

dominance x dominance) were involved in the inheritance of the traits studied including seed yield per plant and 100-seed weight.

Karami and Talebi (2013) from their study on a 5 x 5 half diallel cross in chickpea, reported that both additive and dominance genetic effects were significant for 100 seed weight as well as for seed yield per plant.

Kumhar *et al.* (2013) estimated the gene effects for yield and yield components for five generations in five crosses of chickpea under irrigated and rainfed conditions. They reported that the additive effect was significant in most of the cases, whereas dominance effect was non-significant in all the cases, which indicated the importance of additive effect in the inheritance of 100-seed weight. Among the interaction effects, additive x additive effect was found to be important. In case of seed yield per plant, both the main effects *i.e.,* additive and dominance were important and the magnitudes of dominance were higher than their respective additive effect. Additive x additive and dominance x dominance effects were also reported to be important for seed yield per plant.

Sharma *et al.* (2013) studied the relative importance of additive and non-additive gene effects on seed size in three chickpea crosses (desi x desi, desi x kabuli and kabuli x kabuli) by generation mean analysis. They reported that additive gene effect was controlling the seed size in all the three crosses and additive x additive type of interaction was found to be important in desi x kabuli cross only.

2.3 Correlations study

Phenology time of flowering, podding and maturity are important traits in many region of the world as these are essential component of crop adaptation. For Kabuli chickpea seed weight is an important yield component and a significant yield determinant. Grain yield of chickpea is a quantitative character and affected by many genetic factors as well as environment fluctuations (Muehlbauer and Singh, 1987). The efficiency of selection for phenology and yield component characters mainly depends upon direction and magnitude of association among these characters. Therefore relationships among these characters have been reviewed and presented here under.

Ali (1990) reported positive association of grain yield with plant height and grain mass while studying in six advanced lines of desi chickpea with two checks and suggested

that longer duration of flowering, late maturity and large grain mass should be considered while selecting genotypes for grain yield.

Lal *et al*. (1993) reported that seed yield was positively and significantly correlated with pod number and plant height and negatively correlated with 100-seed weight in chickpea. Pod number exhibited significant and negative correlation with 100-seed weight. They also identified pod number and plant height as important characters for seed yield.

Sandhu and Mangal (1995) computed correlations between seed yield and other traits in 32 genotypes of chickpea and reported significant positive association between yield and days to flowering.

Mathur and Mathur (1996) worked out genotypic and phenotypic correlation for grain yield and yield contributing characters in 34 genotypes of chickpea. They reported positive correlation of yield with 100-seed weight but negative correlation with days to first flowering.

Or *et al.* (1999) studied the phenotypic correlations between days to first flower; pod number and mean grain weight in F_2 populations derived from crosses between early flowering (desi) and late flowering (kabuli) cultivars and observed strong association between the characters studied.

Hovav *et al*. (2003) studied the effect of the major flowering gene (PPD) on seed weight of 450 F_3 families in chickpea from reciprocal crosses between a small-seeded, early-flowering (ppd / ppd) type and a large-seeded, late flowering (PPD/PPD) cultivar. They reported positive and relatively higher correlations coefficients between time to flowering and seed weight.

Arshad *et al*. (2004) conducted a correlation study in 24 advanced lines of chickpea. They reported that the grain yield per plant was positively and significantly correlated with plant height, pods per plant, 100 seed weight and biological yield per plant but it was negatively correlated with days to flowering, number of primary branches and harvest index. Similar results were also reported earlier by Malik *et al.* (1987) and Khan *et al*. (1989). Arshad *et al*.(2004) also indicated positive and strong correlation of days to flowers with number of primary branches while negative and highly significant association with plant height.

Toker and Cagirgan (2004) proposed a yield improvement criterion in chickpea using phenotypic correlations. They noted that grain yield was positively and significantly correlated with biological yield, harvest index, plant height, branches and pods per plant, while it was negatively and significantly associated with grain weight.

Jeena *et al*. (2005), computed correlation coefficients in 80 genetically diverse chickpea genotypes and reported that the seed yield was significantly and positively correlated with plant height, pods per plant, 100-seed weight, biological yield per plant and harvest index.

Ali *et al*. (2010) carried out correlation studies for different characters in chickpea. They observed that biomass per plant, pods per plant, number of secondary branches per plant, seeds per pod and 100-seed weight were positively and strongly correlated to each other at phenotypic level. Grain yield per plant was negatively and non-significantly correlated to days to first flower, while it was positively and highly significantly correlated with 100-seed weight.

A negative but highly significant correlation of 100-seed weight with number of seeds per pod was reported by Dasgupta *et al.* (1992), Saleem *et al.* (2002), Menna *et al.* (2006) and Ali *et al.*(2010).

Jivani *et al.* (2013) investigated a set of 105 diverse genotypes of chickpea to estimate correlation for seed yield per plant and its ten component characters. They reported that seed yield per plant had significant and positive correlation with number of pods per plant, biological yield per plant and harvest index. They also reported that 100-seed weight had significant and positive correlation with biological yield per plant.

Monpara and Dhameliya (2013) conducted an experiment for genetic analysis of five quantitative traits related to earliness and seed yield in chickpea. Experiment was carried out using eight segregating population (F_2 generation) and their parents. Correlation studies revealed that days to flowering and days to maturity had significant positive association between them, but their association with seed yield per plant was non-significant.

Chapter-III

MATERIALS AND METHODS

3.1 Experimental site

The experiment was conducted at International Crop Research Institute for Semi-Arid Tropics (ICRISAT), Patancheru, Andhra Pradesh, situated at an altitude of 545.0 m above the mean sea level. Geographically it lies at latitude of 17.53^0 N and longitude of 78.27^0. It comes under tenth agro-climatic zone of India (Southern plateau and hills region). The experimental field BP-12 (black precision) was solarised and had good soil health with proper drainage system.

3.2 Climate and weather conditions

Hyderabad comes under semi-arid region where annual mean temperature is 26°C with hot and dry summers (March–June). Heavy rain from the south-west summer monsoon falls between June to September. Temperatures in the evening and morning are generally cooler because of the city's moderate elevation. The weather data during the course of investigation was recorded from the meteorological observatory laboratory of ICRISAT, Patancheru, Hyderabad. During the crop growth period the maximum temperature (32.7^0C) was recorded on 11^{th} February 2014 and the minimum temperature (6.8^0C) on 9^{th} December 2013. The weather parameters that prevailed during the crop growth period are given in the Table (3.1)

3.3 Experimental materials

The experimental materials were comprised of five chickpea genotypes (ICC 16644, JGK 2, KAK 2, KRIPA and ICC 17109), F_{1s} developed by crossing common genotype, ICC 16644 with the remaining four genotypes *viz*., JGK 2, KAK 2, KRIPA and ICC 17109, their four F_2 and four F_3 populations. In the study cross between JGK 2 × ICC 16644, KAK 2 × ICC 16644, KRIPA × ICC 16644 and ICC 17109 × ICC 16644 were designated as C_1, C_2, C_3 and C_4 respectively. As the maternal effects were not observed in any of the cross combinations earlier for the traits under study, so reciprocal

Table 3.1. Weather data November 2013 to March 2014

Year	Std. Week	Date			Max. Temp. (^{o}C)	Min. Temp. (^{o}C)	Evap. (mm)	Rel. Humidity1 at 07:17 (%)	Rel. Humidity2 at 14:17 (%)	Wind Velocity (Kmph)	Solar Radiation (mj- m^2)	Bright Sunshine (Hrs)
2013	46	12/Nov	to	18/Nov	27.95	13.02	30.59	90.28	37.71	3.54	18.12	8.57
2013	47	19/Nov	to	25/Nov	28.02	16.18	22.00	93.00	55.42	4.24	13.98	6.05
2013	48	26/Nov	to	2/Dec	28.44	16.05	20.60	93.85	53.28	4.08	14.38	6.41
2013	49	2/Dec	to	9/Dec	27.62	12.18	25.49	95.28	45.28	3.81	16.54	8.07
2013	50	10/Dec	to	16/Dec	28.61	8.31	24.29	94.28	30.00	2.67	18.42	9.85
2013	51	17/Dec	to	23/Dec	28.09	10.82	25.00	92.57	36.00	4.32	16.78	9.50
2013	52	24/Dec	to	31/Dec	26.54	12.42	27.10	93.62	46.37	5.62	15.27	8.00
2014	1	1/Jan	to	7/Jan	28.02	13.40	23.89	95.85	44.42	5.10	15.17	8.19
2014	2	8/Jan	to	14/Jan	28.97	14.91	28.00	91.71	41.00	6.51	15.62	8.18
2014	3	15/Jan	to	21/Jan	28.84	15.37	32.39	91.00	42.57	8.18	15.45	7.80
2014	4	22/Jan	to	28/Jan	27.82	15.59	29.60	89.00	46.85	6.61	14.67	6.25
2014	5	29/Jan	to	4/Feb	28.25	13.52	29.20	90.00	39.28	4.58	16.00	7.78
2014	6	5/Feb	to	11/Feb	32.22	13.71	37.50	84.14	26.00	4.41	17.88	9.70

crosses were not studied. The experimental materials were collected from Chickpea Breeding, Grain Legumes, ICRISAT. The details of parents are given in Table (3.2).

Table 3.2. Description of parental lines used in the study

Characters	JGK 2	KAK 2	KRIPA	ICC 17109	ICC 16644
Biological status	Cultivar	Cultivar	Cultivar	Landrace	Landrace
Maturity	Medium	Medium	Late	Late	Early
Seed size	Medium	Medium	Large	Large	Small
Growth habit	Semi-erect	Semi-erect	Semi-erect	Semi-erect	Semi-spreading
Seed type	Kabuli	Kabuli	Kabuli	Kabuli	Kabuli

3.4 Experimental design

The five generations *viz*., P_1, P_2, F_1, F_2 and F_3 of each of the four crosses were sown in the field on 12th November, 2013 at ICRISAT. The final evaluation of experiment was laid out in Compact Family Block Design with three replications. Each replication was divided into four compact blocks which consists of single cross. Each block was divided into five plots, each comprising of five basic generations of each cross. The crosses were randomly assigned to each block and the five generations of each cross were randomly allotted to individual plot within the block. The plots of various generations contained different number of rows *i.e*., 2 rows of parents, 1 row of F_1, and 6 rows of F_2 and F_3 generations. Seeds were treated before sowing with a mixture of 2 g of Thiram and 1 g of Carbendazim per kilogram of seeds to avoid infestation by soil-borne pathogens. The seeds were sown at a wider spacing of 60 cm x 20 cm with single seed per hill in the row length of 4m. Care was taken to sow the seeds at uniform depth (5 cm). All the recommended agronomical practices and necessary plant protection measures including basal application of 18 kg N and 46 kg P_2O_5 ha^{-1} by

using 100 kg/ha Diammonium phosphate fertilizer, were followed to raise healthy crop. One intercultural operation was done to control the weeds and three sprays of 20 mL/ha Indoxacarb in 300 L water was done to manage pod borer (*Helicoverpa armigera*). One light irrigation was given at 30 DAS to overcome moisture stress conditions.

3.5 Recording of observations

The following observations were recorded on individual plant basis in each replication on randomly selected ten plants of each of the parent and F_{1s} and 70 plants from F_2 and F_3 generations separately.

3.5.1 Pre-harvest observations

The following observations were recorded on individual plant in the field condition.

3.5.1.1 Days to first flower

The number of days was counted from the date of sowing to appearance of first flower on the plant.

3.5.1.2 Days to pod initiation

The number of days was counted from the date of sowing to appearance of first pod on the plant.

3.5.1.3 Plant height at maturity (cm)

The plant height at maturity was measured in centimetre from ground level to the tip of the longest branch at maturity.

3.5.1.4 Days to maturity

This was taken as days after sowing when more than 95% of pods of the plant had changed from green to yellow.

3.5.2 Post-harvest observations

The plants were harvested separately and the following observations were recorded for individual plant.

3.5.2.1 Biological yield per plant (g)

The weight of the fully dried plant was taken and recorded in grams.

3.5.2.2 Number of pods per plant

The number of pods per plant was computed by counting the total number of filled pods on each plant.

3.5.2.3 Number of seeds per plant

The total number of seeds obtained after threshing of all the filled pods of a plant was counted.

3.5.2.4 Number of seeds per pod

The total number of seeds per pod was computed by dividing total number of seeds per plant by total number of filled pods per plant.

$$\text{No. of seeds per pod} = \frac{\text{Total number of seeds per plant}}{\text{Total number of pods per plant.}}$$

3.5.2.5 Grain yield per plant (g)

The total seed from each plant were weighed and recorded in gram (g) after threshing the dried pods.

3.5.2.6 100-seed weight (g)

Weight of 100 seeds expressed in gram. Those plants which had number of seeds less than 100, 100-seed weight was calculated by the following formula:

$$\text{100-seed weight} = \frac{\text{Wt. of total seeds of the plant (g)}}{\text{Total number of seeds of the plant}} \text{ X } 100$$

3.5.2.7 Harvest index (%)

It was calculated by the following formula:

$$\text{Harvest Index} = \frac{\text{Grain yield per plant (g)}}{\text{Biological yield per plant (g)}} \text{ X } 100$$

3.6 STATISTICAL ANALYSES

The values obtained from the observations recorded on representative plant samples for the characters under study were used for various statistical computations on related aspects.

3.6.1 Analysis of variance for experimental design.

3.6.2 Heritability and genetic advance.

3.6.3. Generation mean analysis.

3.6.4 Correlation coefficient analysis.

3.6.1 Analysis of variance for experimental design

The data were subjected to analysis of variance for compact family block design as described by Panse and Sukhatme (1985). Here, crosses and generation within each cross were taken as families and progenies, respectively. The analysis carried out in two stages.

(a) First from the data of main plots, the variance between crosses and the corresponding error was calculated by treating the experiment as one in simple randomized blocks. The structure of ANOVA for families is given below:

Table 3.3. Analysis of variance between families

Sources of variation	**Degrees of freedom**	**Mean sum of squares**	**Expected mean square**
Replications	(r–1)	M_r	$\sigma^2_{e1} + f\sigma^2_r$
Families (crosses)	(f–1)	M_f	$\sigma^2_{e1} + r\sigma^2_f$
Error	(r–1) (f–1)	M_{e1}	σ^2_{e1}

(b) The analysis for progenies under each family was done separately for each character using the data of sub plots to give the variance between different generations

and the corresponding error. The structure of ANOVA for progenies within family is given below:

Table: 3.4 Analysis of variance between progenies

Sources of variation	**Degrees of freedom**	**Mean sum of squares**	**Expected mean square**
Replications	(r–1)	M_r	$\sigma^2_{e2} + p\sigma^2_r$
Progenies within family (generations)	(p–1)	M_p	$\sigma^2_{e2} + r\sigma^2_p$
Error	(r–1) (p–1)	M_{e2}	σ^2_{e2}

Where,

r = Number of replications

f = Number of families (crosses)

p = Number of progenies within each family (generations)

M_r = Mean square due to replications

M_f = Mean square due to families

M_p = Mean square due to progenies within each family

M_{e1} = Error mean square for families

M_{r2} = Error mean square for progenies within each family

3.6.2 Heritability and Genetic Advance

The broad sense heritability (h^2_{bs}) for all the crosses were estimated as a percentage of the ratio of genotypic variance to phenotypic variance as per Allard's formula (1960) as follows:

$$h^2_{bs} = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where,

h^2_{bs}= Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance $= \sigma^2_g + \sigma^2_e$

σ^2_e = Environmental variance

As suggested by Johnson *et al*. (1955a), heritability values are categorized as follows:

Low : Less than 30%

Moderate : 30 – 60 %

High : More than60 %

Genetic advance was computed by using the formula elucidated by Johnson *et al*. (1955a)

$$\text{Genetic Advance} = K \times h^2_{bs} \times \sigma_p$$

Where,

h^2_{bs}= Heritability in broad sense

σ_p = Phenotypic standard deviation

K = Selection differential in standard units which is 2.06 at 5% selection intensity.

Genetic advance as percentage of mean was calculated by the following formula:

$$\text{Genetic Advance as Percentage of Mean} = \frac{GA}{\bar{X}} \times 100$$

Where,

GA = Genetic advance

$\overline{X}$ = General mean of the character in the population

The range of Genetic Advance as per cent of mean was classified according to Johnson *et al*. (1955a):

Low : Less than 10%

Moderate : 10-20%

High : More than 20%

3.6.3 Generation Means Analysis

3.6.3.1 Generation Means and Variances

The standard statistical procedures were used to calculate mean and variances of each generation for each character. Mean (x) = $\frac{\sum xi}{n}$

Variance = $\frac{n}{n-1}\left[\sum x_i^2 - \frac{(\sum xi)^2}{n}\right]$

Variance of mean (V_m) = $\frac{\text{Variance}}{n}$

Standard error mean (S.E) = $\sqrt{\frac{\text{Variance}}{n}}$

n = Total number of observations recorded for respective generation.

3.6.2.2 Simple scaling tests

[(Mather, (1949) and Hayman and Mather, (1955)]

In the presence of simple additive-dominance situations, there exists a simple relationship between the expected values of different generation means. Mather (1949) and Hayman and Mather (1955) constructed scaling test A, B, C and D based on this concept which were used to test the adequacy of simple additive-dominance model and to detect the presence of epistatic interaction. The significance of either of tests would indicate failure of simple additive-dominance model to explain variation in generation means. The calculations of scaling tests are as here under.

A = $2\,\bar{B}_1 - \bar{P}_1 - \bar{F}_1$

B = $2\,\bar{B}_2 - \bar{P}_2 - \bar{F}_1$

C = $4\,\bar{F}_2 - 2\,\bar{F}_1 - \bar{P}_1 - \bar{P}_2$

D = $4\,\bar{F}_3 - 2\,\bar{F}_2 - \bar{P}_1 - \bar{P}_2$

Since in the present study there were five generations *viz*., P_1, P_2, F_1, F_2 and F_3, hence the estimation of scales C and D were done.

The variances of the estimates were computed using following formulae

$V_C = 16V(\bar{F}_2) + 4V(\bar{F}_1) + V(\bar{P}_1) + V(\bar{P}_2)$

$V_D = 16V(\bar{F}_3) + 4V(\bar{F}_2) + V(\bar{P}_1) + V(\bar{P}_2)$

The standard error of each scaling test was calculated as under:

S.E. (C) = $(V_C)^{\frac{1}{2}}$

S.E. (D) = $(V_D)^{\frac{1}{2}}$

The testing of individual scaling test was carried out by using t-test as follows:

t (C) = C/S.E. (C)

t(D) = D/S.E.(D)

The degree of freedom for t-test was equal to the sum of degree of freedom of all the generations involved in the respective scaling test as shown below:

d.f. (C) = d.f of F_2 + d.f. of F_1 + d.f. of P_1 + d.f. of P_2

d.f. (D) = d.f of F_3 + d.f. of F_2 + d.f. of P_1 + d.f. of P_2

However, the calculated values of 't' were compared with the tabulated values of 't' at 5% and 1% levels of significance. The significance of any one of these scales is taken to indicate the presence of non-allelic interaction.

3.6.2.3 Estimation of genetic components

Five-parameter model for estimation of various genetic components proposed by Hayman (1958) was applied using following formulae.

Mean (m) = $\bar{F}_2$

Additive effect (d) = $\frac{1}{2}\bar{P}_1 - \frac{1}{2}\bar{P}_2$

Dominance effect (h) = $(4\bar{F}_1 + 12\bar{F}_2 - 16\bar{F}_3) / 6$

Dominance x Dominance (l) = $(8\bar{F}_1 - 24\bar{F}_2 + 16\bar{F}_3) / 3$

Additive x Additive (i) = $\bar{P}_1 - \bar{F}_2 + \frac{1}{2}(\bar{P}_1 - \bar{P}_2 + h) - \frac{l}{4}$

The variance of each estimate was computed as follows:

$V_m = V(\bar{F}_2)$

$V_d = \frac{1}{4}[V(\bar{P}_1) + V(\bar{P}_2)]$

$V_h = \frac{1}{36}[16V(\bar{F}_1) + 144V(\bar{F}_2) + 256V(\bar{F}_3)]$

$V_l = = \frac{1}{9}[256V(\bar{F}_3) + 576V(\bar{F}_2) + 64V(\bar{F}_1)]$

$V_i = V(\bar{P}_1) + V(F_2) + \frac{1}{4}[V(\bar{P}_1) + V(\bar{P}_2) + V_h] + \frac{1}{16}(V_l)$

The standard error of each of the gene effect was computed as follows:

S.E. (m) = $(V_m)^{\frac{1}{2}}$

S.E. (d) = $(V_d)^{\frac{1}{2}}$

S.E. (h) =$(V_h)^{\frac{1}{2}}$

S.E. (l) = $(V_l)^{\frac{1}{2}}$

S.E. (i) =$(V_i)^{\frac{1}{2}}$

The significance of each parameter was tested by using t-test

t (m) = (m)/S.E.(m)

t (d) = (d)/S.E.(d)

t (h) = (h)/S.E. (h)

t (l) = (1)/S.E. (1)

t (i) = (i)/S.E. (i)

The calculated t value of each parameter was compared with tabulated values of t at 5% and 1% levels of significance.

3.6.4 Correlation coefficient analysis

Phenotypic correlation coefficients between characters were computed utilizing respective components of variance and co-variance, by following formula suggested by Al-Jibouri and Miller *et al*. (1958).

$$r_{xy} = \frac{Cov\,(x,y)}{\sqrt{V_{(x)} \times V_{(y)}}}$$

$$Cov\,(xy) = \frac{1}{n}\left[\sum x \sum y - \frac{(\sum x . \sum y)}{n}\right]$$

$$Var\,(x) = \frac{1}{n}\left[\sum x^2 - \frac{(\sum x)^2}{n}\right]$$

$$Var\,(y) = \frac{1}{n}\left[\sum y^2 - \frac{(\sum y)^2}{n}\right]$$

Where,

r_{xy} = Correlation coefficient between character x and y,

Cov (x, y) = Co-variance of character x and y,

$V_{(x)}$ = Variance of character x, and

$V_{(y)}$ = Variance of character y.

r = correlation coefficient

x and y = two independent variables

To test the significance of correlation coefficients, the estimated values were compared with the tabulated values of Fisher and Yates (1938) at (n-2) d.f. at two levels of probability, *viz.*, 5% and 1%. If the calculated value of correlation coefficient is greater than tabulated value it is considered to be significant and vice-versa.

All the statistical analysis was done by using WINDOSTAT 8.5 software (Indostat services, Hyderabad, India).

Chapter-IV

EXPERIMENTAL FINDINGS

For improvement of any trait, selection of parents on the basis of phenotypic performance alone may not necessarily lead to desirable results (Allard, 1960). Phenotypically superior lines may yield poor recombinants in the segregating generations. It is, therefore, essential that parents should be chosen on the basis of their genetic value. The genetic components of variation are helpful to decipher an overall genetic picture of quantitative characters. Hence, the knowledge of the genetics is essential for simultaneous improvement of different traits. The present experiment was conducted to determine inheritance of phenology, grain size and grain yield along with the association analysis among 11 different traits. The results obtained from the data of present investigation have been presented here under the following headings.

4.1 Analysis of variance.

4.2 Heritability and genetic advance.

4.3. Generation mean analysis.

4.4 Correlation coefficient analysis.

4.1 Analysis of Variance.

Aanlysis of variance was performed for 11 characters as per the design of experiment for comparison of crosses as well as generations of each cross according to Panse and Sukhatme (1985). The mean squares from ANOVA presented in Table-4.1 showed that there were significant differences among the crosses for all the 11 traits except harvest index which indicated that considerable amount of variability were present in the crosses included in the study for ten traits. Likewise the mean sum of square among the progenies (generations) for all the characters studied in all the four crosses revealed that the variations among the five generations of each cross were significant for all the characters except harvest index. Hence, further genetic analysis of generation means were done.

Table 4.1. Analysis of variance for the design of experiment of 11 different characters of five generations and four crosses in chickpea

sources of variation	df	Days to first flower	Days to pod initiation	Days to maturity	Plant height at maturity (cm)	No. of pods/plant	No. of seeds/plant	No. of seeds/pod	Grain yield/ plant (g)	Biological yield/plant (g)	100-seed weight (g)	Harvest index (%)
Analysis of variance between crosses												
Rep	2	3.543	9.484	1.166	33.368	295.507	447.983	0.001	66.897	81.756	0.759	6.172
Cross	3	24.140**	22.444**	50.353**	130.377**	2527.763**	2994.022**	0.017**	36.195*	658.654**	2057.053**	31.148
Error	6	0.784	1.475	0.614	12.042	65.047	91.920	0.001	17.718	35.175	3.996	16.969
Analysis of variance between generations within crosses												
JGK 2 × ICC 16644												
Rep	2	4.312	7.664	1.641	54.802	181.204	259.100	0.001	38.115	100.718	4.660	3.215
Gen	4	170.058**	172.601**	49.186**	22.790**	1236.313**	931.840**	0.005**	66.120*	237.872**	42.731**	12.937
Error	8	3.687	4.113	2.887	13.891	71.795	81.931	0.001	9.530	32.009	1.313	3.550
KAK 2 × ICC 16644												
Rep	2	0.092	2.030	0.031	0.749	191.429	317.435	0.001	55.600	64.426	3.462	4.380
Gen	4	211.524**	208.140**	92.026**	14.769**	564.431**	357.275*	0.023**	52.226*	146.035*	85.275**	45.615
Error	8	1.269	1.348	0.877	3.282	56.337	81.470	0.001	12.475	26.950	3.558	13.053
KRIPA × ICC 16644												
Rep	2	0.354	2.231	0.759	1.148	82.101	113.517	0.001	15.715	7.366	3.316	26.206
Gen	4	203.265**	206.713**	93.984**	73.877**	510.635**	662.011*	0.013*	21.443*	88.067*	142.334**	80.725
Error	8	0.843	1.445	1.243	4.066	81.477	87.194	0.002	11.060	27.777	7.354	41.957
ICC 17109 × ICC 16644												
Rep	2	1.136	1.985	0.576	12.795	35.915	33.692	0.000	10.621	14.769	1.310	23.279
Gen	4	206.224**	203.869**	108.936**	51.349**	546.291**	622.503**	0.007**	43.682*	283.653**	49.995*	94.942
Error	8	1.303	1.182	1.197	6.323	34.238	39.411	0.000	10.281	8.727	11.870	56.032

Rep - replication, Gen - generation, df.- degrees of freedom.* and ** are significant at 5% and 1% respectively.

Table 4.2. Coefficient of variations for 11 different characters in four crosses of chickpea

Genetic parameters	JGK 2 × ICC16644	KAK 2 × ICC16644	KRIPA × ICC16644	ICC17109 × ICC16644
		Days to first flower		
PCV (%)	19.24	19.69	19.67	19.73
GCV (%)	18.63	19.52	19.54	19.54
		Days to pod initiation		
PCV (%)	17.30	17.60	17.79	17.57
GCV (%)	16.70	17.43	17.61	17.42
		Days to maturity		
PCV (%)	4.94	6.31	6.32	6.70
GCV (%)	4.53	6.22	6.20	6.59
		Plant height at maturity		
PCV (%)	9.04	5.62	10.03	9.20
GCV (%)	3.79	4.12	9.26	7.72
		No. of pods per plant		
PCV (%)	22.28	17.36	20.32	21.29
GCV (%)	20.47	15.04	16.22	19.43
		No. of seeds per plant		
PCV (%)	18.77	13.36	20.84	21.04
GCV (%)	16.53	9.73	17.27	19.19
		No. of seeds per pod		
PCV (%)	4.26	7.99	6.79	4.73
GCV (%)	3.91	7.61	5.70	4.37
		Grain yield per plant		
PCV (%)	16.92	16.78	13.26	16.51
GCV (%)	13.79	12.04	9.47	12.91
		Biological yield per plant		
PCV (%)	18.85	14.95	13.88	25.09
GCV (%)	15.57	11.54	9.99	23.98
		100-seed weight		
PCV (%)	12.44	17.25	19.60	8.80
GCV (%)	11.89	16.23	18.17	6.33
		Harvest index		
PCV (%)	4.37	8.77	12.75	13.47
GCV (%)	2.99	6.91	8.19	8.27

GCV- Genotypic coefficient of variation

PCV-Phenotypic coefficient of variation

The estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for all the characters are presented in Table-4.2. A wide range of PCV was observed ranging from 4.26 % (number of seeds per pod in C_1) to 25.09 % (biological yield per plant in C_4), while GCV varied from 3.79 % (plant height at maturity C_1) to 23.98 % (biological yield per plant in C_4).

Higher magnitude of PCV was recorded for biological yield per plant in C_4 (25.09 %), number of pods per plant in all the crosses except C_2, and number of seeds per plant in C_3 (20.84 %) and C_4 (21.04 %), while moderate estimates of PCV were observed for days to first flower, days to first pod formation, grain yield per plant in all the crosses. 100-seed weight and biological yield per plant showed moderate PCV in all the crosses except C_4 where low value of PCV for 100-seed weight was recorded. Moderate estimate of PCV was also exhibited by number of seeds per plant in C_1 (18.77 %) and C_2 (13.36 %); and harvest index in C_3 (12.75 %) and C_1 (14.47 %). For rest of characters like days to maturity, plant height at maturity and number of seeds per pod PCV was found low in all the crosses.

Higher magnitude of GCV was recorded for biological yield per plant in C_4 (23.98 %) and number of pods per plant in C_1 (20.47 %), while moderate estimates were observed for days to first flower and days to first pod formation in all the crosses. Grain yield per plant and 100-seed weight showed moderate GCV in all the crosses except C_3 and C_4. Lower magnitude of GCV was recorded for days to maturity, plant height at maturity, number of seeds per pod and harvest index in all the crosses. For number of seeds per plant moderate value of GCV was recorded for all the crosses except C_2 where low value of GCV was exhibited by this trait.

4.2 Heritability and Genetic advance as percent of mean (GAM)

Heritability has been usually adopted as a reliable indicator for making effective improvement in the character for which selection is practiced. A perusal of data in Table-4.3 it is evident that the heritability (in broad sense) estimated for 11 quantitative characters was, ranged from 17.60% (Plant height at maturity in Cross C_1) to 98.77% (days to flowering in cross C_3). High estimates of heritability were noticed for days to first flower, days to pod initiation, days to maturity, number of pods per plant, number of seeds per plant, number of seeds per pod and 100-seed weight in all the crosses.

Table 4.3. Genetic parameters of 11 different characters in four crosses of chickpea

Genetic parameters	JGK 2 × ICC16644	KAK 2 × ICC16644	KRIPA × ICC16644	ICC17109 × ICC16644
Days to first flower				
Heritability (%)	93.77	98.22	98.77	98.13
GAM	37.16	39.85	40.01	39.88
Days to pod initiation				
Heritability (%)	93.18	98.08	97.93	98.28
GAM	33.20	35.55	35.89	35.58
Days to maturity				
Heritability (%)	84.24	97.19	96.13	96.77
GAM	8.57	12.63	12.51	13.35
Plant height at maturity				
Heritability (%)	17.60	53.84	85.13	70.36
GAM	3.28	6.23	17.60	13.34
No. of pods per plant				
Heritability (%)	84.39	75.04	63.71	83.29
GAM	38.73	26.84	26.68	36.53
No. of seeds per plant				
Heritability (%)	84.39	75.04	63.71	83.29
GAM	38.73	26.84	26.68	36.53
No. of seeds per pod				
Heritability (%)	84.25	90.72	70.35	85.45
GAM	7.40	14.93	9.84	8.33
Grain yield per plant				
Heritability (%)	66.44	51.51	23.84	51.99
GAM	23.15	17.80	6.51	17.69
Biological yield per plant				
Heritability (%)	68.19	59.56	41.98	91.31
GAM	26.48	18.34	12.00	47.19
100-seed weight				
Heritability (%)	91.32	88.45	85.95	61.71
GAM	23.40	31.44	34.71	20.37
Harvest index				
Heritability (%)	46.85	45.40	23.55	18.80
GAM	4.22	8.20	6.18	5.60

GAM- Genetic advance as percent of mean.

Heritability for plant height at maturity was found to be high for the cross C_3 (85.13%) and C_4 (70.36%) while it was moderate in C_2 (53.84%) and low in C_1 (17.60%). For grain yield per plant high magnitude of heritability was exhibited by cross C_1 (66.44%) while it was moderate in cross C_2 (51.51%) and C_4 (51.99%) and low for the cross C_3 (23.84%). High heritability for biological yield per plant was observed in the crosses, C_1 (68.19%) and C_4 (91.31%), while moderate value of heritability was found for the crosses C_2 (59.56%) and C_3 (41.98%). Moderate heritability was noted for harvest index in C_1 (46.85%) and C_2 (45.40%) while low heritability was noted for C_3 (23.55%) and C_4 (18.80%).

A perusal of genetic advance as percent of mean (Table-4.3) for the characters under study revealed that, it ranged between 3.28% (plant height at maturity in C_1) to 40.01% (days to flowering in C_3). High genetic advance was observed for days to first flower, days to pod initiation, number of pods per plant, number of seeds per plant and 100-seed weight in all the crosses. For days to maturity moderate genetic advance as percent of mean (GAM) was reported in all the crosses except C_1 which exhibited low GAM (8.57%). Plant height showed moderate GAM for the cross C_3 (17.16%) and C_4 (17.60%), while low GAM was observed in C_1 (3.28%) and C_2 (6.23%). Number of seeds per pod showed low GAM in all the crosses except C_2 (17.80%), where it was moderate. For grain yield per plant high GAM was exhibited by C_1 (23.15%) while moderate GAM was reported in C_2 (17.80%) and C_4 (17.69%) and it was low for C_3 (6.51%). Biological yield per plant was observed to have high GAM for the crosses C_1 (26.48%) and C_4 (47.19%), while moderate value for C_2 (18.34%) and C_3 (12.00%). Very low estimates of GAM for harvest index were noted in all the crosses.

4.3 Generation mean analysis

Quantitative traits are complex in nature and show involvement of additive, dominance and all types of interaction effects for the expression of these traits. The involvement of environmental effect in higher proportion makes the trait more complex to understand the genetic basis of the trait. Analysis of generation means allow testing of adequacy of different types of genetic models as well as quantification of various genetic parameters in a given model (Mather and Jinks, 1971). The failure of additive-

Table 4.4. Means, variances and standard errors (±) for various 11 characters in five generations of each of the four crosses of chickpea

Characters	P_1	P_2	F_1	F_2	F_3
Days to first flower					
JGK 2 × ICC 16644					
Means	34.950	31.333	50.467	40.124	43.438
Std. errors	±0.178	±0.175	±0.257	±0.530	±0.538
KAK 2 × ICC 16644					
Means	36.767	31.500	51.333	47.300	47.638
Std. errors	±0.184	±0.184	±0.330	±0.764	±0.733
KRIPA × ICC 16644					
Means	38.700	30.700	52.967	42.305	45.476
Std. errors	±0.236	±0.131	±0.265	±0.644	±0.695
ICC 17109 × ICC 16644					
Means	38.200	31.367	53.400	42.510	46.029
Std. errors	±0.242	±0.169	±0.256	±0.638	±0.721
Days to pod initiation					
JGK 2 × ICC 16644					
Means	39.966	36.067	55.400	44.838	48.562
Std. errors	±0.302	±0.244	±0.370	±0.544	±0.571
KAK 2 × ICC 16644					
Means	41.767	36.062	55.667	52.081	52.633
Std. errors	±0.274	±0.252	±0.411	±0.765	±0.723
KRIPA × ICC 16644					
Means	43.267	35.802	58.167	47.290	50.386
Std. errors	±0.267	±0.223	±0.369	±0.642	±0.685
ICC 17109 × ICC 16644					
Means	43.767	35.800	57.900	47.448	51.043
Std. errors	±0.238	±0.222	±0.301	±0.649	±0.734
Days to maturity					
JGK 2 × ICC 16644					
Means	85.500	81.100	92.400	87.062	87.124
Std. errors	±0.306	±0.297	±0.317	±0.405	±0.431
KAK 2 × ICC 16644					
Means	85.533	80.467	90.767	93.148	93.267
Std. errors	±0.287	±0.439	±0.341	±0.541	±0.538
KRIPA × ICC 16644					
Means	89.200	80.634	94.000	90.219	94.610
Std. errors	±0.194	±0.243	±0.392	±0.587	±0.725
ICC17109 × ICC 16644					
Means	90.500	81.367	96.467	91.243	95.362
Std. errors	±0.279	±0.323	±0.331	±0.668	±0.756
Plant height at maturity (cm)					
JGK 2 × ICC 16644					
Means	48.400	41.267	44.500	48.367	45.690
Std. errors	±1.470	±1.269	±0.773	±0.392	±0.386
KAK 2 × ICC 16644					
Means	50.333	44.835	46.300	49.086	46.719
Std. errors	±0.674	±1.108	±1.097	±0.371	±0.447
KRIPA × ICC 16644					
Means	60.033	46.567	50.833	52.710	50.376
Std. errors	±1.005	±0.698	±0.561	±0.410	±0.508
ICC 17109 × ICC 16644					
Means	56.433	44.967	49.533	50.786	49.343
Std. errors	±1.202	±0.987	±1.107	±0.463	±0.534

Table 4.4. (cont.).

Characters	P_1	P_2	F_1	F_2	F_3
No. of pods per plant					
JGK 2 × ICC 16644					
Means	86.700	76.133	130.033	93.000	95.290
Std. errors	±4.754	±3.138	±7.709	±2.719	±3.528
KAK 2 × ICC 16644					
Means	76.933	80.807	109.300	76.414	89.829
Std. errors	±4.191	±3.288	±8.492	±2.744	±3.269
KRIPA × ICC 16644					
Means	55.933	77.234	91.567	71.248	70.643
Std. errors	±2.914	±3.447	±5.724	±2.133	±2.650
ICC 17109 × ICC 16644					
Means	47.967	72.433	85.333	64.462	66.581
Std. errors	±2.376	±3.534	±7.559	±2.194	±2.432
No. of seeds per plant					
JGK 2 × ICC 16644					
Means	91.000	85.633	131.133	99.838	101.400
Std. errors	±4.725	±3.473	±7.771	±2.725	±3.705
KAK 2 × ICC 16644					
Means	85.500	95.600	110.500	92.081	108.824
Std. errors	±4.634	±3.679	±8.718	±3.270	±3.960
KRIPA × ICC 16644					
Means	59.267	95.234	93.833	76.386	75.948
Std. errors	±3.132	±4.281	±5.781	±2.226	±2.831
ICC 17109 × ICC 16644					
Means	50.533	82.667	88.067	69.324	73.181
Std. errors	2.557	3.866	±8.139	±2.373	±2.654
No. of seeds per pod					
JGK 2 × ICC 16644					
Means	1.059	1.127	1.010	1.092	1.076
Std. errors	±0.021	±0.013	±0.006	±0.008	±0.009
KAK 2 × ICC 16644					
Means	1.113	1.194	1.010	1.212	1.223
Std. errors	±0.018	±0.018	±0.004	±0.011	±0.012
KRIPA × ICC 16644					
Means	1.061	1.204	1.027	1.081	1.086
Std. errors	±0.017	±0.021	±0.005	±0.007	±0.010
ICC 17109 × ICC 16644					
Means	1.054	1.148	1.025	1.080	1.103
Std. errors	±0.010	±0.019	±0.006	±0.007	±0.008
Grain yield per plant (g)					
JGK 2 × ICC 16644					
Means	32.883	24.008	36.648	33.233	30.740
Std. errors	±1.882	±1.091	±2.867	±0.865	±1.105
KAK 2 × ICC 16644					
Means	35.551	23.812	33.310	26.760	29.732
Std. errors	±1.938	±0.993	±2.779	±0.862	±1.020
KRIPA × ICC 16644					
Means	28.737	23.396	33.272	28.540	26.323
Std. errors	±1.874	±1.281	±1.967	±0.811	±1.006
ICC 17109 × ICC 16644					
Means	29.939	23.888	33.376	28.751	27.674
Std. errors	±1.883	±1.373	±3.369	±0.882	±0.947

Table 4.4. (cont.).

Characters	P_1	P_2	F_1	F_2	F_3
Biological Yield (g)					
JGK 2 × ICC 16644					
Means	53.792	39.218	63.957	55.534	53.602
Std. errors	±2.963	±1.572	±5.104	±1.380	±1.750
KAK 2 × ICC 16644					
Means	57.324	45.278	60.581	49.294	57.016
Std. errors	±2.998	±1.810	±4.105	±1.412	±1.763
KRIPA × ICC 16644					
Means	49.604	40.582	57.317	51.797	49.936
Std. errors	±2.507	±2.279	±2.941	±1.397	±1.707
ICC 17109 × ICC 16644					
Means	49.539	38.307	61.749	48.719	52.967
Std. errors	±2.836	±2.007	±5.346	±1.554	±1.668
100-seed Weight (g)					
JGK 2 × ICC 16644					
Means	36.008	29.217	26.431	33.852	30.789
Std. errors	±0.544	±0.816	±0.945	±0.440	±0.458
KAK 2 × ICC 16644					
Means	41.623	30.160	30.266	30.149	28.685
Std. errors	±0.585	±0.597	±1.195	±0.504	±0.501
KRIPA × ICC 16644					
Means	47.757	28.981	35.606	37.861	34.334
Std. errors	±1.987	±0.706	±0.591	±0.454	±0.482
ICC 17109 × ICC 16644					
Means	55.563	28.670	37.580	39.279	38.502
Std. errors	±1.706	±0.562	±0.887	±0.534	±0.543
Harvest index (%)					
JGK 2 × ICC 16644					
Means	60.977	60.874	58.321	59.692	55.994
Std. errors	±0.509	±0.967	±1.947	0.527	±0.684
KAK 2 × ICC 16644					
Means	61.906	57.313	53.195	53.539	51.522
Std. errors	±0.602	±0.974	±1.661	±0.818	±0.823
KRIPA × ICC 16644					
Means	59.799	65.531	58.416	55.040	51.768
Std. errors	±2.663	±1.632	±2.165	0.711	±0.945
ICC 17109 × ICC 16644					
Means	59.248	61.196	53.527	55.062	52.021
Std. errors	±1.822	±0.742	±1.690	±0.628	±0.803

dominance model may be incurred from the scaling test and it usually definite the indication of non-additive interaction. In the course of present study, genetic analysis for ten quantitative characters in four crosses of kabuli chickpea was carried out. The detection of epistasis was done through scaling test C and D of Mather (1949) and Hyman and Mather (1955) and to estimate the genetic parameters, five-parameter model [Hyman (1958)] were applied. The analysed data concerning Generation mean analysis have been depicted in Table-4.5. It was observed that estimate of a five-parameter important for a particular trait in one cross was not necessarily found to be significant for the same character in other crosses. This revealed that the genetic behavior was variable for cross to cross and character to character.

Days to first flower

Substantial amount of variability in the mean performance (Table-4.4) for all the basic generations P_1, P_2, F_1, F_2 and F_3 were noticed for days to first flower. The parental divergence was noticed for this trait in all the crosses. The mean performances of F_{1s} were exceeded the duration of late maturing parent suggesting the involvement of over-dominance. For days to first flower the estimates of both the scales C and D were found to be significant for all the crosses which revealed the inadequacy of simple additive-dominance model and the presence of non-allelic interaction for this trait. The mean effect of F_2 performance (m) was highly significant in all the crosses studied for the trait. The main effect additive (d) was found to be important in governing the trait in all the crosses, whereas the dominance gene effect (h) was non-significant. The estimates of additive gene effect (d) was highest in cross C_3 (4.000**) followed by cross C_4 (3.450**) while the lowest estimates of additive gene effect (d) was reported for the cross C_1 (1.583**). The analysis of interaction effects indicated the involvement of both the additive x additive (i) and dominance x dominance (l) interaction in all the crosses except C_2, where only additive x additive (i) interaction effect was important. In the cross C_4 (47.810**) the estimate of dominance x dominance (l) was found to be the highest whereas the lowest value was observed for the crosses C_2 (12.559**). The

Table 4.5. Estimates of scaling test, gene effects (±SE of mean) for various traits in the four crosses of chickpea using five-parameter model (Hayman, 1958)

Characters / Crosses	Scales		Genetic parameters					Gene action
	C	D	m	d	h	l	i	
Days to first flower								
JGK 2 × ICC 16644	–6.271** (±2.195)	27.671** (±2.411)	40.124** (±0.530)	1.583** (±0.125)	–1.943 (±1.791)	45.257** (±5.164)	–16.326** (±1.673)	**Duplicate**
KAK 2 × ICC 16644	18.333** (±3.135)	27.752** (±3.315)	47.300** (±0.764)	2.667** (±0.128)	1.787 (±2.490)	12.559 (±5.305)	–10.113** (±2.349)	**—**
KRIPA × ICC 16644	–6.114* (±2.643)	27.895** (±3.078)	42.305** (±0.644)	4.000** (±0.136)	–1.349 (±2.265)	45.346** (±6.386)	–11.616** (±2.078)	**Duplicate**
ICC 17109 × ICC 16644	–6.262* (±2.621)	29.595** (±3.169)	42.510** (±0.638)	3.450** (±0.149)	–2.124 (±2.315)	47.810** (±6.430)	–13.874** (±2.101)	**Duplicate**
Days to pod initiation								
JGK 2 × ICC 16644	–7.081** (±2.333)	28.938** (±2.559)	44.838** (±0.544)	1.750** (±0.194)	–2.889 (±1.887)	48.025** (±5.405)	–16.972** (±1.772)	**Duplicate**
KAK 2 × ICC 16644	19.157** (±3.191)	28.538** (±3.292)	52.081** (±0.765)	2.850** (±0.184)	0.917 (±2.477)	12.508 (±5.319)	–10.133** (±2.361)	**—**
KRIPA × ICC 16644	–6.238* (±2.695)	27.895** (±3.046)	47.290** (±0.642)	3.733** (±0.172)	–1.003 (±2.247)	45.511** (±6.381)	–12.170** (±2.079)	**Duplicate**
ICC 17109 × ICC 16644	–5.543* (±2.686)	29.743** (±3.228)	47.448** (±0.649)	4.000** (±0.163)	–2.619 (±2.358)	47.048** (±6.555)	–12.752** (±2.140)	**Duplicate**
Days to maturity								
JGK 2 × ICC 16644	–3.152 (±1.791)	7.771** (±1.952)	87.062** (±0.405)	2.200** (±0.213)	3.394* (±1.422)	14.565** (±4.062)	–1.306 (±1.356)	**Complementary**
KAK 2 × ICC 16644	25.057** (±2.329)	20.771** (±2.465)	93.148** (±0.541)	2.533** (±0.263)	–1.905 (±1.811)	–5.714 (±5.271)	–4.605* (±1.732)	**—**
KRIPA × ICC 16644	3.043 (±2.498)	28.167** (±3.145)	90.219** (±0.587)	4.283** (±0.164)	–9.187** (±2.277)	33.198** (±6.173)	–9.704** (±2.022)	**Duplicate**
ICC 17109 × ICC 16644	0.338 (±2.783)	27.262** (±3.334)	91.243** (±0.668)	4.650** (±0.212)	–7.502** (±2.429)	35.898** (±6.750)	–8.818** (±2.211)	**Duplicate**

* and ** are significant at 5% and 1% respectively

estimate of additive x additive (i) was highest in the cross C_1 (–16.326 **) and was the lowest in cross C_2 (–10.113**). The negative sign of additive x additive (i) showed that the alleles of genes pair responsible for the trait were in dispersive form in their respective parents. The gene action was considered to be of duplicate type for the character, since the estimates of dominance (h) and dominance x dominance (l) had opposite signs. (Mather and Jinks, 1982)

Days to pod initiation

F_1 generations derived from the hybridization of all distinct parents for days to pod initiation showed over-dominance gene expression for the trait over late duration parent. Significant differences in the F_2 population in the crosses depicted the chances for isolation of desired segregants.

The estimates of the C and D scale deviated significantly from zero for all the crosses. Significance of both the scaling test revealed the inadequacy of additive-dominance model and presence of epistasis for the character. The main effect additive (d) was found to be important in governing the trait in all the crosses, whereas the dominance gene effect (h) was found to be non-significant, signifying the involvement of additive main effect for governing the trait. The estimates of additive gene effect (d) was highest in cross C_4 (4.000**) while the lowest value was recorded for the cross C_1 (1.750**). Among the interaction effects both the interactions *i.e.*, additive x additive (i) and dominance x dominance (l) were found to be significant in all the crosses except C_2, where only additive x additive (i) interaction was important in governing the trait. In the cross C_1 (48.025**) the estimate of dominance x dominance (l) was found to be the highest whereas the lowest estimates for dominance x dominance was observed for the cross C_3 (45.511**). The estimate of additive x additive (i) was highest in the cross C_1 (−16.972**) and lowest in the cross C_2 (−10.133**). The negative sign of additive x additive (i) revealed the existence of dispersion of alleles in their respective parents. The opposite sign of dominance (h) and dominance x dominance (l) suggested duplicate type of epistasis for the trait.

Days to maturity

Substantial amount of variability in the mean performance for all the basic generations were noticed for days to maturity. The maturity duration of F_{1s} was higher than the late maturing parent suggesting over dominance gene action. Significant variation in F_2 population depicted the chances of selection.

The estimate of C scale was found to be significant for the cross C_2 only, while the estimates of the D scales were found to be significant for all the crosses which revealed the presence of non-allelic interaction for the trait. The main effect additive (d) was found to be significant for all the crosses among which the cross C_4 (4.650**) has the highest estimate of additive gene effect (d) whereas the lowest value was recorded for the cross C_1 (2.200**). The analysis of interaction effect revealed both additive x additive (i) and dominance x dominance (l), were playing important role for governing the trait in all the crosses except C_2. The estimate of dominance x dominance (l) was highest in cross C_4 (35.898**) and the lowest value was reported for the cross C_1 (14.565**). The additive x additive (i) interaction was important for the trait in all the crosses except C_1. The estimate of additive x additive (i) interaction was highest in C_3 (−9.704**) while the lowest estimate was reported for the cross C_2 (−4.605**). The opposite sign of dominance (h) and dominance x dominance (l) component for the crosses C_3 and C_4 indicated duplicate type gene action while similar sign for the cross C_1 showed the involvement of complementary type gene action for this cross.

Plant height at maturity

Plant height at maturity is one of the important traits in chickpea for mechanical harvesting. In the present study the crosses were generated from distinct parents where the character expressions in F_{1s} were closer to the dwarf parent showing partial-dominance. Significant differences in the F_2 population in all the crosses depicted the chances for isolation of desired segregants.

The estimates of C scale showed significant deviation from zero for the crosses C_1 and C_2 only, whereas the estimates of D scale were deviated significantly from zero for all the crosses except C_1. For the cross C_2 both the scaling test were significant while for the rest three crosses either of scaling test was found to be significant, which

Table 4.5 (cont.).

Characters / Crosses	Scales		Genetic parameters					Gene action
	C	D	m	d	h	l	i	
Plant height at maturity								
JGK 2 × ICC 16644	15.900** (±2.936)	–2.538 (±2.602)	48.367** (±0.405)	3.017** (±0.213)	4.559** (±1.422)	–24.584** (±4.062)	10.375** (±1.356)	**Duplicate**
KAK 2 × ICC 16644	8.576** (±2.935)	–6.462** (±2.311)	49.086** (±0.371)	2.917** (±0.632)	4.454** (±1.582)	–20.051** (±4.801)	11.237** (±1.748)	**Duplicate**
KRIPA × ICC 16644	2.571 (±2.338)	–10.514** (±2.512)	52.710** (±0.410)	6.733** (±0.616)	4.971** (±1.626)	–17.448** (±4.519)	20.905** (±1.868)	**Duplicate**
ICC 17109 × ICC 16644	2.743 (±3.277)	–5.533* (±2.799)	50.786** (±0.463)	5.767** (±0.777)	3.013 (±1.852)	–11.035* (±5.524)	15.679** (±2.242)	**Duplicate**
Number of pods per plant								
JGK 2 × ICC 16644	–50.900* (±19.709)	32.329* (±16.159)	93.000** (±2.719)	5.283 (±2.848)	18.581 (±12.019)	110.971** (±35.350)	–19.469 (±12.342)	**Complementary**
KAK 2 × ICC 16644	–70.676** (±20.912)	48.752** (±15.149)	76.414** (±2.744)	–1.993 (±2.662)	–13.848 (±11.755)	159.238** (±36.040)	–48.148** (±12.161)	**Duplicate**
KRIPA × ICC 16644	–33.310* (±15.053)	4.910 (±12.381)	71.248** (±2.133)	–11.650** (±2.384)	15.159 (±9.094)	50.959* (±26.907)	–32.125** (±9.201)	**Complementary**
ICC 17109 × ICC 16644	–32.652 (±18.003)	17.567 (11.505)	64.462** (±2.194)	–11.950** (±2.151)	8.263 (±9.311)	66.959* (±29.709)	–41.053** (±9.588)	**Complementary**
Number of seeds per plant								
JGK 2 × ICC 16644	–39.548* (±19.869)	29.290 (±16.844)	99.838** (±2.725)	2.683 (±2.932)	16.698 (±12.416)	91.784* (±35.990)	–20.752 (±12.964)	**Complementary**
KAK 2 × ICC 16644	–33.776 (±22.590)	–70.033** (±18.135)	92.081** (±3.270)	–5.450 (±2.967)	–32.368* (±13.713)	138.413** (±40.876)	–62.418** (±13.871)	**Duplicate**
KRIPA × ICC 16644	–36.624* (±15.659)	–3.481 (±13.429)	76.386** (±2.226)	–17.983** (±2.839)	12.800 (±9.575)	44.190 (±27.978)	–39.750** (±9.730)	—
ICC 17109 × ICC 16644	–31.605 (±19.411)	21.310 (±12.528)	69.324** (±2.373)	–15.850** (±2.330)	2.210 (±10.102)	70.552* (±32.121)	–51.174** (±10.373)	**Complementary**

* and ** are significant at 5% and 1% respectively

revealed the importance of epistasis for the trait. The main effect additive (d) was found to be important for the trait in all the crosses, among which the cross C_3 (6.733**) had the highest estimate of additive gene effect (d) and lowest value was observed for the cross C_2 (2.917**). The dominance gene effect (h) was important for all the crosses except C_4. The highest estimate of dominance (h) were reported for the cross C_3 (4.971**) while the lowest estimate of dominance gene effect (h) was reported for the cross C_2 (4.454**). The result of interaction components showed both the additive x additive (i) and dominance x dominance (l) gene effects were important for all the crosses. The highest estimate of additive x additive (i) was for C_3 (20.905**) while it was the lowest for C_2 (10.375*). The estimate of dominance x dominance (l) was highest for C_1 (–24.584**) while it was lowest for C_4 (–11.235**). In general, the interaction effects *i.e*., additive x additive (i) and dominance x dominance (l) along with the main effects of additive (d) and dominance (h) was found to be important for the trait expression. The gene action was considered to be of duplicate type for the character, since the estimates of dominance (h) and dominance x dominance (l) had opposite signs.

Number of pods per plant

Substantial amount of variability in the mean performance for all generations developed in the present study were noticed for number of pods per plant. The mean performance of F_{1s} were found higher than the either of the parent for this trait. However mean performance of F_2 and F_3 generations showed significant decline over their respective F_1 for this trait in all the crosses. Significant deviation was observed for the performance of F_2 populations in all the crosses.

The estimates of the C scale deviated significantly for all the crosses except C_4, while the estimates of D scale were also significant only for the crosses C_1 and C_2. Significance of the scaling test revealed the inadequacy of additive-dominance model and presence of epistasis for the character. Only additive effect was found to be important for the crosses C_3 and C_4 whereas none of the main effect was important for other two crosses. Both the interactions components *i.e.*, additive x additive (i) and dominance x dominance (l) were found to be significant in all the crosses except C_1,

where only dominance x dominance (l) interaction was important in governing the trait. In the cross C_2 (159.238**) the estimate of dominance x dominance (l) was found to be highest whereas the lowest estimate was observed for the cross C_3 (15.159**). The estimate of additive x additive (i) was highest in the cross C_2 (−48.148**) and lowest in the cross C_1 (−19.469**). However, relatively higher magnitude of dominance x dominance (l) indicated the preponderance of dominance x dominance (l) over the additive x additive (i) effect. The negative sign of additive x additive (i) revealed that the gene pairs responsible for the trait are in dispersive form in their respective parents. The same sign of dominance (h) and dominance x dominance (l) suggested complementary type of epistasis for all the crosses except C_2 which exhibited duplicate gene action for the trait.

Number of seeds per plant

Character expressions in F_1 generated from all the four crosses involving distinct parent for number of pods per plant were showing over dominance. Significant differences in the F_2 population in all the crosses depicted the chances for isolation of desired segregants. Analysis of interaction component using scaling test revealed that the estimates of C scale deviated significantly from zero for the crosses C_1 and C_3. Scale D was significant for the cross C_2 only which revealed the presence of epistasis in the first three crosses for the character. The result of main effect for number of seeds per plant showed the involvement of both additive and non-additive effects. Additive effect (d) was found to be significant for C_3 (17.983**) and C_4 (15.850**), whereas dominant effect (h) was significant for the cross C_2 (32.368*) only. The result of interaction effect revealed the involvement of both additive x additive (i) and dominance x dominance (l) for the trait. Additive x additive (h) effect was important for the crosses C_2, C_3 and C_4 out of which cross C_2 (62.418**) had highest estimate of additive x additive (i) followed by C_4 (51.174**) and C_3 (39.750**). Dominance x dominance (l) interaction was found significant for all the crosses except C_3. C_2 (138.413**) had highest estimates of dominance x dominance (l) while it was lowest for the cross C_4 (70.552*). The cross C_1 exhibited dominance x dominance (l) interaction only, depicting its major role for governing the traits. However, the cross C_3 exhibited significant additive x additive (i)

gene action. The same sign of dominance (h) and dominance x dominance (l) suggested complementary type of epistasis for the trait in C_1 and C_4.

Number of seeds per pod

The mean performance of F_{1s} derived from two distinct parent for number of seeds per pod were found lower than the either of their respective parent for this trait. However mean performances of F_2 and F_3 generations showed significant decline over their respective F_{1s} for this trait in all the crosses. Results revealed that the performance of F_2 generations (m) was highly significant in all the crosses studied for the trait.

The estimate of C scaling test were significant for C_1 and C_2 and the estimates of D scaling test were significant for C_2 only. The significant estimate of scaling test revealed that there was inadequacy of additive-dominance model and the presence of epistasis for the cross C_1 and C_2. The main effect additive (d) was significant for all the crosses with the highest estimate of additive gene effect (d) in the cross C_3 (−0.071**), while it was lowest for the cross C_1 (−0.034**). The dominance effect (h) was found to be significant for the cross C_2 (−0.163**) and C_4 (−0.099**) only. Among the interactions components dominance x dominance (l) interaction was significant for the C_1 (−0.307**) and C_2 (−0.482**) only. Additive x additive (i) was important for all the crosses except C_1. The highest estimate of additive x additive (i) was found to be for the cross C_4 (−0.120**) while the estimate of additive x additive (i) was lowest for the cross C_3 (−0.088**). The same sign of dominance (h) and dominance x dominance (l) suggested complementary type of epistasis for the trait.

Grain yield per plant

For grain yield per plant the estimated value of both the scale C and D significantly deviated from zero for the cross C_2 only which indicated the inadequacy of additive-dominance model and the presence of epistasis for the trait. For the rest three crosses C_1, C_3 and C_4 both the scaling test were non-significant. Results revealed that the mean effect of F_2 performance (m) was highly significant in all the crosses studied which indicated the fare chances of selection for grain yield.

Table 4.5 (cont.).

Characters / Crosses	Scales C	D	Genetic parameters m	d	h	l	i	Gene action
Number of seeds per pod								
JGK 2 × ICC 16644	0.163** (±0.041)	–0.067 (±0.046)	1.092** (±0.008)	–0.034** (±0.012)	–0.011 (±0.029)	–0.307** (±0.079)	–0.004 (±0.035)	**Complementary**
KAK 2 × ICC 16644	0.524** (±0.052)	0.163** (±0.059)	1.212** (±0.011)	–0.039** (±0.013)	–0.163** (±0.0039)	–0.482** (±0.111)	–0.099* (±0.042)	**Complementary**
KRIPA × ICC 16644	0.006 (±0.041)	–0.081 (±0.050)	1.081** (±0.007)	–0.071** (±0.014)	–0.051 (±0.030)	–0.115 (±0.080)	–0.088* (±0.034)	**Complementary**
ICC 17109 × ICC 16644	0.063 (±0.038)	0.048 (±0.042)	1.080** (±0.007)	–0.049** (±0.011)	–0.099** (±0.026)	–0.019 (±0.074)	–0.120** (±0.028)	**Complementary**
Grain yield per plant								
JGK 2 × ICC 16644	2.745 (±7.042)	–0.398 (±5.223)	33.233** (±0.865)	4.438** (±1.088)	8.925* (±3.916)	–4.191 (±11.879)	–9.598* (±4.258)	**Duplicate**
KAK 2 × ICC 16644	–20.945** (±6.895)	4.064** (±4.937)	26.760** (±0.862)	4.870** (±1.091)	–3.560 (±3.715)	33.321** (±11.491)	3.551 (±4.170)	**Duplicate**
KRIPA × ICC 16644	–7.916 (±5.599)	–7.320 (±4.916)	28.540** (±0.811)	0.371 (±1.156)	9.066** (±3.398)	0.795 (±9.921)	4.303 (±3.814)	—
ICC 17109 × ICC 16644	–12.942 (±7.955)	3.998 (±4.786)	26.751** (±0.882)	2.795* (±1.167)	1.957 (±3.812)	22.587 (±12.489)	0.767 (±4.366)	—
Biological yield per plant								
JGK 2 × ICC 16644	1.213 (±12.080)	10.332 (±8.238)	55.534** (±1.380)	7.287** (±1.677)	10.767 (±6.401)	12.159 (±19.856)	7.888 (±6.956)	—
KAK 2 × ICC 16644	–26.959* (±10.562)	26.875** (±8.364)	49.294** (±1.412)	6.024** (±1.751)	–13.068* (±6.129)	71.287** (±18.325)	–10.301 (±6.665)	**Duplicate**
KRIPA × ICC 16644	2.369 (±8.803)	5.964 (±8.130)	51.797** (±1.397)	4.511* (±1.708)	8.643 (±5.690)	4.793 (±16.410)	1.441 (±6.006)	—
ICC 17109 × ICC 16644	–16.425 (±12.848)	26.627** (±8.412)	48.719** (±1.554)	5.638** (±1.738)	–2.642 (±6.493)	57.403** (±20.905)	–9.214 (±7.165)	**Duplicate**

* and ** are significant at 5% and 1% respectively

The main effect additive (d) was found to be significant in all the crosses except C_3. The highest estimates of additive gene effect (d) was reported for the cross C_2 (4.870**) while it was found to be the lowest for C_4 (2.795**). The dominance gene effect (h) was also important but for the cross C_1 (8.925*) and C_3 (9.066**) only. Among interaction dominance x dominance (l) effect was significant for the C_2 (–33.321**) while additive x additive (i) was important for the cross C_1 (–9.598*) only. For C_1 both the main effects additive (d) and dominance gene effect (h) was important along with additive x additive interaction (i). The additive gene effect (d) and dominance x dominance (l) type epistasis was playing important role in governing the trait in C_2. While for the cross C_3 and C_4, only main effect dominant and additive respectively was important with the absence of epistatic interactions. In most of the cases the interaction was duplicate type for C_1 and C_2.

Biological yield per plant

The mean performances of F_{1s} were found higher than that of their respective parents for this trait. Both the scaling tests C and D were significant for C_2 while for the cross C_4 only D scale was significant indicating the presence of epistasis for the trait in both the crosses. Additive gene effect (d) was important for all the crosses while dominance gene effect (h) was important for the cross C_2 (–13.068**) only. Highest estimates of additive gene effect (d) was noticed for the cross C_1 (7.287**) while the lowest estimate was recorded for C_3 (4.511**). Dominance gene effect (h) was playing important role in governing the trait in C_2 only. Among the interaction effects dominance x dominance (l) interaction was important for the crosses C_2 (71.287**) and C_4 (7.403**). The cross C_2 exhibited both, the main effect *i.e.*, additive (d) and dominance (h) and interaction effect dominance x dominance (l) for the inheritance of this trait. The opposite signs of dominance (h) and dominance x dominance (l) revealed that duplicate epistasis was involved in controlling the trait in the crosses C_2 and C_4.

100-seed weight

The mean performance of F_{1s} generated from the crosses revealed that smaller seed size was partially dominant over larger seed size. Present study showed that the F_2 performance (m) was highly significant in all the crosses studied. The estimates of scale

Table 4.5 (cont.).

Characters / Crosses	Scales		Genetic parameters					Gene action
	C	D	m	d	h	l	i	
100-seed weight								
JGK 2 × ICC 16644	17.323** (±2.761)	–9.772** (±2.256)	33.852** (±0.440)	3.395** (±0.490)	3.220* (±1.631)	–36.127** (±4.969)	16.192 (±1.714)	**Duplicate**
KAK 2 × ICC 16644	–11.718** (±3.328)	–17.340** (±2.393)	30.149** (±0.504)	5.708** (±0.418)	3.982* (±1.854)	–7.496 (±5.794)	21.070** (±1.931)	**Duplicate**
KRIPA × ICC 16644	3.494 (±3.025)	15.127** (±3.001)	37.861** (±0.454)	9.388** (±1.056)	7.904** (±1.623)	–24.828** (±4.722)	29.443** (±2.706)	**Duplicate**
ICC 17109 × ICC 16644	–2.318 (±3.306)	–8.823** (±3.015)	39.279** (±0.534)	13.426** (±0.897)	0.939 (±1.895)	–8.672 (±5.679)	32.346** (±2.630)	**Duplicate**

* and ** are significant at 5% and 1% respectively

C showed significant deviation from zero for the crosses C_2 and C_3 while the estimates of D scale were deviated significantly from zero for all the crosses. Significance of either of scaling test or both in the crosses revealed the importance of epistasis for the trait. Both the main effects *i.e*., additive (d) and dominance (h) were significant for the trait in all the crosses except C_4 where only additive (d) gene action was important. Among the crosses, C_4 (13.426**) had the highest estimate of additive gene effect (d) while the lowest was observed for the cross C_1 (3.395**). The analysis of dominance gene effect showed highest estimate for C_3 (7.904**) while the lowest estimate was reported for C_1 (3.220**). The relative magnitude of additive (d) effect than the dominance (h) indicated the importance of additive (d) effect in governing the trait in all the four crosses. With regards to interaction effects both the interactions *i.e*., additive x additive (i) and dominance x dominance (l) were found to be important in all the crosses except cross C_2 and C_4, where only dominance x dominance (l) interaction effect was found to be important. An interaction of duplicate type was recorded for all the crosses for 100-seed weight.

Harvest index

No parental divergence was noticed for this trait in any of the crosses since the difference between the mean performances of parents for harvest index was non-significant. Hence this character was not considered for generation mean analysis.

4.4 Correlation Coefficient Analysis

In the present investigation phenotypic correlation coefficients among 11 different characters were computed for the F_2 and F_3 generations of the four crosses to estimate the association of phenology with grain size and grain yield, and inter-relationship among the characters studied. The phenotypic correlation coefficients of the characters under study have been depicted in Table-4.6. The two values of correlation coefficients of the characters for different crosses mentioned below in the parenthesis are of F_2 and F_3 generations, respectively.

Table 4.6. Phenotypic correlation coefficients among 11 characters in F_2 and F_3 generations of the four crosses in chickpea

Characters	Crosses	Generations	Days to pod initiation	Days to maturity	Plant height at maturity	No. of pods/ plant	No. of seeds/ plant	No. of seeds/ pod	Biological yield/plant	100–seed weight	Harvest index	Grain yield/plant
Days to first flower	JGK 2 × ICC 16644	F_2	0.9879**	0.8231**	–0.2365**	0.2882**	0.2485**	–0.2849**	0.1532*	–0.3450**	–0.2418**	0.0528
		F_3	0.9860**	0.7502**	–0.2298**	0.1551*	0.1015	–0.2425**	0.0690	–0.2593**	–0.2116**	– 0.0066
	KAK 2 × ICC 16644	F_2	0.9950**	0.8942**	0.0562	0.1594*	0.0882	–0.3790**	0.1378*	–0.2999**	–0.4374**	–0.0460
		F_3	0.9944**	0.8833**	0.0269	0.0857	0.0189	–0.3223**	0.1255	–0.2396**	–0.4085**	–0.0679
	KRIPA × ICC16644	F_2	0.9917**	0.8910**	0.1800**	0.0263	–0.0330	–0.3391**	0.0926	–0.1426*	–0.4731**	–0.0774
		F_3	0.9921**	0.9131**	0.1256	–0.0636	–0.1045	–0.2108**	0.0317	–0.1005	–0.4319**	–0.1320
	ICC 17109 × ICC 16644	F_2	0.9943**	0.8870**	0.0640	–0.0101	–0.0549	–0.2328**	0.0260	–0.0975	–0.3946**	–0.0904
		F_3	0.9956**	0.9449**	0.2096**	–0.1602*	0.2073**	–0.2895**	–0.0549	–0.0095	–0.4129**	–0.1898**
Days to pod initiation	JGK 2 × ICC16644	F_2		0.8231**	-0.2262**	0.2844**	0.2492**	–0.2615**	0.1486*	–0.3466**	–0.2283**	0.0535
		F_3		0.7552**	-0.2341**	0.1636*	0.1131	–0.2226**	0.0768	–0.2687**	–0.2100**	–0.0018
	KAK 2 × ICC 16644	F_2		0.8944**	0.0521	0.1489*	0.0816	–0.3681**	0.1254	–0.3028**	-0.4410**	–0.0568
		F_3		0.8903**	0.0292	0.0831	0.0180	–0.3255**	0.1201	–0.2270**	-0.4063**	–0.0714
	KRIPA × ICC16644	F_2		0.8846**	0.1784**	0.0216	–0.0368	–0.3292**	0.0797	–0.1370*	-0.4425**	–0.0780
		F_3		0.9048**	0.1351	–0.0674	–0.1102	–0.2266**	0.0348	–0.0853	-0.4308**	–0.1315
	ICC17109 × ICC16644	F_2		0.8823**	0.0517	–0.0114	–0.0539	–0.2228**	0.0244	–0.0846	–0.3831*	–0.0877
		F_3		0.9422**	0.2041**	–0.1722*	-0.2172*	–0.2759**	–0.0661	–0.0105	–0.4114*	–0.1980**

* and ** are significant at 5% and 1% respectively.

Table 4.6 (cont.).

Characters	Crosses	Generations	Days to pod initiation	Days to maturity	Plant height at maturity	No. of pods/ plant	No. of seeds/ plant	No. of seeds/ pod	Biological yield/plant	100–seed weight	Harvest index	Grain yield/plant
Days to maturity	JGK 2 × ICC16644	F_2			– 0.1297	0.2469**	0.2236**	–0.1936**	0.1849**	–0.2098**	–0.2085**	0.0957
		F_3			– 0.0485	0.1732*	0.1438*	– 0.1371*	0.1375*	– 0.1542*	– 0.1305	0.0851
	KAK 2 × ICC16644	F_2			0.0835	0.1929**	0.1165	–0.3642**	0.1563*	–0.2789**	–0.4170**	–0.0248
		F_3			0.0604	0.0363	–0.0235	–0.3073**	0.1084	–0.1467*	–0.3954**	–0.0799
	KRIPA × ICC16644	F_2			0.1589*	–0.0012	–0.0439	–0.2582**	0.0856	–0.1246	–0.4450**	–0.0808
		F_3			0.1590*	0.0063	–0.0287	–0.1591*	0.0939	–0.0941	–0.3706**	–0.0530
	ICC17109 × ICC16644	F_2			0.0902	0.0407	0.0039	–0.2056**	0.0738	–0.0753	–0.3567**	–0.0330
		F_3			0.2119**	–0.1198	–0.1612*	–0.2623**	–0.0411	–0.0423	–0.4053**	–0.1701*
Plant height at maturity	JGK 2 × ICC16644	F_2				0.2164**	0.2559**	0.0978	0.2926**	0.1859**	0.2069**	0.3259**
		F_3				0.2049**	0.2214**	0.0196	0.2809**	0.1416*	0.0747	0.2939**
	KAK 2 × ICC16644	F_2				0.0896	0.0918	–0.0012	0.2108**	0.2321**	–0.0321	0.1808**
		F_3				0.0987	0.1100	0.0636	0.2662**	0.1527*	–0.0637	0.2199**
	KRIPA × ICC16644	F_2				0.2659**	0.2287**	–0.2819**	0.2906**	0.1407*	–0.0210	0.2642**
		F_3				0.1670*	0.1441*	–0.1175	0.2249**	0.0575	–0.0866	0.1657*
	ICC17109 × ICC16644	F_2				0.1111	0.1239	0.0533	0.2211**	0.1251	–0.1136	0.1813**
		F_3				0.1645*	0.1356	–0.1733*	0.1888**	0.1016	–0.0544	0.1628*

* and ** are significant at 5% and 1% respectively.

Association of phenology with 100-seed weight

The association analysis revealed that phenological traits *i.e.*, days to flowering, days to pod initiation and days to maturity were significantly and positively correlated among each other. Days to flowering exhibited significantly negative association with 100-seed weight for both F_2 and F_3 generations in the crosses C_1 (–34.50**, –25.93**) and C_2 (–0.2999**, –0.2396**), respectively in parenthesis, while significantly negative association was observed for the cross C_3 (–0.1426*) only in F_2 generation. For the remaining generations of C_3 and C_4 it showed non-significant association. Days to first pod formation expressed significant but negative association with 100-seed weight in both the segregating generations of C_1 (–0.3466**, –0.2687**) and C_2 (–0.3028**, –0.2270**), and F_2 generation of C_3 (–0.1370*). For rest of the populations the association was non-significant. Significant and negative correlation was also observed between days to maturity and 100-seed weight in both F_2 and F_3 generations of C_1 (–0.2098**, –0.1542*) and C_2 (–0.2789**, –0.1467*). For rest of the populations the association was non-significant with negative magnitude.

Association of phenology with seed yield per plant

Non-significant association was observed between days to flowering and seed yield per plant in F_2 and F_3 generations of all the four crosses under study except in F_3 generation of the cross C_4 (–0.1898**) where significant negative association was noted. Similarly, the association between days to pod initiation and seed yield per plant was non-significant in both the segregating generations of all the crosses except F_3 generation of C_4 (–0.1980**) which exhibited weak significant negative association. Days to maturity was not significantly correlated with seed yield per plant in both the segregating generations of all the crosses studied except in F_3 generation of cross C_4 (–0.1701**) where significantly negative association with low magnitude was observed.

Association among other characters

Seed yield per plant showed positive and significant association with plant height at maturity, number of pods per plant, number of seeds per plant, biological yield per plant, and harvest index in both the segregating generations of all the crosses studied. A positive and significant association was noted for 100-seed weight in both

Table 4.6 (cont.).

Characters	Crosses	Generations	Days to pod initiation	Days to maturity	Plant height at maturity	No. of pods/ plant	No. of seeds/ plant	No. of seeds/ pod	Biological yield/plant	100–seed weight	Harvest index	Grain yield/plant
No. of pods/plant	JGK 2 × ICC16644	F_2					0.9832**	– 0.4009**	0.8743**	– 0.2370**	0.0610	0.8355**
		F_3					0.9797**	– 0.1684*	0.9132**	– 0.117	0.3149**	0.8942**
	KAK 2 × ICC16644	F_2					0.9646**	–0.0873	0.8777**	–0.2365**	0.3128**	0.8882**
		F_3					0.9559**	–0.1232	0.8616**	–0.2067**	0.3332**	0.8889**
	KRIPA × ICC16644	F_2					0.9799**	–0.2011**	0.8934**	–0.1559*	0.1909**	0.8972**
		F_3					0.9796**	–0.1439*	0.8879**	0.1146	0.3776**	0.9339**
	ICC17109 × ICC16644	F_2					0.9810**	–0.0842	0.9181**	–0.1568*	0.1052	0.9156**
		F_3					0.9805**	–0.0640	0.8665**	–0.1271	0.2476**	0.8861**
No. of seeds/plant	JGK 2 × ICC16644	F_2						– 0.2513**	0.8889**	– 0.2252**	0.0910	0.8603**
		F_3						0.0038	0.9338**	– 0.1104	0.3273**	0.9165**
	KAK 2 × ICC16644	F_2						0.1502*	0.8450**	–0.2907**	0.3915**	0.8945**
		F_3						0.1326	0.8311**	–0.2704**	0.3758**	0.8839**
	KRIPA × ICC16644	F_2						–0.0189	0.8875**	–0.1802**	0.2398**	0.9085**
		F_3						0.0163	0.8866**	0.0869	0.3948**	0.9379**
	ICC17109 × ICC16644	F_2						0.0854	0.9139**	–0.1807**	0.1398*	0.9267**
		F_3						0.1152	0.8470**	–0.1669*	0.2847**	0.8839**

* and ** are significant at 5% and 1% respectively.

the segregating generations of all the crosses except C_2 where association was positive but non-significant.

The phenological traits, *i.e*., days to flowering, podding and maturity exhibited significantly negative association with harvest index and number of seeds per pod in both the segregating generations studied except in the F_2 generation of cross C_1 in which the association between days to maturity and harvest index was reported to be non-significant.

Days to flowering was observed to have significant and positive association with biological yield per plant in the F_2 generation of cross C_1 (0.1532*) and C_2 (0.1378*). It was also significantly and positively associated with number of pods per plant in F_2 and F_3 generations of C_1 (0.2882**, 0.1551*) and only F_2 generation of C_2 (0.1594*). With plant height the days to first flower showed significantly negative association in F_2 (–0.2365**) and F_3 (–0.2298**) generations of C_1, while significantly positive in case of F_2 (0.1800**) of C_3 and F_3 (0.2096**) of C_4. Days to pod initiation had no significant correlation with biological yield per plant in any of the generation of the four crosses under study except F_2 (0.1486*) generation of cross C_1 in which a significant weak positive association was observed. Days to maturity showed positive significant association with number of pods per plant in both the segregating generations of cross C_1 (0.2469**, 0.1732**) and also in F_2 generation of C_2 (0.1929**). It exhibited positive association with number of seeds per plant in F_2 (0.2236**) and F_3 (0.1438**) generation of cross C_1, while it was significantly negative in F_3 (–0.1612*) generation of C_4.

Plant height at maturity exhibited significant positive association with 100-seed weight in both the segregating generations of C_1 (0.1859**, 0.1416*) and C_2 (0.2321**, 0.1527*) while only in F_2 (0.1407*) generation of C_3. A significant positive association was also noted with seed yield per plant in all the generations of all the crosses studied.

Number of pods per plant exhibited significantly strong positive association with number of seeds per plant, biological yield per plant in both F_2 and F_3 generations of all the crosses, while it showed significant negative association with number of seeds per pod in both F_2 and F_3 generation of C_1 (–0.4009**, –0.1684*) and C_3 (–0.2011**, –

Table 4.6 (cont.).

Characters	Crosses	Generations	Days to pod initiation	Days to maturity	Plant height at maturity	No. of pods/ plant	No. of seeds/ plant	No. of seeds/ pod	Biological yield/plant	100–seed weight	Harvest index	Grain yield/plant
No. of seeds/pod	JGK 2 × ICC16644	F_2							– 0.2582**	0.0575	0.0625	– 0.2110**
		F_3							– 0.0002	0.0011	0.0296	0.0018
	KAK 2 × ICC16644	F_2							–0.1124	–0.2154**	0.3912**	0.0553
		F_3							–0.1042	–0.3099**	0.1386*	–0.0156
	KRIPA × ICC16644	F_2							–0.1637*	–0.1296	0.2661**	–0.0639
		F_3							–0.0757	–0.1269	0.1314	–0.0413
	ICC17109 × ICC16644	F_2							–0.0336	–0.1968**	0.1875**	0.0316
		F_3							–0.0718	–0.1903**	0.3076**	0.0328
Biological yield/plant	JGK 2 × ICC16644	F_2								0.1328	0.0549	0.9538**
		F_3								0.1286	0.2899**	0.9711**
	KAK 2 × ICC16644	F_2								0.0614	0.1525*	0.9115**
		F_3								0.0206	0.1175	0.9119**
	KRIPA × ICC16644	F_2								0.0648	0.0149	0.9124**
		F_3								0.2531**	0.1400*	0.9029**
	ICC17109 × ICC16644	F_2								0.0632	–0.0365	0.9458**
		F_3								0.1686*	0.0428	0.9183**

* and ** are significant at 5% and 1% respectively.

Table 4.5 (cont.).

Characters	Crosses	Generations	Days to pod initiation	Days to maturity	Plant height at maturity	No. of pods/ plant	No. of seeds/ plant	No. of seeds/ pod	Biological yield/plant	100–seed weight	Harvest index	Grain yield/plant
100–seed weight	JGK 2 × ICC16644	F_2									0.4900**	0.269**
		F_3									0.5296**	0.2423**
	KAK 2 × ICC16644	F_2									0.1829**	0.1112
		F_3									0.2877**	0.1130
	KRIPA × ICC16644	F_2									0.3812**	0.2089**
		F_3									0.4753**	0.3852**
	ICC17109 × ICC16644	F_2									0.3093**	0.1578*
		F_3									0.2663**	0.2453**
Harvest index	JGK 2 × ICC16644	F_2										0.3153**
		F_3										0.4702**
	KAK 2 × ICC16644	F_2										0.5050**
		F_3										0.4689**
	KRIPA × ICC16644	F_2										0.3885**
		F_3										0.4999**
	ICC17109 × ICC16644	F_2										0.2600**
		F_3										0.3891**

* and ** are significant at 5% and 1% respectively.

0.1439*). Significantly positive association were also noted with harvest index in F_2 and F_3 generations of C_2 (0.3128**, 0.3332**) and C_3 (0.1909**, 0.3776**), while only in F_3 generations of C_1 (0.3149**) and C_4 (0.2476**).

Number of seeds per plant expressed positive significant association with harvest index in both the generations of all the four crosses except F_2 generation of C_1 where the association was non-significant. It also showed significantly positive association with biological yield per plant and seed yield per plant in both the generations of all the crosses studied. Negative and significant association was observed between number of seeds per plant and 100-seed weight and in both F_2 and F_3 generations of the cross C_2 (–0.2907**, –0.2704**) and C_4 (–0.1807**, –0.1669*), and only in F_2 generation of C_1 (–0.2252**) and C_3 (–0.1802**).

Number of seeds per pod exhibited significant negative association with 100-seed weight in both the generations of cross C_2 (–0.2154**, –0.3099**) and C_4 (–0.1968**, –0.1903*), while significantly positive association was observed with harvest index in both F_2 and F_3 of C_2 (0.3912**, 0.1386*) and C_4 (0.1875**, 0.3076**), and in only F_2 (0.2661**) of C_3. It was observed to have significantly negative association with biological yield per plant (–0.2582**) and seed yield per plant (–0.2110**) of C_1 cross in F_2 generation.

The correlation of biological yield per plant with harvest index was significantly positive in F_3 (0.2899**) of C_1, F_2 (0.1525*) of C_2 and F_3 (0.1400**) of C_3. Non-significant association between biological yield per plant and 100-seed weight was noted for all the crosses studied in both the generation except F_3 of C_3 (0.2531**) in which association was significantly positive.

100-seed weight expressed highly significant and positive association with harvest index in all the four crosses of both the segregating generations studied.

Chapter-V

DISCUSSION

5.1 Analysis of variance

The analysis of variance between families (crosses) and among progenies of each cross revealed that there were significant differences among crosses as well as generation for all the traits except harvest index and indicated the presence of genetic variability among the genotypes and revealed that there is ample scope for selection. The results of the present investigation are in a line with the observations of Kumar *et al.* (2013) for Days to maturity, Plant height at maturity (cm), Number of pods per plant, Grain yield per plant (g), Biological yield per plant (g) and 100-Seed weight (g).

In general the estimates of phenotypic coefficient of variation (PCV) were higher than their corresponding genotypic coefficient of variation GCV. The high estimates of GCV and PCV was observed for biological yield per plant in C_4 and number of pods per plant in all the crosses. These findings are in conformity with the results of Shivkumar *et al.* (2013). However, Ali *et al.* (2010) reported moderate value of both GCV and PCV for these traits. Days to first flower, days to first pod formation, and grain yield per plant had moderate estimates of GCV and PCV. Similar results were also reported by Singh *et al.* (1995), Yadav *et al.* (1999) and Arora and Jeena (2000), while Ali *et al.* (2010) reported that PCV and GCV both were high for grain yield per plant and low for days to first flower. For days to maturity, plant height at maturity and number of seeds per pod estimates of PCV and GCV were found low in all the crosses. These results are in consonance with the finding of Ali *et al.* (2010) and Monpara and Dhameliya (2013). Moderate estimate of coefficients of variation for 100-seed weight were recorded in all the cross except C_4 where both the PCV and GCV was recorded to be low, results are in agreement with the result of Singh *et al.* (2004). However, Vijayalakshmi *et al.* (2000) reported high estimate of coefficients of variation for 100-seed weight.

5.2 Heritability and Genetic Advance

According to Johnson (1955) high heritability should be accompanied with high genetic advance to arrive at desired level of improvement in a particular character, but it may not be necessary that a character exhibiting high heritability will give high genetic advance. Several researchers (Malik *et al.,* 1983; Malik *et al.,* 1988; Ghafoor *et al.,* 1990 and Ghafoor *et al.,* 2000) have emphasized the utility of the estimates of heritability and genetic advance for the prediction of response of quantitative characters to selection in chickpea. In the present study high heritability along with high genetic advance as % of mean was exhibited by days to first flower, days to pod initiation, number of pods per plant, number of seeds per plant and 100-seed weight for all the crosses indicated that selection based on mean values would be effective in improving these traits. Arshad *et al.* (2004), Anbessa *et al*. (2006), Bicer and Sakar (2008) and Srinivasan *et al.* (2011) also reported high broad-sense heritability and GAM for days to first flower in contrast to Deb and Khaleque (2009) and Ali *et al* (2010) who proposed low and moderate value of the broad sense heritability respectively in chickpea. High broad sense heritability for 100-seed weight in chickpea was also reported by Burli *et al.* (2004), Arshad *et al.* (2004), Dubey and Srivastava (2007), Baber *et al.* (2008), Bicer and Sakar (2008), Sharma and Saini (2010), Ali *et al.* (2010), Hossain *et al.* (2010), Srinivasan *et al.* (2011), Karami and Talebi (2013), Sharma *et al.* (2013) and Shivkumar *et al.* (2013) in chickpea. High broad-sense heritability coupled with moderate GAM was noted for days to maturity in three crosses (C_2, C_3 and C_4). High heritability along with moderate GAM was exhibited by C_3 and C_4 for plant height at maturity. Number of seeds per pod showed high heritability along with low GAM in all the crosses except C_2. For grain yield per plant high heritability coupled with high GAM exhibited by C_1, while moderate heritability with moderate GAM was reported for the cross C_2 and C_4. Shivkumar *et al.* (2013) also reported high broad-sense heritability along with high GAM for grain yield, while Ali *et al.* (2010), reported high broad-sense heritability along with low GAM for the same. Biological yield per plant had high heritability associated with high genetic advance in the cross C_1 and C_4, while moderate value of heritability as well as GAM was observed for the crosses C_2 and C_3.

These results get support with the findings of Dubey and Srivastava (2007), Bicer and Sakar (2008), Baber *et al.* (2008), Sharma and Saini (2010) and Karami and Talebi (2013).

5.3 Generation mean analysis

Days to first flower

The variability for days to first flower in F_2 and F_3 generations for all the four crosses signify the scope for improvement through selection. In all the crosses epistasis was playing important role. The main effect, additive gene effect (d), was important for the trait in all the crosses. Importance of additive gene action for days to flowering was also reported by Jahagirdar *et al*. (1994), Jha *et al*. (1997) and Bicer and Sakar (2008), in chickpea, Craufurd *et al.* (2001) in pigeonpea while, dominance gene effect (h) was also reported to be important for days to flowering in chickpea along with additive gene effect (d) by Karami and Talebi (2013) and Kumar *et al.* (2013). Among interactions, both the interactions were important for the trait in all the crosses except in C_2, where only additive x additive (i) gene action was important. Relatively higher magnitude of dominance x dominance (l) indicated the preponderance of dominance x dominance (l) over additive x additive (i). Present study revealed the duplicate type gene action in almost all the crosses. Negative sign of additive x additive reflects the dispersion of allele in the parents for the trait. Dispersion of allele along with duplicate type epistasis may lead to the faulty selection in the early generation of segregants. Duplicate type of epistasis for the trait was also reported by Gumber and Saravjeet (1996), Girase and Deshmukh (2000) and Bhardwaj and Sandhu (2007) while complementary type of epistasis was suggested for days to flowering by Kumar and Rao (1996) in chickpea.

Days of pod initiation

Significance of both the scaling test revealed the importance of epistasis in governing the trait in all the crosses. Main effect additive (d) as well as both the interactions were playing important role in governing the trait in all the crosses except C_2 where dominance x dominance (l) was not important. Relatively higher magnitude of dominance x dominance (l) than additive x additive (i) indicated the preponderance of dominance x dominance (l) interaction. Duplicate type of epistasis was also observed

for the trait in all the crosses except C_2. Estimates of gene effect reveled that both the additive as well as non-additive gene action was important in governing the trait. According to Bicer and Sakar (2007) both the additive as well as non-additive gene effects was important with duplicate type of epistasis for the trait in chickpea.

Days to maturity

Significance of either or both of the scaling tests revealed the inadequacy of additive-dominance model and presence of epistasis in governing the days to maturity in all the crosses. Both the main effects *i.e*., additive effect (d) and dominance effect (h) were important for the trait in all the crosses except C_2 where additive gene action (d) and additive x additive (i) interaction was important. Similar results were also reported by Girase and Deshmukh (2000). For rest of the three crosses both the main effect and interaction effect were important except C_1 where additive x additive (i) effects was not important in governing the trait. However the relative magnitude of dominance effect (h) over additive effect (d) and dominance x dominance (l) over additive x additive (i) indicated the preponderance of non-additive gene action. Duplicate type of epistasis was reported for the trait in C_3 and C_4. Similar findings were also reported by Bhardwaj and Sandhu (2007) and Kumar *et al*. (2013) in chickpea. In the cross C_1, complementary epistasis was observed. Srinivasan *et al*. (2011) reported complementary epistasis for days to maturity in control condition while the type of epistasis for the same was found to be duplicate in saline condition in chickpea.

Plant height at maturity

Scaling test revealed the importance of epistasis in governing the trait. The main effect additive (d) and dominance (h) as well as interaction effects additive x additive (i) and dominance x dominance (l) were important for all the crosses except for the cross C_4 where dominance (h) effect was not important. The gene action was considered to be of duplicate type for the character. Negative sign of dominance x dominance (l) showed ambidirectional dominant but the positive sign of additive x additive reflects the association of alleles in the parental lines. Similar result were found by Bhardwaj and Sandhu (2007) and Kumar *et al*. (2013), on the other hand Girase and Deshmukh (2000) reported only main effects were important for plant height in chickpea. In the cross C_4

additive (d), dominance x dominance (l) and additive x additive (i) were important for the trait which was in accordance with the result of Kidambi *et al*. (1988).

Number of pods per plant

Either or both of the scaling tests were significant which indicated the presence of epistasis for the trait in all the crosses studied except C_4 for which neither of the scaling tests was significant, while the interaction components recorded were significantly higher for the cross C_4. Mather and Jinks (1971) pointed out some conditions in which one or more of these generations means (*i.e.*, B_1, B_2, F_2 and F_3 means those referred as A, B, C and D scales) may not deviate significantly even when non-allelic interactions are present. These conditions are, (a) with a dispersed pair of genes, the three groups of interactions, additive x additive (i), additive x dominance (j) and dominance x dominance (1) interactions may partly cancel out, and (b) with more than two interacting genes, cancellation can arise because of dispersion and because the individual i's, j's and l's may differ from one pair of interacting genes to another. Main effect additive was found important for the crosses C_3 and C_4 while dominance gene effect (h) was not important for this trait. Among the interaction components both the additive x additive and dominance x dominance (l) were important for all the crosses except C_1 where only additive x additive was significant. But higher magnitude of dominance x dominance (l) interaction effect showed its significance for governing the number of pods per plant. Negative sign of additive x additive interaction showed the dispersion of alleles in the parents. Sharma *et al.* (1990), Pundhir *et al*. (1991) and Panchhbhai *et al.* (1992) also reported non-additive gene action for this character. Duplicate type of epistasis was considered for the trait, since the estimates of dominance (h) and dominance x dominance (l) had opposite signs. Similar results were also reported for the crosses *i.e*, PBG5 X ICCV93929 and IPC-94-19 X RSG-888 among the crosses taken for study by Bhardwaj and Sandhu (2007) and Kumar *et al.* (2013) respectively. Khodambashi *et al*. (2012) also reported duplicate type of epistasis for this trait in lentil. However, according to Girase and Deshmukh (2000) and Srinivasan *et al*. (2011) only the main effects were important and there was no epistasis for the trait.

Number of seeds per plant

Significance of either of the scale in all the crosses except C_4 indicated the presence of epistasis for the trait. Different type of gene interaction was found for different crosses analysed in the present study. For the cross C_1 only dominance x dominance (l) was governing the trait and positive sign of dominance x dominance (l) indicated that dominance direct was unidirectional. Additive gene effect (d) and additive x additive (i) interaction were important for the cross C_3. Srinivasan *et al.* (2011) reported that additive effect (d) was important but no epistasis was found for this trait. Earlier Kumar *et al.* (2013) reported similar result in one of the crosses they studied *i.e.*, in IPC-94-94 x RSG-888 in rainfed condition the number of seed per pod was governed by additive x additive (i) gene effect only. For C_2 dominance effect (h) and both the interaction effect were important while in C_4 additive effect (d) and both the interactions were important. Girase and Deshmukh (2000), reported dominance as well as interaction were important in governing this trait in one of the crosses they studied while in other crosses only main effect was important. Kumar *et al.* (2013) reported for the cross RSG-895 x RSG-888 dominance effect (h) as well as both the interaction effect were important for the trait. Complementary type of epistasis was found important for the crosses C_1 and C_4, while for the cross C_2 it was duplicate type of epistasis. On the parental line allele dispersion was found in almost all the crosses. On parental line alleles dispersion was found in almost all the crosses. Duplicate gene action was also reported by Kumar *et al.* (2013), Girase and Deshmukh (2000) in chickpea; and Khodambashi *et al*. (2012) in lentil.

Number of seeds per pod

All the components of gene action were found to be important for governing the trait. Among the main effect additive gene action (h) was playing important role for expression of trait in all the crosses. Negative sign of additive gene action suggested the higher proportion of negative allele in the parents. Among interactions, dominance x dominance (l) was important for C_1 and C_2 while additive x additive (i) was governing the trait in all the crosses except C_1 depicting the major role played by additive x additive gene action. Complementary type of epistasis was reported for the trait.

Preponderance of additive effect (d), additive x additive interaction (i), along with complementary type of interaction showed effectiveness of selection for improving the trait. Similar results were found by Bhardwaj and Sandhu (2007) and Kumar *et al*. (2013) in chickpea.

Grain yield per plant

Differential role of individual genes and their interactions were found important for grain yield per plant in different crosses. Additive effect (d), dominance effect (h) and additive x additive interaction (i) were important for C_1 crosses with preponderance of dominance effect (h) and additive x additive interaction (i). In contrast to that additive effect (d) and dominance x dominance interaction (l) were found to have important role in cross C_2. Bhardwaj and Sandhu (2007) in their study in two crosses of chickpea also reported that dominance gene effects (h) as well as additive x additive (i) interaction were important for this trait. In both the above crosses C_1 and C_2 both the additive as well as non-additive gene action was important and duplicate type of epistasis was governing the trait. Importance of additive as well as non-additive gene actions for seed yield per plant was also reported by Bhardwaj *et al.* (2005), Deb and Khaleque (2009) and Karami and Talebi (2013). Khattak *et al.* (2004) reported complementary type of gene action for this trait in mungbean. For the crosses C_3 and C_4 only dominance gene effect (h) and additive gene effect (d) respectively were found significant and the absence of epistasis confirmed the results of scaling test for this trait. Srinivasan *et al*. (2011) reported dominance effect (h) in control condition while additive effect (d) in saline condition were governing the seed yield per plant in chickpea. Ahir *et al.* (2006) reported additive effect (d), dominance effect (h) and both in first cross, second cross and third cross respectively in pigeonpea. However, Girase and Deshmukh (2000) and Bhardwaj and Sandhu (2007) reported interactions effect and duplicate type of epistasis was playing important role along with main effects for grain yield per plant in chickpea.

Biological yield per plant

Scaling test for crosses C_2 and C_4 indicated the presence of epistasis in governing the trait. The main effect additive (d) was found to be important in governing

biological yield per plant in all the crosses while dominance effect (h) was important for C_2 only. Both, additive gene effect (d), dominance effect (h) along with dominance x dominance (l) was also important for this trait in C_2. However the magnitude of dominance x dominance (l) was highest among all the estimates in both the crosses. For the cross C_4 additive effect (d) and dominance x dominance (l) was important. Duplicate type of epistasis was reported for the trait in both the crosses. Similar result was reported by Kumar et al. (2013) for the cross RSG-888 x ICC4958 in irrigated condition in chickpea. Whereas, Bhardwaj and Sandhu (2005) suggested that both the main effect and all the interaction effects was important in governing the trait in chickpea. For the cross C_1 and C_3 only main effect, additive effect (d) and dominance effect (h) respectively was found to be important.

100-Seed weight

The mean performance of F_{1s} generated from the crosses revealed that smaller seed size was partially dominant over larger seed size. Significance of either or both of the scales for all the crosses revealed the presence of epistasis for the trait. Both the main effect *i.e.*, additive (d) and dominance (h) were important in all the crosses except C_4 where only additive effect (d) was important. However relative higher magnitude of additive gene effects revealed the preponderance of additive gene action. The positive sign of dominance effect (h) showed that increasing alleles were involved in dominant phenotype *i.e.,* small seed size. Among interactions, dominance x dominance (l) was governing the trait in C_1 and C_3 only. In the all crosses additive x additive (i) interaction was important except C_1. Duplicate epistasis was evident from the opposite signs of dominance effect (h) and dominance x dominance effect (l) in all the crosses except C_4. Positive sign for additive x additive (i) in all the crosses showed that there was association of alleles in parents for the trait in all the crosses. However negative sign of dominance x dominance effect (l) indicated ambidirectional dominant. For the cross C_2 and C_4 mainly additive gene effect (d) and additive x additive (i) interaction effect were governing the seed size. Sharma *et al*. (2013) also reported the similar result in their desi x kabuli cross. In contrast Khodambashi *et al*. (2012) suggested dominance gene effect (h) as well as dominance x dominance (l) interaction was important for the trait in lentil whereas, Girase and Deshmukh (2000) reported only dominance effect was

important for this trait in chickpea. In C_3 both the main effects as well as both the interaction effects were important. Similar results were proposed by Bhardwaj and Sandhu (2005) and they also reported duplicate gene action for the trait, Khattak *et al.* (2004) also reported duplicate type of epistasis in mungbean in contrast, Hossain *et al.* (2010) reported complementary genes for the character in chickpea.

5.4 Correlation coefficient analysis.

Correlation analysis was carried out to assess the information on the nature and extent of association of phenology (days to first flower, days to pod initiation and days to maturity) with seed size and seed yield per plant and among other characters. The inter-correlations among phenology and other character are also important to find out the relative importance of individual character which influences the phenology.

In the present study phenology exhibited significant but negative association with 100-seed weight in both the segregating generations of the crosses C_1 and C_2 while for the both F_2 and F_3 of C_3 and C_4 the association was non-significant. Arshad *et al.* (2004) and Ali *et al*. (2010) also reported non-significant association between 100-seed weight and days to first flowering. For days to maturity, Jivani *et al*. (2013) found non-significant association for 100-seed weight. While according to Hovav *et al.* (2003) correlation between time to flowering and seed weight were positive. Negative association between phenology and 100-seed weight in C_3 and C_4 suggested that in certain genetic background it might be possible to breed early flowering genotypes with large seed size.

Phenology of two segregating generations of each of the four different crosses showed non-significant association with seed yield per plant in all the segregating generations studied except in F_3 generation of the cross C_4 in which negative significant association of seed yield per plant with days to flowering, days to pod initiation and days to maturity was recorded. One of the possible causes may be the ambidirectional distribution of alleles in the parental population and accumulation of positive alleles in later generations. Nevertheless, the data suggested that one or more component of phenology may be associated in certain genetic backgrounds with seed yield per plant. From the result it may be concluded that selection for early phenology may increase

seed yield per plant but it depends on the genetic background of the parent used in the hybridization programme and the selection should be practiced in later generations. These findings are corroborative with the findings of Arshad *et al.* (2004), Ali *et al.* (2010) and Monpara and Dhameliya (2013).

Yield per plant was positively associated with biological yield per plant, number of seeds per plant, number of pods per plant, harvest index and plant height at maturity. Such positive interrelationship between these attributes had also been reported in chickpea by Arshad *et al*. (2004), Vaghela *et al.* (2009) and Jivani *et al*. (2013). The 100-seed weight was positively correlated with grain yield per plant in all the crosses except C_2. Mathur and Mathur (1996) and Ali *et al.* (2010) also reported similar results while Lal *et al*. (1993) reported a negative correlation between seed yield and 100-seed weight.

Plant height at maturity showed positive and significant association with number of pods per plant, number of seeds per plant, biological yield per plant and 100-seed weight in both the segregating generations of C_1 and C_3 which was in accordance with the findings of Jadhav and Mane (1991), Jethwa (1994) and Jivani *et al.* (2013) in chickpea.

Number of pods per plant, number of seeds per plant and biological yield per plant were highly interrelated among each other in both F_2 and F_3 generations of all the crosses. These results get support with the findings of Ali *et al*. (2010).

Number of seeds per plant revealed significant positive correlation with biological yield per plant and harvest index but negative association with 100-seed weight. Vijayalaxmi *et al*. (2000) also reported negative association of number of seeds per plant with 100-seed weight in chickpea. Regarding relationship between number of seeds per plant and 100-seed weight Ali *et al.* (2010) reported contrast result.

Number of seeds per pod exhibited positive correlation with harvest index and negative correlation with 100-seed weight. 100-seed weight expressed significant positive correlation with harvest index while Arshad *et al*. (2004) and Jivani *et al*. (2013) reported non-significant association between them.

Biological yield per plant showed positive correlation with harvest index. The present findings had been credence with the observations made by Arshad *et al*. (2004) while Jeena *et al.* (2005) reported negative association between them. According to Jivani *et al.* (2013) there was non-significant correlation between biological yield per plant and harvest index.

From the results it can be concluded that all the three phenological traits were not associated with yield *per se.* In general, it is difficult to improve both the yield as well as phenological traits simultaneously through selection. However, phenological traits were associated with yield *per se* in F_3 generation of cross C_4 which suggested that improvement may be possible by using specific parent in the cross and selection should be practiced in later generations. Results also suggested that in certain genetic background it might be possible to breed early flowering genotypes with large seed size.

SUMMARY AND CONCLUSION

The present investigation "Effect of phenology on grain size and grain yield in kabuli chickpea (*Cicer arietinum* L.)." was undertaken to study the inheritance of time to flowering, seed size and seed yield and to study the association of phenology with seed size and seed yield in kabuli chickpea. The materials for study comprised of one early maturing small-seeded landrace (ICC 16644); two medium maturing medium-seeded cultivars (JGK 2 and KAK 2) and two late maturing large-seeded genotypes (KRIPA and ICC 17109), four F_{1s} derived from the crosses namely, JGK 2 x ICC 16644 (C_1), KAK 2 x ICC 16644 (C_2), KRIPA x ICC 16644 (C_3) and ICC 17109 x ICC 16644 (C_4); four F_2 and four F_3 generations; which were collected from Chickpea Breeding, ICRISAT, Patancheru, Hyderabad. The experiment was undertaken in vertisol at ICRISAT on 12th Nov 2013 in compact family block design with three replications. The observations were recorded on 11 characters *viz*., days to first flower, days to pod initiation, days to maturity, plant height at maturity (cm), number of pods per plant, number of seeds per plant, number of seeds per pod, biological yield per plant (g), grain yield per plant (g), harvest index (%) and100-seed weight (g).

For the inheritance study of traits, to decide the adequacy of additive-dominance model, simple scaling test [(Mather, (1949) and Hayman and Mather, (1955)] and to estimate the genetic parameters, five-parameter model [Hyman (1958)] were applied. Heritability [Allard's formula (1960)] and genetic advance as percent of mean [Johnson *et al*. (1955a)] were calculated to study the possibility and extent to which improvement is possible through selection. Correlation studies were undertaken to determine whether the phenology affect the seed size and seed yield and also to study the association among other characters. Salient findings of the present study and conclusion drawn are summarized below.

The analysis of variance between families (crosses) and among the generations of each cross revealed that there were significant differences among crosses as well as generations for all the traits except harvest index which indicated the chances of improvement through selection. Moderate magnitude of genotypic coefficient of variation and phenotypic coefficient of variation was observed for days to first flower, days to pod initiation, number of pods per plant,

grain yield per plant and 100-seed weight. High heritability along with high genetic advance as percent of mean was exhibited by days to flowering, days to pod initiation, number of pods per plant, number of seeds per plant and 100-seed weight for all the crosses indicating that selection based on mean values would be effective in improving these traits in respective crosses. For grain yield per plant high heritability coupled with high GAM exhibited by C_1, while moderate heritability with moderate GAM was reported for the cross C_2 and C_4.

The result of generation mean analysis revealed that estimate of a genetic parameter significant for a particular trait in one cross was not necessarily found to be significant for the same character in other cross. The mean effect of F_2 performance (m) was highly significant for all the characters in all the crosses. Main effect, additive (d) and both the interaction effects *i.e.*, dominance x dominance (l) and additive x additive (i) effects were important for days to first flower, days to pod initiation and days to maturity. Relatively higher magnitude of dominance x dominance over additive x additive indicated the preponderance of dominance x dominance gene action in governing the phenological traits, with duplicate type of epistasis. For grain yield per plant, additive effect, dominance effect and additive x additive interaction for C_1; additive effect and dominance x dominance interaction in C_2; only dominance gene effect in C_3 and only additive gene effect in C_4 were contributing significantly in governing the phenology. Both the main effect *i.e.*, additive and dominance were important for seed size with the preponderance of additive gene action in all the crosses. For the cross C_2 and C_4 mainly additive gene effect and additive x additive interaction were governing the seed size whereas for C_1 and C_3 both the main effects as well as interaction effects were important with duplicate type epistasis.

Phenology (time to flowering, podding and maturity) exhibited significantly negative association with 100-seed weight in both the segregating generations of C_1 and C_2 while for both F_2 and F_3 of C_3 and C_4 the association non-significant. The negative association of phenology with seed size in the two crosses (C_1 and C_2) suggested that in certain genetic background it might be possible to breed early-flowering cultivars with larger seed size.

Phenology showed non-significant association with seed yield per plant in all the segregating generations studied, except in F_3 generation of the cross C_4 where significant and negative association of seed yield per plant with days to

first flower, days to pod initiation and days to maturity was noted. Nevertheless, the data suggested that one or more component of phenology may be associated in certain genetic backgrounds with yield per plant, though the associations were weak. It envisages clear that selection for early phenology would not be effective to increase the seed yield per plant directly.

From the result it can be concluded that additive (d), dominance x dominance (l) and additive x additive (i) gene actions played significant role for the inheritance of phenological traits (time of flowering, podding and maturity) in chickpea. Main effect additive and both the interactions were important for governing the trait grain yield per plant in almost all the crosses. However for 100-seed weight additive (d), dominance (h) and additive x additive (i) were important for most of the crosses. Duplicate type of interaction was found for all the phonological traits along with grain yield and 100-seed weight. Phenology exhibited significant negative correlation with 100-seed weight in two crosses suggesting that in certain backgrounds it might be possible to breed early-flowering genotypes with larger seed size. Phenology showed non-significant association with seed yield per plant in all the segregating generations studied except F_3 generation of C_4. The result suggested that selection for early phenology may not be effective to increase the seed yield per plant directly.

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APPENDIX

Appendix: i. Range of 11 characters in different generations of each of the four crosses in chickpea					
Traits / Generations		**JGK 2 × ICC16644**	**KAK 2 × ICC16644**	**KRIPA × ICC16644**	**ICC17109 × ICC16644**
Days to first flower	P_1	34–36	35–39	36–41	36–41
	P_2	30–33	30–33	30–33	30–33
	F_1	48–52	49–56	51–57	51–58
	F_2	29–58	30–72	29–63	29–61
	F_3	29–61	28–75	28–73	29–71
Days to pod initiation	P_1	37–43	39–44	40–46	42–47
	P_2	34–39	34–39	34–38	34–39
	F_1	51–57	52–60	55–61	55–62
	F_2	33–65	34–76	33–68	34–69
	F_3	33–67	33–78	32–77	33–75
Days to maturity	P_1	82–88	83–88	87–90	87–94
	P_2	79–84	79–84	79–84	79–84
	F_1	90–95	90–98	91–100	93–99
	F_2	78–103	78–110	77–110	76–111
	F_3	78–110	79–107	78–111	79–101
Plant height at maturity (cm)	P_1	36–60	43–58	48–70	42–70
	P_2	32–55	32–55	33–52	32–54
	F_1	33–55	30–58	43–56	40–61
	F_2	33–65	34–64	34–63	33–71
	F_3	33–63	27–61	26–66	30–68
No. of pods per plan	P_1	50–150	45–110	23-89	26–83
	P_2	48–108	50–118	45–120	40–160
	F_1	89–150	55–183	33–64	28–145
	F_2	14–208	14–211	12–200	16–201
	F_3	10–275	15–250	13–198	14–248
No. of seeds per plant	P_1	52–150	46–150	23–89	26–85
	P_2	48–134	58–141	45–154	40–119
	F_1	89–214	56–230	35–169	28–115
	F_2	26–213	14–253	12–200	16–239
	F_3	11–275	15–269	13–252	14–290
No. of seeds per pod	P_1	1–1.15	1–1.22	1–1.11	1–1.11
	P_2	1–1.28	1.1–1.29	1.09–1.30	1.05–1.27
	F_1	1–1.07	1–1.12	1–1.08	1–1.13
	F_2	1–1.12	1–1.16	1–1.25	1–1.15
	F_3	1–1.20	1.02–1.29	1.01–1.26	1.02–1.17
Grain yield per plant (g)	P_1	23.67–49.87	17.30–61.29	12.20–45.85	16.80–56.63
	P_2	21.06–38.30	18.26–38.43	15.90–39.90	15.89–41.00
	F_1	21.03–52.64	14.92–62.23	11.9–60.00	10.80–61.90
	F_2	9.09–67.88	8.95–71.88	7.3–74.12	7.27–85.91
	F_3	8.81–78.37	8.30–77.10	8.29–76.20	6.08–75.53
Biological yield per plant (g)	P_1	32.10–94.30	30.20–96.30	29.90–79.23	32.31–97.92
	P_2	36.44–60.52	32.28–68.71	29.00–73.50	33.60–62.20
	F_1	38.76–103.22	33.30–120.47	35.58–106.40	20.90–124.46
	F_2	20.10–110.00	15.50–128.14	18.25–138.78	12.40–138.47
	F_3	19.31–128.43	15.50–146.48	18.26–138.40	12.69–137.58
100-seed weight (g)	P_1	28.87–40.67	30.45–41.84	31.64–61.87	29.56–70.56
	P_2	22.56–30.67	23.68–33.87	24.74–29.44	22.85–31.64
	F_1	22.67–42.88	27.75–45.74	28.74–46.54	27.33–48.55
	F_2	14.33–51.66	15.78–57.67	21.45–54.78	21.98–62.88
	F_3	11.66–63.66	14.26–54.20	18.34–55.94	21.33–62.87
Harvest index %	P_1	54.00–68.33	52.47–67.78	37.54–83.01	26.23–82.00
	P_2	49.32–79.49	49.22–75.63	48.22–80.00	47.47–78.23
	F_1	38.62–81.26	33.41–62.28	26.36–78.40	28.47–69.23
	F_2	40.02–85.54	25.56–77.86	22.77–78.86	25.30–77.29
	F_3	24.00–76.55	27.24–82.01	29.26–83.88	30.30–83.17

APPENDIX