GENETIC STUDIES OF QUALITATIVE AND QUANTITATIVE TRAITS IN CHICKPEA (*Cicer arietinum* L.)

By

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CERTIFICATE

Mr Sayyed Hossain Sabaghpour has satisfactorily prosecuted the course of research and that the thesis "**GENETIC STUDIES OF QUALITATIVE AND QUANTITATIVE TRAITS IN CHICKPEA (*Cicer arietinum* L.)**" submitted is the result of original research work and is of sufficiently high standard to warrant its presentation to the examination. I also certify that the thesis or part thereof has not been previously submitted by him for a degree of any university.

Date: 14 Ve 2001

Dr Jagdish Kumar

Major Advisor

CERTIFICATE

This is to certify that the thesis entitled, "**GENETIC STUDIES OF QUALITATIVE AND QUANTITATIVE TRAITS IN CHICKPEA (*Cicer arietinum* L.)**" submitted in partial fulfillment of the requirements for the degree of ' **Doctor of Philosophy**' of the Acharya N G Ranga Agricultural University, Hyderabad, is a record of the bonafide research work carried out by **Mr SAYYED HOSSAIN SABAGHPOUR** under my guidance and supervision. The subject of the thesis has been approved by the Student's Advisory Committee.

No part of the thesis has been submitted for any other degree or diploma. The published part has been fully acknowledged. All assistance and help received during the course of investigations have been duly acknowledged by the author of the thesis.

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Abbreviations (s)	Description (s)
BC_1P_1	F_1 x ICCV2
BC_1P_2	F_1 x JG62
cm	Centimeter
cm^2	Square centimeter
C^o	Degree centigrade
et al.	And others
FAO	Food and Agriculture Organization
Fig	Figure
F_1	First filial generation
F_2	Second filial generation
F_4	Forth filial generation
g	gram
hr	Hour
kg/ha	Kilogram per hectare
m	meter
m^2	square meter
No.	number
p	probability
P_1	parent 1
P_2	parent 2
QTLs	Quantitative trait locus/loci

Contd..

Abbreviations (s)	Description (s)
%	percent
NS	Not Significant
vs.	Versus
χ^2	Chi-square

Dedicated

to my parents with high regards and respect

and

to my wife with special gratitude

and

to my children, Azadeh, Arman and Alaleh with great affection

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DECLARATION

I, Mr Sayyed Hossain Sabaghpour hereby declare that the thesis entitle "**GENETIC STUDIES OF QUALITATIVE AND QUANTITATIVE TRAITS IN CHICKPEA (*Cicer arietinum* L.)**" submitted to Acharya N G Ranga Agricultural University for the Degree of **Doctor of Philosophy in Agriculture** is a result of original research work done by me. I also declare that material contained in the thesis has not been published earlier.

Date: 14. 10. 2000

Sayyed Hossain Sabaghpour

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ABSTRACT

Investigations were carried out to study the genetics of qualitative and quantitative characters of a cross between kabuli type ICCV2 and desi type JG62 chickpea (*Cicer arietinum* L.) varieties at the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, near Hyderabad, A.P., during the *Rabi* season 1998-1999 and 1999-2000.

The experimental material comprised of parents, F_1, F_2, F_3, BC_1 BC_2 generations and 126 RILs. The experimental design to test 126 recombinant inbred lines, parents, F_1 and three checks (Annigeri, ICCV10 and ICCV96029) was an Alpha design with three replications. Each replication consisted of 12 blocks with 11 genotypes appeared in each block. Each plot in RILs and F_3 consisted of two rows of 4 m length and spacing between rows were 60 cm and plant to plant distance were 10 cm. The seven generations (P_1, P_2, F_1, F_2, F_3, BC_1P_1 and , BC_1P_2) of same cross were planted without replication. The generations were planted as single row of 4 m with 60 cm spacing between rows and 20 cm spacing between plants within the row.

Inheritance of seven qualitative characters; flower colour, stem colour, double pod traits, seed type, seed surface, initial growth vigour and seed coat colour was determined. Heritability, genetic advance, coheritability, correlated genetic gain, heterosis, inbreeding depression and superiority of RILs over either parent were studied for days to first flowering, days to 50% flowering, days to first podding, days to maturity, 100-seed weight,

plant height, plant width, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per plant, number of seeds per pod, leaf size, leaf weight, specific leaf weight, seed fibre, seed yield per plant and seed yield per plot.

Monogenic inheritance was obtained for three characters, pink vs. white flowers, pigmented vs. non-pigmented stem colours and single podded vs. double podded peduncles. Genotype of ICCV2 for flower colour is determined as PPbbCC and of JG62 as PPBBCC. Seed surface is governed by two pairs of genes (Sr_1 and Sr_2) in which dominant inhibitory epistasis is operating for this character. Seed type is controlled by two pairs of genes. Plants with dominant genes at both loci produce desi type ($St_1St_1St_2St_2$) and intermediate type is due to dominant gene at one locus ($St_1St_1st_2st_2$ or $st_1st_1St_2St_2$) and kabuli type has recessive alleles at both loci ($st_1st_1st_2st_2$). Early growth vigour is controlled by two pairs of genes. This character appears to be governed by duplicate dominant epistasis. Plants with dominant gene in one or two loci have high growth vigour (Gv_1Gv_2, Gv_1gv_2 or gv_1Gv_2) and recessive alleles in both the loci produce low growth vigour (gv_1gv_2). Early growth vigour character had significant negative correlation with days to first flowering, days to 50% flowering, days to first podding and days to maturity. Seed coat colour is controlled by at least three pairs of genes (Ysc, Bsc, Rsc). If the three loci are present in dominant condition, the seed coat colour will be yellow brown. The genotypes with two loci in dominant condition will have brown, reddish brown or light brown colours. If dominant gene is present at one locus, seed coat colours are yellow beige, dark beige and dark brown. Three recessive genes condition light yellow seed coat colour.

Interrelationships between pairs of characters flower colour, stem colour, seed coat colour, seed type and seed surface showed that gene 'b' controlling flower colour has a pleiotropic effect on stem colour. There is linkage between genes governing flower colour and seed type, flower colour and seed coat colour, and also between seed type and seed coat colour and between stem colour and seed coat colour and seed type. Distance between one of the gene governing flower colour and seed type, seed type and seed coat colour, and stem colour and seed type were 29, 35 and 29 cM respectively.

100-seed weight followed by leaf weight and specific leaf weight showed very high narrow sense heritability and genetic advance. Very high heritability values by regression were for days to first pod followed by days to first flower and 100 seed weight.

The correlated genetic gain estimates of different traits revealed that number of pods per plant, followed by number of seeds per plant and number of secondary branches per plant had high correlated response with seed yield per plant. Number of secondary branches per plant, number of pods per plant, seed yield per plant and number of seeds per plant exhibited high correlated response to selection with yield per plot.

The coheritability estimates of different characters indicated that days to first pod followed by number of pods per plant and number of seeds per plant had high coheritability with seed yield per plot.

Number of pods per plant had positive and maximum values for heterosis over mid parent and better parent heterosis while inbreeding depression value was obtained negative.

RIL numbers 8 and 67 were superior to either parent for most of characters. Using these RILs in a breeding programme, new varieties can be obtained with desirable characters.

For QTL, an association is sought between marker variants (genotypes) and different trait values (phenotypes). Study on 25 qualitative and quantitative characters in F_2, BC_2 and RILs in this investigation may be useful for making map of chickpea.

Introduction

CHAPTER I

INTRODUCTION

Chickpea (*Cicer arietinum* L.) belongs to genus *Cicer*, tribe *Cicereae*, family Fabaceae, and subfamily *Papilionacea* (Singh *et al.* 1997). It originated in southeastern Turkey (Ladizinsky, 1975). Cultivated chickpea is a diploid (2n=2x=16), highly self pollinated, leguminous crop that ranks second in area and third in production among the pulses (Singh *et al.*, 1997). It is grown over an area of nearly 11 million ha in the world and productivity with 820 kg/ha. India, Pakistan, Turkey and Iran together account for about 88% of world chickpea production and 88% of chickpea area. (FAO, 1999). It is cultivated primarily for its protein-rich seed. The plant is an efficient symbiotic-fixer of nitrogen, playing an important role in farming system. Two types of chickpea are grown: desi, with angular and coloured seeds, primarily grown in South Asia; and kabuli, with large, owl-head shape and beige-coloured seeds, grown in the Mediterranean region (Singh *et al.*, 1997). This crop is used predominantly as a pulse, but the manner of use varies with seed type and between regions. In the Indian subcontinent, the desi types are generally milled to remove the testa and produce a split pea composed solely of cotyledonary tissue known as `dhal`. Dhal is utilized either in the preparation of a thin spiced porridge of the same name, which forms an accompaniment to most Indian meals, or further ground to flour (`*besan*`) for the preparation of fried, sweet or savoury snacks or besan curry. Whole chickpea seeds are spiced, soaked, roasted or fried and eaten in North Indians as `chhole`. Kabuli and green-seeded desi types are principally utilized whole in soups, curries and stews. Outside the Indian subcontinent, the predominantly kabuli types are consumed as whole seeds in soups and stews or, increasingly, in developed countries, in salads as a

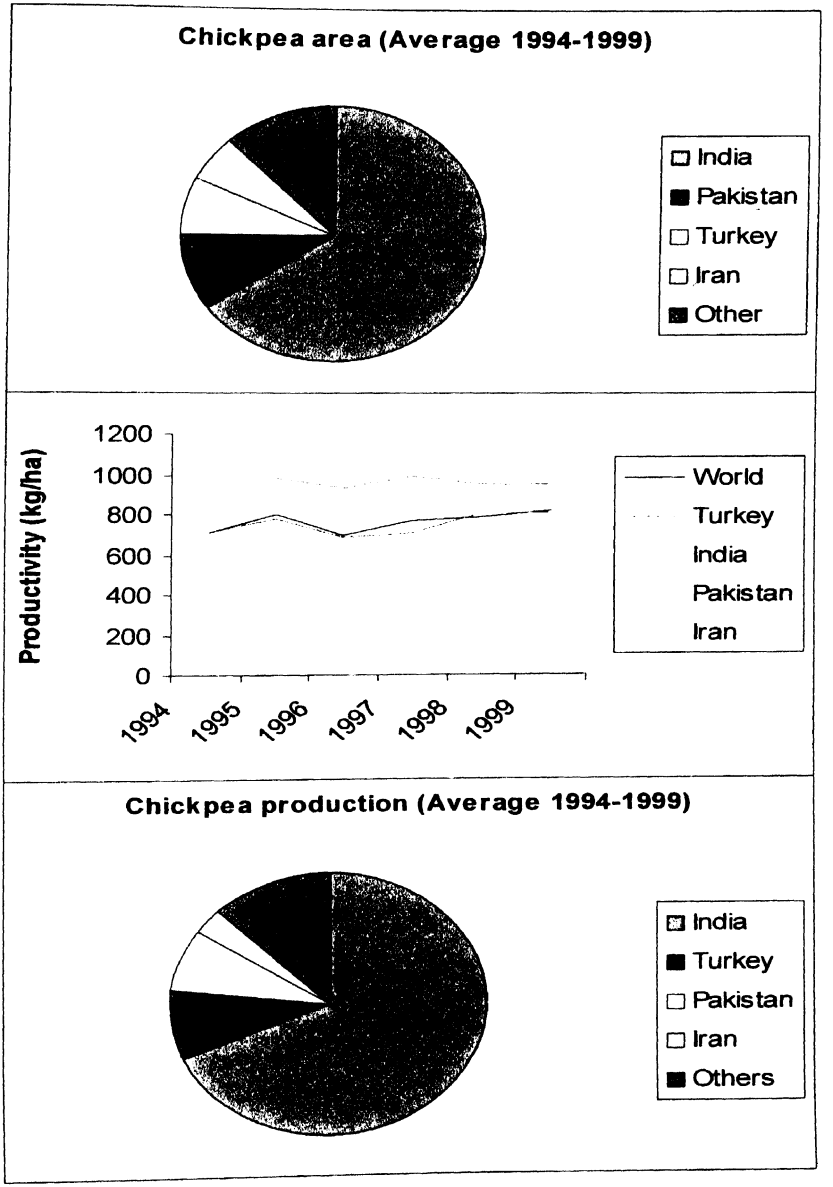

Fig 1. Contribution chickpea area, productivity and production of India, Pakistan, Turkey and Iran to World

'health' food. In the Mediterranean area, cooked seeds are mixed with sesame oil and other flavouring to prepare a savory paste ('*hommos* bi-tehineh') served as a side-dish and eaten with unleavened bread as an accompaniment to main meals (Smithson *et al.*, 1985).

The effectiveness of selection for a trait depends on the relative importance of genetics and nongenetic factors in the expression of phenotypic differences among genotypes in a population, a concept referred to as heritability (Fehr, 1987). Knowing the degree of heritability of a characteristic is very helpful in choosing an efficient breeding system in estimating the gain to be expected under mass selection and in constructing a selection index (Kempthorne and Tandon, 1953). Information on heritability, and genetic advance of yield-attributing traits and their association with seed yield helps to identify characters for more effective selection (Misra, 1991). Estimate of coheritability and correlated genetic gain help in identifying those secondary traits that could be effectively used as basis for indirect selection for improved seed yield.

Assessment of genetic linkage relationships among agronomically important genes is a major component of the genetic characterization of agronomic crops (Davis, 1991). Linkage is of considerable value in plant breeding, when two favourable genes are linked, they tend to be transmitted together, and are easily combined in the progeny. In case of tight linkage (crossing over less than one percent), selection for only one of the two characters may be necessary (Singh, 1997).

Plant yield is a complex character being dependent upon a number of genetical factors interacting with the environment. The average productivity of chickpea is very low

(786 kg/ha). For improvement of the chickpea yield, the breeder has to select superior individuals from their phenotypic expression. Selection based on the phenotypic expression is some times misleading as development of the character is the result of interaction of the heritable and non-heritable. This highlights the imperative need for partitioning the overall variability into its heritable and non-heritable components of heritability, coheritability and genetic advance over the mean of each character. The present investigation was carried out to increase the yield potential of chickpea with the following objectives:

1- To estimate genetic variance and covariance components of important quantitative traits in chickpea;
2- To estimate heritability and coheritability of quantitative characters;
3- To estimate genetic gain and correlated genetic gain;
4- To determine linkage among qualitative traits;
5- To measure the extent of heterosis and inbreeding depression for different traits; and
6- To determine superiority of RILs over parents

Review of literature

CHAPTER II

REVIEW OF LITERATURE

Two main types of chickpea are recognized, namely "desi" and "kabuli". Desi or "indigenous" type is usually of small size, angular shape, and variously coloured and fibrous; while the "kabuli" type is characterized by its large seed size, ram- head shape, and beige/cream coloured seeds with low percentage of fibre (Singh *et al.*, 1985). According to Singh (1987) and Jambunathan *et al.* (1994) the "desi" type accounts for about 80-85% of total world chickpea production.

One of the most important decisions a plant breeder must make involves the selection of parents for population development. The decision-making process includes identifying the characters to be improved, understanding how the characters are inherited. The inheritance of characters ranges from control by one major gene whose expression is not influenced by the environment (qualitative characters) to control by many genes and much influence by the environment (quantitative characters) (Fehr, 1987).

Review of literature pertaining to genetic study of qualitative characters such as flower colour, plant pigmentation, growth vigour, pod number per peduncle, seed-coat colour, seed surface and seed type and quantitative characters such as seed yield plant^{-1}, seed size, number of pods plant^{-1}, number of primary branches plant^{-1}, number of secondary branches plant^{-1}, Plant height, plant width, leaf area, dry leaf weight, specific leaf weight, number of seeds plant^{-1}, seed fibre, seed weight, number of seeds pod^{-1}, days to flowering, days to first pod, days to maturity, and seed yield plot^{-1}.

Inheritance of qualitative characters in chickpea vary from study to study. Some workers reported that one gene and other workers concluded two or three gene control the character. Therefore, the segregation for one, two or three gene pairs is mainly due to the use of difference in the genetic constitution of the parents.

2.1 INHERITANCE OF QUALITATIVE TRAITS IN CHICKPEA:

2.1.1 Flower colour:

Chickpea flowers are complete and bisexual, and have papilionaceous corolla. Their petals are white, pink, and purple or blue in colour. In coloured flowers, the peduncles may be of different colours, the floral part purplish and the racemal green. The axillary inflorescence is shorter than the subtending leaf (Cubero, 1987). Flower colour is a reliable morphological marker in chickpea (*Cicer arietinum* L.). There are different reports of gene action for controlling flower colour in chickpea. Pimplikar (1943), Khan *et al.* (1950), Bhapkar and Patil (1962, 1963), Tendulkar (1965), More (1976) and Gil and Cubero (1993) reported that a single locus is responsible for pink and white flower colour in chickpea. Eight flower colours have bean reported in this species (Pundir *et al.*, 1988). Khosh-Khui and Niknejad (1971a) and Gil and Cubero (1993) reported purple flower is dominant over white flower. Mian (1971) observed monofactorial inheritance for flower colour with pink flower being dominant over white. Whereas Khan and Akhtar (1934), Kadam *et al.* (1941), Pawar and Patil (1979), Ghatge (1994) and Kumar (1997) reported that two genes control this character. Ayyar and Balasubramanian (1936), D' Cruz and Tendulkar (1970), Phadnis (1976) and Vijayalakshmi Satya (1998) reported trigenic inheritance for flower colour. Davis *et al.* (1985) reported that Twenty-two genes are

responsible for flower colour in genus *Pisum*. The gene symbols have given by Ayyar and Balasubramanian (1936) are C, B and P. Their data indicated that C is complementary to B and that P is supplementary to B. Thus, when all these were present together the colour was pink, when CB alone were present it was blue while in six combination viz., cbp, cbP, Cbp, CbP, cBp, and cBP was white. Therefore, the segregation for one, two or three gene pairs governing the flower colour will depend on the genotype of the parents.

2.1.2 Stem colour

The use of markers in crop cultivar classification gives an added advantage in characterizing and maintaining the genetic purity. Many morphological markers for shape, size and pigmentation are used in different crops (Muehlbauer and Singh, 1987). Such pigmentation markers could be used for studying the metabolic pathways of anthocyanin synthesis in chickpea. An ICRISAT line, ICC 5763, which develops purple pigmentation in the whole plant, stem, branches, leaves and flower has been in used as a flagging markers (Mathur, 1989). Mathur (1998) reported that in a chickpea cultigen (ICC-5763) which turns the plant surface purple in the light exposed portions of the plant. The unexposed or diffusely exposed portions of the plant remained green. Another chickpea line 6071 is with purple pigmentation on the whole plant (stem, leaves and flowers) which the pigmentation remains stable from the seedling stage to plant maturity (Sandhu *et al.*, 1993).

Argikar (1955), Argikar and D'Cruz (1963) reported F_2 ratio of 3:1 for stem colour. The same was confirmed by Tendulkar (1965) and More (1976). Whereas Pawar and Patil

(1979), Ghatge *et al.* (1985) and Ghatge (1994) observed a ratio of 9 purple: 7 green for stem colour. Ghatge (1994) and Mathur (1998) reported that purple stem colour was dominant over green stem and found two genes controlling this character (9:7). Thus, the segregation for one and two gene pairs may be due to use of different genotypes of the parents.

2.1.3 Pod number per peduncle:

Flowers are borne singly on pedicels subtended by single peduncles in the axils of the leaves. The normal condition is one pedicel (and flower) per peduncle but double-flowered genotype is quite common. The proportion of double-flowers which set fruit varied with genotypes and environment but, when well expressed, the 'double-podded 'character contributes to slightly improved and more stable yield (Smithson *et al.*, 1985). Normally chickpea have one flower or pod on each peduncle. Many workers reported double-poddedness is controlled by single recessive gene (Khan and Akhtar, 1934; Ahmad, 1964; Singh, 1965; Yadav *et al.*, 1978, Singh and Rheenen, 1994 and Kumar *et al.*, 2000).

The potential for a significant increase in pods and yield in double-podded genotypes has been emphasized, although the gene could also have a negative effect on seed size- an important characters, especially in western Mediterranean countries (Singh, 1987). To date, little information is available about the nature of double pod gene on both yield and seed size. Sheldrake *et al.* (1978) obtained 6-13% higher yield in double podded plants compared with single-podded plants of the same genotype, in which the second flower had been removed. Srivastava (1998) found the gene for double podding exhibits

unstable penetrance and variable expressivity in cross ICCV2 x JG62. The penetrance as well as expressivity of the gene for double podding in highly influenced by environment conditions and also reported that high number of double pods can contribute significantly towards increased seed yield when it is well expressed. Knight (1987) did not find in general differences in yield between single and double-podded F_4 lines on three different genetic background. Singh and Rheenen (1994) suggested double-poddedness can contribute positively to higher productivity in chickpea through a rapid increase in the sink capacity of the plant and additional photosynthetic activity that takes place in the pods and also found mean seed yield of double-podded plants was highest than that of single-podded plants. Rubio *et al.* (1998) reported that the double-pod gene has a positive effect on the stability yield and is not linked to any other gene responsible for seed size in chickpea. Therefore, the double pod character will not decrease seed size in chickpea, a result which allows for the introduction of character in most breeding programs. However, these results clearly indicate that the double pod character is fully compatible with the large seeds characteristic of the high-quality chickpea used for human consumption in western Mediterranean countries. Therefore, several workers reports indicated that double pod per peduncle is controlled by one gene and single pod per peduncle is dominant over double pod per peduncle. But reports about association between number of pods per peduncle with seed yield were different. Therefore, it is necessary to study more about this association.

2.1.4 Seed surface

Singh and Ekbote (1936), Balasubramanian (1937) More and D'Cruz (1970) and Deshmukh (1972) reported that roughness and smoothness of the testa were governed by a

single gene. Later, Tendulkar (1965), Deshmukh *et al.* (1972), More and D'Cruz (1976a), More (1976) and Pawar and Patil (1979) reported two complementary loci (*Rsa* and *Rsb*) for seed surface. Little information for this character is available, thus it needs further studies.

2.1.5 Seed type

Mitosis in *Cicer arietinum* L. was first studied by Dombrowsky-Sludsky (1927), who found the 2n number to be 14. Dixit (1932a) reported that the desi type of *Cicer* with small brown seeds had 14, while the kabuli varieties, which he called *C. Kabulium*, having large white seeds, had 16 chromosomes. Subsequently, Dixit (1932b) reported that the desi type 2 Pusa No.22 having 14 chromosomes, gave rise to a mutant having 16 chromosomes, which he named *Cicer gigas*.

Desi and Kabuli chickpea differ not only in seed morphology including size, colour, shape and testa texture and thickness (Smithson *et al.*, 1985) but also in nutrition such as crude fibre (Jambunathan and Singh, 1980 and Singh, 1984), acid detergent fibre and neutral detergent fibre (Singh, 1984). The protein and oil were similar in these two groups (Jambunathan and Singh, 1980). Breeders have found it convenient to classify chickpea into two main types, namely desi (characterized by small size, angular shape, and coloured seed with a high percentage of fibre) and kabuli (characterized by large size, ram-head shape and beige coloured seeds with a low percentage of fibre). A third type, designated the intermediate, is characterized by medium to small size, pea shape and cream coloured seeds. The intermediate type is found more often in germplasm collection than in

farmer' fields. The desi type accounts for about 85% of the world production, the remainder being kabuli (Singh *et al.*, 1985). In general, the kabuli types are well adapted to spring sowing from Afghanistan westwards into Middle East, Southern Europe and north Africa and desi types are mostly planted in winter from Pakistan eastwards and also in Ethiopia, Sudan, Mexico and Chile (Auckland and Singh, 1977).

It is commonly accepted that kabuli chickpea originated from desi (Moreno and Cubero, 1978 and Salimath *et al.*, 1984). But how did this transformation from desi to kabuli take place? Moreno and Cubero (1978) suggested that the change from *microsperma* to *macrosperma* was a gradual one in which, seed size and suitability for human consumption (e.g., cookability, digestibility) increased and white flower phenotype begun to be more acceptable as a consequence of a correlated response which is very common in legumes where by white flowered cultivars usually show low or zero tannin content and/or they other possesses antinutritional factors.

Hawtin and Singh (1980) reported that there is a fairly clear distinction between the two types, which is generally agreed upon by breeders but is difficult to define systematically. This distinction is based almost entirely on seed shape and colour but also takes account of geographical origin and uses. A third group having round pea-like seeds with the characteristic *Cicer* beak, is also to be found in world collections. These are comparatively rare in local markets. Such round-seeded types (which may be any colour from light beige to black, including green) are generally designed "intermediate" or "pea " type by breeders. Knights (1980) found that pea type (intermediate) was dominant to both

desi and kabuli types and desi was dominant to kabuli. He concluded that seed type is under the control of only a few major genes. Tefera (1998) found 1:2:1 ratio in F_{10} RILs for seed shape and suggested additive gene action for this character. Information about inheritance of seed type is little. Therefore, it is necessary to study more about this character.

2.1.6 Seed coat colour

The inheritance of seed characters is rather more complex than corolla colour. Parents and methods of classification used and gene symbols assigned vary among studies, while seed coat colour is known to change during seed development and ageing. It is clear that several factors are involved, that each interacts with others, and that some have pleiotropic effects (Smithson *et al.*, 1985). For example several genes are involved in seed coat colouration, and pleiotropic effects on flower, stem, and leaf colouration (Muehlbauer and Singh, 1987).

Pimplikar (1943), Bhapkar and Patil (1962) D'Cruz and Tendulkar (1970) obtained a monogenic behavior for seed-coat colour. Argikar and D'Cruz (1962), Bhapkar and Patil (1962), More and D'Cruz (1970), More (1976) and Pawar and Patil (1979) reported that this character is controlled by two pairs of genes. Reddy and Chopde (1977) found black seed-coat colour was dominant over brown and in F_2 the population segregated in 9 black: 7 brown. Alam (1935) reported that seed-coat colour in chickpea is determined by the presence or the absence of at least four different factors and there was strong correlation between flower colour and seed-coat colour. Ayyar and Balasubramanyan (1936) found

that seed coat colour was dependent on five gene pairs, Bb, Pp, T^1t^1, T^2t^2, F^1f^1, all of them showed dominance and none were linked. Brar and Athwal (1970) reported that five loci are involved in the production and expression of different seed colour in chickpea and they designed P/p, $S1/s_1$, $S2/s_2$, $S3/s_3$, and $S4/s_4$, controlling seed-coat colour. Ayyar and Balasubramanian (1936, 1937) and Balasubramanian (1950a, 1950b) described 13 colour classes of chickpea ranging from yellow to dark brown. The genes T^1, T^2, T^3, and T^4 darken testa colour. Three other genes *B/b*, *P/p* and *Fr/fr* also effect testa colour. Different reports from study to study for number of genes to control seed colour is due to use of different genotypes of parent and methods for classification of seed coat colour. Therefore, it is difficult to relate between inheritance of seed colour in different studies.

2.1.7 Growth vigour

Initial seedling vigour plays an important role for establishment of normal crop. Raje (1992) has reported positive association of seed size with vigour index in gram. Seedling vigour is a complex character which it is governed by many parameters and an important attribute in seed technology. Initial seedling vigour plays an important role for high planting value of seed lot and early establishment of crops (Jain *et al.*, 1998). In chickpea, early growth and vigour can be important in providing increased biomass. Considerable losses are observed because of stiff competition of the crop with weeds, particularly in irrigated and late-sown conditions (Lather *et al.*, 1997). Oudhia *et al.* (1997) reported early establishment of the crop to reduce early crop weed competition.

The establishment of healthy seedling is important for successful production of any crop (Matthews *et al.*, 1988). Poor vigour can decrease yields in two ways: first, decreased emergence may lead to sub-optimal populations of irregularly distributed plants: secondly, those seedlings which do emerge grow more slowly and, under some circumstances, this can effect final yields, even when anticipated sub-optimal emergence is compensated by increased sowing rates (Roberts and Osei-Bonsu, 1988).

Most seed crops of legumes would not be deliberately grown at low plant populations; but this discussion emphasises the double jeopardy that can arise when low vigour seed lots results in both reduced establishment and reduced early plant growth, since plants from low vigour seeds are less able to take advantage of the reduced competition in sub-optimal plant populations. Because of the two separate but interacting effects of low vigour seed on crop yield, they are best investigated in the field using a range of plant population densities and applying standard yield/ density equation (Roberts, 1986).

It seemed possible that in pigeonpea and chickpea selection for seed size would have important consequences for seedling growth, which could in turn influence stand establishment, especially under adverse environmental conditions. The selection of larger-seeded varieties seem likely to result in better seedling vigour (Narayanan *et al.*, 1981).

Large-seeded varieties of chickpea produce larger and more vigour seedling, which will have an advantage in stand establishment under adverse conditions. (van der Maesen,

1972). Seedling characters such as root and shoot lengths and their ratio have an important effect on seed quality and seedling vigour. Rapid seedling growth has been found to be associated with early seedling establishment and early maturity in chickpea; which in turn contribute favourably to high yield under drought condition, because plant completes its life cycle before the onset of drought (Gupta, 1985). Singh *et al.* (1997) reported that seed yield under drought condition was positively correlated with early flowering, maturity, early plant vigour, shoot biomass yield, and short plant stature. Due to major breeding successes for drought resistance have been achieved, only in the selection for escape. Association between early growth vigour and early maturity have been reported by earlier workers. Therefore, it needs to study more about inheritance and association between this trait and other characters.

2.2 INHERITANCE OF QUANTITATIVE TRAITS

Plant characters often are referred to as qualitative or quantitative, depending on the number of genes that control them and the importance of the environment in expression of the genes. Qualitative characters have phenotypes that can be divided in to discrete classes. They are controlled by one or a few major genes whose expression is not influenced markedly by the environment.

A quantitative character displays a continuous distribution of phenotypes. The variability is associated with the segregation of multiple minor genes or polygenes, which have small individual effects and are influenced markedly by the environment. Seed yield is a quantitative character controlled by polygenes and strongly influenced by environment.

Some plant characters exhibit aspects of both qualitative and quantitative inheritance. These are characters that are controlled by one or a few major genes and additionally by multiple genes with small effects. The genes with small effects sometimes referred to as modifying genes, and the effect of the environment contribute to a phenotypic distribution that is continuous. The phenotypic distribution of segregates can have several modes, each of which represents the expression of a major gene (Fehr, 1987).

2.2.1 Heritability, Genetic advance

The genes cannot cause a character to develop unless they have the proper environment, and conversely, no amount of manipulation of the environment will cause a characteristic to develop unless the necessary genes are present. Nevertheless, we must recognize that the variability observed in some characters is caused primarily by differences in the genes carried by different individuals and that the variability in other characters is due primarily to differences in the environments to which individuals have been exposed. It would therefore be useful to have a quantitative statement of the relative importance of heredity and environment in determining the expression of characters (Allard, 1960). The effectiveness of selection for a trait depends on the relative importance of genetic and nongenetic factors in the expression of phenotypic difference among genotypes in a population, a concept referred to as heritability. The heritability of a character has a major impact on the methods chosen for population improvement, inbreeding, and other aspects of selection (Fehr, 1987). In crop improvement, only the genetic component of variation is important since only this component is transmitted to the

next generation. The ratio of genetic variance to the phenotypic variance, is known as heritability (Singh, 1997).

Heritability is generally expressed in percent. Thus it is the heritable portion of phenotypic variance. It is a good index of the transmission of characters from parents to their off spring (Falconer, 1989). The estimates of heritability help the plant breeder in selection of elite genotypes from diverse genetic populations. Depending on the components of variance used as numerator in the calculation, heritability is of two types, namely broad sense heritability and narrow heritability. (Phundan Singh and Narayanan, 1997).

Improvement in the mean genotypic value of selected plants over the parental population is known as genetic advance. It is the measure of genetic gain under selection. The success of genetic advance under selection depends on the three main factors such as genetic variability, heritability and selection intensity (Allard, 1960).

For developing superior varieties for agronomic characters and yield, the breeders have to deal with polygenic characters showing continuous variation. Therefore, the success of any plant improvement programme lies in careful management of this variability. Heritability and genetic advance are two importance selection parameters, of which the former is used to estimate the expected genetic advance through selection (Sharma *et al.*, 1990). Studies of quantitative variation in *Cicer* have shown that economic traits such as yield, branch and pod number, plant height and seed size are quantitatively

inherited. A thorough understanding of the inheritance of traits, their heritabilities and relationship with other important characteristics is important for the choice of breeding and selection methods.

In chickpea, though there are several reports on heritability and genetic advance, some of them contradict each other. This may be due to differences in genetic architecture of the parents, number of parents involved, mating designs employed and the environments sampled.

2.2.1.1 Days to Flowering

Days to flowering seems to be a highly heritable character (Pandey and Tiwari, 1983; Jivani and Yadavendra, 1988; Sharma *et al.*, 1990; Uddin *et al.*, 1990; Misra, 1991; Pundir *et al.*, 1991; Panchbhai *et al.*, 1992; Chavan *et al.*, 1994; Jahagirdar *et al.*, 1994, and Mathur and Mathur 1996).

Raju *et al.* (1978), Pandey and Tiwari (1983), Misra (1991), Sharma *et al.* (1990) and Rao *et al.* (1994) recorded lower value of genetic advance for days to flowering while Chandra (1968) Jivani and Yadavendra (1988) and Jahagirdar *et al.* (1994) observed it to be high.

For days to flowering some workers like Pandey and Tiwari (1983), Sharma *et al.* (1990), Misra (1991), Pundir *et al.* (1991) Panchbhai *et al.* (1992) and Chavan *et al.* (1994) reported nonadditive gene action whereas Chandra (1968), Jivani and Yadavendra (1988)

Uddin *et al.* (1990) Pandey *et al.* (1990), and Jahagirdar *et al.* (1994) suggested additive gene action for the character.

Or *et al.* (1999) reported that flowering time in chickpea is controlled by a major gene, suggested a gene symbol of *Ppd* for this gene.

2.2.1.2 Days to maturity

For maturity duration, moderate (Rastogi and Singh, 1977 and Setty *et al.*, 1977) to high (Uddin *et al.*, 1990; Sharma *et al.*, 1990; Misra, 1991; Panchbhai *et al.*, 1992; Chavan *et al.*, 1994; Mishra *et al.*, 1994, and Mathur and Mathur, 1996) heritability have been observed.

Mishra *et al.* (1988), Sharma *et al.* (1990), Misra (1991), Panchbhai *et al.* (1992), Chavan *et al.* (1994), Rao *et al.* (1994), and Mathur and Mathur (1996) recorded lower value of genetic advance for day to maturity, while Mishra *et al.* (1994) reported it to be high.

For days to maturity Uddin *et al.* (1990), Misra (1991), Chavan *et al.* (1994), and Mathur and Mathur (1996) concluded nonadditive gene action whereas Mishra *et al.* (1994) reported that additive gene action for the character.

2.2.1.3 100-seed weight

Seed size is not only one of the most important yield component (Singh and Paroda, 1986) but also an important criterion for consumer preference (Singh, 1987). It has also been consideration an important factor in germination, seedling vigour, seedling mass, and subsequent plant growth (Narayanan *et al.*, 1981 and Dahiya *et al.*, 1985).

New cultivar released in 18 countries for winter sowing have small to medium seed size, whereas the local markets demand large seeds. Small-seeded cultivars are a major hurdle in the large-scale introduction of winter sowing of chickpea (Malhotra *et al.*, 1997). Therefore improvement in seed size is an important goal in chickpea breeding programmes. This in turn requires a better understanding of the inheritance pattern and type of gene action governing seed size. Though, heritability of seed size has been found to be generally high (Chandra, 1968; Sandhu and Singh 1970; Niknejad *et al.*, 1971; Gupta *et al.*, 1972; Patil and Phadnis, 1977; Setty *et al.*, 1977; Ram *et al.*, 1978; Mandal and Bahl, 1980; Pandey and Tiwari, 1983; Jivani and Yadavendra, 1988; Sharma *et al.*, 1990; Pundir *et al.*, 1991; Rana *et al.*, 1995; Mathur and Mathur, 1996; Misra, 1991; Rao *et al.*, 1994, and Malhotra *et al.*, 1997). However, Sandha and Chandra (1969), Chand *et al.* (1975), Rastogi and Singh (1977) and Sandhu *et al.* (1991) observed seed weight to be moderately heritable.

Estimates of genetic advance for seed size have been reported from low Sandhu *et al.* (1991), to moderate Misra (1991) to high (Sandhu and Singh, 1970; Ram *et al.*, 1978;

Jivani and Yadavendra, 1988; Sharma *et al.*, 1990; Mathur and Mathur 1996; Misra, 1991, and Rao *et al.*, 1994).

Sandhu and Singh (1970), Ram *et al.* (1978), Jivani and Yadavendra (1988), Sharma *et al.* (1990), Rao *et al.* (1994), and Mathur and Mathur (1996) reported that additive gene action for 100-seed weight while Sandhu *et al.* (1991) found nonadditive gene action and Misra (1991) suggested both additive and nonadditive gene action for the character.

Information on genetics of seed size of chickpea is limited. Argikar (1956) reported this character was controlled by a single recessive gene, while Patil and D'Cruz (1964) found it to be under the control of two genes. Ghatge (1993) found medium (normal) seed size was dominant over bold and small and reported that it was controlled by two pairs of genes having supplementary action. The genes *Bsd. Smsd* (medium), *Bsd. smsd* (bold) and *bsd smsd* (small) were symbolized. But Rastogi (1979) supported the results of Jagtap *et al.* (1973) and Reddy and Chopde (1977) and further stated that more than two genes are involved in the inheritance of seed size. Results obtained by Athwal and Sandha (1967) and Kumar and Singh (1995) that small-seed size was partially dominant over large-seed size. In contrast, Niknejad *et al.* (1971) stated that large-seed size was partially dominant over the small and was controlled by eight genes.

2.2.1.4 Plant height

Estimates of heritability for plant height varied from moderate (Khosh-khui and Niknejad, 1972b; Rastogi and Singh, 1977; Setty *et al.*, 1977; and Sandhu *et al.*, 1991; Panchbhai *et al.*, 1992) to high (Sharma *et al.*, 1990; Misra, 1991; Rao, 1994; Chavan *et al.*, 1994, and Mathur and Mathur 1996).

The expected genetic advance for plant height is reported to be low (Sandhu *et al.*, 1974; Misra, 1991; Sandhu *et al.* 1991, and Panchbhai *et al.*, 1992) moderate (Sharma *et al.*, 1990) and high (Rao *et al.*, 1994).

Misra (1991), Sandhu *et al.* (1991), Panchbhai *et al.* (1992), Chavan *et al.* (1994), and Mathur and Mathur (1996) suggested nonadditive genetic effects for plant height while Gowda and Bahl (1978) Singh and Mehra (1980) and Rao *et al.* (1994) concluded additive genetic effects for the character.

2.2.1.5 Plant width

Chavan *et al.* (1994) reported low heritability and with low genetic advance for plant breadth whereas Mishra *et al.* (1988) found high heritability with low genetic advance for this character.

Chavan *et al.* (1994) and Mishra *et al.* (1988) reported that width of plant is governed by genes having epistatic and dominant gene effects while Bhatt and Singh, (1980a), and Ugale (1980) reported additive gene action for the character.

2.2.1.6 Number of primary branches per plant

For number of primary branches per plant have been reported low (Sandhu *et al.*, 1991; Panchbhai *et al.*, 1992; Rao *et al.*, 1994, and Rana *et al.*, 1995) to high (Sharma *et al.*, 1990 and Jha *et al.*, 1997) heritability.

The expected genetic advance for number of primary branches per plant is reported to be low (Sandhu *et al.*, 1991 and Rao *et al.*, 1994) to moderate (Sharma *et al.*, 1990).

Sandhu *et al.* (1991), and Rao *et al.* (1994) concluded nonadditive gene action for number of primary branches per plant whereas Sharma *et al.* (1990) found the presence of both additive and nonadditive gene action for the character.

2.2.1.7 Number of secondary branches per plant

Estimates of heritability for secondary branches per plant varied from low (Sandhu *et al.*, 1991 and Rao *et al.*, 1994) to high (Mishra, 1988; Jahagirdar *et al.*, 1994 and Rana *et al.*, 1995).

Expected genetic advance reported for number of secondary branches per plant from low (Sandhu *et al.*, 1991) to high (Mishra, 1988; Jahagirdar *et al.*, 1994; Rao *et al.*, 1994 and Sharma *et al.*, 1990).

Mishra *et al.* (1988), Jahagirdar *et al.* (1994) and Rao *et al.* (1994) suggested additive genetic effect for number of secondary branches per plant whereas Sandhu *et al.* (1991) reported nonadditive gene action for the character.

2.2.1.8 Number of pods per Plant

Estimate of heritability for number of pods per plant varied from low (Sharma *et al.*, 1990; Sandhu *et al.*, 1991; Pundir *et al.*, 1991; Panchbhai *et al.*, 1992; Mishra *et al.*, 1994; Rao *et al.*, 1994; Rana *et al.*, 1995 to high (Setty *et al.*, 1977; Raju *et al.*, 1978; Mishra *et al.*, 1988; Jivani and Yadavendra, 1988; Mishra, 1991; Chavan *et al.*, 1994, and Mathur and Mathur, 1996).

Expected genetic advance for pod number per plant has also been reported to be low (Sharma *et al.*, 1990; Misra, 1991; Sandhu *et al.*, 1991; Panchbhai *et al.*, 1992) to high (Mishra *et al.*, 1988; Jivani and Yadavendra, 1988; Rao *et al.*, 1994; Mishra *et al.*, 1994, and Chavan *et al.*, 1994).

Mishra *et al.* (1988), Jivani and Yadavendra (1988), Misra (1991), Rao *et al.* (1994) and Chavan *et al.* (1994) suggested additive gene action for number of pods per plant whereas Sharma *et al.* (1990), Sandhu *et al.* (1991), Pundir *et al.* (1991), and Panchbhai *et al.* (1992) reported that non additive gene action for the character.

2.2.1.9 Number of seeds per plant

Pandey *et al.* (1990) found moderate heritability with high genetic advance for seed per plant and they reported that nonadditive with appreciable additive gene effects were

predominant for the character whereas Panchbhai *et al.* (1992) observed low heritability with low genetic advance for this character and reported nonadditive gene action.

2.2.1.10 Number of seeds per pod

Estimate of heritability for number of seeds per pod varied from low (Sandha and Chandra, 1969; Mandal and Bahl, 1980; Sandhu *et al.*, 1991 and Rana *et al.*, 1995) to high (Chandra, 1968; Gupta *et al.*, 1972; Raju *et al.*, 1978; Ram *et al.*, 1978, and Sharma *et al* 1990). Mishra *et al.* (1994) and Pundir *et al.* (1991) observed moderate heritability with low genetic advance for number of seeds per pod whereas Sharma *et al.* (1990) reported high heritability and moderate genetic advance for the character.

Sandhu *et al.* (1991) and Pundir *et al.* (1991) suggested nonadditive genetic effects for number of seeds per pod while Sharma *et al.* (1990) observed the presence of both additive and nonadditive gene actions for the character. Jha *et al.* (1997) reported that seed number per pod is controlled by additive genetic effect.

2.2.1.11 Seed yield

Seed yield is influenced by a number of factors. Environment has a great influence upon many of economically important characters which are quantitatively inherited. Thus it becomes difficult to judge whether the observed variability is heritable or is due to the environment. It becomes therefore, necessary to break up the observed variability into its heritable and non-heritable component as this proves useful to the plant breeder in selecting suitable plants.

Seed yield per plant is reported to have low heritability (Rao *et al.*, 1994; Sharma *et al.*, 1990; Misra 1991 and Panchbhai *et al.*, 1992) to moderate (Chand *et al.*, 1975; Mandal and Bahl, 1980; and Mandal and Bahl, 1983a) and high (Setty *et al.*, 1977; Patil and Phadnis, 1977; Sandhu *et al.*, 1991; Mishra *et al.*, 1994; Chavan *et al.*, 1994, and Mathur and Mathur, 1996).

The expected genetic advance for seed yield per plant has been estimated to be low (Misra, 1991; Sharma *et al.*, 1990; and Panchbhai *et al.*, 1992) to high (Mishra *et al.*, 1988; Mishra *et al.*, 1994; Sandhu *et al.*, 1991; Rao *et al.*, 1994; Chavan *et al.*, 1994, and Mathur and Mathur, 1996).

Setty *et al.* (1977), Patil and Phadnis (1977), Chavan *et al.* (1994), Rao *et al.* (1994) Mishra *et al.* (1994), and Mathur and Mathur (1996) concluded that the genotypic variation for seed yield is due to additive genetic effects whereas Misra (1991) and Panchbhai (1992) suggested nonadditive genetic effects for such character.

2.2.1.12 Leaf size

Pundir *et al.* (1991) and Katiyar and Katiyar (1994) found high heritability with high genetic advance for leaf size and concluded additive genetic effect for the character.

Ghatge (1992) reported that leaf/leaflet size was due to three factors of which two are supplementary in action producing bold leaflet size (*Ovlt* and *Smlt*) while third gene (*I-Ovlt-Smlt*) was having inhibitory action.

2.2.1.13 Leaf weight

Katiyar and Katiyar (1994) reported high heritability coupled with high genetic advance for leaf weight per plant and suggested additive genetic effect for this character.

2.2.1.14 Specific leaf weight

Katiyar and Katiyar (1994) reported high heritability coupled with high genetic advance for specific leaf weight and suggested additive genetic effect for this character.

2.2.1.15 Seed fibre

Desi and kabuli chickpea can be characterized by the seed fibre content and seed coat thickness: desi types have a higher fibre content and a thicker seed coat, up to 80% of seed fibre being in the seed coat (Singh 1984). Fibre content shows considerable variation. Comparisons of random sets of desi and kabuli genotypes have shown a much lower fibre content in kabuli seeds, although the effect of seed type on protein is less clear (Jambunathan and Singh, 1979; Saini and Knights, 1984). Knights (1980) reported that kabuli seeds have a fibre content of approximately 5-6% compared to 17-18% for desi seeds. Knights and Mailer (1989) reported seed type had its greatest effect on testa fraction and fibre content, desi seeds having 2.34 time more testa and 2.38 time more fibre than kabuli seeds. They also reported that presence of a coloured testa, which in the kabuli material studied was pleiotropic to the expression of pigmented foliage and corolla, was associated with a small increase in testa content.

2.2.2 Parent-offspring regression

Heritability of a metric character is an important parameter which aids the plant breeder in predicting the genetic advance that can be achieved by exercing necessary selection pressure. This procedure involves the regression of the mean value of a characteristic in the progeny upon the value for the same character in the parent (Sumathi and Ramanathan, 1995). The estimation of the heritability from the regression of offspring on parents is comparatively straight forward (Falconer, 1989).

Heritability in broad sense include the variance due to all types of gene expressions (additive, dominance, epistasis) while in narrow sense it includes only the additive fraction (Luciano *et al.*, 1965).

One of the most useful methods is based on the resemblance between parents and offspring. In general, this method is less likely to have been seriously affected by environmental contributions than are estimates based on the resemblance of two contemporary relatives or the resemblance of two maternal sibs who have had a common prenatal environment (Kempthorne and Tandon, 1953).

One of the common methods of determining the heritability percentages of attributes in plants is by the progeny-parent regression procedure proposed by Lush (1940). This procedure involves the regressing of the mean value of a characteristic in the progeny upon the value for the same characteristic in the parent. To obtain heritability values in cross pollinated crops, it is necessary to double the regression values obtained by this

procedure, but in the self-pollinated crops the regression values are converted directly to heritability percentage by multiplying by 100 (Frey and Horner, 1957).

The two most commonly used regression estimators appeared to be $2b=h^2$ and $b=h^2$. The first of these is an appropriate estimator for the regression of offspring on parent in a bisexual population when the parent is noninbred as in a random-mating population. To the extent that the parents are inbred or related, the use of twice the regression coefficient will result in an overestimate of the heritability.

Similarly $b=h^2$ is appropriate for estimating heritability in a self-pollinated population if the parent is noninbred as with regression of F_2 on its single cross F_1 parent. However, this estimator will overestimate heritability if the inbreeding coefficient of the parent is greater than zero as with regression of F_3 progeny on F_2 parents (Smith and Kinman, 1965).

Correlation of the performance of a parent with that of its offspring was proposed by Frey and Horner (1957) as an alternative to the parent-offspring regression methods for computing heritability. When parents are measured in one season and their off-spring in another, environmental differences between the two seasons can cause the range in phenotypes among the parents to be greater or less than for the offspring. As a result heritability percentages obtained by parent-offspring regression could have maximum values greater than 100 percent. To eliminate this effect of environment, the use of standard unit heritabilities obtained by calculating parent-offspring regressions on data

coded in terms of standard deviation units was suggested. Such a procedure leads to results equivalent to the coefficient obtained from a simple parent-offspring correlation (Fehr, 1987).

In practice progeny-parent regression for characteristics in plant crops often involve regressing the data obtained from the progeny in one year upon the parental data obtained in the previous year. Obviously, any environmental factor or factors which tended to reduce or increase the range of phenotypic variation of the progenies, could materially effect the heritability percentage obtained even though the ratio of the component variances remained similar to that of the parents (Frey and Horner, 1957).

Sumathi and Ramanathan (1995) reported that heritability estimates by parent-offspring regression method in groundnut were moderate for all characters such as pod yield, plant height, number of flowers and 100 pod weight.

Seed weight, seed yield, pod per plant, seed per pod and plant height varied from the highest and lowest heritability values estimated by the regression method in chickpea (Salimath and Patil, 1990).

2.3 LINKAGE

Genes often show a tendency to be inherited together, that is, a tendency to pass to the same gamete during segregation, and do not show independent segregation. This phenomenon is known as linkage. The genes that show linkage are situated in the same

chromosome. Each chromosome is transmitted intact as a unit during meiosis. Consequently, the genes situated in the same chromosome are also transmitted together. But during meiosis, there is exchange of chromatin material between homologous chromosomes; this is known as crossing over. Crossing over, therefore, leads to recombination between linked genes. The frequency of recombination between any two linked genes depends upon the distance between them. Thus the chief effect of linkage is to reduce the frequency of recombination between linked genes (Singh, 1997).

Linkage may be in coupling phase in which two dominant genes or two recessive genes are linked together, e.g., AB/ab or in repulsion phase where one dominant and one recessive genes are linked e.g., Ab/aB. The coupling or repulsion phases alter drastically the frequencies of various phenotypes in F_2 and other segregating generations but have no effect on the frequency of recombination.

Several methods of estimating this fraction from the observed data have been proposed from time to time and which method to choose for estimation is a problem which naturally puzzles the research worker. From the point of view of the problem on hand the following two are important. One is that the estimate obtained should tend to the theoretical value as the sample is enlarged and the other is that the estimate should have the lowest possible variance for the type of data. The first criterion, known as the criterion of consistency, ensures that any bias in the estimate decreases to a negligible magnitude as the sample size becomes large, while the second, the criterion of efficiency, ensures that

the estimate will be as precise as possible, under the particular conditions (Panse and Sukhatme, 1989).

If two traits have high phenotypic and genotypic correlation it is possible to select one of them through selection of the associated trait. This is useful when a trait is economically important, but has low heritability comparatively to the associated trait. In this case, the trait of interest should be selected using the trait with high heritability and lesser economic importance. Also, if two traits are associated and one is easier to assess and select, selection pressure should be applied to this trait to improve the other (Falconer, 1989).

Three methods such as Emerson's, maximum likelihood and product ratio methods would be found adequate for the simpler types of experiments generally conducted. Their merits and demerits and their suitability in particular case should be noted carefully. Emerson's method is generally less efficient than the other two methods, as it gives an estimate with a larger standard error. When the linkage is tight, however, the standard, the standard error of this estimate is nearly the same as those of other two estimates and this method may then be preferred on account of its simplicity. The other two methods are equally efficient as can be seen from the fact that they have the same variance for the estimate obtained. The product-ratio method has the advantage of being less influenced by viability disturbances which cannot be taken in to account by the maximum likelihood method. With tight linkage, however, the recombination classes may have very few members and one class may at times be absent. In such a case the product-ratio methods

gives zero as the estimate of the recombination fraction while the other class shows that recombination has occurred. In this situation the maximum likelihood estimate is definitely superior and even the estimate obtained by Emerson's methods is preferable. Wherever the frequencies expected in the different classes can be calculated exactly, the maximum likelihood method is superior (Panse and Sukhatme, 1989).

The linkage of genes for economically important traits with easily identified markers, can improve the efficiency of breeding and hasten the development of improved cultivars. Linkage relationships can also be used to study gene systems and genetic mechanisms (Muehlbauer and Singh, 1987).

Several cases of linkage have been reported in *Cicer*. The first was by Bhat and Argikar (1951) for the genes for branching habit, alternate leaflet arrangement and earliness. Later Bhapkar and Patil (1963) reported that factor P for flower colour is linked with one of the two factors (F^1 and T^2) governing the expression of seed coat colour. Brar and Athwal (1970) found linkage between bunchy habit with one of the loci controlling seed coat colour. A linkage group involving corolla colour, flower number per axil, seed coat colour and seed shape reported by D'Cruz and Tendulkar (1970) and Pundir and van der Maesen (1983). Reddy and Chopde (1977) observed linkage between tiny leaf and corolla colour. According to Aziz *et al.* (1960) gene P for flower colour is linked to the gene for rough seed. They also found that P was linked to R (seed coat colour). The linkage of P and R may be the same linkage recognized by Bhapkar and Patil (1963) who reported that P was linked with either F^1 or T^2. The use of different symbols makes it

difficult to draw conclusion. Nayeem *et al.* (1977) reported that one of the spinate seed loci was linked with a locus affecting seed coat colour. Pawar and Patil (1979) found linkage group corolla (Lvco) , seed surface (R) and seed coat colour (Bsc). Rao and Pundir (1983) reported that close linkage between lobed vexillum and broad leaflets and double-flower per peduncle, appeared loosely linked to lobed vexillum.

Davis (1991) reported that fil (filiform leaf) and w2 (white flower or colour) genes were linked, with recombination frequencies of 0.05 and 0.14 estimated from results of coupling and repulsion phase crosses, respectively and he found rn3 (root nodulation) was closely linked to slv (simple leaf), with recombination frequency of 0.05 and 0.11 were estimated from results of coupling and repulsion phase crosses respectively. A loose linkage detected between the w2-fil and the rn3-slv linkage groups will be the subject of further scrutiny. Kumar *et al.* (1991) found that gene P (flower and seed colour) closely linked to resistance to Damping-off (*Phythium ultimu*). Linkage was found between seed coat thickness and flower colour, the recombinant fraction being 0.19. No relationship was found between seed coat thickness and seed size (Gil and Cubero, 1993). Pundir and Reddy (1998) reported flower type and leaf size showed recombination fraction of 0.34, meaning that linkage exits between the genes governing these two traits and also they reported that no linkage between flower colour and flower type. Singh (1987) suggested that 'double pod' decrease seed size in chickpea whereas Rubio *et al.* (1998) found that single-/double podded gene is not linked to any other gene related to seed size. Therefore they suggested, the double-pod character will not decrease seed size in chickpea.

There are some reports of association of traits in *Cicer*, such as cotyledon and foliage colour (More and D'Cruz, 1976c), stem and pedical colour (Patil and Deshmukh, 1975; Pawer and Patil, 1979), testa colour and pigmentation foliage and corolla (Knights and Malier, 1989) corolla, seed coat and cotyledon colour (Ayyar and Balasubrahmanyan, 1936 and Argikar and D'Cruz, 1962) and stem and corolla colour (Ghatge *et al.*, 1985). These associations are most likely due to pleiotropy and do not represent cases of useful linkages. Ghatge (1992) reported that factor (*Ovlt*) for leaf/leaflet shape was found to be common with one of flower (*Ovlt-Smlt* and *I-Ovlt-Smlt*) for leaf/leaflet size. Ghatge (1994) reported that presence of a common gene *Bco* in stem and corolla colour.

2.4 CORRELATED GENETIC GAIN

When selection is applied by plant breeders, change are likely to occur, not only in the trait for which selection is being practiced but in other traits as well. (Dudley, 1997). The improvement of one character by selection frequently causes simultaneous changes in other characters. The effect is the result of correlations between characters, which may be genetic or environmental in nature. Genetic correlation arise from pleiotropy, from linkages between loci controlling the characters or from random genetic drift. According to Falconer (1989) and Simmonds (1979), pleiotropy is the chief cause of genetic correlations, while Mather and Jinks (1982) have argued that linkage is the more likely explanation. A subsequent study by Jinks *et al.* (1985) indicated that either or both factors may be important, depending on the pair of characters considered. The response of a correlated character can be predicted if the genetic correlation and the heritabilities of the two characters are known (Falconer, 1989). Godawat and Choudhary (1990) reported that

maximum correlated response in yield were expected through selection on component traits like harvest index, panicle weight, 100-seed weight and productive tiller per plant in proso millet. Menendez and Hall (1995) suggested that early-generation selection for isotope discrimination using F_2 plants may not be as efficient as family selection cowpea. Mishra *et al.* (1992) found that number of pods per plant had the highest correlated response with seed yield per plant, followed by harvest index and biological yield per plant in chickpea.

2.5 COHERITABILITY

The concept of heritability obtained from ordinary one-trait analysis, will be extended to include the information gained from covariance analysis of pairs of traits. The principle is implicitely contained in the multi-trait selection index as developed by Smith (1936). More recently, Gallais (1973) introduced the notion of 'heritabilite' generallisee partielle' which corresponds to the partial regression coefficient of the genetic values of a given trait onto the phenotypic values of a set of traits. Baradat (1976) suggested a similar idea i.e. 'the coefficient of genetic prediction' of which the values are smaller than unity. He defined the coefficient of genetic prediction between two traits as the ratio of the additive genetic covariance over the product of the phenotypic standard deviation of either trait. In any crop improvement programme, the essential pre-requisite is to know the joint heritability of a pair of characters and prediction of response to selection (Mishra, 1992). Coheritability which refers to joint transmission of different character pairs, is a better genetic parameter for improving selection efficiency as it permits the study of simultaneous changes in different characters (Srivastava and Jain, 1994). It deals with

simultaneous inheritance of two characters (Phundan Singh and Narayanan, 1997). Coheritability takes both genotypic as well as phenotypic covariances into account and helps in understanding changes taking place in pairs of polygenic characters. The high values of coheritability estimate suggest that increase in one polygenic trait will lead to simultaneous increase in another coheritable character. Thus coheritability may from a more meaningful index for achieving the breeding objectives (Biswas and Sasmal, 1989).

Parthasarathy and Medhi (1983) reported that root length in radish showed better coheritability estimates with all the characters including root diameter. Srivastava and Jain (1994) found that biological yield and number of pods per plant, harvest index and duration of reproductive phase in soybean exhibited substantial coheritability estimates with seed yield. Mishra *et al.* (1992) reported that the coheritability estimates of different components with economic yield in chickpea revealed that number of pods per plant had the highest coheritability with economic yield (0.7319) followed by harvest index (0.7084), number of secondary branches per plant (0.5430) and biological yield per plant (0.4296). However, moderate estimates of coheritability values were observed for number of primary branches per plant with seed yield (0.3879), plant spread with seed yield (0.3679) and pod bearing length with seed yield (0.2009). The coheritability values of number of pods per plant, number secondary branches per plant and plant spread were found to be positive and relatively high in magnitude with economic yield, biological yield and harvest index. Among the yield components, none of the character combination had a very high magnitude of negative coheritability estimates. Hence, they concluded that the

selection for number of pods per plant, number of secondary branches per plant, harvested index and biological yield per plant simultaneously improve the economic yield.

2.6 HETEROSIS AND INBREEDING DEPRESSION

Heterosis is the superiority in performance of hybrid individuals compared with their parents. The occurrence of heterosis is common in plant species, but its level of expression is highly variable (Fehr, 1987). Self- and often cross-pollinated crops show little or no loss in vigour or yield due to inbreeding. But F_1 hybrids in such crops are generally more vigorous and higher yielding than either of their parents. They are also more stable phenotypically than the parental pure lines.

The superiority of an F_1 over its parents is known as heterosis or hybrid vigour. Heterosis is commercially utilised by using F_1 hybrids as commercial varieties, i.e., hybrid varieties (Singh, 1997). Exploitation of heterosis appears to be cheap and easy method for increasing yield in many crops and considerable success has been achieved in this direction in crop exhibiting an appreciable degree of cross pollination. Comparatively, little use has been made of heterosis breeding, owing to its cleistogamic nature and absence of male sterility (Kamatar *et al.*, 1996). Self-pollinated species do not show inbreeding depression, but may exhibit considerable heterosis (Singh, 1997). While considerable success has been achieved in this direction in taxa which exhibit an appreciable degree of cross-pollination, comparatively little use has been made of heterosis breeding in self-pollinated crops. Two factors have been responsible for this: (i) the practical difficulties in exploiting hybrid vigour in plants with prefect flowers, especially when each act of pollination produces very

few seeds and (ii) doubts as to whether hybridity by itself will have any advantage over the pure lines which may be isolated from the particular combination or other combinations (Ramanujam *et al.*, 1964). Chickpea is a highly self-pollinated crop and the scope for exploitation of hybrid vigour will depend on the direction and magnitude of heterosis, biological feasibility, and type of gene action. (Shinde and Deshmukh, 1990). Study of heterosis and inbreeding depression will have a direct bearing on the breeding methodology to be employed for varietal improvement (Tewari and Pandey, 1987).

The review of literature for heterosis and inbreeding depression in chickpea is follows:

The first report of heterosis in number of pods per plant in chickpea was given by Pal (1945), he did not find any hybrid vigour in height of plant, number of branches plant^{-1}, time of flowering and rate of germination.

Ramanujam *et al.* (1964) studied of nine crosses involving seven varieties of gram. They reported that comparison of the parental and F_1 performance in respect of the components of grain yield, suggested that the observed heterosis is due to the combination of favourable expression present in the two parents, the F_1 not differing significantly from the superior parent in respect of either grain number per plant or grain weight.

Singh and Singh (1976) studied 38 F_1 hybrids of Bengal-gram and reported that heterosis for yield and number of pods was quite high whereas negative heterosis was

present for the 100-seed weight and days to 50% flowering. Similarly Singh and Jain (1970) also reported heterosis for yield was in most cases associated with heterosis for pod number.

Bhatt and Singh (1980) studied in 45 crosses in chickpea and observed that the maximum values for heterosis over the mid parent and better parent were 70.0 and 70.0% for primary branches per plant, 62.2 and 40.7% for pods per plant, 25.1 and 19.6% for seeds per pod, and 188.9 and 168.0% for yield per plant. Significant better parent heterosis for yield was observed in 20 crosses and 5 of these gave higher mean yields than the best parent.

Kunadia and Singh (1980) studied 28 hybrids from kabuli type and obtained heterosis in most crosses for yield and pods per plant further indicated high inbreeding depression for these characters.

Deshmukh and Bhapkar (1982) reported that high heterosis for grain yield was coupled with high heterosis for number of branches per plant, number of pods per plant and biological yield. Extent of heterosis over better parent was highest for number of pods per plant (111.31%) and was followed by grain yield (72.11%), biological yield (65.77%) and number of branches per plant (49.16%). None of the hybrid combinations was significantly earlier in blooming or maturity than the corresponding early parent. They reported that generally hybrids showing high heterosis also showed high inbreeding depression.

Tewari and Pandey (1987) observed in many crosses which have exhibited moderate to high manifestation of better parent heterosis for pods and seeds per plant, and seed yield. The estimates of heterosis for seeds per pod and 100-seed weight were mostly negative. They reported that all the crosses showing maximum estimates of heterosis for seed yield also had significant heterotic effects for some of the yield component. Inbreeding depression was significant in all cases except in one cross. They suggested the importance on nonadditive genes in chickpea, because of crosses showing high heterosis also showed high inbreeding depression.

Arora and Pandey (1987) reported significant and positive better-parent heterosis for yield in 19 crosses. Nine of them had mean yields significantly greater than that of the best parent and also these crosses had significant positive heterosis for other components of yield. They obtained higher magnitudes of heterosis in indigenous x exotic and desi x kabuli crosses.

Mian and Bahl (1989) studied relationship between divergence of the parents and heterosis in the hybrids. They found parental clusters separated by medium D^2 values, exhibited significant and positive mid parental heterosis for seed yield and some of its components.

Bahl and Kumar (1989) studied 25 chickpea hybrids and reported that manifestation of heterosis was maximum for seed yield and minimum for 100-seed weight. High heterosis for trait was generally accompanied by significant inbreeding depression.

They suggested importance of nonadditive gene action in chickpea due to parallel relationship between heterosis and inbreeding depression.

Rao and Chopra (1989) obtained high positive values average heterosis and heterobeltiosis in seed yield from number of primary branches per plant, number of secondary branches per plant as well as whole plant: number of pods per plant; number of seeds per plant; and plant weight. Similarly Mandal and Bahl (1984) concluded that yield could be improved by desi x kabuli crosses. But floral biology of chickpea poses difficulty in obtaining large quantities of hybrid seed.

Pandey and Tiwari (1989) studied five crosses and found no uniform trend in the manifestation of heterosis all the crosses for different characters. Three crosses exhibited significant heterosis over better parent for pod number, seed number and yield. The maximum heterosis (29.02% and 16.76%) associated with maximum inbreeding depression for yield was noted in one cross. They reported that the low heterosis might be due to interconcellation of gene effects.

Shinde and Deshmukh (1990) obtain maximum heterosis over better parent in number of pods per plant (54.95%) which was followed by the grain yield (53.69%), number of fruiting branches per plant (46.92%), number of grains per pod (21.94%), 100-grain weight (15.83%) and days to maturity (11.26%). The overall mean heterosis was the highest for the grain yield per plant (25.25%) followed by the number of pods per plant (23.96%) and number of fruiting branches per plant (21.30%). High heterosis for grain

yield was associated with a high heterosis for number of fruiting branches and number of pods per plant. Most of the characters showed nonadditive gene action with over dominance as indicated by close relationship between heterosis and inbreeding depression and potence ratios.

Khan *et al.* (1991) reported that hybrids of seven genotypes exhibited high midparent heterosis for grain yield. There was no relationship between heterosis over midparent and genetic distance between the parents. Therefore, they suggested for improvement yield and desirable characters, traditional approach of making a large number of crosses in chickpea. Similarly Singh and Ramanujum (1981) reported no association between heterosis and inbreeding depression.

Gumber *et al.* (1992) selected seven parents with moderate genetic divergence and comparatively high *per se* performance and produced 21 crosses. Five crosses had high mean performance for important yield components. Seven out of 21 crosses showed heterobeltiosis ranging from 12.1 to 50.1 percent for seed yield.

Mandal (1992) studied eight chickpea crosses and reported that none of the crosses exhibited significant heterosis and inbreeding depression in F_1 and F_2 generations for harvest index and low values of heterosis for harvest index was earlier reported by Sadhu and Mandal (1987).

Patil *et al.* (1996) studied in intra (desi x desi and kabuli x kabuli) and inter (desi x kabuli) group of crosses in chickpea. They found the magnitude of heterosis for seed yield and components was higher in inter than intragroup crosses. Heterosis for number of pods per plant contributed considerably to yield heterosis. Inbreeding depression from F_1, to F_2, to F_3, for yield and yield component was low in intragroup crosses and moderate in intergroup cross.

Kamatar *et al.* (1996) studied in 66 crosses in chickpea. They reported that maximum positive heterosis was observed for pod number (144.3%), followed by grained yield per plant (130.5%), total number of branches per plant (120.46%) and protein content (47.1%). They obtained heterosis for yield was mainly associated with heterosis for number of primary branches per plant, total number of branches per plant and number of pods per plant.

Materials and methods

CHAPTER III

MATERIALS AND METHODS

The present investigations were carried on the genetic studies of qualitative and quantitative traits in seven different generations and 126 recombinant inbred line (RILs) derived from cross between ICCV2 and JG62 in chickpea. The experiments were conducted during the *Rabi* (post-rainy season) 1998-1999 and 1999-2000 at the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) Patancheru, A.P., which is situated at an altitude of 545 m above the mean sea level at a latitude of 17°' 32 'N and longitude of 78° 16' E. The weather data during the crop growth period is given in Figure 2.3.

3.1 MATERIALS

The experimental material comprised 126 recombinant inbred lines (RILs), five generations (P_1, P_2, F_1, F_2, and F_3) in first year (1998-1999) and seven generations (P_1, P_2, F_1, F_2, F_3, BC_1P_1 and BC_1P_2) in second year (1999-2000) obtained from a cross between two chickpea varieties kabuli type ICCV2 (P_1) and desi type JG62 (P_2). Characteristics of parental lines and F_1, BC_1P_1, and BC_1P_2 are given in Table 1.

3.2 METHODS

3.2.1 Experiment I

The 126 F_{10} RILs along with the parents, F_1 and three checks (Annigeri, ICCV10 and ICCV 96029) were sown on deep vertisol with conserved soil moisture on 4 November 1998 and 12 October 1999. The experimental design to test these materials was

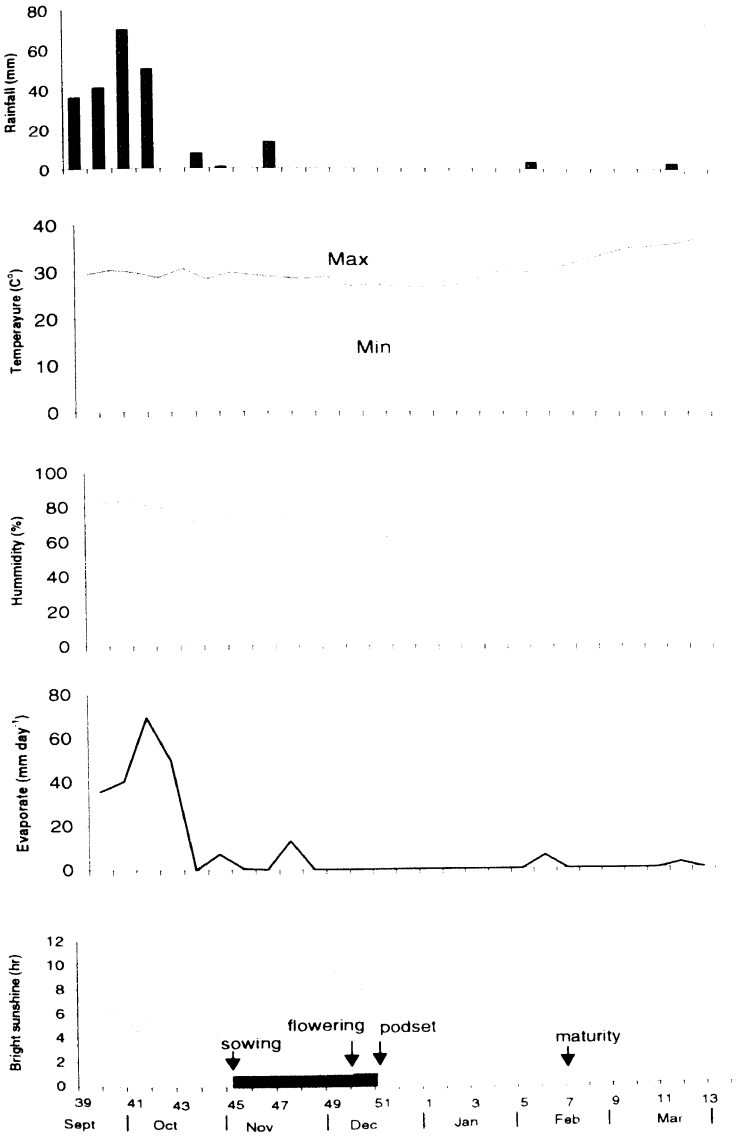

Fig. 2 Weather conditions at ICRISAT during 1998-1999

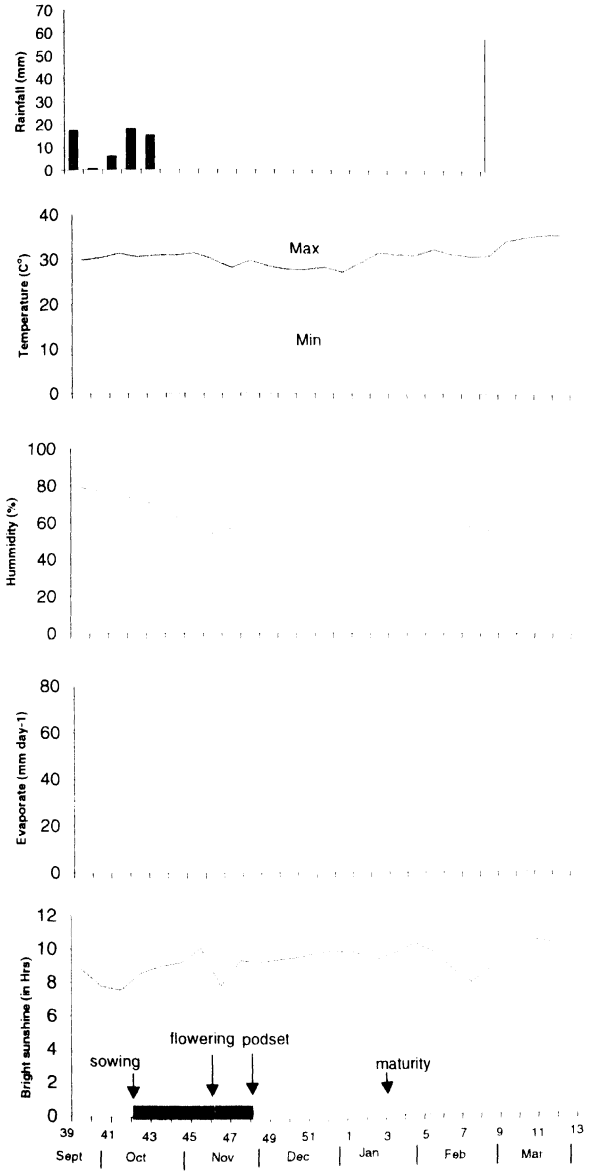

Fig. 3 Weather conditions at ICRISAT during 1999-2000

Table 1. Characteristic feature of parents, their F_1, $BC_1P_1$and BC_1P_2 in 1998-1999 and 1999- 2000.

Characters	ICCV2	JG62	F_1	BC_1P_1	BC_1P_2
Varietal status	Released	Released	Not App.	Not App.	Not App.
Flower colour	White	Pink	Pink	Seg	Pink
Seed type	Kabuli	Desi	Desi	Seg	Desi
Seed colour	Yellow beige	Yellow brown	Yellow brown	Seg	Yellow brown
Seed size	23 g /100	14 g/100	13 g/100	21 g/100	16 g/100
Seed surface	Smooth	Rough	Rough	Seg	Rough
Growth vigour	High	Low	High	High	Seg
Seed fibre	Low	High	Medium	-	-
Anthocyanin pigment	Absent	Present	Present	Seg	Present
Fusarium wilt	Resistant	Susceptible	Susceptible	-	-
Flowering	37 days	46 days	46 days	40 days	45 days
Maturity	83 days	94 days	95 days	88 days	94 days
No. of pods/ peduncle	One	Two	One	One	Seg
No. of pods/ plant	74	64	114	110	117
No. of primary branches	2	3	3	3	4
No. of secondary branches	4	7	7	5	7
Width	35 cm	36 cm	37 cm	43 cm	43 cm
Pod size [a]	Bold	Small	-	-	-
Drought	Escape	Tolerant	-	-	-
Leaf size	6.8 cm^2	5.9 cm^2	5.7 cm^2	6 cm^2	4 cm^2
Sugar content [a]	High	Low	NA	-	-
Plant height	28 cm	39 cm	38	34 cm	35 cm
Seed yield/ plant	17 g	17 g	21 g	24 g	21 g
Malic acid [a]	Low	High	-	-	-

[a] Source: Chickpea Breeding ICRISAT
- = Information was not available
Seg = Segregating
Data of BC_1P_1 and BC_1P_2 are from 1999-2000
Not App. = Not applicable

Alpha design with three replications. Each replication consists of 12 blocks and 11 treatments (lines) appeared in each. Each entry were planted in 2 rows of 4 meter length with 60 cm spacing between rows and 10 cm spacing between plants within the rows.

3.2.2 Experiment II

The seven generations (P_1, P_2, F_1, F_2, F_3, BC_1P_1, and BC_1P_2) the same cross were planted without replication with spacing of 60 cm between rows 20 cm between plants in P_1, P_2, F_1, F_2, BC_1P_1, and BC_1P_2. In F_3 progeny, one row consisted of 4 meters length with 10 cm distance between plants.

The population of P_1, P_2, F_1, F_2, F_3, BC_1P_1, and BC_1P_2 in first year and second year are given in Table 2.

Table 2. Population size of P_1, P_2, F_1, F_2, F_3, BC_1P_1 and BC_1P_2 in first year and second year experiment.

Generations	1998-1999	1999-2000
P_1 (ICCV2)	15	15
P_2 (JG62)	15	16
F_1 (ICCV2♀ X JG62♂)	-	20
F_1 (JG62♀ X ICCV2♂)	5	15
F_2	202	306
F_3	240	202
BC_1P_1	-	39
BC_1P_2	-	37

3.2 CHARACTERS STUDIED

In the present investigation, data on the following characters were recorded for Experiment I and Experiment II.

1- growth vigour (score)

2- stem colour (anthocyanin pigmentation)

3- flower colour

4- number of pods per peduncle

5- days to first flower

6- days to 50% flower

7- days to first pod

8- days to maturity

9- number of primary branches per plant

10- number of secondary branches per plant

11- plant height (cm)

12- plant width (cm)

13- number of pods per plant

14- number of seeds per plant

15- number of seeds per pod

16- 100-seed weight (g)

17- yield per plant (g)

18- yield per plot (g)

19- leaf size (cm^2)

20- seed surface

21- seed type

22- seed-coat colour

23- seed fibre

24- dry leaf weight (g)

25- Specific leaf weight

3.3.1 Observational procedures

Observations were recorded on five competitive random plants per plot in each of the RILs, parents and checks and F_1 and also for each progeny in F_3. The characters for P_1, P_2, F_1, F_2, BC_1P_1, and BC_1P_2 were recorded in each individual plant (as detailed in Table 2). The particulars of characters studied are as follows:

3.3.1.1 Growth vigour

Visual observation of growth was recorded at 15-20 days after germination based on 1-5 scale where 1 indicated plants with low vigour and score 5 was assigned high vigour. Plant having ratings of 1 and 2 were grouped as low growth vigour and those with 3 to 5 as high growth vigour. The Chi-square test was used to test the goodness of fit to different genetic ratios.

3.3.1.2 Flower colour

Observation on flower colour was recorded on individual plant basis at the time of flowering. Flower colour was recorded as white and pink.

3.3.1.3 Stem colour

Observation on stem colour was made twice on single plants basis, first before flowering and next at the time of flowering when the stem pigmentation was much clear. Stem colour (anthocyanin pigmentation) was recorded as present or absent.

3.3.1.4 Number of pods per peduncle

The number of flowers or pods on each peduncle were recorded as single or double.

3.3.1.5 Days to first flower

The number of days from time of planting up to observe first flower in plant or plot.

3.3.1.6 Days to 50% flowering

Number of days from sowing to the date when 50% of the plants in the plots had at least one open flower.

3.3.1.7 Leaf size (cm^2)

Leaf size was measured on two leaves per plant in P_1, P_2, F_1, BC_1P_1, BC_1P_2 and F_2 on fifth or sixth leaf from the top of primary branches for this measurement and sampling done at the time of 50% flowering. In F_3 and RILs were selected in 10 plants in each progeny and 5 plants per plot respectively. Leaf areas were measured with the help of a LI-COR LI-3100 Area meter, LI-COR Inc. Nebroske, USA and the observations were recorded as cm^2.

3.3.1.8 Leaf weight (g)

Leaf weight was recorded after drying the leaves in oven at 80° C for 72 hours.

3.3.1.9 Days to first pod

The number of days from time of planting up to observe first pod in plant or plot.

3.3.1.10 Days to maturity

Number of days taken from sowing to the time when more than 90 per cent of pods on the chickpea plant had turned from green to light yellow or brown (dry pod) was recorded as days to maturity

3.3.1.11 Number of primary branches per plant

The number of branches originating directly from main stem of a plant counted at time of maturity.

3.3.1.12 Number of secondary branches per plant

At the time of maturity total number of branches arising from primary branches per plant was counted.

3.3.1.13 Plant height (cm)

At the time of maturity height of plant was measured from the ground level to the tip of tallest branch.

3.3.1.14 Plant width (cm)

The width of fully mature plant was measured in cm, at the time of maturity.

3.3.1.15 Number of pods per plant

Total number of pods (filled and unfilled) on a individual plant was counted.

3.3.1.16 Number of seeds per plant

Total number of seeds per plant was counted after threshing the dried pods.

3.3.1.17 Number of seeds per pod

Number of seeds per pod was calculated by following formula.

$$\frac{\text{Total number of seeds per plant}}{\text{Total number of pods per plant}}$$

3.3.1.18 Seed yield per plant (g)

Total seed from individual plant were weighted and recorded in grams.

3.3.1.19 100-seed weight (g)

The weight of 100-seed in gram was obtained by the following formula.

$$\frac{\text{Seed yield per plant (g)}}{\text{Total number of seeds per plant}} \times 100$$

3.3.1.20 Yield per plot (g)

All the seeds of plant per plot were weighted in grams.

3.3.1.21 Seed surface

Observations on seed surface were recorded on individual seed in each plant. Seed surface was categorised as rough and smooth.

3.3.1.22 Seed type

Seed type observation was made on individual seed in each plant. Seed type was recorded as desi, intermediate or kabuli type.

3.3.1.23 Seed-coat colour

Seed-coat colour was recorded based on colour chart. It was found to be difficult due to continuos variation.

3.3.1.24 Specific leaf weight

Specific leaf weight was determined by following formula suggested by Radford (1967).

Leaf weight (g)

Leaf area (cm^2)

3.4 CHEMICAL ANALYSIS

3.4.1 Crude fibre content (%)

Crude fibre content (%) was determined by estimating the fibre content of the seed as follows:

Crude fibre estimation:

Clean chickpea seeds were taken and ground by Udy cyclone mill. This flour was passed through 0.4 mm mesh. Weighed 2 g of chickpea flour and 1 g of asbestos and were transferred in to a crude fibre beaker (special type beaker for fibre estimation). 200 ml hot solution of 0.255 N sulphuric acid and boiling chips were added. The beaker was put on a preheated plate of the digestion apparatus and digested the sample for 30 min, rotating the beaker periodically to keep the solids or material from adhering to the sides. The sample was filtered through a California modified Buchner funnel by using a vaccum pump. The residue was washed with hot water until washings were free from acid. The residue was transferred back into the beaker with hot 0.313 N sodium hydroxide solution. The beaker was placed on the heater and sample was digested for 30 min. The sample was filtered through California modified funnel and the residue was washed with hot water until the washings were free from alkali. Finally the residue was washed with alcohol (about 25 ml). The residue was transferred into a clean porcelain crucible and dried at 100°C overnight. The crucible was transferred into a desiccator and cooled to room temperature and weighed (W1). The residue was ignited in a muffle furnace at 600° C for 30 min. Then the crucible was transfer into a desiccator and cooled to room temperature and weighed it (W2). A blank also run along with the samples.

Weight of the crude fibre = (W1-W2) - Blank

$$\% \text{ Crude fibre} = \frac{\text{Weight of the crude fibre (g)} \times 100}{\text{Weight of the sample (2 g)}}$$

3.5 STATISTICAL ANALYSIS

The recorded data were subjected to following statistical analyses.

3.5.1 χ^2 test of goodness of fit

χ^2 test was used to test the goodness of fit of the observed ratio of segregation for flower colour, plant pigmentation, pod number per peduncle, seed-coat colour, seed surface, seed type and growth vigour based on data for F_2 population. Further results were confirmed with F_3, BC_1P_1, BC_1P_2, and RILs. To test the goodness of fit, suggested formula by Panse and Sukhatme (1989) was used.

$$\chi^2 = \Sigma \frac{(O-E)^2}{}$$

Where O stands for the observed and E for the expected frequency in any particular class of the distribution and Σ for the summation over all classes.

3.5.2 Heritability

Heritability was estimated for of seed yield per plot, seed yield per plant, days to first flower, days to 50% flowering, number of seeds per pod, days to maturity, plant

height, plant width, number of seeds per plant, number of pods per plant, number of primary branches per plant, number of secondary branches per plant, seed fibre, leaf size, leaf weight, specific leaf area and seed size. Depending on the components of variance used as numerator in the calculation, heritability is of two types, viz, broad sense heritability and narrow sense heritability.

3.5.2.1 Broad-sense heritability

3.5.2.1.1 heritability in RILs

Broad sense heritability is the ratio of the total genotypic variance to the phenotypic variance. It was computed as per Falconer, 1989.

$$h^2 = \frac{VG}{VP} \times 100$$

h^2 = heritability

VG = genotypic variance

VP = phenotypic variance

3.5.2.1.2 Heritability in generations

For estimating broad sense heritability variance of different generations were worked out by utilising the following formula given by Waldia *et al.* (1992).

$$h^2_{bs} = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}} \times 100 = \frac{}{VF_2} \times 100$$

$$Vg = VF_2 - VE$$

$$VE = \frac{VP_1 + VP_2 + VF_1}{}$$

VE = Variance of environment

VP_1 = Variance of parent one

VP_2 = Variance of parent two

VF_1= Variance of F_1

VF_2 = Variance of F_2

3.5.2.2 Narrow- sense heritability

The heritability in narrow sense was worked out utilising the following formula suggested by Warner (1952).

$$h^2_n = \left[\frac{1/2\ D}{VF_2} \right] \times 100$$

D = additive variance

VF_2 = phenotypic variance of a trait in generation F_2

The calculation of additive variance were done by following the suggested by Fehr (1987).

$(1/2)\ VD = 2VF_2 - (V\ BC_1P_1 + V\ BC_1P_2)$

VF_2 = variance among F_2 plants of the single-cross population

BC_1P_1 = total within variance of the back crosses of the F_1 to the parent one

BC_1P_2 = total within variance of the back crosses of the F_1 to the parent two

3.5.3 Parent- offspring regression

Parent-offspring regression between F_2 and F_3 on days to first flowering, days to first pod, date of maturity, plant height, number of pods per plant, yield per plant, number of primary branches per plant, number of secondary branches per plant, number of seeds per plant, plant width and 100-seed weight, were worked out by using standardized data Z obtained as follows (Frey and Horner, 1957).

$$Z_{F3} = \frac{Yi - \bar{Y}_{F3}}{\sigma_{F3}}$$

Yi = observed data in F_3

Y_{F3} = mean of F_3 data

σ_{F3} = standard deviation on F_3 data

$$Z_{F2} = \frac{Xi - \bar{X}_{F2}}{\sigma_{F2}}$$

Xi = observed data in F_2

$\bar{X}_{F2}$ = mean of F_2 data

σ_{F2} = standard deviation of F_2 data

$$h^2 = b_{F3,\,F2} = \frac{Cov\,(F_3, F_2)}{\sigma^2 F_2}$$

b = regression coefficients

Cov (F_3, F_2) = covariance between individuals of generation F_2 and the mean of their progenies in F_3.

$\sigma^2 F_2$ = phenotypic variance of a trait in generation F_2.

3.5.4 Genetic advance

The 'genetic advance' and 'genetic advance as percentage of mean' were calculated by the following formula given by Singh (1997).

$$GS = K \sqrt{Vp} \times \frac{VG}{VP}$$

GS = genetic advance

K = intensity of selection

Vp = phenotypic standard deviation of base population

$$GS\ (\%mean) = \frac{GS}{\bar{X}} \times 100$$

$\bar{X}$ = mean of base population

3.5.5 Recombination frequencies

3.5.5.1 Recombination frequencies from F_2 data

Method of maximum likelihood is a method of unique importance, for it has been shown that in large samples no other method will give an estimate with a smaller sampling variance than the one given by this method (Fisher, 1921). This is based on the principle that a recombination value (p), whose variance is minimum, will be the best estimate of recombination frequency.

The recombination frequencies from F_2 data were calculated following formula suggested by Gupta (1997)

$$P^2 = \frac{-S \pm \sqrt{S^2 - 4nt}}{2n}$$

S = -(a-2b -2c-d)

t =-2d

n =(a+b+c+d)

a =A-B-

b = A-bb

c = aaB-

d = aabb

3.5.6 Correlated genetic gain

The extent of correlated response is a function of the heritabilities of the primary and correlated characters, as well as the genetic correlation between the characters. (Dudley, 1997).

The calculations of correlated genetic gain were worked out utilising the following formula suggested by Falconer (1989).

$CRy = ih_x h_y r_g \sigma p_y$

CRy = correlated response of character Y when selection is based on character X

i = intensity of selection

h_x = square-root of the heritability of character X

h_y = square- root of the heritability of character Y

r_g = genetic correlation between two characters X and Y

σp_y = phenotypic standard deviation of character Y

The genotypic correlation coefficient was obtained by estimating the variance and covariance components for each character and character pairs using the formula given by Menendez and Hall (1995).

$$r_g = \frac{Cov_g\ (X,Y)}{\sqrt{Var_g\ (X)\ Var_g\ (Y)}}$$

r_g = genetic correlation

Cov_g (X,Y) = genetic covariance between characters X,Y

Var_g (X) = genetic variance in character X

Var_g (Y) = genetic variance in character Y

The variance and covariance components were estimated using the REML procedure.

3.5.7 Coheritability

Coheritability deals with simultaneous inheritance of two characters. The calculation for coheritability was done utilising formula suggested by Janssens (1979).

$$\text{Coheritability } (X_1,X_2) = \frac{\text{Gcov } (X_1X_2)}{\text{Pcov } (X_1X_2)} \times 100$$

GCov = genotypic covariance of characters X_1 and X_2

PCov = phenotypic covariance of character X_1 and X_2

3.5.8 Test of significance of means

For testing of significance of means, the following formula given by Singh and Chaudhary (1996) was used.

If Ho: $\sigma_1^2 = \sigma_2^2$ was not rejected by the F-test t was computed as

$$t = \frac{\bar{X}_1 - \bar{X}_2}{s\sqrt{\frac{1}{n_1} + \frac{1}{n_2}}}$$

where, $s^2 = \frac{(n_1-1)s_1^2 + (n_2-1)s_2^2}{n_1 + n_2 - 2}$

$$t = \frac{\bar{X}_1 - \bar{X}_2}{\sqrt{\frac{s^2_1}{n_1} \quad \frac{s^2_2}{n_2}}}$$

where, $s^2_1 = \frac{\sum (xi_1 - \bar{X}_1)^2}{n_1 - 1}$

$$s^2_2 = \frac{\sum (xi_2 - \bar{X}_2)^2}{n_2 - 1}$$

3.5.9 Heterosis

The performance of a hybrid relative to its parents can be expressed in two ways. Mid-parent heterosis (average heterosis) is the performance of a hybrid compared with the average performance of its both parents. High-parent heterosis (heterobeltiosis) is a comparison of the performance of the hybrid with that of the better parent in the cross.

Heterosis is usually expressed as a percentage and computed by using following formula suggested by Fehr (1987).

$$\text{Mid-parent heterosis (\%)} = \frac{\bar{F}_1 - \overline{MP}}{\overline{MP}} \times 100$$

$$\text{High-parent heterosis (\%)} = \frac{\bar{F}_1 - \overline{HP}}{\overline{HP}} \times 100$$

$\bar{F}_1$ = Average performance of hybrid
$\overline{MP}$= Average performance of both parents
$\overline{HP}$ = Average performance of best parent

3.5.10 Inbreeding depression

The inbreeding depression refers to decrease in fitness and vigour due to inbreeding. Inbreeding depression was calculated using following formula given by Phundan Singh and Narayanan (1997).

$$\text{Inbreeding depression} = \frac{\bar{F}_1 - \bar{F}_2}{\bar{F}_1} \times 100$$

Where $\bar{F}_1$ and $\bar{F}_2$ are the mean values of F_1 and F_2 progeny, respectively of the same cross for a given character.

3.5.11 Superiority of RILs over parents

The calculation of superiority of RILs over parents were worked out utilising the following formula.

$$S_1 = \frac{\overline{RIL} - \bar{P}_1}{\bar{P}_1} \times 100$$

$$S_2 = \frac{RIL - \bar{P}_2}{\bar{P}_2} \times 100$$

S_1 = Superiority to ICCV2

S_2 = Superiority to JG62

$\bar{P}_1$ = Mean of parent 1

$\bar{P}_2$ = Mean of parent 2

Results

CHAPTER IV

RESULTS

Experiments were conducted during the *Rabi* (Post-rainy) seasons of 1998/1999 and 1999/2000 to investigate inheritance of qualitative and quantitative traits in chickpea (*Cicer arietinum* L.). The studies were carried out on parents, F_1, F_2, F_3, BC_1P_1 and BC_1P_2 generations and recombinant inbred lines (RILs) of a cross between two chickpea varieties ICCV2 (P_1) and JG62 (P_2). The data were recorded on individual plants for parents, F_1, F_2, BC_1P_1, BC_1P_2 and 5 competitive random plants for each of the F_3 progenies and RILs.

The generations under study were evaluated for seven qualitative and 18 quantitative characters. These were flower colour, stem colour, number of pods per peduncle, seed surface, seed type, seed coat colour, growth vigour, days to first flower, days to 50% flower, days to first pod, days to maturity, number of primary branches per plant, number of secondary branches per plant, plant height, plant width, number of pods per plant, number of seeds per plant, number of seeds per pod, 100-seed weight, yield per plot, leaf size, leaf weight, specific leaf weight, yield per plot and seed fibre. The results for these are presented under the following headings:

4.1 INHERITANCE OF QUALITATIVE TRIATS

4.2 4.1.1 Flower colour

4.1.2 Stem colour

4.1.3 Number of pods per peduncle

4.1 INHERITANCE OF QUALITATIVE TRAITS

4.1 .1 Flower colour

The inheritance of pink and white flower colour (Plate 1) was studied. The observations obtained in F_2 in the first year (153 pink: 49 white) and second year experiments (239 pink: 67 white) indicated that the flower colour in this cross was controlled by a single gene. This corresponds with the expected 3:1 ratio (Table 3).

The inheritance of flower colour was also observed in RILs and BC_1P_1. Among the 114 RILs studied 55 showed pink colour while 59 exhibited white colour. In the BC_1P_1 these were 20 pink and 19 white coloured plants. These results correspond with the expected 1:1 ratio (Table 3).

4.1.2 Stem colour

The observations on the anthocyanin pigmentation of the stem (Plate 2) in the F_2 generation gave a good fit to the expected 3:1 ratio (Table 4).

The results for RILs and BC_1P_1 showed a good fit to the expected 1:1 ratio for pigmented and non-pigmented stem colour (Table 4).

4.1.3 Number of pods per peduncle

ICCV2 is single podded and JG62 double podded parent used in the present investigation (Plate 3). The F_2 Population in the first year experiment did not show a good fit to the expected 3 single pod: 1 double pod ratio (Table 5), because out of 310

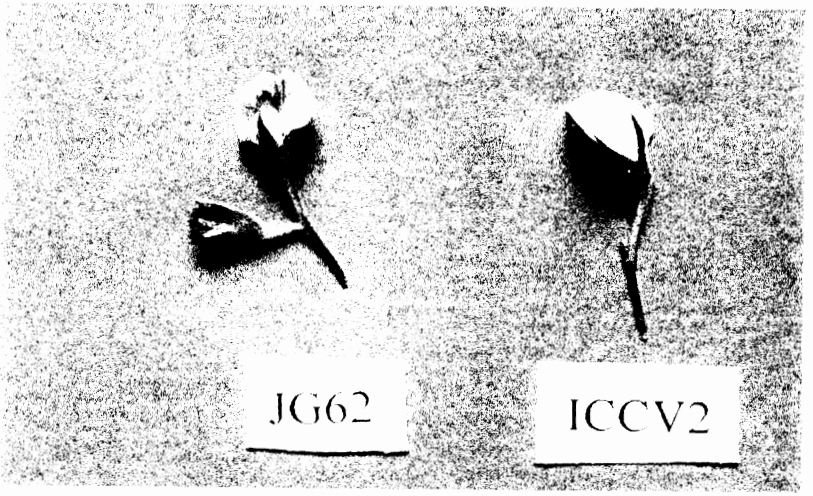

Plate 1. Flower characters of parents JG62

Plate2. Stem colour of pigmented and non-pigmented plants.

ICCV2
single pod

JG62
double pods

Plate 3. Podding trait of the parental lines, single podded: ICCV 2 And double podded: JG62.

Table 3. Segregation for flower colour in F_2, BC_1P_1, BC_1P_2 and RILs of ICCV2 x JG62 cross of chickpea during 1998-1999 and 1999-2000.

Year	Generation	Phenotype	Observed number	Appropriate ratio	χ^2	P
1998-1999	F_2	Pink	153	3:1	0.104^{ns}	0.75
		White	49			
1999-2000	F_2	Pink	239	3:1	1.569^{ns}	0.21
		White	67			
1999-2000	BC_1P_1[a]	Pink	20	1:1	0.024^{ns}	0.88
		White	19			
1999-2000	BC_1P_2[b]	All flowers were Pink				
1998-1999	RILs[c]	Pink	55	1:1	0.14^{ns}	0.71
		White	59			
1999-2000	RILs[c]	Pink	55	1:1	0.14^{ns}	0.71
		White	59			

[a] $BC_1P_1 = F_1$ x ICCV2

[b] $BC_1P_2 = F_1$ x JG62

[c] 2 out of 116 still were segregating.

χ^2 = Chi-square

^{ns} = Non-significant

Table 4. Segregation for stem colour in F_2, BC_1P_1, and RILs of ICCV2 x JG62 cross of chickpea during 1998-1999 and 1999-2000.

Year	Generations	Phenotype	Observed number	Appropriate ratio	χ^2	p
1998-1999	F_2	Pigmented	153	3:1	0.104^{ns}	0.75
		Non-pigmented	49			
1999-2000	F_2	Pigmented	239	3:1	1.569^{ns}	0.21
		Non-pigmented	67			
1999-2000	BC_1P_1	Pigmented	20	1:1	0.024^{ns}	0.88
		Non-pigmented	19			
1999-2000	BC_1P_2	All stems were pigmented				
1998-1999	RILs[a]	Pigmented	55	1:1	0.14^{ns}	0.71
		Non-pigmented	59			
1999-2000	RILs[a]	Pigmented	55	1:1	0.14^{ns}	0.71
		Non-pigmented	59			

[a] 2 out of 116 still were segregating.

Table 5. Segregation for pod number per peduncle in F_2, BC_1P_2, and RILs of ICCV2 x JG62 cross of chickpea during 1998-1999 and 1999-2000.

Year	Generations	Phenotype	Observed number	Appropriate ratio	χ^2	P
1999-2000	F_2	Single pod	237	3:1	1.19^{ns}	0.28
		Double pod	68			
1999-2000	BC_1P_1	All plants had single pod				
1999-2000	BC_1P_2	Single pod	15	1:1	1.32^{ns}	0.25
		Double pod	22			
1998-1999	RILs	Single pod	59	1:1	0.034^{ns}	0.85
		Double pod	57			
1999-2000	RILs	Single pod	59	1:1	0.034^{ns}	0.85
		Double pod	57			

individual plants, 108 plants were killed before flowering due to fusarium wilt disease. Therefore, probably may be due the susceptibility of double pod genotype to fusarium biased the results and lack inadequate population size expected results could not be achieved. The second year F_2 population produced 237 single podded and 68 double podded plants.

The inheritance of pod number per peduncle was also studied in RILs and BC_1P_1 generation. Of the 116 RILs 59 were single podded and 57 were double podded and in BC_1P_1 these were 15 single podded and 22 were double podded plants. These results gave a good fit to the expected 1:1 ratio based on one gene segregation (Table 5).

There were no effect of double pods over single pods per peduncle on yield and yield components in F_2 and RILs, except for number of seeds per pod character in the F_2 in the second year experiment (Tables 6.7).

4.1.4 Seed surface

ICCV2 seed has smooth while JG62 has rough testa. In the present study a segregation pattern of 13:3 in the F_2 in both the year experiments was observed (Table 8).

Similarly, the inheritance of seed surface in RILs and BC_1P_1 was studied. The results gave a good fit to the expected 3:1 for roughness and smoothness of the testa (Table 8).

Table 6. Comparison by' t' test of single and double podded in F_2 plants of ICCV2 x JG62 cross of chickpea.

Character	Type of pod	1998-1999		1999-2000	
		Mean	P value	Mean	P value
Pod number/ plant	Single pod	110.7	0.506	138.7	0.377
	Double pod	121.4		147.8	
Seed number/plant	Single pod	116.4	0.713	153.4	0.920
	Double pod	122.4		152.2	
Seed number/pod	Single pod	1.06	0.133	1.11	0.003
	Double pod	1.01		1.04	
100-seed weight	Single pod	15.93	0.589	19.93	0.722
	Double pod	15.45		19.33	
Seed yield/plant	Single pod	19.06	0.957	28.64	0.94
	Double pod	18.89		28.79	

Table 7. Comparison by t test of single and double podded in RILs of ICCV2 x JG62 cross of chickpea.

Character	Type of pod	1998-1999		1999-2000	
		Mean	P value	Mean	P value
Pod number/ plant	Single pod	71.18	0.225	67.21	0.202
	Double pod	74.95		71.25	
Seed number/plant	Single pod	75.72	0.385	72.48	0.559
	Double pod	78.64		74.48	
Seed number/pod	Single pod	1.07	0.389	1.08	0.068
	Double pod	1.05		1.05	
100-seed weight	Single pod	17.80	0.269	20.32	0.582
	Double pod	17.10		19.92	
Seed yield/plant	Single pod	12.97	0.691	14.15	0.709
	Double pod	12.98		14.29	

Table 8. Segregation data for seed surface in F_2, BC_1P_1, and RILs of ICCV2 x JG62 cross of chickpea during 1998-1999 and 1999-2000.

Year	Gen[a]	Phenotype	Observed number	Appropriate ratio	χ^2	P	Gene symbol
1998-1999	F_2	Rough	163	13:3	0.032^{ns}	0.86	Sr_1Sr_2
		Smooth	39				
1999-2000	F_2	Rough	248	13:3	0.395^{ns}	0.53	
		Smooth	52				
1999-2000	BC_1P_1	Rough	26	3:1	0.44^{ns}	0.51	
		Smooth	11				
1999-2000	BC_1P_2	All seeds were rough					
1998-1999	RILs	Rough	93	3:1	1.66^{ns}	0.20	
		Smooth	23				
1999-2000	RILs	Rough	93	3:1	1.66^{ns}	0.20	
		Smooth	23				

[a] Gen= Generation

4.1.5 Seed type

ICCV2 has kabuli seed type, beige colour and owl's head shape and JG62 has desi seed type with angular shape (Plate 4). The F_1 generation from this cross was desi type (Plate 4). The F_2 population of this cross was segregated into 9 desi: 6 intermediate: 1 kabuli type as shown in Table 9. This result indicates the presence of two of pair genes. Thus the character is controlled by polymeric gene action.

Inheritance of seed type was also observed in BC_1P_1 and RILs. The results gave a good fit to the expected 1 desi: 2 intermediate: 1 kabuli ratio for seed type in chickpea (Table 9).

The mean seed fibre content of desi type (8.92%) was significantly higher than that of kabuli type (4.20%) as indicated by 't' test which was significant at 1% level of probability. The crude fibre content of desi type (8.92%) differed significantly with the crude fibre of intermediate type (5.96%) at 1% level of probability. Also 't' test showed significance at 1% level of probability between the crude fibre content of kabuli type (4.20%) and intermediate type (Table 10). Desi type seeds had 2.12 and 1.5 times more fibre than kabuli and intermediate types respectively. Intermediate seeds showed 1.42 time more fibre than kabuli type. The mean crude fibre contents of ICCV2 and JG62 were 3.84 and 10.32 percent respectively. Mean of F_1 seeds showed 7.65 percent crude fibre while hybrid seed of crosses ICCV2 x JG62 and JG62 x ICCV2 had 3.91 and 11.67 percent respectively.

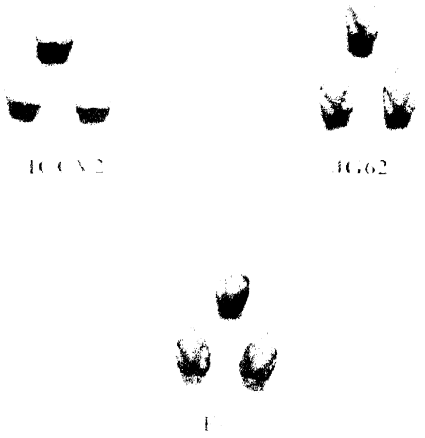

Plate 4. Seed type of the parental lines and F_1. ICCV2 yellow beige, smooth and owl's head shape, and JG62 yellow brown, rough and angular shape. F_1 yellow brown, rough and angular.

Table 9. Segregation for seed type in F_2, BC_1P_1, and RILs of ICCV2 x JG62 cross of chickpea during 1998-1999 and 1999-2000.

Year	Generation	Phenotype	Observed number	Appropriate ratio	χ^2	p	Gene symbol
1998-1999	F_2	Desi Intermediate Kabuli	118 78 6	9:6:1	3.75^{ns}	0.15	St_1, St_2
1999-2000	F_2	Desi Intermediate Kabuli	165 117 18	9:6:1	0.273^{ns}	0.87	
1999-2000	BC_1P_1	Desi Intermediate Kabuli	9 22 6	1:2:1	1.81^{ns}	0.40	
1999-2000	BC_1P_2	All seeds were desi type					
1998-1999 1999-2000	RILs	Desi Intermediate Kabuli	40 52 24	1:2:1	5.65^{ns}	0.059	

Table 10. Comparison by ' t' test of crude fibre concentration in desi, kabuli and intermediate seed type on RILs derived from the ICCV2 x JG62 cross in chickpea

Type of seed	Mean	P value
Desi type	8.919	< 0.001
Kabuli type	4.202	
Desi type	8.919	< 0.001
Intermediate type	5.956	
Intermediate type	5.956	< 0.001
Kabuli type	4.203	

4.1.6 Seed coat colour

JG62 has yellow brown and ICCV2 has yellow beige seed coat colours. Eight phenotypic classes as shown in Plate 5. The F_2 generations in the first year and second year showed a good fit to the expected 27:9:9:9:3:3:3:1 ratio for yellow brown, brown, reddish brown, light brown, yellow beige, dark beige, dark brown and light yellow colours respectively (Table 11). This result indicates that the seed colour of chickpea is controlled by at least 3 major genes.

The seed coat colours in RILs and BC_1P_1 were studied. The results gave a good fitness to the expected 1:1:1:1:1:1:1:1 and 1:1:1:1 ratioes respectively (Table 11). The seeds of all plants of the cross between F_1 and JG62 (BC_1P_2) were yellow brown.

4.1.7 Growth vigour

ICCV2 has high initial seedling vigour and JG62 has low initial seedling vigour (Plate 6). The observation obtained in the first year (191 high growth vigour: 11 low growth vigour) and second year (279 high growth vigour: 27 low growth vigour) indicate that growth vigour is controlled by two genes and this trait is governed by duplicate dominant epistasis (Table 12).

Inheritance of growth vigour also was studied in BC_1P_1 and RILs. The results gave a good fit to the expected 3:1 for high growth vigour and low growth vigour (Table 12). Growth vigour was also studied in F_1 (JG62 x ICCV2 and ICCV2 x JG62) and BC_1P_1 (F_1

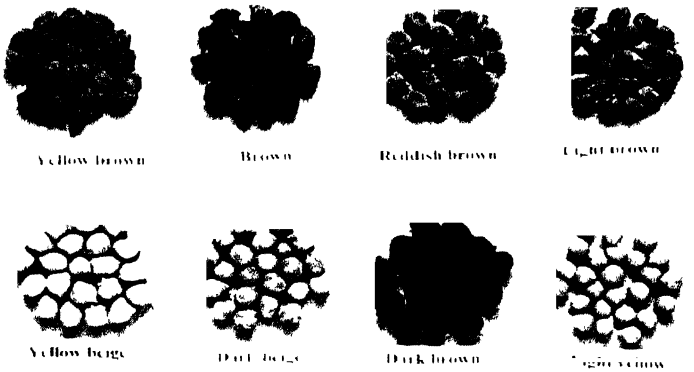

Plate 5. Phenotypic classes for seed coat colour in generations and RILs.

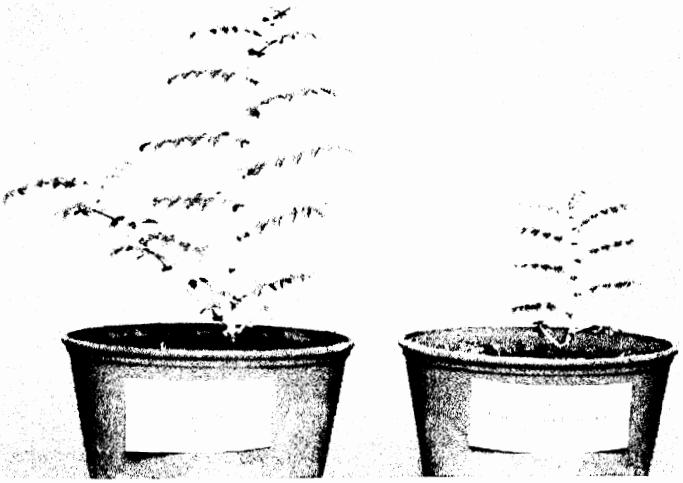

Plate 6. Initial growth vigour of parental varieties 20 days after sowing. ICCV2 high growth vigour and JG62 low growth vigour.

Plate 7a. General view of the experiment II in 1999-2000.

Plate 7b. Over all view of the RIL experiment in 1999-2000.

Table 11. Segregation for seed coat colour in F_2, BC_1P_1, and RILs of ICCV2 x JG62 cross of chickpea during 1998-1999 and 1999-2000.

Year	Generation	Phenotype	Observed Number	Appropriate ratio	χ^2	p	Gene symbol
1998-1999	F_2	Yellow brown	71	27	8.31^{ns}	0.31	**Ysc, Bsc, Rsc**
		Brown	36	9			
		Reddish brown	32	9			
		Light brown	31	9			
		Yellow beige	14	3			
		Dark beige	9	3			
		Dark brown	7	3			
		Light yellow	2	1			
1999 -2000	F_2	Yellow brown	126	27	1.50^{ns}	0.98	
		Brown	44	9			
		Reddish brown	41	9			
		Light brown	46	9			
		Yellow beige	12	3			
		Dark beige	15	3			
		Dark brown	13	3			
		Light yellow	3	1			
1999 -2000	BC_1P_1	Yellow brown	5	1	4.29^{ns}	0.75	
		Brown	6	1			
		Reddish brown	4	1			
		Light brown	6	1			
		Yellow beige	4	1			
		Dark beige	5	1			
		Dark brown	6	1			
		Light yellow	1	1			
1999-2000	BC_1P_2	Seeds of all plants were yellow brown					
1998 -1999 and 1999-2000	RILs	Yellow brown	13	1	6.76^{ns}	0.45	
		Brown	12	1			
		Reddish brown	21	1			
		Light brown	13	1			
		Yellow beige	20	1			
		Dark beige	12	1			
		Dark brown	12	1			
		Light yellow	13	1			

Table 12. Segregation for growth vigour in F_2, BC_1P_2, and RILs of ICCV2 x JG62 cross of chickpea during 1998-1999 and 1999-2000.

Year	Generations	Phenotype	Observed number	Appropriate ratio	χ^2	P	Gene symbol
1998-1999	F_2	High growth vigour	191	15:1	0.22^{ns}	0.64	**Gv_1Gv_2**
		Low growth vigour	11				
1999-2000	F_2	High growth vigour	279	15:1	3.45^{ns}	0.06	
		Low growth vigour	27				
1999-2000	BC_1P_2	High growth vigour	32	3:1	2.60^{ns}	0.11	
		Low growth vigour	5				
1998-1999	RILs	High growth vigour	91	3:1	0.73^{ns}	0.39	
		Low growth vigour	25				
1999-2000	RILs	High growth vigour	81	3:1	1.66^{ns}	0.20	
		Low growth vigour	35				

x ICCV2) as shown in Table 13. The results confirmed that high growth vigour is dominant over low growth vigour.

In the present study, correlation between growth vigour and other quantitative characters was studied for F_2 and RILs. The results showed that high growth vigour had significant negative correlation with days to first flower, days to 50% flowering, days to first pod and days to maturity. In the RILs, highly significant positive correlation was observed between initial growth vigour and 100-seed weight, leaf size and leaf weight, also showed significant negative correlation with number of seeds per plant, number of pods per plant, number of primary branches per plant, number of secondary branches per plant and number of seeds per pod. The correlation between yield per plant and growth vigour was not significant in RILs and F_2 generation (Table 14).

4.2 INHERITANCE OF QUANTITATIVE TRAITS

4.3 4.2.1 Heritability and genetic advance

The estimates of heritable and non-heritable variance give a clue on possible improvement for the character under study. Heritability and genetic advance are two important selection parameters, of which the former is used to estimate the expected genetic advance through selection.

The present investigation was planned to estimate broad sense heritability, narrow sense heritability and genetic advance in segregating populations and recombinant inbred line (RILs) of the cross ICCV2 x JG62.

Table 13. Segregation for growth vigour in F_1 and BC_1P_1 of ICCV2 x JG62 cross of chickpea during 1998-1999 and 1999-2000.

Year	Generation	Phenotype	Observed number
1998-1999	F_1 (JG62♀ x ICCV2♂)	High growth vigour	29
		Low growth vigour	0
1999-2000	F_1 (JG62♀ x ICCV2♂)	High growth vigour	14
		Low growth vigour	1
1999-2000	F_1 (ICCV2♀ x JG62♂)	High growth vigour	19
		Low growth vigour	0
1999-2000	BC_1P_1 (F_1♀ x ICCV2♂)	High growth vigour	38
		Low growth vigour	1

Table 14. Correlation coefficient between initial growth vigour and some other characters in F_2 and RILs.

Year	Gen	DFF	DFP	DFPF	DM	HSDW	POD	SDNO	SD/PD	PBR	SBR	SDYLD	HT	WID	LS	LW	SPLWT
1998-1999	F_2	-0.98**	-0.98**	-	-0.91*	-0.71	0.92*	0.83	-0.26	-0.44	0.34	0.69	0.79	0.98**	-	-	-
1999-2000	F_2	-0.89*	-0.87*	-	-0.71	-0.84*	0.61	0.46	-0.31	0.58	0.56	0.60	0.57	0.48	0.95**	-0.67	-0.81
1998-1999	RILs	-0.98**	-0.98**	-0.98**	-0.95*	0.99**	-0.90*	-0.92*	-0.85	-0.83	-0.98**	0.37	0.92*	0.86	-	-	-
1999-2000	RILs	-0.99**	-0.99**	-0.99**	-0.99**	0.99**	-0.98**	-0.99**	-0.82*	-0.95*	-0.98**	-0.30	0.12	-0.13	0.98**	0.98**	-0.95**

Gen= Generation.EV= Early growth vigour. DFF= Days to first flower, HT= Plant height, WID= Plant width. PDNO= Number of pods per plant, PBR= Number of primary branches per plant, SBR= Number of secondary branches per plant. SD/PD= Number of seeds per pod. SDNO= Number of seeds per plant, SD/PD= Number of seeds per pods, SDYD= Yield per plant. HSDWT= 100-seed weight. DFP= Days to first pod. DFPF= Days to 50% flowering. DM= Days to maturity. LS = Leaf size. LW = Leaf weight. SPLWT = Specific leaf weight

* Significant at 5% level of probability
** Significant at 1% level of probability
- Data not available

4.2.1.1 Days to first flower

The estimates of broad sense heritability for days to first flower were high in RILs and segregating populations while narrow sense heritability for this character was moderate (Table 15).

Genetic advance estimates as percent of mean for days to first flower in RILs was high while in segregating populations it was low (Table 16).

4.2.1.2 Days to 50% flowering

The broad sense heritability estimate was high for days to 50% flowering in RILs (Table 15).

Days to 50% flowering had high genetic advance as percent of mean in RILs (Table 16).

4.2.1.3 Days to first pod

The estimates of broad sense heritability for days to first pod were high in RILs and segregating populations while narrow sense heritability was moderate for this trait (Table 15).

Genetic advance estimate for days to first pod was high in RILs while it was low in segregating populations for this character (Table 16).

Table. 15 Heritability estimates for different characters for RILs and segregating populations.

Characters	RILs	Segregating populations		
	h^2(bs)	h^2(bs)		h^2 (ns)
	pooled	1998-1999	1999-2000	1999 -2000
Days to first flower	94	93	74	54
Days to 50% flowering	96	-	-	-
Days to first pod	94	89	81	60
Days to maturity	89	91	69	40
100-seed weight	89	63	98	97
Plant height	85	40	58	28
Primary branches	24	71	38	33
Number of pods/plant	56	65	64	37
Secondary branches	37	50	34	14
Number of seeds/ plant	57	70	67	41
Width of plant (canopy)	16	41	41	11
Number of seeds/pod	71	0	75	45
Yield/plant	55	74	57	36
Seed fibre	89	-	-	-
Leaf size [a]	87	-	70	4
Leaf weight [a]	88	-	96	87
Specific leaf weight [a]	60	-	99	94

[a] Computed on 1999-2000 data

- Data not available

Table 16. Genetic advance (GS) for RILs and segregating populations.

Characters	RILs[a]		Segregating populations	
	GS	GS (%mean)	GS	GS (%mean)
Days to first flower	14.52	39.57	8.7	19.66
Days to first pod	16.37	35.79	9.3	19.1
Days to 50% flowering	16.02	40.29	-	-
Days to maturity	12.64	14.29	5.2	5.6
100-seed weight	6.97	37.2	23.5	118.5
Plant height	10.62	29.27	3.5	10.3
Primary branches	0.22	8.6	0.58	16.5
Number of pods/ plant	22.62	31.61	54	38
Secondary branches	0.84	18.12	0.7	10.3
Number of seeds/plant	24.78	32.56	66.5	43.4
Number of seeds /pod	0.16	14.54	0.14	12.83
Seed yield/plant	5.62	40.52	10.12	35.21
Width of plant	1.68	5.28	2.42	5.51
Leaf size[b]	3.69	58	1.23	25.49
Seed fibre	4.03	60.5	-	-
Leaf weight (dry)[b]	0.026	58.7	0.07	184.21
Specific leaf weight[b]	0.000769	10.94	0.0116	145

[a] Pooled analysis

[b] Computed on 1999-2000 data

- Data not available

4.2.1.4 Days to maturity

The estimates of broad sense heritability for days to maturity were high in RILs and segregating populations while narrow sense heritability was moderate for this trait (Table 15).

Days to maturity showed low genetic advance in RILs and segregating populations (Table 16).

4.2.1.5 100-seed weight

The broad sense estimates for heritability were high for 100-seed weight in RILs and in segregating populations. This character had very high narrow sense estimate of heritability (Table 15).

High genetic advance was recorded for 100-seed weight in RILs and segregating populations (Table 16).

4.2.1.6 Plant height

Plant height had high broad sense heritability in RILs but moderate in segregating populations. Narrow sense heritability was low for this character (Table 15). This may be due to low variation for the trait in this cross.

The estimate of genetic advance for plant height was moderate for RILs and low for segregating populations (Table 16).

4.2.1.7 Width of plant

Width of plant had low broad sense heritability for RILs and moderate for segregating populations. Narrow sense heritability for this trait was low (Table 15).

Genetic advance estimates for this trait were low in RILs and segregating populations (Table 16).

4.2.1.8 Number of primary branches per plant

Broad sense heritability estimates for number of primary branches per plant were low for RILs and moderate in segregating population in the second year experiment while it was high in the first year experiment (segregating populations). Narrow sense heritability was moderate for this character (Table15).

Genetic advance estimates for primary branches per plant were moderate for RILs and low for segregating populations (Table 16).

4.2.1.9 Number of secondary branches per plant

Number of secondary branches per plant showed moderate broad sense heritability estimates for RILs and segregating populations. Narrow sense heritability was low for this character (Table 15).

Estimates of genetic advance for secondary branches per plant were moderate for RILs but were low in segregating populations (Table 16).

4.2.1.10 Number of pods per plant

The estimates of broad sense heritability for number of pods per plant were moderate for RILs but were relatively high for segregating populations. Narrow sense heritability was moderate for this character (Table 15).

Genetic advance estimates were high and moderate for RILs and segregating populations (Table 16).

4.2.1.11 Number of seeds per plant

Broad sense heritability estimates were moderate for RILs and were relatively high for segregating populations. Narrow sense heritability estimate was moderate for this trait (Table 15).

Number of seeds per plant had relatively high genetic advance for RILs but it was moderate for segregating populations (Table 16).

4.2.1.12 Number of seeds per pod

The estimate of broad sense heritability for number of seeds per pod were high for RILs and second year experiment for segregating populations while it was low in the first year experiment of segregating populations. Narrow sense heritability was moderate for this character (Table 15).

Genetic advance estimates were low for RILs and segregating populations (Table 16).

4.2. 1. 13 Yield per plant

Yield per plant had moderate broad sense heritability in RILs. It was relatively high and moderate in first and second year experiments of segregating populations. The estimate of narrow sense heritability was moderate for this character (Table 15).

Genetic advance estimate obtained high for RILs while was moderate for this character in segregating populations (Table 16).

4.2.1. 14 Leaf size

The estimates for broad sense heritability for leaf size were high in RILs and segregating populations but narrow sense heritability was low for this character (Table 15).

Genetic advance was high for this character for RILs while it was moderate for segregating population (Table 16).

4.2.1.15 Leaf weight

Broad and narrow sense heritability estimates were high for leaf weight for RILs and segregating populations (Table 15).

The estimates of genetic advance were high for RILs and segregating populations (Table 16).

4.2.1.16 Specific leaf weight

Specific leaf weight had high broad sense heritability for RILs and segregating populations. The estimate of narrow sense heritability was also high for this character (Table 15).

Genetic advance was low for RILs while it was very high in segregating populations (Table 16).

4.3.1.17 Seed fibre

Broad sense heritability for seed fibre was high for RILs. Genetic advance was also high in RILs for this character (Tables 15, 16).

4.2.2 Parent-offspring regression

The result of parent-offspring correlation indicated that days to first pod had high heritability (59%) followed by days to first flower (57%) and days to maturity (46%). Plant height and 100-seed weight showed moderate heritability in the first year while it was relatively high in the second year . Very low heritability was observed for seed yield per plant. Moderate heritability was obtained for number of primary branches per plant and number of seeds per pod in the second year whereas these characters had low

heritability in the first year experiment. Heritability estimates were low for number of seeds per plant, number of secondary branches per plant and plant width (Table 17).

4.3 LINKAGE

The joint segregations for each pair of characters was investigated in order to find out the relative position of genes involved. When flower colour and stem pigmentation were studied together, the F_2 population did not show any recombination. It has been considered to be a case of pleiotropy or two genes responsible for the two characters are tightly linked (Table 18).

The χ^2 for joint segregation between flower colour and number of pods per peduncle in first year experiment was significant while in the second year it was non-significant. It appears that the F_2 population did not show a good fit to the expected 3:1 ratio for pod per peduncle as 108 out of 310 plants were killed by fusarium wilt in the first year. Most probably genes for flower colour and number of pods per peduncle are independent from each other (Table 19).

The χ^2 for segregation for flower colour and seed type was significant. Therefore, these results indicate that the genes governing flower colour and seed type are linked (Table 20). However, when seed type ratio (9:6:1) is grouped into two classes desi and kabuli (3:1) recombination values were 27.2 and 31.7 percent in 1998-1999 and 1999-2000 (Table 37). These results indicate one of the genes for flower colour (B) is linked with one of the genes for seed type (St_1, St_2).

Table 17. Generation means and heritability estimates by parent-offspring regression method.

Characters	Mean		Heritability %	Mean		Heritability %
	1997	1998		1998	1999	
	F_2	F_3		F_2	F_3	
Days to first flower	-	-	-	43.6	31	57
Days to first pod	-	-	-	51.6	40.9	59
Days to maturity	-	-	-	91.6	88.6	46
100-seed weight	23.4	17.0	25	15.9	21.3	47
Plant height	45.8	39.2	30	33.3	36.3	44
Primary branches	3.5	2.3	0	2.0	2.8	22
Secondary branches	8.6	4.2	10	6.1	6.6	0
Pods number/plant	79.5	92.8	16	112.3	65.5	7
Seed number/plant	69.7	93.9	13	117.3	86.2	6
Plant width	-	-	-	38.7	30.0	7
Seed/pod	0.9	1.0	7	1.1	1.1	27
Yield/plant	14.7	15.5	3	19.1	14.2	2

- Data for F_2 1997 not available
- 1997 data from F. Tefera/R. Srivastava

Table 18. Joint segregation for flower and stem colours among F_2 plants.

Year	Character	Appropriate ratio	Segregation	obs	exp	χ^2	P
1998-1999	Flower colour	3:1	Pink with pigmented	153	113.6	94.14**	<0.001
	(3:1)		Pink with non-pigmented	0	37.88		
	Stem colour		White with pigmented	0	37.88		
	(3:1)		White with non-pigmented	49	12.63		
1999-2000	Flower colour	3:1	Pink with pigmented	239	172.12	260.53**	<0.001
	(3:1)		Pink with non-pigmented	0	57.38		
	Stem colour		White with pigmented	0	57.38		
	(3:1)		White with non-pigmented	67	19.13		

Table 19. Joint segregation of flower colour and pod number per peduncle in F_2 generation.

Year	Character	Appropriate ratio	Segregation	obs	exp	χ^2	P
1998-1999	Flower colour	9:3:3:1	Pink with single pod	141	113.6	26.69**	< 0.001
	(3:1)		Pink with double pod	12	37.9		
	Pod number/peduncle		White with single pod	41	37.9		
	(3:1)		White with double pod	8	12.6		
1999-2000	Flower colour	9:3:3:1	Pink with single pod	187	172.9	2.72^{ns}	0.44
	(3:1)		Pink with double pod	51	57.7		
	Pod number/peduncle		White with single pod	52	57.7		
	(3:1)		White with double pod	17	19		

Table 20. Joint segregation of flower colour and seed type in F_2 generation.

Year	Character	Appropriate ratio	Segregation	obs	exp	χ^2	p
1998-1999	Flower colour (3:1) Seed type (9:6:1)	27:18:3:9:6:1	Desi with pink	110	85.5	51**	<0.001
			Intermediate with pink	43	56.8		
			Kabuli with pink	0	9.5		
			Desi with white	8	28.4		
			Intermediate with white	35	18.9		
			Kabuli with white	6	3.2		
1999-2000	Flower colour (3:1) Seed type (9:6:1)	27:18:3:9:6:1	Desi with pink	155	126.6	47**	<0.001
			Intermediate with pink	73	84.4		
			Kabuli with pink	9	14.1		
			Desi with white	10	42.2		
			Intermediate with white	44	28.1		
			Kabuli with white	9	4.7		

The joint segregation for flower colour and seed surface within each year showed non-significant χ^2 values (Table 21). The results indicate the gene for flower colour segregating in this cross and the genes for seed roughness are independent from each other.

The χ^2 for the first year joint segregation of number of pods per peduncle and seed surface was significant due to effect of fusarium wilt disease, pod number per peduncle did not give good fit to the expected 3:1 ratio. But results of the joint segregation of these two traits in second year showed these characters are segregating independently (Table 22).

The result of first year for joint segregation for seed type and number of pods per peduncle was significant. Because of number of pods per peduncle due to effects of fusarium wilt did not show a good fit to expected 3:1 ratio, while the results of the joint segregation in the second year experiment, showed independence for these two traits (Table 23).

Joint segregation between stem colour and number of pods per peduncle, seed type and seed surface showed similar results as between flower colour and other characters due to pleiotropic effect of the same gene for the two characters (Tables 24, 25, 26).

The results of joint segregation for flower colour and seed coat colour were significant (Tables 27, 28). It is clear that there are linkages between the genes controlling

Table 21. Joint segregation of flower colour and seed surface in the F_2 generation.

Year	Character	Appropriate ratio	Segregation	obs	exp	χ^2	P
1998-1999	Flower colour (3:1) Seed surface (13:3)	39:13:9:3	Pink with rough	120	123.1	3.14^{ns}	0.37
			Pink with smooth	33	28.4		
			White with rough	44	41		
			White with smooth	5	9.5		
1998-1999	Flower colour (3:1) Seed surface (13:3)	39:13:9:3	Pink with rough	190	182.8	6.81^{ns}	0.08
			Pink with smooth	47	42.2		
			White with rough	58	60.9		
			White with smooth	5	14.1		

Table 22. Joint segregation of pod number per peduncle and seed surface in F_2 generation.

Year	Character	Appropriate ratio	Segregation	obs	exp	χ^2	p
1998-1999	Pod number/peduncle	39:13:9:3	Single pod with rough	147	123.1	22**	<0.001
	(3:1)		Single pod with smooth	35	28.4		
	Seed surface		Double pod with rough	16	41		
	(13:3)		Double pod with smooth	4	9.5		
1999-2000	Pod number/peduncle	39:13:9:3	Single pod with rough	190	182.8	1.597^{ns}	0.66
	(3:1)		Single pod with smooth	42	42.2		
	Seed surface		Double pod with rough	58	60.9		
	(13:3)		Double pod with smooth	10	14.1		

** = Significant at 1% level of probability

Table 23. Joint segregation of seed type and pod number per peduncle in F_2 generation.

Year	Character	Appropriate ratio	Segregation	obs	exp	χ^2	p
1998-1999	Seed type	27:18:3:9:6:1	Desi with single pod	107	85.5	29**	<0.001
	(9:6:1)		Intermediate with single pod	70	56.8		
	pod number/peduncle		Kabuli with single pod	5	9.5		
	(3:1)		Desi with double pod	11	28		
			Intermediate with double pod	8	18.9		
			Kabuli with double pod	1	3.2		
1999- 2000	Seed type	27:18:3:9:6:1	Desi with single pod	125	126.6	1.7^{ns}	0.89
	(9:6:1)		Intermediate with single pod	93	84.4		
	pod number/peduncle		Kabuli with single pod	14	14.1		
	(3:1)		Desi with double pod	40	42.2		
			Intermediate with double pod	24	28.1		
			Kabuli with double pod	4	4.7		

Table 24. Joint segregation for stem colour and pod number per peduncle in F_2 population.

Year	Character	Appropriate ratio	Segregation	obs	exp	χ^2	p
1998-1999	Stem colour (3:1)	9:3:3:1	Pigmented with single pod	141	113.6	26.69**	<0.001
	Pod number/peduncle		Pigmented with double pod	12	37.9		
	(3:1)		Non-pigmented with single pod	41	37.9		
			Non-pigmented with double pod	8	12.6		
1999-2000	Stem colour (3:1)	9:3:3:1	Pigmented with single pod	187	172.9	2.72^{ns}	0.44
	Pod number/peduncle		Pigmented with double pod	51	57.7		
	(3:1)		Non-pigmented with single pod	52	57.7		
			Non-pigmented with double pod	17	19		

Table 25. Joint segregation for stem colour and seed type in F_2 population.

Year	Character	Appropriate ratio	Segregation	obs	exp	χ^2	p
1998-1999	Stem colour (3:1)	27:18:3:9:6:1	Desi with pigmented	110	85.5	51.11**	<0.001
	Seed type (9:6:1)		Intermediate with pigmented	43	56.8		
			Kabuli with pigmented	0	9.5		
			Desi with non-pigmented	8	28.4		
			Intermediate with non-pigmented	35	18.9		
			Kabuli with non-pigmented	6	3.2		
1999-2000	Stem colour (3:1)	27:18:3:9:6:1	Desi with pigmented	155	126.6	47.23**	<0.001
	Seed type (9:6:1)		Intermediate with pigmented	73	84.4		
			Kabuli with pigmented	9	14.1		
			Desi with non-pigmented	10	42.2		
			Intermediate with non-pigmented	44	28.1		
			Kabuli with non-pigmented	9	4.7		

Table 26. Joint segregation for stem colour and seed surface in F_2 population.

Year	Character	Appropriate ratio	Segregation	obs	exp	χ^2	p
1998-1999	Stem colour (3:1) Seed surface (13:3)	39:13:9:3	Pigmented with rough	120	123.1	3.14^{ns}	0.37
			Pigmented with smooth	33	28.4		
			Non-pigmented with rough	44	41		
			Non-pigmented with smooth	5	9.5		
1999-2000	Stem colour (3:1) Seed surface (13:3)	39:13:9:3	Pigmented with rough	190	182.8	6.81^{ns}	0.08
			Pigmented with smooth	47	42.2		
			Non-pigmented with rough	58	60.9		
			Non-pigmented with smooth	5	14.1		

Table 27. Joint segregation for flower colour and seed coat colour in F_2 generation in 1998-1999

Character	Appropriate ratio	Segregation	obs	exp	χ^2	p
Flower colour (3:1)	81:27:27:27:9:9:9:3:27:9:9:9:3:3:3:1	Pink with yellow brown	50	63.9	97.39**	<0.001
		Pink with reddish brown	25	21.3		
		Pink with light brown	31	21.3		
Seed coat colour (27:9:9:9:3:3:3:1)		Pink with brown	36	21.3		
		Pink with yellow beige	2	7.1		
		Pink with dark beige	1	7.1		
		Pink with dark brown	7	7.1		
		Pink with light yellow	1	2.36		
		White with yellow brown	21	21.3		
		White with reddish brown	7	7.1		
		White with light brown	0	7.1		
		White with brown	0	7.1		
		White with yellow beige	12	2.36		
		White with dark beige	8	2.36		
		White with dark brown	0	2.36		
		White with light yellow	1	0.79		

Table 28 Joint segregation for flower colour and seed coat colour in F_2 Plants in 1999-2000.

Character	Appropriate ratio	Segregation	obs	exp	χ^2	p
Flower colour (3:1) Seed coat colour (27:9:9:9:3:3:3:1)	81:27:27:27:9:9:9:3:27:9:9:9:3:3:3:1	Pink with yellow brown	105	94.92	123.12**	<0.001
		Pink with reddish brown	27	31.64		
		Pink with light brown	46	31.64		
		Pink with brown	44	31.64		
		Pink with yellow beige	0	10.55		
		Pink with dark beige	0	10.55		
		Pink with dark brown	13	10.55		
		Pink with light yellow	2	3.52		
		White with yellow brown	21	31.64		
		White with reddish brown	14	10.55		
		White with light brown	0	10.55		
		White with brown	0	10.55		
		White with yellow beige	12	3.5		
		White with dark beige	15	3.5		
		White with dark brown	0	3.5		
		White with light yellow	1	1.17		

flower and seed coat colours. When seed coat colour ratio (27:9:9:9:3:3:3:3:1) is grouped into two classes 27:9:9:3 and 9:3:3:1. On the other hand, when yellow brown, brown, reddish brown and dark brown in one group and light brown, yellow beige, dark beige, light yellow, in other group, recombination values were 28 and 19.3 in 1998-1999 and 1999-2000 experiments respectively (Table 37). This result showed that one of the genes for flower colour (B) is linked with one of the genes for seed coat colour (Ysc, Bsc, Rsc).

The χ^2 for segregation for stem and seed coat colours was significant. Therefore this result indicated that there is linkage between genes controlling stem and seed coat colours (Table 29, 30). When the seed coat colour ratio was (27:9:9:9:3:3:3:3:1) grouped into two classes 27:9:9:3 and 9:3:3:1. On the other hand, when yellow brown, brown, reddish brown and dark brown in were grouped as one class and light brown, yellow beige, dark beige, light yellow, in another class. The recombination values were 28 for 1998-1999 and 19.3 for 1999-2000 experiments (Table 37). This result shows that the gene for stem colour (B) is linked with one of the genes for seed coat colour (Ysc, Bsc, Rsc).

The χ^2 for joint segregation between number of pods per peduncle and seed coat colour was significant for the first year while it was non significant for the second year experiment (Table 31, 32). This is due to were killed 108 plants out of 310 plants in F_2 population by fusarium wilt in the first year and did not give a good fit to the expected 3:1 for pod number per plant in first year experiment. The results of the second year indicate that these traits are segregating independently.

Table 29. Joint segregation for stem colour and seed coat colour in F_2 generation in 1998-1999.

Character	Appropriate ratio	Segregation	obs	exp	χ^2	p
Stem colour (3:1) Seed coat colour (27:9:9:9:3:3:3:1)	81:27:27:27:9:9:9:3:27:9:9:9:3:3:3:1	Pigmented with yellow brown	50	63.9	97.4**	<0.001
		Pigmented with reddish brown	25	21.3		
		Pigmented with light brown	31	21.3		
		Pigmented with brown	6	21.3		
		Pigmented with yellow beige	2	7.1		
		Pigmented with dark beige	1	7.1		
		Pigmented with dark brown	7	7.1		
		Pigmented with light yellow	1	2.36		
		Non-pigmented with yellow brown	21	21.3		
		Non-pigmented with reddish brown	7	7.1		
		Non-pigmented with light brown	0	7.1		
		Non-pigmented with brown	0	7 1		
		Non-pigmented with yellow beige	12	2.36		
		Non-pigmented with dark beige	8	2.36		
		Non-pigmented with dark brown	0	2 36		
		Non-pigmented with light yellow	1	0 79		

Table 30. Joint segregation for stem colour and seed coat colour in F_2 generation in 1999 -2000.

Character	Appropriate ratio	Segregation	obs	exp	χ^2	p
Stem colour (3:1) Seed coat colour (27:9:9:9:3:3:3:1)	81:27:27:27:9:9:9:3:27:9:9:9:3:3:3:1	Pigmented with yellow brown	105	94.92	123**	<0.001
		Pigmented with reddish brown	27	31.64		
		Pigmented with light brown	46	31.64		
		Pigmented with brown	44	31.64		
		Pigmented with yellow beige	0	10.55		
		Pigmented with dark beige	0	10.55		
		Pigmented with dark brown	13	10.55		
		Pigmented with light yellow	2	3.52		
		Non-pigmented with yellow brown	21	31.64		
		Non-pigmented with reddish brown	14	10.55		
		Non-pigmented with light brown	0	10.55		
		Non-pigmented with brown	0	10.55		
		Non-pigmented with yellow beige	12	3.5		
		Non-pigmented with dark beige	15	3.5		
		Non-pigmented with dark brown	0	3.5		
		Non-pigmented with light yellow	1	1.17		

Table 31. Joint segregation for number of pods per peduncle and seed coat colour in F_2 generation in 1998-1999.

Character	Appropriate ratio	Segregation	obs	exp	χ^2	p
Number of pod per peduncle (3:1) Seed coat colour (27:9:9:9:3:3:3:1)	81:27:27:27:9:9:9:3:27:9:9:9:3:3:3:1	Single pod with yellow brown	64	63.9	34.35**	0.003
		Single pod with reddish brown	29	21.3		
		Single pod with light brown	29	21.3		
		Single pod with brown	32	21.3		
		Single pod with yellow beige	11	7.1		
		Single pod with dark beige	8	7.1		
		Single pod with dark brown	7	7.1		
		Single pod with light yellow	2	2.36		
		Double pod with yellow brown	7	21.3		
		Double pod with reddish brown	3	7.1		
		Double pod with light brown	2	7.1		
		Double pod with Brown	4	7.1		
		Double pod with yellow beige	3	2.36		
		Double pod with dark beige	1	2.36		
		Double pod with dark brown	0	2.36		
		Double pod with light yellow	0	0.79		

Table 32. Joint segregation for number of pod per peduncle and seed coat colour in F_2 generation in 1999-2000.

Character	Appropriate ratio	Segregation	obs	exp	χ^2	p
Number of pod per peduncle (3:1) Seed coat colour (27:9:9:9:3:3:3:1)	81:27:27:27:9:9:9:3:27:9:9:9:3:3:3:1	Single pod with yellow brown	96	94.92	5.02^{ns}	0.99
		Single pod with reddish brown	33	31.64		
		Single pod with light brown	38	31.64		
		Single pod with brown	33	31.64		
		Single pod with yellow beige	9	10.55		
		Single pod with dark beige	10	10.55		
		Single pod with dark brown	11	10.55		
		Single pod with light yellow	2	3.52		
		Double pod with yellow brown	30	31.64		
		Double pod with reddish brown	8	10.55		
		Double pod light brown	8	10.55		
		Double pod with brown	11	10.55		
		Double pod with yellow beige	3	3.5		
		Double pod with dark beige	5	3.5		
		Double pod with dark brown	2	3.5		
		Double pod with light yellow	1	1.17		

The estimates of chi-square test for joint segregation between seed surface and seed coat colour were non-significant (Table 33, 34). The results of this investigation revealed seed surface and seed coat colour segregate independently.

The study of interrelationship between seed type and seed coat colour showed that χ^2 for joint segregation was significant (Table 35, 36). This findings indicated that the presence of linkage between genes governing seed type and seed coat colour. When the seed type ratio (9:6:1) is grouped into two classes, desi and kabuli (3:1) and also seed coat colour ratio (27:9:9:9:3:3:3:1) in two classes 27:9:9:3 and 9:3:3:1. On the other hand when it is classified yellow brown, reddish brown, brown and dark brown in one group and light brown, yellow beige, dark beige and light yellow in other group in seed coat colour. The estimate of percent cross over was 35% for 1998-1999 and 1999-2000 experiments (Table 37).

4.4 CORRELATED GENETIC GAIN

The present investigation was carried out to estimate the correlated response to selection for different characters in chickpea. The correlated genetic gain estimates of different traits with seed yield per plant and plot indicated that the number of pods per plant (0.82) followed by number of seeds per plant (0.65) and number of secondary branches per plant (0.51) exhibited high correlated response with seed yield per plant and number of secondary branches per plant (107.80), pod number per plant (54.34), seed yield per plant (38.75), seed number per plant (35.34), days to first pod (29.63), days to 50% flowering (18.80) and days to first flowering (19.21) showed high correlated

Table 33. Joint segregation for seed surface and seed coat colour in F_2 generation in 1998-1999.

Characters	Appropriate ratio	Segregation	obs	exp	χ^2	p
Seed surface (13:3) Seed coat colour (27:9:9:9:3:3:3:1)	351:117:117:117:39:39:39:13:81:27:27:27:9:9:9:3	Rough with yellow brown	66	69.38	21.81^{ns}	0.11
		Rough with reddish brown	22	23.12		
		Rough with light brown	24	23.12		
		Rough with brown	26	23.12		
		Rough with yellow beige	10	7.71		
		Rough with dark beige	7	7.71		
		Rough with dark brown	6	7.71		
		Rough with light yellow	2	2.6		
		Smooth with yellow brown	5	16		
		Smooth with reddish brown	10	5.34		
		Smooth with light brown	7	5.34		
		Smooth with brown	10	5.34		
		Smooth with yellow beige	4	1.78		
		Smooth with dark beige	2	1.78		
		Smooth with dark brown	1	1.78		
		Smooth with light yellow	0	0.59		

Table 34. Joint segregation for seed surface and seed coat colour in F_2 generation in 1999-2000.

Characters	Appropriate ratio	Segregation	obs	exp	χ^2	p
Seed surface (13:3) Seed coat colour (27:9:9:9:3:3:3:1)	351:117:117:117:39:39:39:13:81:27:27:27:9:9:9:3	Rough with yellow brown	115	103	22.84	0.088
		Rough with reddish brown	34	34.34		
		Rough with light brown	31	34.34		
		Rough with brown	33	34.34		
		Rough with yellow beige	8	11.45		
		Rough with dark beige	15	11.45		
		Rough with dark brown	10	11.45		
		Rough with light yellow	2	3.82		
		Smooth with yellow brown	11	23.78		
		Smooth with reddish brown	7	7.93		
		Smooth with light brown	15	7.93		
		Smooth with brown	11	7.93		
		Smooth with yellow beige	4	2.64		
		Smooth with dark beige	0	2.64		
		Smooth with dark brown	3	2.64		
		Smooth with light yellow	1	0.88		

Table 35. Joint segregation for seed type and seed coat colour in F_2 generation in 1998-1999.

Characters	Appropriate ratio	Segregation	obs	exp	χ^2	p
Seed type (9:6:1) Seed coat colour (27:9:9:9:3:3:3:1)	243:81:81:81:27:27:27:9:162:54:54:54 18:18:18:6:27:9:9:9:3:3:3:1	Desi with yellow brown	49	47.94	117.10**	<0.001
		Desi with reddish brown	11	15.98		
		Desi with light brown	29	15.98		
		Desi with brown	22	15.98		
		Desi with yellow beige	2	5.33		
		Desi with dark beige	0	5.33		
		Desi with dark brown	3	5.33		
		Desi with light yellow	2	1.78		
		Intermediate with yellow brown	22	31.96		
		Intermediate with reddish brown	21	10.65		
		Intermediate with light brown	2	10.65		
		Intermediate with brown	14	10.65		
		Intermediate with yellow beige	6	3.55		
		Intermediate with dark beige	9	3.55		
		Intermediate with dark brown	4	3.55		
		Intermediate with light yellow	0	1.18		
		Kabuli with yellow brown	0	5.33		
		Kabuli with reddish brown	0	1.78		
		Kabuli with light brown	0	1.78		
		Kabuli with brown	0	1.78		
		Kabuli with yellow beige	6	0.59		
		Kabuli with dark beige	0	0.59		
		Kabuli with dark brown	0	0.59		
		Kabuli with light yellow	0	0.29		

Table 36. Joint segregation for seed type and seed coat colour in F_2 generation in 1999-2000.

Characters	Appropriate ratio	Segregation	obs	exp	χ^2	p
Seed type (9:6:1) Seed coat colour (27:9:9:9:3:3:3:1)	243:81:81:81:27:27:27:9:162:54:54:54 18:18:18:6:27:9:9:9:3:3:3:1	Desi with yellow brown	97	71.9	160.30**	<0.001
		Desi with reddish brown	15	23.73		
		Desi with light brown	26	23.73		
		Desi with brown	18	23.73		
		Desi with yellow beige	1	7.91		
		Desi with dark beige	0	7.91		
		Desi with dark brown	5	7.91		
		Desi with light yellow	3	2.64		
		Intermediate with yellow brown	28	47.46		
		Intermediate with reddish brown	26	15.82		
		Intermediate with light brown	18	15.82		
		Intermediate with brown	20	15.82		
		Intermediate with yellow beige	2	5.27		
		Intermediate with dark beige	15	5.27		
		Intermediate with dark brown	8	5.27		
		Intermediate with light yellow	0	1.75		
		Kabuli with yellow brown	1	7.91		
		Kabuli with reddish brown	0	2.64		
		Kabuli with light brown	2	2.64		
		Kabuli with brown	6	2.64		
		Kabuli with yellow beige	9	0.87		
		Kabuli with dark beige	0	0.87		
		Kabuli with dark brown	0	0.87		
		Kabuli with light yellow	0	0.29		

Table 37. Joint segregation of characters in the F_2 generation.

Character	Ratio	Year	Segregation				C.O%
			XY[a]	Xy	xY	xy	
Flower colour and seed type	9:3:3:1	1998-1999	132	25	21	24	27.2
		1999-2000	192	32	45	31	31.7
Stem colour and seed type	9:3:3:1	1998-1999	132	25	21	24	27.2
		1999-2000	192	32	45	31	31.7
Flower colour and seed coat colour	9:3:3:1	1998-1999	124	99	21	28	28
		1999-2000	208	29	21	42	19.3
Stem colour and seed coat colour	9:3:3:1	1998-1999	124	99	21	28	28
		1999-2000	208	29	21	42	19.3
Seed type and seed coat colour	9:3:3:1	1998-1999	124	33	21	19	35
		1999-2000	183	40	46	31	35

[a] XY=a Xy=b xY=c xy=d

response with yield per plot (Table 38). Number of seeds per pod (-0.69) and plant height (-0.42) had high and negatively correlation with seed yield per plant. Number of seeds per pod (-43.91) followed by plant width (-40.68), days to maturity (-14.80) and plant height (-10.37) had high and negatively correlation with seed yield per plot (Table 38).

4.5 COHERITABILITY

In this investigation, an attempt was made to know the joint heritability of character pairs in experiment I for quantitative characters by estimates of coheritability.

4.5.1 Days to first flower

The coheritability estimates for different characters with days to first flower showed that plant height (0.998), number of seeds per pod (0.983), number of primary branches per plant (0.974), days to first pod (0.970), days to 50% flowering (0.968), days to maturity (0.968), number of pods per plant (0.924) and number of seeds per plant (0.704) had high coheritability with days to first flower (Table 39).

4.5.2 Days to 50% flowering

The estimate of coheritability for different traits with days to 50% flowering revealed that number of seeds per pod (0.999), plant width (0.994), plant height (0.993), days to first pod (0.992), number of secondary branches per plant (0.991), number of primary branches per plant (0.972), days to first flower (0.968), and number of pods per plant (0.930) had high coheritability with days to 50% flowering. The estimate of

Table 38. Estimates for correlated genetic gain for different characters.

Character	DFF	HT	WID	PDNO	PBR	SBR	SD/PD	SDNO	SDYD	HSDWT	DFP	DFPF	DM	YLD/PT
DFF	-	11.13	1.59	3.85	6.08	6.59	-0.05	0.41	-0.25	-0.51	16.29	15.86	12.48	19.21
HT		-	0.98	-6.08	0.20	0.50	-0.04	-10.63	-0.42	2.20	12.34	12.27	0.32	-10.37
WID			-	2.84	0.09	0.09	0.02	2.64	-0.07	-0.23	1.79	1.69	10.46	-40.68
PDNO				-	7.44	12.67	-3.04	22.88	0.82	-4.27	5.14	3.76	6.30	54.34
PBR					-	0.71	-0.01	6.63	0.29	-1.51	0.36	0.36	0.34	18.30
SBR						-	-0.01	12.35	0.51	-2.09	1.04	0.99	1.00	107.80
SD/PD							-	9.70	-0.69	-2.62	0.06	0.05	-0.05	-43.91
SDNO								-	0.65	-4.98	1.31	0.07	2.26	35.34
SDYD									-	0.05	0.05	0.15	0.11	38.75
HSDWT										-	-0.59	-0.47	-0.51	4.93
DFP											-	16.43	12.77	29.63
DEPF												-	12.67	18.80
DM													-	-14.80

DFF= Days to first flower. HT= Plant height, WID= Plant width, PDNO= Number of pods per plant. PBR= Number of primary branches per plant, SBR= Number of secondary branches per plant. SD/PD= Number of seeds per pod. SDNO= Number of seeds per plant. SDYD= Yield per plant. HSDWT= 100-seed weight. DFP= Days to first pod. DFPF= Days to 50% flowering. DM= Days to maturity

Table 39. Coheritability estimates among different characters.

Character	HT	WID	PDNO	PBR	SBR	SD/PD	SDNO	SDYD	HSDWT	DFP	DFPF	DM	YLD/PT
DFF	0.998	1.124	0.924	0.974	1.008	0.983	0.704	4.113	1.041	0.970	0.968	0.968	1.105
HT	-	0.633	1.626	0.901	0.987	0.990	1.341	-29.2	0.981	0.992	0.993	0.984	-1.02
WID		-	0.230	0.229	0.369	2.031	0.199	-0.04	0.666	1.140	0.994	1.045	-0.53
PDNO			-	0.618	0.694	1.017	0.557	0.163	0.983	0.963	0.930	1.049	0.588
PBR				-	0.642	21.22	0.542	0.201	0.933	0.980	0.972	0.899	0.449
SBR					-	3.271	0.638	0.255	0.847	1.018	0.991	1.032	0.209
SD/PD						-	0.749	0.337	0.924	0.960	0.999	0.972	1.077
SDNO							-	0.169	0.963	0.974	0.201	1.033	0.495
SDYD								-	0.123	1.099	1.263	0.356	0.409
HSDWT									-	0.965	1.002	1.063	0.074
DFP										-	0.992	1.140	0.963
DFPF											-	0.968	1.664
DM												-	0.255

DFF= Days to first flower. HT= Plant height. WID= Plant width. PDNO= Number of pods per plant. PBR= Number of primary branches per plant. SBR= Number of secondary branches per plant. SD PD= Number of seeds per pod. SDNO= Number of seeds per plant. SDYD= Seed yield per plant. HSDWT= 100-seed weight. DFP= Days to first pod. DFPF= Days to 50% flowering. DM= Days to Maturity. YLD PT= Seed yield per plot

coheritability between days to 50% flowering and number of seeds per plant (0.201) was moderate (Table 39).

4.5.3 Days to first pod

Days to first pod exhibited high coheritability with days to 50% flowering (0.992), plant hight (0.992), number of primary branches per plant (0.980), number of seeds per plant (0.974), 100- seed weight (0.965), number of pods per plant (0.963) and number of seeds per pod (0.960) (Table 39).

4.5.4 Days to maturity

Days to maturity had high coheritability with plant height (0.984), number of seeds per pod (0.972), days to first flower (0.968), days to 50% flowering (0.968) and number of primary branches per plant (0.899). The estimate of coheritability between days to maturity and yield per plant (0.356) and plot (0.255) were moderate (Table 39).

4.5.5 100- seed weight

The coheritability estimates of different characters with this trait revealed that number of pods per plant (0.983), plant height (0.981), days to first pod (0.965), number of seeds per plant (0.963), number of primary branches per plant (0.933), number of seeds per pod (0.924), number of secondary branches per plant (0.847) and plant width (0.666) had high coheritability with 100-seed weight. The estimate of coheritability between 100-seed weight and yield per plant (0.123) and yield per plot (0.074) were low (Table 39).

4.5.6 Plant height

Plant height had high coheritability with days to first flower (0.998), days to 50% flowering (0.993), days to first pod (0.992), number of secondary branches per plant (0.987), days to maturity (0.984), 100-seed weight (0.981), number of primary branches per plant (0.901) and plant width (0.633) (Table 39).

4.5.7 Plant width

Plant width showed high coheritability with days to 50% flowering (0.994), 100-seed weight (0.666) and plant height (0.633). This character had moderate coheritability with number of secondary branches per plant (0.369), number of pods per plant (0.230) and number of primary branches per plant (0.229). It had low coheritability with number of seeds per plant (0.199). This trait had high and negative coheritability with yield per plot (-0.53) (Table 39).

4.5.8 Number of primary branches per plant

The number of primary branches per plant had high coheritability with days to first pod (0.980), days to first flower (0.974), days to 50% flowering (0.972), 100-seed weight (0.933), plant height (0.901), number of secondary branches per plant (0.642), number of pods per plant (0.618), number of seeds per plant (0.542) and seed yield per plot (0.449). This character had moderate coheritability with plant width (0.229) and yield per plant (0.201) (Table 39).

4.5.9 Number of secondary branches per plant

The estimate of coheritability of different traits with the character showed that days to 50% flowering (0.991), plant height (0.987), 100-seed weight (0.847), number of pods per plant (0.694), number of primary branches per plant (0.642) and number of seeds per plant (0.638) had high coheritability with number of secondary branches per plant. The observed estimates for coheritability were moderate between this trait and plant width (0.369) and yield per plant (0.255) and seed yield per plot (0.209) (Table 39).

4.5.10 Number of pods per plant

The number of pods per plant exhibited high coheritability with 100-seed weight (0.983), days to first pod (0.963), days to 50% flowering (0.930), days to first flowering (0.924), number of secondary branches per plant (0.694), number of primary branches per plant (0.618), yield per plot (0.588) and number of seeds per plant (0.557). The estimate of coheritability observed moderate between this character and plant width (0.233) (Table 39).

4.5.11 Number of seeds per plant

Coheritability estimate for 100-seed weight (0.963), number of seeds per pod (0.749) , days to first flower (0.704) number of secondary branches per plant (0.638), number of pods per plant (0.577), number of primary branches per plant (0.542), seed yield per plot (0.495) were high with number of seeds per plant. The coheritability estimate of number of seeds per plant with days to 50% flowering (0.201) was moderate (Table 39).

4.5.12 Number of seeds per pod

This character showed high coheritability with days to 50% flowering (0.999), plant height (0.990), days to first flower (0.983), days to maturity (0.972), days to first pod (0.960), 100-seed weight (0.924) and number of seeds per plant (0.749). The coheritability value of number of seeds per pod with yield per plant was moderate (0.337) (Table 39).

4.5.13 Yield per plant

The coheritability estimates for different characters with yield per plant indicated that yield per plot had coheritability with yield per plot (0.409). Days to maturity (0.356), number of seeds per pod (0.377), number of secondary branches per plant (0.255) and number of primary branches per plant (0.201) had moderate coheritability with yield per plant. The coheritability value of yield per plant with number of seeds per plant (0.169) and number of pods per plant (0.163) and 100-seed weight (0.123) were low (Table 39).

4.5.14 Yield per plot

Yield per plot exhibited high coheritability with days to first pod (0.963), number of pods per plant (0.588), number of seeds per plant (0.495) and seed yield per plant (0.409). The coheritability value of yield per plot with days to maturity (0.255) and number of secondary branches per plant (0.209) were moderate. Low coheritability obtained between 100-seed weight and yield per plot. High and negative coheritability was between plant width and yield per plot (-0.53) (Table 39).

4.6 HETEROSIS AND INBREEDING DEPRESSION

The present investigation was undertaken to determine magnitudes of heterosis and inbreeding depression in the cross between ICCV2 and JG62. The performance of F_1 hybrids as compared to their F_2 generation are presented in Table 40.

4.6.1 Days t o first flower

Days to first flower showed positive mid parent heterosis (9.2%) and better parent heterosis (22.85%). The estimate of inbreeding depression for this character also was positive (6.83%) (Table 40).

4.6.2 Days to first pod

The results of this study indicated that days to first pod had positive mid parent heterosis (6.88%) and better parent heterosis (17.45%). The inbreeding depression estimate (2.07%) observed also was positive for this trait (Table 40).

4.6.3 Days to maturity

Positive mid parent heterosis (5.32%) and high parent heterosis (11.95%) observed for days to maturity. The inbreeding depression of this character was positive (2.07%) (Table 40).

Table 40. Mid parent and better parent heterosis and inbreeding depression in ICCV2 x JG62 cross in chickpea

Characters	Mean of parents	High parent	Mean of F_1	Mean of F_2	Mid parent heterosis %	High parent heterosis %	Inbreeding depression %
Days to first flower [a]	41.59	36.97	45.42	42.48	9.2	22.85	6.83
Days to first pod [a]	50.11	45.6	53.56	50.25	6.88	17.45	6.6
Days to maturity [a]	88.75	83.49	93.47	91.63	5.32	11.95	2.07
Pod number/plant	69.06	73.57	113.74	126.38	64.7	54.6	-18.30
Seed yield/plant (g)	17.68	17.86	22.5	23.89	27.26	26	-7.86
Primary branches	2.88	3.45	3.09	2.79	7.29	-10.43	10.42
Secondary branches	5.53	6.75	6.73	6.5	21.7	-0.29	4.16
Seed number/plant	93.95	115.69	128.26	135.02	36.52	10.87	-7.20
Plant width (cm)	35.33	35.74	38.50	41.34	8.97	7.72	-8.03
Plant height (cm)	33.89	39.32	38.63	33.53	13.99	-1.75	15.05
100-seed weight (g)	19.28	23.89	17.46	17.85	-9.4	-26.91	-2.02
Seed number/pod	1.03	1.08	1.19	1.08	15.15	9.40	10.78

[a] early flowering, podding and maturity considered as high parent.

4.6.4 Number of pods per plant

Number of pods per plant had positive and maximum values for heterosis over mid parent (64.7%) and better parent heterosis (54.6%) while inbreeding depression values obtained negative (-18.30%) (Table 40).

4.6.5 Seed yield per plant

The positive values of heterosis (27.26%) and heterobeltiosis (26%) were observed for seed yield per plant. The inbreeding depression estimate was negative for this character (-7.86%) (Table 40).

4.6.6 Number of primary branches per plant

Number of primary branches per plant had positive mid parent heterosis (7.29%) while high parent heterosis was negative (-10.43%). Positive inbreeding depression values (10.42%) obtained for this trait (Table 40).

4.6.7 Number of secondary branches per plant

Positive mid parent heterosis (21.7%) and negative high parent heterosis (-0.29%) were observed for secondary branches per plant. The estimate of inbreeding depression was positive (4.16%) for this character (Table 40).

4.6.8 Number of seeds per plant

The result of this investigation revealed that number of seeds per plant had positive mid parent heterosis (36.52%) and high parent heterosis (10.87%). Inbreeding depression values for this trait was negative (-7.20%) (Table 40).

4.6.9 Plant width

Mid parent heterosis (8.97%) and high parent heterosis (7.72%) were positive for plant width whereas inbreeding depression values for this character was negative (-8.03%) (Table 40).

4.6.10 100-seed weight

Negative values of mid parent heterosis (-9.4%), high parent heterosis (-26.91%) and inbreeding depression (-2.02%) were obtained for 100-seed weight (Table 40).

4.6.11 Number of seeds per pod

The heterotic response for both mid parent heterosis (15.15%) and better parent heterosis (9.40%) were positive for number of seeds per pod. The inbreeding depression estimate was positive (10.78%) for this character (Table 40).

4.6.12 Plant height

Positive mid parent heterosis (13.99%) and negative better parent heterosis (-1.75%) were observed for plant height. Positive inbreeding depression value (15.05%) was obtained for this trait (Table 40).

4.7 SUPERIORITY OF RILs OVER PARENTS

In this study 126 RILs were compared with their parents for 19 characters. 47 percent of the RILs showed higher growth vigour than ICCV2 and 87 percent over JG62 (Table 43). Thirty five and 81 percent of RILs flowered earlier than ICCV2 and JG62. With regard to days to first pod 41 percent were earlier than ICCV2 and 70 percent earlier than JG62. For days to 50% flowering 32 percent and 77 percent were earlier than ICCV2 and JG62 respectively. The estimate of superiority showed 45 percent and 60 percent of RILs matured earlier than ICCV2 and JG62. The result of superiority RILs over parents revealed that 38 and 10 percent of RILs produced more pods than ICCV2 and JG62 respectively. With regard to number of seeds per plant 51 and 12 percent of RILs had more seeds than ICCV2 and JG62 respectively. Nine and 89 percent of RILs had more 100-seed weight than ICCV2 and JG62 respectively. Three percent of RILs had higher yield than ICCV2 and 89 percent more than JG62. Seed fibre contents in RILs were 92 and 2 percent higher than ICCV2 and JG62.

Among the 126 RILs 4 RILs (#s 8, 49, 67 and 108) were superior to ICCV2 for most of yield component characters. RILs number 8, 67 showed 13 and 14 out of 19 characters superior than ICCV2. Also 11 RILs (#s13, 41, 48, 67, 69, 73, 85, 96, 99, 109 and 116) were superior to JG62 for most characters. RII numbers 13, 73, 85 and 109 were superior to JG62 for 13, 14, 13 and 14 out of 19 characters studied.

Table 41. Performance of RILs compared to ICCV2 based on their mean performance in 1998-1999 and 1999-2000.

RILs	EV	DFF	HT	WID	POD	PBR	SBR	SD	SDNO	SDWT	HSD	DFP	DFL	DM	YDP	FR	LS	LW	SPLWT
1	-	-	-	-	-	+	-	+	-			-	-	-	-	+	-	-	+
2	+	+	-	-	-	-	-	+	-			+	-	+	-	-	-	-	+
3	-	+	-	-	-	-	-	+	+			+	+	-	-	-	-	-	+
4	+	-	-	-	-	+	-	+	-			+	-	+	-	+	-	-	+
5	+	-	+	-	+	+	-	+	+			+	-	+	-	+	-	-	+
6	-	-	+	-	-	+	+	+	-			-	-	-	-	+	-	-	+
7	+	-	-	-	-	+	+	+	-			-	-	-	-	+	-	-	+
8	+	+	-	+	+	-	+	+	+			+	+	+	-	+	-	-	+
9	-	+	-	+	-	+	-	+	-			+	+	+	-	+	-	-	+
10	+	-	+	-	-	-	-	+	-			-	-	-	-	+	+	+	+
11	-	-	+	+	-	+	+	+	-			-	-	-	-	+	+	+	+
12	+	+	+	-	-	-	-	+	-			+	+	+	-	+	-	-	-
13	-	-	+	+	+	+	-	+	+			-	-	-	-	+	-	-	+
14	-	-	-	+	+	+	-	+	+			-	-	+	-	+	-	-	+
15	-	-	-	-	+	+	+	+	+			-	-	+	-	+	-	-	+
16	-	-	+	+	+	+	+	+	+			-	-	-	-	+	-	-	+
17	+	-	+	+	-	+	+	+	-			-	-	-	-	+	-	-	-
18	-	-	+	-	-	-	+	+	-			-	-	-	-	+	+	+	+
19	-	-	+	+	+	+	+	+	+			-	-	-	-	+	-	-	+
20	-	-	+	-	+	+	+	+	+			-	-	-	-	+	-	-	+
21	+	-	+	-	-	+	+	+	-			-	-	-	-	+	-	+	+
22	+	+	-	-	-	-	-	+	-			+	+	+	-	+	-	-	+
23	+	+	-	+	-	+	-	+	-			+	+	+	-	+	-	-	+
24	+	+	+	-	-	+	-	+	-			+	+	+	-	+	-	-	-
25	+	+	-	-	-	-	-	+	-			+	+	+	-	+	-	-	+
26	-	+	-	-	+	-	-	+	+			+	+	+	-	+	-	-	+
27	-	-	+	-	-	+	+	+	-			-	-	-	-	+	+	+	+
28	-	-	+	+	+	+	+	+	+			-	-	-	-	+	-	-	+
29	+	-	+	+	-	+	-	-	-			-	-	-	-	+	+	+	+
30	+	-	+	+	-	+	-	-	-			-	-	-	-	+	+	+	+
31	-	+	-	+	+	+	-	+	+			+	+	+	-	+	-	-	+
32	-	+	-	-	+	-	-	+	+			+	+	+	-	+	-	-	+
33	-	+	-	-	+	+	-	+	+			+	+	+	-	+	-	-	+
34	+	+	-	-	-	-	-	+	-			+	+	+	-	+	-	-	+
35	-	-	+	+	+	+	+	+	+			-	-	-	-	+	-	-	+
36	-	-	-	+	+	-	+	+	+			-	-	-	-	+	-	-	+
37	+	-	+	-	-	+	-	+	-			-	-	-	-	+	-	+	+

\+ Superiority of RILs over ICCV2
\- Superiority of ICCV2 over RILs
0 Equal to ICCV2

Contd..

RILs	EV	DFF	HT	WID	POD	PBR	SBR	SD	SDNO	SDWT	HSD	DFP	DFL	DM	YDP	FR	LS	LW	SPLWT
38	-	-	+	-	+	+	+	+	+	-	-	-	-	-	-	+	-	-	+
39	-	-	+	+	+	+	+	+	+	-	-	-	-	-	-	+	-	-	+
40	+	+	-	-	-	-	-	+	-	-	-	+	+	+	-	-	-	+	+
41	+	+	+	+	-	-	-	+	-	-	-	+	+	+	-	-	+	+	+
42	+	+	-	-	+	-	+	+	+	-	-	+	+	+	-	+	-	-	+
43	-	-	+	+	+	+	+	+	+	-	-	-	-	-	-	+	-	-	+
44	+	-	+	-	-	+	+	+	-	-	+	-	-	-	-	+	+	+	+
45	+	+	-	+	-	+	-	+	-	-	-	+	+	+	-	-	-	-	+
46	+	+	+	-	-	-	-	+	-	-	-	+	+	+	-	-	-	-	-
47	-	+	-	-	-	-	-	+	+	-	-	+	+	+	-	+	-	-	+
48	+	0	+	+	-	-	-	+	-	-	-	+	-	+	-	+	+	+	+
49	+	+	+	+	-	-	-	+	-	-	-	+	+	+	-	+	+	+	+
50	+	-	+	-	-	-	-	+	-	-	-	+	-	-	-	+	+	+	+
51	+	-	+	+	-	+	-	+	-	-	-	-	-	+	-	+	+	+	+
52	-	+	-	-	+	-	-	+	+	-	-	+	+	+	-	+	-	-	+
53	-	-	+	-	-	+	-	+	-	-	-	-	-	-	-	+	-	-	+
54	-	-	+	+	+	+	+	+	+	-	-	-	-	-	-	+	-	-	+
55	+	-	+	+	-	+	+	-	-	-	-	-	-	-	-	+	-	-	-
56	+	-	+	+	-	+	-	0	-	-	-	-	-	-	-	+	-	-	+
57	+	-	+	+	-	+	+	+	-	-	-	-	-	-	-	-	+	+	+
58	-	+	-	-	+	+	-	+	+	-	-	+	+	+	-	+	-	-	+
59	-	-	+	+	+	+	+	+	+	+	-	-	-	-	-	+	-	-	+
60	-	-	+	-	-	+	+	+	+	-	-	-	-	-	-	+	-	-	+
61	+	-	+	+	-	+	+	+	-	-	-	-	-	-	-	+	-	-	-
62	-	-	+	+	-	+	+	+	-	-	-	-	-	-	-	+	-	-	+
63	-	-	+	-	-	+	+	+	-	-	-	-	-	-	-	+	-	-	+
64	+	+	-	-	-	-	-	+	-	-	-	+	+	+	-	+	-	-	+
65	+	-	+	-	-	+	-	-	-	-	-	-	-	-	-	+	+	+	+
66	+	-	+	+	-	+	-	+	-	-	+	-	-	-	-	+	-	+	+
67	+	+	+	+	-	+	-	+	-	-	+	+	+	+	-	+	+	+	+
68	+	-	+	-	-	-	-	+	-	-	+	+	-	-	-	+	+	+	+
69	+	-	+	+	-	-	-	+	-	-	+	-	-	+	-	+	+	+	+
70	-	-	+	-	+	+	+	+	+	-	-	-	-	-	-	+	-	-	+
71	-	-	+	-	+	+	+	+	+	+	-	-	-	-	-	+	-	-	+
72	-	-	+	+	-	+	+	+	-	-	-	-	-	-	-	+	+	+	+
73	+	-	+	+	+	+	+	-	+	+	-	-	-	-	-	+	-	-	-
74	+	+	-	-	+	+	-	+	+	-	-	+	+	+	-	+	-	-	+
75	-	+	-	-	+	+	-	+	+	-	-	+	+	+	-	+	-	-	+

Contd..

RILs	EV	DFF	HT	WID	POD	PBR	SBR	SD	SDNO	SDWT	HSD	DFP	DFL	DM	YDP	FR	LS	LW	SPLWT
76	+	+	+	-	-	-	-	+	-					+	-	+	-	-	-
77	+	+	-	-	-	-	-	+	-					+	-	+	-	+	+
78	-	+	-	+	-	-	-	+	+					+	-	+	-	-	+
79	+	-	+	-	-	-	-	+	-					+	-	+	+	+	+
80	-	-	-	-	+	+	+	+	+					-	-	+	-	-	+
81	-	+	-	-	+	+	+	+	+					-	-	+	-	-	+
82	-	-	+	-	+	+	+	+	+					-	-	+	-	-	+
83	+	+	+	+	+	+	+	+	+			+	+	-	-	-	-	-	-
84	-	+	-	+	-	+	-	+	+			+	+	+	-	+	-	-	+
85	-	-	+	+	+	+	+	+	+					-	-	+	-	-	+
86	-	-	-	-	-	+	-	+	+					+	-	+	-	-	+
87	-	+	-	-	+	+	+	+	+					+	-	+	-	-	+
88	-	-	-	-	-	-	-	+	+					+	-	-	-	-	+
89	-	-	+	+	+	+	+	+	+					-	-	+	-	-	-
90	-	+	-	+	+	+	-	+	+					-	-	+	-	-	+
91	+	-	+	-	-	+	+	+	-					-	-	+	+	+	+
92	+	-	+	+	-	+	+	+	-					-	-	+	-	-	-
93	-	-	-	-	+	+	+	+	+					-	-	+	-	-	+
94	+	-	+	-	-	+	+	-	-					-	-	+	-	-	+
95	-	-	-	-	-	+	+	+	+					-	-	+	-	-	+
96	-	-	+	+	+	+	0	+	+					-	-	+	-	-	+
97	-	+	-	-	-	+	-	+	+					+	-	+	-	-	+
98	-	-	+	-	-	+	-	+	-					-	-	+	+	+	+
99	+	+	-	+	-	-	-	+	-					+	-	+	-	-	+
100	-	-	+	-	-	+	+	-	-					-	-	+	-	-	-
101	+	-	+	+	-	-	-	+	-					+	-	+	-	-	+
102	-	-	+	-	+	+	+	+	+					-	-	+	-	-	+
103	-	+	-	-	+	+	-	+	+					+	-	+	-	-	+
104	-	-	-	-	-	+	+	+	+					+	-	+	-	-	+
105	-	+	-	+	-	+	+	+	+					+	-	+	-	-	+
106	+	-	+	+	-	-	-	+	-					+	-	+	+	+	+
107	+	-	-	+	+	-	-	+	+					+	-	+	-	-	+
108	+	+	+	+	+	-	-	+	+					+	-	+	+	+	+
109	-	-	+	+	+	+	+	+	+					-	-	+	-	-	+
110	-	-	+	+	+	+	+	+	+					-	-	+	-	-	+
111	-	-	+	-	+	+	+	+	+					-	-	+	-	-	+
112	-	-	+	-	-	+	-	+	-					-	-	+	-	-	-
113	+	-	+	-	-	-	-	+	+					+	-	+	-	-	+
114	-	-	-	-	-	+	-	+	+					+	-	+	-	-	+

Contd..

RILs	EV	DFF	HT	WID	POD	PBR	SBR	SD	SDNO	SDWT	HSD	DFP	DFL	DM	YDP	FR	LS	LW	SPLWT
115	-	-	+	+	+	+	+	+	+	-	-	-	-	-	-	+	-	-	+
116	+	+	-	+	-	-	-	+	+	-	-	+	+	+	-	+	-	-	+
117	+	+	-	-	-	-	-	-	-	-	+	+	+	+	-	+	+	-	-
118	+	+	-	-	-	+	-	+	-	-	-	+	+	+	-	+	-	-	+
119	+	-	+	-	-	+	+	+	-	-	-	-	-	-	-	+	+	+	+
120	+	-	+	-	-	+	+	-	-	-	-	+	-	-	-	+	-	-	+
121	+	-	+	-	-	+	-	-	-	-	-	-	-	-	-	+	-	-	-
122	-	-	-	-	-	+	-	+	-	-	-	-	-	+	-	+	-	-	+
123	-	+	-	-	-	+	-	+	+	-	-	+	-	+	-	+	-	-	+
124	-	-	+	+	+	+	+	+	+	-	-	-	-	-	-	+	-	-	-
125	+	-	-	+	+	+	-	-	+	-	-	-	-	-	-	+	-	-	+
126	-	-	+	+	-	+	+	+	+	-	-	-	-	-	-	+	-	-	+

EV= Early vigour, DFF= Days to first flower, HT= Plant height, WID= Plant width, POD= Number of pods per plant, PBR= Number of primary branches per plant, SBR= Number of secondary branches per plant, SD= Number of seeds per pod, SDNO= Number of seeds per plant, SDYD= Yield per plant, HSD= 100-seed weight, DFP= Days to first pod, DFL= Days to 50% flowering, DM= Days to maturity, YDP= Yield per plot, FR= Seed fibre, LS= Leaf Size, LW= Leaf weight., SPLWT= Specific leaf weight

Table 42. Performance of RILs compared to JG62 based on their mean performance in 1998-1999 and 1999-2000.

RILs	EV	DFF	HT	WID	POD	PBR	SBR	SD	SDNO	SDYD	HSD	DFP	DFL	DM	YDP	FR	LS	LW	SPLWT
1	+	+	-	-				-	-	-	+	+	+	+	-	-	+	+	+
2	+	+	-	-				+	-	-	+	+	+	+	+	-	+	+	+
3	+	+	-	-				+	-	-	+	+	+	+	-	-	+	+	+
4	+	+	-	-				+	-	+	+	+	+	+	-	-	+	+	+
5	+	+	-	-				+	-	+	+	+	+	+	-	-	+	+	+
6	0	-	-	-				-	-	-	+	-	-	-	-	-	-	-	+
7	+	+	-	-				-	-	+	+	+	+	+	+	-	+	+	+
8	+	+	-	+				-	-	+	+	+	+	+	-	-	+	+	+
9	+	+	-	+				+	-	-	+	+	+	+	-	-	+	+	+
10	+	+	+	-				-	-	-	+	+	+	+	-	-	+	+	+
11	+	-	+	+				+	-	-	+	-	-	-	-	-	+	+	+
12	+	+	-	-				+	-	+	+	+	+	+	-	-	+	+	+
13	+	+	+	+				+	+	+	+	+	+	-	-	-	+	+	+
14	-	+	-	+				+	-	-	+	+	+	+	-	-	+	+	+
15	+	+	-	-				+	-	-	-	+	+	+	-	-	+	+	+
16	-	+	-	+				-	+	-	-	+	+	-	-	-	-	-	+
17	+	-	-	+				-	-	+	+	-	0	-	-	-	+	+	+
18	+	-	+	-				-	-	-	+	-	-	-	-	-	+	+	+
19	+	+	+	+				+	+	-	-	-	+	-	-	-	-	+	+
20	+	+	+	-				+	-	-	+	-	-	-	-	-	-	+	+
21	+	-	+	-				+	-	-	+	-	-	-	-	-	+	+	+
22	+	+	-	-				-	-	-	+	+	+	+	-	-	+	+	+
23	+	+	-	+				+	-	-	+	+	+	+	-	-	+	+	+
24	+	+	-	-				-	-	+	+	+	+	+	-	-	+	+	-
25	+	+	-	-				+	-	-	+	+	+	+	-	-	+	+	+
26	+	+	-	-				+	-	+	+	+	+	+	-	-	-	-	+
27	+	-	+	-				-	-	-	+	-	-	-	-	-	+	+	+
28	+	-	+	+				+	+	+	+	-	-	-	-	-	+	+	+
29	+	+	+	+				-	-	-	+	+	+	-	-	-	+	+	+
30	+	+	+	+				-	-	-	+	+	+	-	-	-	+	+	+
31	+	+	-	+				+	-	+	+	+	+	+	-	-	-	+	+
32	+	+	-	-				+	-	+	+	+	+	+	-	-	+	+	+
33	+	+	-	-				+	-	-	+	+	+	+	-	-	+	+	+
34	+	+	-	-				-	-	-	+	+	+	+	-	-	+	+	+
35	0	+	-	+				+	+	+	+	-	+	-	-	-	-	+	+
36	0	+	-	+				-	+	+	-	+	+	+	-	-	-	-	+
37	+	+	+	-				+	-	-	+	-	-	-	-	-	+	+	+

+ Superiority of RILs over JG62
- Superiority of JG62 over RILs
0 Equal to JG62

Contd..

RILs	EV	DFF	HT	WID	POD	PBR	SBR	SD	SDNO	SDYD	HSD	DFP	DFL	DM	YDP	FR	LS	LW	SPLWT
38	0	+	+	-	-	-		-	-	-	+	-	+	-	-	-	+	+	+
39	+	+	-	+	+	+		-	+	+	-	+	+	-	-	-	-	-	+
40	+	+	-	-	-	-		+	-	-	+	+	+	+	-	-	+	+	+
41	+	+	-	+	-	-		+	-	+	+	+	+	+	-	-	+	+	+
42	+	+	-	-	-	-		-	-	+	+	+	+	+	-	-	+	+	+
43	0	-	+	+	-	+		+	+	+	+	-	-	-	-	-	-	+	+
44	+	-	+	-	-	-		-	-	-	+	-	-	-	-	-	+	+	+
45	+	+	-	+	-	-		-	-	-	+	+	+	+	-	-	+	+	+
46	+	+	-	-	-	-		-	-	-	+	+	+	+	-	-	+	+	-
47	+	+	-	-	-	-		+	-	-	+	+	+	+	-	-	-	-	+
48	+	+	-	+	-	-		+	-	-	+	+	+	+	-	+	+	+	+
49	+	+	-	+	-	-		+	-	-	+	+	+	+	-	-	+	+	+
50	+	+	-	-	-	-		+	-	-	+	+	+	+	-	-	+	+	+
51	+	+	-	+	-	-		-	-	+	+	+	+	+	-	-	+	+	+
52	+	+	-	-	-	-		+	-	-	-	+	+	+	-	-	-	-	+
53	+	-	+	-	-	-		-	-	-	+	-	-	-	-	-	+	+	+
54	0	-	-	+	+	-		-	+	-	-	-	-	-	-	-	-	-	+
55	+	+	+	+	-	+		-	-	+	+	-	+	-	-	-	+	+	+
56	+	+	+	+	-	-		-	-	+	+	+	+	-	-	-	+	+	+
57	+	-	+	+	-	-		+	-	-	+	-	-	-	-	-	+	+	+
58	+	+	-	-	-	-		+	-	-	+	+	+	+	-	-	-	-	+
59	+	+	-	+	+	-		-	+	+	+	+	+	-	-	-	-	-	+
60	-	-	+	-	-	+		+	-	-	-	-	-	-	-	-	-	-	+
61	+	+	+	+	-	-		-	-	-	+	+	+	-	-	-	+	+	-
62	+	-	+	+	-	+		-	-	-	+	-	-	-	-	-	+	+	+
63	+	+	+	-	-	+		-	-	-	+	-	-	-	-	-	+	+	+
64	+	+	-	-	-	-		+	-	+	+	+	+	+	-	-	+	+	+
65	+	-	+	-	-	-		-	-	-	+	-	-	-	-	-	+	+	+
66	+	+	+	-	-	+		-	-	-	+	-	+	-	-	-	+	+	+
67	+	+	-	+	-	-		+	-	+	+	+	+	+	-	-	+	+	+
68	+	+	+	-	-	-		-	-	+	+	+	+	+	-	-	+	+	+
69	+	+	+	+	-	-		+	-	-	+	+	+	+	-	-	+	+	+
70	-	-	+	-	-	+		+	-	-	-	-	-	-	-	-	-	+	+
71	+	+	-	-	+	+		-	+	+	+	+	+	-	+	-	-	-	+
72	+	-	+	+	-	-		+	-	-	+	-	-	-	-	-	+	+	+
73	+	+	+	+	+	+		-	-	+	+	+	+	+	-	-	+	+	+
74	+	+	-	-	-	-		+	-	+	+	+	+	+	-	-	+	+	+
75	+	+	-	-	-	-		+	-	-	+	+	+	+	-	-	-	-	+

Contd..

RILs	EV	DFF	HT	WID	POD	PBR	SBR	SD	SDNO	SDYD	HSD	DFP	DFL	DM	YDP	FR	LS	LW	SPLWT
76	+	+	-	-				-	-	+	+	+	+	+	-	-	+	+	-
77	+	+	-	-				-	-	+	+	+	+	+	-	-	+	+	+
78	+	+	-	+				+	-	-	+	+	+	+	-	-	+	+	+
79	+	+	-	-				+	-	-	+	+	+	+	-	-	+	+	+
80	-	+	-	-				-	+	-	-	+	+	+	-	-	-	-	+
81	+	+	-	-				+	-	-	-	+	+	+	-	-	-	-	+
82	+	+	+	-				-	-	+	+	-	+	-	+	-	-	+	+
83	+	+	-	+				-	-	+	+	+	+	-	-	-	+	+	-
84	+	+	-	+				+	-	-	+	+	+	+	-	-	+	+	+
85	0	+	-	+				+	+	+	+	+	+	-	-	-	-	+	+
86	+	+	-	-				+	-	-	-	+	+	+	-	-	+	+	+
87	+	+	-	-				-	-	-	+	+	+	+	-	-	-	-	+
88	+	+	-	-				+	-	+	+	+	+	+	-	-	+	+	+
89	+	+	-	+				-	-	-	+	-	+	-	-	+	0	-	-
90	+	+	-	+				-	-	-	+	+	+	+	-	-	-	+	+
91	+	-	+	-				-	-	-	+	-	-	-	-	-	+	+	+
92	+	-	+	+				-	-	-	+	-	-	-	-	-	+	+	-
93	0	+	-	-				-	+	-	-	+	+	+	-	-	-	-	+
94	+	+	+	-				-	-	-	+	-	-	-	-	-	+	+	+
95	0	-	+	+				-	-	-	+	+	+	+	-	-	-	-	+
96	+	+	-	+				-	-	+	+	+	+	+	-	-	+	+	+
97	+	+	-	-				+	-	-	+	+	+	+	-	-	-	-	+
98	+	+	-	-				+	-	-	+	+	+	+	-	-	+	+	+
99	+	+	-	+				+	-	+	+	+	+	+	-	-	+	+	+
100	+	-	+	-				-	-	-	+	-	-	-	-	-	+	+	-
101	+	+	-	-				-	-	+	+	+	+	+	-	-	+	+	+
102	+	+	-	-				-	-	+	+	-	-	-	-	-	-	-	+
103	+	+	-	-				+	-	-	+	+	+	+	-	-	-	+	+
104	+	+	-	-				+	-	-	+	+	+	+	-	-	+	+	+
105	+	+	-	+				+	-	-	+	+	+	+	-	-	+	+	+
106	+	+	-	+				-	-	-	+	+	+	+	-	-	+	+	+
107	+	+	-	+				-	-	+	+	+	+	+	-	-	+	+	+
108	+	+	-	+				-	-	+	+	+	+	+	-	-	+	+	+
109	+	+	+	+				+	-	+	+	+	+	-	+	-	+	+	+
110	+	+	-	+				-	-	+	+	-	+	-	+	-	-	+	+
111	0	-	+	-				+	-	-	+	-	-	-	-	-	+	+	+
112	+	-	+	-				-	-	-	+	-	0	-	-	-	+	+	-
113	+	+	-	-				+	-	+	+	+	+	+	-	-	+	+	+
114	+	+	-	-				+	-	-	+	+	+	+	-	-	+	+	+

Contd..

RILs	EV	DFF	HT	WID	POD	PBR	SBR	SD	SDNO	SDYD	HSD	DFP	DFL	DM	YDP	FR	LS	LW	SPLWT
115	+	+	-	+	-	+	-	-	-	+	+	+	+	-	-	-	+	+	+
116	+	+	-	+	-	-	-	+	-	+	+	+	+	+	-	-	+	+	+
117	+	+						-	-	-	+	+	+	+	-	-	+	+	+
118	+	+						+	-	-	+	+	+	+	-	-	-	+	+
119	+	+						-	-	-	+	+	+	+	-	-	+	+	+
120	+	+						-	-	-	+	+	+	+	-	-	+	+	+
121	+	-						-	-	-	+	-	-	-	-	-	+	+	-
122	+	+						+	-	-	+	+	+	+	-	-	+	+	+
123	+	+						+	-	-	+	+	+	+	-	-	-	+	+
124	0	+						-	+	+	-	-	+	-	-	-	-	-	-
125	+	+						-	-	+	+	+	+	+	-	-	+	+	+
126	+	0						+	-	+	+	-	-	-	+	-	+	+	+

EV= Early vigour, DFF= Days to first flower, HT= Plant height, WID= Plant width, POD= Number of pods per plant, PBR= Number of primary branches per plant, SBR= Number of secondary branches per plant, SD= Number of seeds per pod, SDNO= Number of seeds per plant, SDYD= Yield per plant, HSD= 100-seed weight, DFP= Days to first pod, DFL= Days to 50% flowering, DM= Days to maturity, YDP= Yield per plot, FR= Seed fibre, LS= Leaf Size, LW= Leaf weight., SPLWT= Specific leaf weight

Table 43. Percent superiority of RILs over ICCV2 and JG62.

Character	ICCV2	JG62
Early growth vigour	47	87
Days to first flower	35	81
Days to first pod	41	70
Days to 50% flowering	32	77
Days to maturity	45	60
Plant height	60	33
Plant width	44	42
Number of pods/plant	38	10
Primary branches/plant	71	25
Secondary branches/plant	44	3
Number of seeds/pod	90	50
Number of seeds/plant	51	12
Yield/plant	3	38
100-seed weight	9	89
Yield/plot	0	5
Seed fibre	92	2
Leaf size	20	72
Leaf weight	23	83
Specific leaf weight	87	91

Discussion

CHAPTER V

DISCUSSION

The inheritance and linkage relationships of seven qualitative and 18 quantitative characters were determined in chickpea using the data for F_2, F_3, BC_1P_1, BC_1P_2, generations and RILs of the chickpea cross ICCV2 and JG62. The results and their implications are discussed here.

5.1 INHERITANCE OF QUALITATIVE TRAITS

5.1.1 Flower colour

The flower colour is an important trait because it is a reliable morphological marker in chickpea. The two main types of chickpea desi and kabuli can usually be distinguished by their flower colours. Kabuli types always have white flower colour. The results indicated that the difference in pink and white colours is controlled by a single gene is dominant to white colour. These results confirmed monogenic behaviour for flower colour suggested by Pimplikar (1943), Khan *et al.* (1950), Bhapkar and Patil (1962, 1963), Tendulkar (1965), Khosh-khui and Niknejad (1971a), and Gil and Cubero (1993) reported pink flower is dominant over white flower and controlled by single gene. Whereas Khan and Akhtar (1934), Kadam *et al.* (1941), Pawar and Patil (1979), Ghatge (1994) and Kumar (1997) reported that two genes control this character. Ayyar and Balasubramanian (1936), D'Cruz and Tendulkar (1970), Phadnis (1976), Vijalakshmi Satya (1998) and Kumar *et al.* (2000) suggested trigenic inheritance for this character. Ayyar and Balasubramanian (1936) suggested gene symbols C,B, P for this trait. They suggested when all the three genes C, B, P are present in the dominant condition, pink colour is

produced. Flower colour is blue when C and B are in dominant condition and white colour when either B or C is in homozygous recessive form. Thus the segregation for one, two or three gene pairs is based upon the genetic constitution of the parents. Based on the gene symbols suggested by Ayyar and Balasubramanian, and those of Pimplikar (1943), Khan *et al.* (1950), Bhapkar and Patil (1962, 19630), Tendulkar (1965), Khosh- khui and Niknejad (1971a), Gil and Cubero (1993) and in the present study either gene C or B was segregating. Kumar *et al.* (2000) showed that both ICCV2 and JG62 produce pink flower when crossed to a blue flowered line T 39-1 the genotype of which was determined as ppBBCC. Therefore the genotype of ICCV2 is PPBBcc or PPbbCC and that of JG62 is PPBBCC. According to their results ICCV2 when crossed to another white flowered line RS11 produces pink flower colour. They determined the RS11 genotype is PPBBcc. Therefore the ICCV2 genetic constitution should be PPbbCC.

5.1.2 Stem colour

The use of markers in crop varieties gives an added advantage in characterizing and in maintaining their genetic purity. In chickpea purple foliage could be used as a marker to identify true hybrids between desi and its inter varietal crosses (Sandhu *et al.*, 1993). In some varieties such as ICC5763, pigmentation depends upon direct sunlight, and no anthocyanin synthesis takes place unless the plants are exposed to sunlight (Mathur, 1989). In other pigmented lines such as line, 6071, pigmentation remains stable from seedling stage to plant maturity (Sandhu *et al.*, 1993). Mathur (1989) concluded that the whole spectrum of visible light (400-700 A^{o}) is required to produce pigmentation.

The results of the present study revealed that stem colour is controlled by single gene and pigmentation is dominant to non-pigmentation. Similar results were also obtained by Argikar (1955), Argikar and D'Cruz (1963), Tendulkar (1965), More (1976) and Tafera (1998). Whereas Pawar and Patil (1979), Ghatge *et al.* (1985), Ghatge (1994) and Mathur (1998) observed a ratio 9 purple: 7 green for stem colour and they reported that the pigmented stem colour was dominant over green stem.

Some genotypes clearly differ from one another, for their pigmentation. Some are slightly pigmented. The pigmented will appear clearly on pedicel at the time of flowering. Therefore, different reports for the number of genes controlling stem colour may be due to the stage at which the pigmented was recorded and also due to different genetic constitutions of the parents used in studies.

5.1.3 Pod number per peduncle

Flowers are borne singly on pedicels subtended by single peduncles in the axils of the leaves in chickpea. The normal condition is one pedicel (and flower) per peduncle but double- flowered genotypes are quite common (Smithson *et al.*, 1985). The proportion of double-flowers which set fruit vary with genotypes and environment but, when well expressed, the 'double-podded' character contributes to slightly improved and more stable yield (Smithson *et al.*, 1985).

The results obtained in this study indicated single gene control for number of pods per peduncle. This result agrees with those of several workers (Khan and Akhtar, 1934;

Ahmad, 1964; Singh, 1965; Yadav *et al.*, 1978, Singh and Rheenen, 1994 and Kumar *et al.* 2000) who found a single recessive gene controlling the double podded character.

The potential for a significant increase in pods and yield in double-podded genotype has been emphasized, although the gene could also have a negative effect on seed size which is an important character, especially in western Mediterranean countries (Singh, 1987). Sheldarke *et al.* (1978) obtained 6-13% higher yield in double podded plants compared with single-podded plants of the same genotype, in which the second flower had been removed. Singh and van Rheenen (1989) found the double-podded character to have only a stability effect on grain yield under a condition of late-sowing. Srivastava (1998) found that the gene for double podding exhibits unstable penetrance and variable expressivity in the same cross in this study. The penetrance as well as expressivity of the gene for double podding was highly influenced by environmental conditions. He also reported that high number of double pods can contribute significantly towards increased seed yield when the double podded nature is well expressed.

In the present study there was no effect of double pod and single pod per peduncle on yield and yield components. This result indicate the absence of significant differences for number of pods per plant, number of seeds per plant, 100-seed weight and seed yield per plant in single and double-podded genotypes. However, the number of seeds per pod differed significantly at 1% level in F_2 in the second year. Although number of seeds per pod were not significant difference in F_2 generation for first year and RILs but number of seeds per pod in single podded were more than double pod and number of pods per plant in

double podded genotypes were more than single podded genotypes (Tables 6.7). Therefore this may be due to double pod genotypes sink for number of pods per peduncle and single pod genotypes has more capacity sink for number of seeds per pod. Knight (1987) did not find any general differences in yield between single and double-podded F_4 lines having three different genetic backgrounds. Rubio *et al.* (1998) reported that the gene for double-podding had a positive effect on the stability of yield and was not linked to any other gene responsible for seed size in chickpea. However, the results obtained in this investigation suggest that the 'double pod' character does not affect significantly seed size and seed yield. Lack of significant effect of double pod character on seed yield may be due to the absence of significant differences between the two parents for seed yield.

5.1.4 Seed surface

Present investigation showed that seed surface was controlled by two pairs of genes as F_2 ratio of 13:3 was observed for rough and smooth surface. The result can be explained by dominant inhibitory epistasis. Singh and Ekbote (1936); Balasubramanian (1937); More and D'Cruz (1970) and Deshmukh (1972) found that roughness and smoothness of the testa were governed by a single gene. Later, Tendulkar (1965), Deshmukh *et al.* (1972) and More and D'Cruz (1976), More (1976), Pawar and Patil (1979) reported two complementary loci (*Rsa* and *Rsb*) for this trait.

Rough and smooth seed surfaces are distinguished from one another clearly but the intermediate grades are sometime difficult to determine. Thus, different ratioes for this character may be caused by this problem or may be due to the use of parents with different

genetic constitution. On the basis of the segregation pattern in the cross, the genomic symbols could be designated as Sr_1Sr_1 Sr_2Sr_2, $sr_1sr_1Sr_2Sr_2$ and $sr_1sr_1sr_2sr_2$ for the seed rough surface and $Sr_1Sr_1sr_2sr_2$ for smooth surface.

5.1.5 Seed type

Two main types of chickpea are recognized desi and kabuli. There are price differences between the two types. Hawtin and Singh (1980) reported that there is a fairly clear distinction between the two types, which is generally agreed upon by breeders but it is difficult to define systematically. A third group with pea shape and a beak, is also found in the world collections. It is comparatively rare in local markets. Such round-seeded types (which may be any colour from light beige to black, including green) are generally designed "intermediate" or "pea " type by breeders. Knights (1980) found pea type (intermediate) dominant to both desi and kabuli types and desi was dominant to kabuli. He concluded small number of segregation classes is under the control of only a few major genes for seed type character. The F_2 segregations from desi x kabuli crosses generally produces up to five classes namely pea, desi, kabuli, and the two intermediate forms (pea-desi and pea-kabuli). Frequencies of these classes are variable and dependent up on the parental lines used. Knight (1980) observed that in the F_2 generation, recovery of desi type ranged from 2.3 to 53.3% and that of kabuli type from 0 to 9.8%. There is further segregation of desi and kabuli from pea and intermediate types. The variable frequencies of segregation classes, together with the stability of desi and kabuli types in early generations, indicate epistasis (Knight, 1980). The results obtained from F_2, BC_1P_1 and RILs in the present study indicated that seed type is controlled by two pairs of gene. In the reciprocal

crosses of desi type and kabuli type, the F_1 seeds were desi type and the F_2 population also showed similar segregation pattern. This indicates the character is governed by nuclear genes and there is no cytoplasmic effect.

On the basis of the segregation pattern in the cross, the genomic symbols for the seed type could be designated as St_1St_1 St_2St_2 for desi type, St_1 St_1 st_2 st_2 and st_1st_1 St_2St_2 for intermediate types and st_1st_1 st_2st_2 for kabuli type. Plants with dominant genes at both the loci will produce desi type. Intermediate types are produced by dominant gene in one locus. Recessive alleles at both the loci produce kabuli type. The results of this study differ with Knight (1980) because F_1 seed from desi x kabuli cross was desi type. Furthermore desi type seed is dominant to kabuli type and the cross of homozygous dominant with four alleles with pure intermediate produce desi types.

The results of this study indicated that crude fibre content among desi and kabuli, desi and intermediate, and kabuli and intermediate types differed. These results are in agreement with earlier reports (Jambunathan and Singh, 1979; Saini and Knights, 1984 and Singh, 1984) that suggested desi type had higher fibre content than kabuli type. In the present investigation, desi seeds had 2.12 and 1.5 times more fibre than kabuli types and intermediate types respectively. Intermediate type seeds had 1.42 time more fibre content than kabuli type. Knights (1980) found kabuli seeds had a fibre content of approximately 5-6% compared to 17-18% for desi seeds. Knights and Mailer (1989) reported desi type had 2.34 time more fibre than kabuli seeds. This suggests that there is difference within desi types and within kabuli types for seed fibre concentration.

5.1.6 Seed coat colour

Seed coat colour is an important character as it is a major trait that determines chickpea price in the market. Results of the present findings revealed that the seed coat colour in this cross is controlled by at least three gene pairs. Pimplikar (1943), Bhapkar and Patil (1962) D'Cruz and Tendulkar (1970) obtained a monogenic behavior for seed-coat colour. Bhapkar and Patil (1962), More and D'Cruz (1970), More (1976) and Pawar and Patil (1979) reported that this character is controlled by two pairs of genes. Reddy and Chopde (1977) found that black seed-coat colour was dominant over brown and F_2 population segregated into 9 black: 7 brown seeds. Alam (1935) reported that seed coat colour in chickpea is governed by at least four different factors whereas Ayyar and Balasubramanian (1936) and Brar and Athwal (1970) found that five loci are involved in the production and expression of different seed colours in chickpea. Different reports for number of genes controlling seed colour are due to the use of parents different genotypes slight variations in methods for classification of seed coat colour can also influence the results. Therefore, it is difficult to relate between the results for inheritance of seed colours in different studies. Some colours such as yellow brown, reddish brown, brown, dark brown and light brown exhibited variation even among the seeds of a single plant. This variability in colour may also be cased by forced maturity. In a few cases some seeds were greenish and this colour was not real colour. This kind of colour may be due to improper by developed seeds. The seed colour also darkens with the age of seed, therefore it is suggested this character should be evaluated when seeds are fresh. Ayyar and Balasubramanian (1936, 1937) and Balasubramanian (1950a, 1950b) described 13 different seed colour classes of chickpea ranging from yellow to dark brown. In the present

investigation eight phenotypic classes were obtained. Therefore conclude that ICCV2 and JG62 differ for three genes. If all the three genes are present in dominant condition, the seed coat colour is yellow brown. Therefore JG62 has three dominant genes for seed coat colour. Yellow brown seed coat of the back cross seeds with JG62 confirmed this finding. If dominant genes are present at two loci, seed coat colours are brown, reddish brown or light brown. The genotypes with one gene in dominant condition for seed coat colour have yellow beige, dark beige and dark brown seed coat colours. All three recessive genes condition light yellow seed coat colour. Therefore, these genes are symbolized as Ysc, Bsc, Rsc.

5.1.7 Growth vigour

Initial seedling vigour plays an important role in the establishment of a normal crop. In chickpea, early growth and vigour can be important in providing increased biomass. Oudio *et al.* (1997) observed that early establishment helped the crop to compete well with weeds. Considerable losses are observed because of stiff competition of the crop with weeds, particularly in irrigated and late-sown conditions (Lather *et al.* 1997). Jain *et al.* (1998) reported that initial seedling vigour plays an important role for high planting value of seed lot and early establishment of the crop. Early growth vigour will also help utilize moisture better. Therefore, in the present investigation an attempt was made to know the inheritance of growth vigour and its association with other characters.

The results of the present finding indicate that growth vigour is controlled by two pairs of genes. Homozygous recessive condition for both is necessary for low growth

vigour. This character appears to be governed by duplicate dominant epistasis. In the reciprocal crosses of high vigour and low growth vigour, the F_1 plants had high growth vigour but the mean scores of crosses ICCV2♀ x JG62♂ and JG62♀ x ICCV2♂ were 4.15 and 3.33 respectively. The difference between the reciprocal F_1s, indicate the character may also be governed by cytoplasmic genes.

The information on the number of genes controlling this character is not available. Seedling vigour is a complex character. It is governed by many parameters (Jain *et al.*, 1998). One plant in F_1 (JG62♀ x ICCV2♂) and BC_1P_1 (F_1♀ x ICCV2♂) were low growth vigour (Table 9), probably effects of some factor such as seed size and depth of sowing did not show proper phenotype. In chickpea, the larger seedlings produced by large seeded varieties may emerge better after deep sowing, which is often necessary when the crop is sown in seed-beds which are drying out (van der Maesen, 1972). Raje (1992) found positive association of seed size with vigour index in gram. Breeding efforts to increase drought resistance in chickpea are limited, despite the fact that drought is the most important yield-reducing factor in production (van Rheenen *et al.*, 1990). A major reason for this has been a lack of reliable screening techniques for large-scale evaluation of germplasm and breeding materials. Although chickpea is more drought-resistant than other cool-season food legumes, drought is the most important yield reducer in this crop (Saxena, 1987; Singh, 1993 and Johansen *et al.*, 1994a, 1994b).

Drought resistance is classified by Singh *et al.* (1997) as escape and avoidance (e.g. early flowering and better water extraction from soil through a larger root system) and

desiccation tolerance (continuation of metabolism at low tissue water potential). Drought escape is a particularly important strategy for matching phenological development with the period of soil moisture availability to minimize the impact of drought stress on crop production in environments where the growing season is short and terminal drought stress predominates (Turner, 1986a,b). Abiotic stress factors contribute significantly to the generally low yields (<0.8 t/ha) of chickpea and pigeonpea achieved in farmer fields. Development of short duration genotypes of both chickpea and pigeonpea has increased options of escaping terminal drought stress (Chauhan *et al.*, 1992). Development of shorter duration varieties that are better assured of reaching maturity within a limited growing period, as determined by available soil moisture, is the most promising avenue for genetic improvement for droughted environments (Johansen *et al.*, 1997). Water availability is a major yield-limiting factor in semi-arid regions. Hence, efficient utilization of soil water for grain production depends on the correct timing of flowering (Or *et al.*, 1999).

Landraces of chickpea, pigeonpea, and groundnut growing in their natural environments often face terminal drought stress, as evidenced by a yield increase if irrigation is given during the reproductive phase (Singh and Subba Reddy, 1986). This suggests that, despite their evolution and selection in specific environments, the duration to maturity of these landraces is too long in relation to the amount of the available stored soil moisture (Singh and Subba Reddy, 1986). For instance, newly bred short-duration genotypes of groundnut are generally more successful compared with traditional long-duration genotypes in West African regions characterized by short growing seasons (Virmani and

Singh, 1986). There are many examples of development of short- duration pulses with the potential to increase yield and yield stability in drought-prone environments viz, chickpea (Gupta, 1985; Singh *et al.*, 1990; Kumar *et al.*, 1996; Singh *et al.*, 1997, cowpea; Hall and Patel, 1985; pigeonpea (Hall and Grantz, 1981 and Laxman Singh *et al.*, 1990) and soybean (McBlain and Hume, 1980 and Rose *et al.*, 1992). For most crop species, breeding for shorter duration is a major objective, not only to match the phonology to length of growing season, but also for other reasons such as to fit crops/genotypes into more intensive crop rotations. Also, the use of early maturity as an escape strategy is limited in some environments, such as for chickpea and lentil in the Mediterranean environments, where too early flowering could expose the crop to low temperature and frost damage (Subbarao *et al.*, 1995).

The present study revealed that high growth vigour had significant negative correlation with days to first flower, days to 50% flowering, days to first pod and days to maturity. The genotypes with high growth vigour flowered, podded and matured earlier than those with low growth vigour. The 1-5 scale was used in this study appears effective in finding materials resistant to drought by a mass-screening exercise. Therefore, most of the susceptible types were unable to 'escape' the terminal drought. However, the method also identifies the truly resistant lines within the early-flowering group. These results confirmed association between rapid seedling growth with early maturity as suggested by Gupta (1985). There was a positive correlation between growth vigour and 100-seed weight, leaf size and leaf weight in RILs in this investigation. These results support the findings of Black (1959) in herbage legume, Haskins and Gorz (1975) in sweet clover,

Kneebone and Cramer (1955) in some grass species and Raje (1992) in chickpea, who observed that the seed size influenced seedling growth. It is possible that in chickpea and pigeonpea selection for seed size would have important consequences for seedling growth, which could in turn influence stand establishment, especially under adverse environmental conditions. The selection of large-seeded varieties appear to result in better seedling vigour (Narayanan *et al.*, 1981). Van der Maesen (1972) suggested that large-seeded varieties of chickpea produce larger and more vigourous seedling, that will have advantage in stand establishment under adverse conditions. Singh *et al.* (1997) reported that seed yield under drought conditions was positively correlated with early plant vigour. It is clear that in drought conditions, early maturing genotypes have higher yield than late maturity. But in general in normal condition and irrigated field late maturity have higher yield than early maturity. Therefore, non- significant correlation between early growth vigour and yield per plant may be due to absence of drought condition in the two year experiments. On the basis of segregation pattern in this cross, the genomic symbols for growth vigour could be designed as Gv_1 Gv_2, Gv_1gv_2 and gv_1Gv_2 for high growth vigour and gv_1gv_2 for low growth vigour.

5.2 INHERITANCE OF QUANTITATIVE TRAITS

5.2.1 Heritability and genetic advance

The estimates of heritable and non-heritable variance give a clue on possible improvement for the characters under study (Rao *et al.*, 1994). The estimates of heritability help the plant breeder in selection of elite genotypes from diverse genetic populations (Phundan Singh and Narayanan, 1997). One of the major contributions of

quantitative genetics to plant breeding is the development of an equation for predicting gain from selection. (Dudley, 1997). High heritability alone does not guarantee large gain from selection unless sufficient genetic advance attributable to additive gene action is present (Srivastava and Jain, 1994). Heritability and genetic advance are two important selection parameters of which the former is used to estimate the expected genetic advance through selection (Sharma *et al.*, 1990).

Most of the studies on heritability and genetic advance in chickpea are based on estimates of broad sense heritability. There are discussed with the results of the present study in the following sections:

5.2.1.1 Days to first flower

The estimates of broad sense heritability for days to first flower and days to 50% flowering exhibited high heritability in this study. This is in agreement with earlier reports (Mishra *et al.*, 1988; Sharma *et al.*, 1990; Misra, 1991; Pundir *et al.*, 1991; Sandhu *et al.*, 1991; Panchbhai *et al.*, 1992; Rao *et al.*, 1994; Chavan *et al.*, 1994; Mathur and Mathur, 1996 and Samal and Jagadev, 1996). In the present study Narrow sense heritability estimate for days to first flower was moderate whereas Pandey *et al.*, (1990) reported high value for this trait. Narrow sense heritability is more useful concept because it measures the relative importance of the additive portion of the genetic variance that can be transmitted to the next generation offspring. This is particularly important when heritability is used to predict gain expected from selection for a character (Fehr, 1987).

Narrow sense heritability is more reliable than broad sense heritability. Therefore, days to flowering have moderate heritability.

Genetic advance estimates (% of mean) for days to first flower and days to 50% flower were high in RILs while these were low for segregating populations for days to first flower. Raju *et al.* (1978), Pandey and Tiwari (1983), Misra (1991), Sharma *et al.* (1990) and Rao *et al.* (1994) found lower value of genetic advance for days to flowering. Moderate narrow sense heritability and low genetic advance were obtained for this character. This result shows that nonadditive genes may be influencing this character. Nonadditive gene action is in accordance with the finding of Pandey and Tiwari (1983), Sharma *et al.* (1990), Mishra (1991), Pundir *et al.* (1991), Panchbhai *et al.* (1992) and Chavan *et al.* (1994). Hence, it would be desirable to carry earlier generations of the population derived from crosses by bulk method and postpone selection to later generation till maximum homozygosity is attained by the populations where the gene complex are fixed.

5.2.1.2 Days to first pod

In the present investigation estimates of broad sense heritability for days to first pod were high for RILs and segregating populations. Narrow sense heritability was also high for this trait.

Genetic advance was high for days to first pod in RILs while it was low in segregating populations. I could not find any published information on heritability for this

character. High narrow sense heritability along with low genetic advance (percent of mean) in the character suggest that the genotypic variation for such character is probably due to nonadditive gene action. Since nonadditive components of variation are more predominant, therefore selection in early generations may be less effective.

5.2.1.3 Days to maturity

The estimates of broad sense heritability for days to maturity were high in RILs and segregating population. These results supported finding of Mishra *et al.* (1988), Sharma *et al.* (1990), Panchbhai *et al.* (1992), Mishra *et al.* (1994), Chavan *et al.* (1994) and Mathur and Mathur (1996) who also reported high broad sense heritability for this character. Narrow sense heritability estimate was moderate for days to maturity.

The estimates of genetic advance were low for RILs and segregating populations. Similar results were found by Mishra *et al.* (1988), Sharma *et al.* (1990), Misra (1991), Panchbhai *et al.* (1992), Chavan *et al.* (1994), Rao *et al.* (1994) and Mathur and Mathur (1996).

Moderate heritability coupled with low genetic advance indicated that nonadditive gene effects play an important role in the expression of days to maturity. Nonadditive gene action is in accordance with the findings of Mishra *et al.* (1988), Sharma *et al.* (1990), Misra (1991), Chavan *et al.* (1994) Rao *et al.* (1994) and Mathur and Mathur (1996). Therefore the results indicated that selection for this character may be less effective in early generations.

5.2.1.4 100-seed weight

In the present study broad sense estimates of heritability were high for 100-seed weight in RILs and segregating populations. 100-seed weight had very high narrow sense heritability. High broad and narrow sense heritability obtained in this investigation are in accordance with the findings of Chandra (1968), Sandhu and Singh (1970), Niknejad *et al.* (1971), Gupta *et al.* (1972), Setty *et al.* (1977), Patil and Phadnis (1977), Ram *et al.* (1978), Mandal and Bahl (1980), Pandey and Tiwari (1983) Jivani and Yadavendra (1988), Sharma *et al.* (1990), Pundir *et al.* (1991), Misra (1991), Rao *et al.* (1994), Rana *et al.* (1995), Mathur and Mathur (1996), and Malhotra *et al.* (1997).

High genetic advance was recorded for 100-seed weight in the RILs and segregating populations. Results of this study supported the findings of Sandhu and Singh (1970), Ram *et al.* (1978), Jivani and Yadavendra (1988), Sharma *et al.* (1990), Misra (1991), Rao *et al.* (1994), Kumar and Singh (1995) and Mathur and Mathur (1996) who also reported high genetic advance for this trait.

High heritability estimates coupled with high expected genetic advance observed in this investigation confirm the findings of Sandhu and Singh (1970), Ram *et al.* (1978), Jivani and Yadavendra (1988), Sharma *et al.* (1990), Rao *et al.* (1994), Kumar and Singh (1995) and Mathur and Mathur (1996). High heritability along with high genetic advance in a character is indicative of high genetic effects. Therefore, this character is least influenced by environmental effects and selection in F_2 generation could lead to a substantial improvement in 100-seed weight.

5.2.1.5 Plant height

In the present study, plant height had relatively high broad sense heritability in RILs but moderate for segregating populations. High broad sense heritability were reported by Mishra *et al.* (1988), Sharma *et al.* (1990), Misra (1991), Sandhu *et al.* (1991), Chavan *et al.* (1994), Mathur and Mathur (1996) and Sarral and Jagadev (1996) whereas Mishra *et al.* (1994) reported moderate broad sense heritability for this character. Estimate for narrow sense heritability was low for plant height. Pandey *et al.* (1990) found moderate narrow sense heritability for plant height.

The results of present study showed that genetic advance for plant height was moderate in RILs but was low in segregating populations. The expected genetic advance for plant height obtained was low by Sandhu *et al.* (1974), Misra (1991), Sandhu *et al.* (1991) and Panchbhai *et al.* (1992) while Sharma *et al.* (1990) reported moderate genetic advance for this character.

Low narrow sense heritability along with low genetic advance in segregating populations indicated nonadditive genetic effects for this character. Nonadditive gene action were also suggested by Misra (1991), Sandhu *et al.* (1991), Panchbhai *et al.* (1992), Chavan *et al.* (1994) and Mathur and Mathur (1996).

5.2.1.6 Plant width

In the present investigation, width of plant had low broad sense heritability in RILs and moderate in segregating populations. Narrow sense heritability for plant width

observed was low. Mishra *et al.* (1988) found high broad sense heritability for plant width whereas Chavan *et al.* (1994) did not find high broad sense heritability for this character.

The estimates of genetic advance were low in RILs and segregating populations. These results are in agreement with the findings of Mishra *et al.* (1988) and Chavan *et al.* (1994) for genetic advance for plant width.

Low narrow sense heritability coupled with low genetic advance indicate a significant contribution of nonadditive gene action for this character. These results indicate that plant width is governed by genes having epistatic and dominant gene effects. Mishra *et al.* (1988) Chavan *et al.* (1994) reported nonadditive gene action while Bhatt and Singh (1980) and Ugale (1980) reported additive gene action for the trait.

5.2.1.7 Number of primary branches per plant

The results of present study indicated that broad sense heritability for number of primary branches per plant was low in RILs and moderate in segregating populations (second year) while it was high in the first year in segregating populations. The estimate of narrow sense heritability was moderate for this trait. High broad sense heritability was reported by Mishra *et al.* (1988) and Sharma *et al.* (1990) whereas Sandhu *et al.* (1991) Rao *et al.* (1994), Rana *et al.* (1995) and Samal and Jagadev (1996) obtained low broad sense heritability for this character.

Genetic advance estimate was moderate for number of primary branches per plant in RILs and low for segregating populations. Similar results were observed by Sandhu *et al.* (1991) and Rao *et al.* (1994).

Moderate narrow sense heritability along with low genetic advance in the present study, suggest nonadditive gene action for number of primary branches. Thus, it indicates that the character is highly influenced by environmental effects and selection would be ineffective. Sandhu *et al.* (1991) and Rao *et al.* (1994) concluded nonadditive gene action for number of primary branches per plant whereas Sharma *et al.* (1990) found the presence of both additive and nonadditive gene actions for the character.

5.2.1.8 Number of secondary branches per plant

Estimates of broad sense heritability for number of secondary branches per plant were moderate for RILs and segregating populations. Narrow sense heritability was low for this character. Low broad sense heritability for this trait were suggested by Sandhu *et al.* (1991) and Rana *et al.* (1995) while Rao *et al.* (1994) found moderate broad sense heritability for this trait. Mishra *et al.* (1988) and Sharma *et al.* (1990) observed high broad sense heritability for this character.

Genetic advance estimate for secondary branches per plant observed moderate in RILs whereas exhibited low amount of genetic advance in segregating populations. Present result confirmed low genetic advance for number of secondary branches as reported by Sandhu *et al.* (1991).

Low amount of narrow sense heritability for number of secondary branches along with low genetic advance in segregating populations suggest that the genotypic variation for such character is probably due to nonadditive gene action. Similar results were reported by Sandhu *et al.* (1991). Contrary to the present findings, Mishra *et al.* (1988), Jahagirdar *et al.* (1994) and Rao *et al.* (1994) suggested the importance of additive genetic effect for number of secondary branches per plant.

5.2.1.9 Number of pods per plant

Broad sense heritability estimates for number of pods per plant was moderate for RILs but were relatively high in segregating populations. This result confirmed high broad sense heritability suggested by Misra (1991), Chavan *et al.* (1994) and Mathur and Mathur (1996) for this character. Mishra *et al.* (1994), and Rao *et al.* (1994) found moderate broad sense heritability. Moderate narrow sense heritability for number of pods per plant obtained in this investigation is in accordance with the finding of Pandey *et al.* (1990).

The estimates of genetic advance were high and moderate in RILs and segregating populations respectively. Mishra *et al.* (1988), Jivani and Yadavendra (1988), Chavan *et al.* (1994), Mishra *et al.* (1994) and Rao *et al.* (1994) suggested high genetic advance while Sharma *et al.* (1990), Misra (1991), Sandhu *et al.* (1991) and Panchbhai *et al.* (1992) found low genetic advance for number of pods per plant.

Moderate narrow sense heritability coupled with moderate genetic advance indicated the presence of both additive and nonadditive gene actions for number of pods

per plant. Mishra *et al.* (1988), Jivani and Yadavendra (1988), Misra (1991), Rao *et al.* (1994), Chavan *et al.* (1994) and Jha *et al* (1997) suggested additive gene action for number of pods per plant whereas Sharma *et al.* (1990), Pundir *et al.* (1991), Sandhu *et al.* (1991), and Panchbhai *et al.* (1992) reported that non additive gene actions for the character.

5.2.1.10 Number of seeds per plant

The estimate of broad sense heritability for number of seeds per plant was moderate in RILs but were relatively high in segregating populations. Narrow sense heritability was relatively high for number of seeds per plant. Pandey *et al.* (1990) observed moderate narrow sense heritability while Panchbhai *et al.* (1992) obtained low broad sense heritability for this character.

Number of seeds per plant had relatively high genetic advance in RIls while had moderate in segregating populations. Pandey *et al.* (1990) found high genetic advance for this character whereas Panchbhai *et al.* (1992) reported low genetic advance for number of seeds per plant.

Moderate narrow sense heritability along with moderate genetic advance indicating the present of both additive and non-additive gene actions for number seeds per plant. Pandey *et al.* (1990) suggested non-additive as well as appreciable additive gene effects while Panchbhai *et al.* (1992) reported non-additive gene action for this trait.

5.2.1.11 Number of seeds per pod

The estimate of broad sense heritability for number of seeds per pod was high in RILs and second year experiment in segregating populations while it was low in first year experiment in segregating populations. Narrow sense heritability was moderate for this character. Sharma *et al.* (1990) found high broad sense heritability for this trait. Contrary to present findings, Misra (1991) and Rana *et al.* (1995) obtained low broad sense heritability for this character. Mishra *et al.* (1994) observed moderate broad sense heritability for the character. Singh and Rheenen (1994) obtained relatively high narrow sense heritability for number of seeds per pod.

Estimates of genetic advance for number of seeds per pod were low in RILs and segregating populations. Pundir *et al.* (1991) and Sandhu *et al.* (1991) obtained low genetic advance while Sharma reported moderate genetic advance for this character.

Moderate narrow sense heritability along with low genetic advance indicating nonadditive gene action for number of seeds per pod. These results are in agreement with findings of Sandhu *et al.* (1991) and Pundir *et al.* (1991). Sharma *et al.* (1990) suggested presence of both additive and nonadditive gene actions whereas Jha *et al.* (1997) reported that number of seeds per pod was predominantly under the control of additive genetic effects.

5.2.1.12 Seed yield per plant

In the present study seed yield per plant had moderate broad sense heritability in RILs. The broad sense heritability was relatively high and moderate in first and second year experiments in segregating populations respectively. The estimate of narrow sense heritability was moderate for this character. High broad sense heritability were noticed by Mishra *et al.* (1988), Sandhu *et al.* (1991), Mishra *et al.* (1994), Chavan *et al.* (1994) and Mathur and Mathur (1996). Contrary to these reports, Sharma *et al.* (1990), Misra (1991), Panchbhai *et al.* (1992), Rao *et al.* (1994) and Rana *et al.* (1995) found low heritability for seed yield per plant. Pandey *et al.* (1990) reported relatively high narrow sense heritability for yield per plant.

Genetic advance value obtained high in RILs while in segregating populations was moderate for this character. Sharma *et al.* (1990) reported that moderate genetic advance for this character while Mishra *et al.* (1988), Pandey *et al.* (1990), Sandhu *et al.* (1991), Chavan *et al.* (1994), Mishra (1994), Rao *et al.* (1994), and Mathur and Mathur (1996) reported high genetic advance for this trait. Contrary to these reports, Misra (1991) and Panchbhai *et al.* (1992) reported low genetic advance for this character.

Moderate of narrow sense heritability coupled with moderate genetic advance in segregating populations for seed yield per plant indicated the presence of both additive and nonadditive gene actions for this character. This result is in accordance with the findings Mishra (1991) and Panchbhai *et al.* (1992) who reported that non-additive gene effects play an important role in the expression of seed yield per plant. Mishra *et al* (1988),

Sandhu (1991), Chavan *et al.* (1994), Mishra *et al.* (1994) and Mathur and Mathur (1996) suggested the importance of additive gene effects for this character. The relative magnitudes of the different reports vary from study to study, may be due to differences in genetic architecture of the parents and the environments sampled.

5.2.1.13 Leaf size

In the present investigation, estimate of broad sense heritability for leaf size was high in RILs and segregating populations but narrow sense heritability was low in this character. Pundir *et al.* (1991) and Katiyar and Katiyar (1994) reported high broad sense heritability for this character.

Genetic advance observed high for this character in RILs while it was moderate in segregating populations. Pundir *et al.* (1991) and Katiyar and Katiyar (1994) reported high genetic advance for this trait.

Low narrow sense heritability along with moderate genetic advance in segregating populations suggests the importance of non-additive gene action for this character. Contrary to present findings reported by Pundir *et al.* (1991) and Katiyar and Katiyar (1994) may be due to estimate of heritability and genetic advance based on broad sense heritability.

5.3.1.14 Leaf weight

Leaf weight exhibited high amount of broad and narrow sense heritability in RILs and segregating populations, which are in agreement to earlier report (Katiyar and Katiyar, 1994).

High genetic advance observed in this investigation is in accordance with finding of Katiyar and Katiyar (1994).

The high heritability coupled with high genetic advance in a character suggested that the genotypic variation for such character is probably due to high additive genetic effects and this character is least influenced by environmental effects. Similar the findings were reported by Katiyar and Katiyar (1994).

5.3.1.15 Specific leaf weight

Specific leaf weight had high broad sense and narrow sense heritabilities for RILs and segregating populations. Katiyar and Katiyar (1994) also observed high broad sense heritability for this character.

Genetic advance was low for RIls while it was very high for segregating populations for this trait. High genetic advance was also reported by Katiyar and Katiyar (1994) for specific leaf weight.

High narrow sense heritability along with high genetic advance in segregating populations indicated the substantial contribution of additive genetic advance for the expression of this character. This result supports the findings of Katiyar and Katiyar (1994) observed high heritability and high genetic advance for this character.

5.2.1.16 Seed fibre

The present investigation revealed that seed fibre had high broad sense heritability and also genetic advance was high for this character in RILs. High heritability coupled with high genetic advance indicated additive gene effect to play an important role in the expression of seed fibre. Therefore, the results revealed that selection for seed fibre can be more effective in early generations. The F_1s mean of crude fibre content (7.65%) was similar to the mid parental value (7.08%) indicating the absence of dominance.

5.2.2 Parent-offspring regression

Estimating heritability from relationship between two generations (e.g between generations F_2 and F_3), one should always take into account the fact that parent-offspring regression is a biased estimate of heritability when the two generations have different means and variances. Such differences, caused by environmental or experimental changes, are common in experiments with plants. In such situations parent-offspring correlation rather than regression is recommended as the measure of heritability in a random-mating population (Frey and Horner, 1957).

The estimates of heritability by parent off- spring correlation revealed that a very high heritability was obtained for days to first pod and followed by days to first flower and days to maturity. Low value of heritability estimates obtained in 1997-1998 may be due to the effect of fusarium wilt in 1998-1999 experiment and plants could not obtain their genetic potential. For example means of F_2 and F_3 in 1998 were less than the F_2 in 1997 and F_3 in 1999. The fusarium wilt reduced seed weight (Table 37). A very low heritability estimate was observed for seed yield per plant. Sumathi and Ramanathan (1995) reported that heritability estimates by parent offspring regression method were moderate for all characters such as pod yield, plant height, number of flowers and 100-seed weight in groundnut. Salimath and Patil (1990) found moderate heritability value by regression method for seed weight (33%) followed by seed yield (28%) and number of pods per plant (20%). They observed low heritability for number of seeds per pod (6%) and plant height (0%) in chickpea. Whereas Kumar (1998) reported a high heritability value by regression method for seed yield (55.98) followed by number of pods per plant (48.20) and 100-seed weight (41.06). He obtained the moderate heritability for number of seeds per pod (31.54). The estimates of heritability by different methods would not give same results. For example Kumar (1998) used three different methods such as components of variance, regression of progeny on parent and realized heritability. His estimates of heritability by components of variance method were higher than obtained by the regression method for all characters except seed yield. With component of variance the heritability for seed yield had a low value, whereas with the regression method the seed yield had very high heritability. Similar results were reported by Johnson *et al.* (1983) in oats.

5.3 LINKAGE

Genes often show a tendency to be inherited together, that is to pass to the same gamete during segregation, and therefore may not show independent segregation. The frequency of recombination between any two linked genes depends upon the distance between them. Thus the chief effect of linkage is to reduce the frequency of recombination between linked genes (Singh, 1997). If two traits have high phenotypic and genotypic correlation it is possible to select one of them through selection of the associated trait. This is useful when a trait is economically important, but has low heritability comparatively to the associated trait. In this case, the trait of interest should be selected using the trait with high heritability and lesser economic importance. Also, if two traits are associated and one is easier to assess and select, selection pressure should be applied to this trait to improve the other (Falconer, 1989). The linkage of genes for economically important traits with easily identified markers, can improve the efficiency of breeding and hasten the development of improved cultivars. Linkage relationships can also be used to study gene systems and genetic mechanisms (Muehlbauer and Singh, 1987).

The segregation of flower colour and stem colour did not show any recombination which indicated that the same single gene was involved in controlling these two characters. Pleiotropic action of the same gene seems to be more probable rather than a tight linkage between the two factors. Therefore, gene (B) governs the flower colour, also controls the stem colour in chickpea. Ayyar and Balsubrahmanyam (1936), Argikar (1955), D'Cruz and Tendulkar (1970), and More and D'Cruz (1976) have stated that the expression of these

two characters was due to the pleiotropic action of a single gene. Argikar and D'Cruz (1963) also reported pleiotropy for these two characters and foliage colour.

The results of the present investigation also showed that genes for flower colour and number of pods per peduncle, flower colour and seed surface, pod number per peduncle and seed surface, and seed type and pod number per peduncle were independent of each other. Khan and Akhtar (1934), D'Cruz and Tendulkar (1970), and More and D'Cruz (1976a) reported that the genes governing flower colour and number of flowers per axil were independent of each other. While Aziz *et al.* (1960) found that the factor P (flower colour) was linked with M (seed surface) with 18.2 percent cross over. Bhapkar and Patil (1963) reported that the factor responsible for foliage colour is different and independent from the factors responsible for flower and seed colour. Pawar and Patil (1979) determined a linkage group for corolla colour (*Lvco*), seed surface (*Rs*) and seed coat colour (*Bsc*).

The segregation for flower colour and seed type, and stem colour and seed type gave a probability that was lower than the expected limit of five percent. Thus, these genes controlling the characters appear to be linked. The result of this study indicated that one of the genes for flower colour (B) is linked with one of the genes for seed type (St_1, St_2) and distance between two genes is about 29 cM. The allele responsible for pink flower colour is linked with factor governing angular shape and the allele that controlled white flower colour is linked with the gene responsible for owl's head shape. Recombination values between the two genes indicate that they are not very tightly linked, That's why,

some angular shaped seed had white flower and also owl's head shape seed had pink flower. Since published information about linkage of these characters is not available therefore, it could not be reported.

The results of the present study indicate that there is linkage between genes controlling flower colour and seed coat colour. Colour of seed coat is highly variable and sometimes difficult to classify. Therefore, different values were observed recombinant frequency in two years may be due to sampling error. The result of this study revealed that one of the genes for flower colour (*B*) is linked with one of the genes for seed coat colour (*Ysc, Bsc, Rsc*). On the other hand gene or genes responsible for white flower colour were linked with those that control yellow beige and dark beige colour, these genes governing pink flower colour were linked with factors responsible for brown, light brown and dark brown in seed coat colour (See Tables 24, 25). Linkage between flower colour and seed colour reported earlier by Shaw (1932), Aziz *et al.* (1960), Bhapkar and Patil (1963), D'Cruz and Tendulkar (1970), Pundir and van der Maesen (1983) and Pawar and Patil (1979). Shaw (1932), Bhapkar and Patil (1963) and Pawar and Patil (1979) reported that percent cross over value between the gene responsible for flower colour and the factors governing seed coat colour were 18.4, 18.47 and 40.62 respectively. For the same characters Aziz *et al.* (1960) have found recombination values of 18.4 and 30.4 percent in two crosses.

The χ^2 for segregation for stem colour and seed coat colour was significant. Due to the pleiotropic effect of the gene that control stem colour and flower colour, the chi-square

value for joint segregation is same for the traits. The result of the present study indicated that the gene for stem colour (*B*) is linked with one of the genes for seed coat colour (*Ysc, Bsc, Rsc*). Therefore the allele governing non-pigmentation was linked with the gene responsible for yellow beige and dark beige seed coat colour. However, supporting reports about linkage between stem colour and seed coat colour are not available.

Investigation of joint segregation between number of pods per peduncle and seed coat colour showed that all colours were inherited independently of the locus for number of pods per peduncle. Research reports on number of pods per peduncle and seed coat colour are not available in literature.

The estimate of chi-square for joint segregation between seed surface and seed coat colour revealed that these traits segregate independently. In contrast to this result, Aziz *et al.* (1960) and Pawar and Patil (1979) found a linkage group comprising of corolla colour, seed surface and seed coat colour. Seed coat (testa) colour in chickpea is a highly variable and complex character and may be governed by several genes. Some times even the coat of a single seed develops patches in which more than one colour or shade gets intermixed, making gradation of the seed coat colour extremely difficult (Tefera 1998). Rough and smooth surfaces are clearly marked from one another but the intermediate grades such as slightly rough, slightly smooth are sometime difficult to distinguish. Therefore, high values of chi-square in joint segregation between seed coat colour and seed surface may be caused by such problems.

A study of interrelationship between seed type and seed coat colour indicated linkage between genes governing these traits. The estimate of recombination value revealed that one of the genes responsible for seed type (St_1, St_2) was linked with one of the genes for seed coat colour (*Ysc, Bsc Rsc*) and distance between two genes is 35 cM. The distance between the two genes is relatively long as the recombination value was 35 percent. I could not find any published information for linkage of these two characters.

5.4 CORRELATED GENETIC GAIN

When selection is applied by plant breeders, changes are likely to occur, not only in the trait for which selection is being practiced but in other traits as well. (Dudley, 1997). The improvement of one character by selection frequently causes simultaneous changes in other characters. The effect is the result of correlations between characters, which may be genetic or environmental in nature. Genetic correlation arises from pleiotropy, from linkages between loci controlling the characters or from random genetic drift. Selection for morphological or physiological character is of no value if the characters performance is not correlated with performance of primary character (Fehr, 1987). The response of a correlated character can be predicted if the genetic correlation and the heritabilities of the two characters are known (Falconer, 1989). The results of correlated response to selection estimates of different characters with seed yield per plant showed that number of pods per plant followed by number of seeds per plant and number of secondary branches per plant had high correlated response with seed yield per plant. Number of secondary branches per plant, number of pods per plant, seed yield per plant and number of seeds per plant exhibited high correlated response to selection with yield per plot. The highest correlated

response for number of pods per plant with seed yield per plant in present study is in accordance with the finding of Mishra *et al.* (1992) in chickpea. Therefore, the results of this study indicate that selection of number of pods per plant, number of secondary branches per plant and number of seeds per plant can improve seed yield per plant and per plot in this cross combination of chickpea.

5.5 COHERITABILITY

Coheritability refers to joint transmission of different character pairs, is a better genetic parameter for improving selection efficiency as it permits the study of simultaneous changes in different characters (Srivastava and Jain, 1994). Coheritability takes both genotypic as well as phenotypic covariances into account and helps in understanding changes taking place in pairs of polygenic characters. A high value of coheritability estimate suggests that increase in one polygenic trait will lead to simultaneous increase in another coheritable character. Thus coheritability may form a more meaningful index for achieving breeding objectives (Biwas and Sasmal, 1989). Coheritability is considered a more general genetic parameter for raising the efficiency of plant selection as it permits the study of changes in pairs of characters (Mehan *et al.*, 1982). In any crop improvement program, an essential pre-requisite is to know the joint heritability of a pair of characters and prediction of response to selection (Mishra, 1992).

The yield of a plant is a composite trait, thus it is controlled by many genes having small individual effects. The present study was planned to know the joint heritability of pairs of characters through estimates of coheritability. The coheritability estimates of

different characters with yield per plant revealed yield per plot had high coheritability with yield per plant. Days to maturity, number of seeds per pods, number of secondary branches per plant and number of primary branches per plant had moderate coheritability with seed yield per plant. Seed yield per plot exhibited high coheritability with days to first pod, number of pods per plant, number of seeds per plant, number of primary branches per plant and seed yield per plant. The coheritability value of yield per plot with days to maturity and number of secondary branches per plant were moderate. Mishra *et al.* (1992) reported that number of pods per plant had the highest coheritability with economic yield (0.732) followed by harvest index (0.708), number of secondary branches per plant (0.543). High coheritability estimates of pod number per plant have bean earlier reported by Rao *et al.* (1981) and Srivastava and Jain (1994) in soybean. These workers did not record days to first pod, seed number per plant in chickpea and soybean. High magnitude of coheritability estimates of days to first pod and number of pods per plant expected due to low magnitude of environmental variances. According to Janssens (1979), coheritability includes not only the phenotypic variability of either traits, as does coefficient of genetic prediction between both traits. A high coheritability value of yield per plot with days to first pod, number of pods per plant and number of seeds per plant suggested that latter is probably the best indicator of selection for yield. Coheritability of a character combination based on linkage is evanescent and reverses its sign with crossing over. Such coheritability is not of much value unless linkage is tight (Rao *et al.* 1981). The coheritability values of days to first pod, pod number per plant, number of seed per plant and number of primary branches per plant were found to be positive whereas plant width with yield per plot was high and negative. The coheritability values of 100-seed weight with seed yield per plant and plot

were low and positive. Rao *et al.* (1981) and Mishra *et al.* (1992) obtained low and negative coheritability values of 100-seed weight with yield per plant in chickpea and soybean respectively. Low coheritability between these characters probably is due to the absence of existence of genetic correlation among characters. On the other hand the absence of coheritable variation among pairs of characters. Genotypic covariances, error covariances and phenotypic covariances of days to first flower, plant height and days to 50% flowering in this investigation had different signs therefore interpretation of coheritability is complex. Whenever the genetic and environmental covariance components have different signs, the interpretation of the coheritability becomes awkward as the estimates may be smaller than the narrow sense estimates (Janssens, 1979). The result of present study indicates that the selection for days to first pod, number of pods per plant and number of seeds per plant can simultaneously improve seed yield of chickpea.

5.6 HETEROSIS AND INBREEDING DEPRESSION

The scope for exploitation of hybrid vigour will depend on the direction and magnitude of heterosis, biological feasibility and type of gene action involved. Study of heterosis and inbreeding depression will also have a direct bearing on the breeding methodology to be employed for varietal improvement (Shinde and Deshmukh, 1990). Exploitation of heterosis appears to be cheap and easy method for increasing yield in many crops and considerable success has bean achieved in this direction in the crops exhibiting an appreciable degree of cross pollination. No use has been made of heterosis breeding in chickpea owing to cleistogamic nature of its flowers and small quantity of pollen grains and absence of male sterility (Kamatar *et al.*, 1996) Self-pollinated species do not show

inbreeding depression, but may exhibit considerable heterosis (Singh, 1997). The estimates of heterobeltiosis for yield and its components will give an idea about the crosses to isolate the transgressive segregates. Arora and Pandey (1987) and Rao and Chopra (1989) suggested that improved yield could be obtained through crosses between desi x kabuli chickpea.

5.6.1 Days to flower

Days to first flower showed positive mid parent heterosis and better parent heterosis. The hybrid was not earlier in flowering than mean of parents and corresponding early parent (ICCV2). From this finding it indicated that late flowering is dominant over early flowering. Deshmukh and Bhapkar (1982) observed none of the hybrid combinations was significantly earlier in blooming than early parent. Pal (1945) who published the first report on heterosis in chickpea, he did not find any hybrid vigour for time of flowering, whereas Singh and Singh (1979) reported negative heterosis for days to 50% flowering. Katiyar and Katiyar (1993) found out of 15 hybrids, 14 crosses had significant heterosis for days to flower. The estimate of inbreeding depression for days to first flower was positive.

5.6.2 Days to first pod

The results of this study revealed days to first pod had positive mid parent heterosis and better parent heterosis. The hybrid did not set to podding before mean of parents. The inbreeding depression estimate observed also positive for this trait. For support the result no such work was done elsewhere.

5.6.3 Days to maturity

Positive mid parent heterosis and high parent heterosis observed for days to maturity. The time of maturity for ICCV2 and JG62 was earlier than F_1s. Deshmukh and Bhapkar (1982) and Shinde and Deshmukh (1990) reported that none of the hybrid combinations was significantly earlier in maturity than the corresponding early parent. Kamatar *et al.* (1996) obtained majority of the crosses were late in maturity than their better parent but were earlier than mid parent. The inbreeding depression of this character was positive. Deshmukh and Bhapkar (1982) and Shinde and Deshmukh (1990) found positive inbreeding depression in majority of hybrid.

5.6.4 Number of pods per plant

The highest values for heterosis over mid parent and better parent heterosis observed for number of pods per plant. Pal (1945) Singh and Singh (1976), Bhatt and Singh (1980), Kunadia and Singh (1980), Deshmukh and Bhapkar (1982), Tewari and Pandey (1987), Rao and Chopra (1989), Pandey and Tiwari (1989), Shinde and Deshmukh (1990), Kamatar *et al.* (1996), Patil *et al.* (1996), and Vijayalakshmi Satya (1998) reported heterosis for this character. Majority of worker suggested heterosis for pods per plant contributed considerably to yield heterosis. The estimate of inbreeding depression for number of pods per plant was negative. High heterosis with negative inbreeding depression which could be due to the occurrence of a high proportion of transgressive segregants for number of pods per plant. Kunadia and Singh (1980) and Tewari and Pandey (1987) found in all crosses positive inbreeding depression for this character whereas Deshmukh and

Bhapkar (1982) and Shinde and Deshmukh (1990) obtained in some crosses negative values of inbreeding depression.

5.6.5 Number of primary and secondary branches per plant

Number of primary and secondary branches per plant had positive mid parent heterosis while better parent heterosis was negative. On the other hand F_1s plant had more vigour than mid parents whereas F_1s plant had less vigour than better parent. Heterosis were found for these traits by Bhatt and Singh (1980), Pandey and Tiwari (1989), Rao and Chopra (1989), Shinde and Deshmukh (1990) and Kamatar *et al.* (1996). The estimate of inbreeding depression for these characters was positive in this study. Deshmukh and Bhapkar (1982) and Shinde and Deshmukh (1990) observed in most of crosses high and positive inbreeding depression for these characters.

5.6.6 Number of seeds per plant

The results of this investigation revealed that number of seeds per plant had positive mid parent heterosis and high parent heterosis. Bhatt and Singh (1980), Tewari and Pandey (1987), Pandey and Tewari (1989) and Rao and Chopra (1989) obtained heterosis for number of seeds per plant. Inbreeding depression values for this trait was negative. Tewari and Pandey (1987) found in most of crosses significant inbreeding depression. High heterosis with negative inbreeding depression which may be due to take place of a high proportion transgressive segregants for number of pods per plants.

5.6.7 Plant width

Mid parent heterosis and high parent heterosis were positive for plant width. On the other hand F_1s had more vigour than mean of parent and better parent. Pandey and Tewari (1989) reported heterosis for this character. Inbreeding depression values for this character was negative. High heterosis with negative inbreeding depression for this trait probably is due to transgressive segregants.

5.6.8 Plant height

Positive mid parent heterosis and negative better parent heterosis were observed for plant height. Pal (1945) did not find any hybrid vigour in plant height whereas Pandey and Tewari (1989) and Rao and Chopra (1989), reported heterosis for this character. Vijayalakshmi Satya (1998) noticed no increment in plant height when taller parents are involved in the cross combination. However, when tall and short parents were crossed there is a marked increase in hybrid vigour for plant height.

5.6.9 100-seed weight

Negative values of mid parent heterosis and high parent heterosis for 100-seed weight were observed in this study. Singh and Singh (1976), Arora and Pandey (1987), Tewari and Pandey (1987), Rao and Chopra (1989), Pandey and Tewari (1989) and Shinde and Deshmukh (1990) found in majority of crosses negative heterosis for this trait. Minimum and negative inbreeding depression exhibited for this character. Tewari and Pandey (1987) and Shinde and Deshmukh (1990) Obtained in some crosses negative inbreeding depression.

5.6.10 Number of seeds per pod

The heterotic response for both mid parent heterosis and better parent heterosis were positive for number of seeds per pod. Kunadia and Singh (1980), Tewari and Pandey (1987), Arora and Pandey (1987), Bahl and Kumar (1989), Main and Bahl (1989), Rao and Chopra (1989), Shinde and Deshmukh (1990), Katiyar and Katiyar (1993) and Kamatar *et al.* (1996) reported heterosis for this character. The results of inbreeding depression estimate showed positive for this trait. Parallel relationship between heterosis and inbreeding depression suggests the importance of nonadditive gene action for number of seeds per pod.

5.6.11 Seed yield per plant

The positive values of heterosis and heterobeltiosis were observed for seed yield per plant. High heterosis for grain yield was associated with high heterosis for number of pods per plant, number of seeds per plant and number of seeds per pod. Singh and Singh (1976), Bhatt and Singh (1980), Kunadia and Singh (1980), Deshmukh and Bhapkar (1982) Arora and Pandey (1987), Tewari and Pandey (1987), Bahl and Kumar (1989), Main and Bahl (1989), Pandey and Tiwari (1989), Rao and Chopra (1989), Shinde and Deshmukh (1990), Khan *et al.* (1991), Gumber *et al.* (1992), Kamatar *et al.* (1996), Patil *et al.* (1996) and Vijayalakshmi Satya (1998) reported heterosis for this character. Inbreeding depression estimate was negative for seed yield per plant. High heterosis and negative value of inbreeding depression was noticed in the present investigation. In a few crosses Deshmukh and Bhapkar (1982), Tewari and Pandey (1987) and Shinde and Deshmukh (1990) also observed such results in segregant populations in their studies. Although these

workers obtained high and significant of inbreeding depression for seed yield per plant in most of crosses.

5.7 SUPERIORITY OF RILs OVER PARENTS

The results showed that the cross between high growth vigour parent (ICCV2) and low growth vigour parent (JG62), could give rise 87 percent RILs population more vigour than low growth vigour parent and 47 percent more vigour than the high growth vigour parent. Estimates of superiority obtained by 35 and 81 percent of RILs set to first flower earlier than early flowering parent (ICCV2) and medium flowering parent (JG62), respectively. With regard to days to maturity 45 and 60 percent of RILs matured earlier than ICCV2 and JG62 respectively.

Drought escape is a particularly important strategy of matching phenological development with the duration of soil moisture availability to minimize the impact of drought stress on crop production in environments where the growing season is short and terminal drought stress predominates (Turner, 1986a, b). Abiotic stress factors contribute significantly to the generally low yields (<0.8 t/ha) of chickpea and pigeonpea in farmer fields. Development of short duration genotypes of both chickpea and pigeonpea has increased options of escaping terminal drought stress (Chauhan *et al.*, 1992). For most crop species, breeding for shorter duration is a major objective, not only to match phonology to season length, but also for other reasons such as to fit crops/genotypes into more intensive crop rotations (Subbarao *et al.*, 1995).

Association between high growth vigour and early maturity can escape the terminal drought stress. In the present study, RIL number 8, 49, 67 and 108 exhibited high growth vigour and early maturity, these RILs may prove to be good varieties for drought situations.

ICCV2 has medium while JG62 has small seed size. Estimates of superiority indicated that 9 percent of RILs had more 100-seed weight than ICCV2. Seed size is not only one of the most important yield components (Singh and Paroda, 1986) but also an important criterion for consumer preference (Singh, 1987). It has also been considered as an important factor in germination, seedling vigour, seedling mass, and subsequent plant growth (Narayanan *et al.* 1981; Dahiya *et al.* 1985). Results of the present study indicate that additive gene effects play an important role in the expression of 100-seed weight. Improvement in seed size is an important objective in chickpea breeding programs. Therefore, selection of RILs with large seed size in crossing program can further improvement this character in chickpea.

In the present investigation out of 126 RILs studied, two RILs namely numbers 8 and 67 were superior to either parent for most characters. It is suggested that, these two RILs should be crossed to realize good recombinants for further improvement of the population for realizing with pure lines superior characteristics.

Summary

CHAPTER VI

SUMMARY

The present investigations were taken up (i) to study the inheritance of flower colour, stem colour, number of pods per peduncle, seed surface, seed type and seed coat colour, (ii) to determine linkage among these characters, and (iii) to estimate heritability, genetic advance, coheritability, correlated genetic gain, heterosis, inbreeding depression and superiority of RILs over parents for days to first flowering, days to first podding, days to 50% flowering, days to maturity, 100-seed weight, plant height, plant width, number of pods per plant, number of seeds per plant, number of seeds per pod, number of primary branches per plant, number of secondary branches per plant, seed yield per plant, leaf size, leaf weight, specific leaf weight, seed fibre and seed yield per plot.

The material for investigation comprised of parents, F_1, F_2, F_3, BC_1P_1 and BC_1P_2 generations and F_{10} random recombinant inbred lines (RILs) of a cross between a popular kabuli variety (ICCV2) and a desi variety (JG62) of chickpea (*Cicer arietinum* L.). The studies were carried out during the *Rabi* season 1998-1999 and 1999-2000 at the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, near Hyderabad A. P. 502 324, India.

The experimental design to test 126 RILs, the two parental lines, F_1 and three checks (Annigeri, ICCV10, ICCV96029) was Alpha design with three replications. Each replication consisted of 12 blocks and 11 treatments appeared in each block. The plot size for RILs were 2 rows of 4 meter length with spacing 60 cm spacing between rows and 10

cm spacing between plants within the rows. The seven generations of the cross: P_1, P_2, F_1, F_2, F_3, BC_1P_1 and BC_1P_2 were planted unreplicated. The generations were planted as single row with spacing of 60 cm between rows and 20 cm between plants. The following results were obtained.

Monogenic inheritance was obtained for three characters, pink vs. white flowers, pigmented vs. non-pigmented stem colour and single podded vs. double podded characters. The flower colour genotype for ICCV2 was determined as PPbbCC and that for JG62 as PPBBCC. Seed surface was governed by two pairs of genes (Sr_1 and Sr_2) in which dominant inhibitory epistasis is operating for this character. Seed type was controlled by two pairs of genes. Plants with dominant genes at both loci ($St_1St_1St_2St_2$) produce desi type and dominant gene in one locus ($St_1St_1st_2st_2$ or $st_1st_1St_2St_2$) produce intermediate type and recessive alleles at both loci ($st_1st_1st_2st_2$) produce kabuli type. Crude fibre content among desi, kabuli and intermediate types differed with desi having the highest and kabuli the lowest. Early growth vigour was controlled by two pairs of genes. This character appears to be governed by duplicate dominant epistasis. Plants with dominant gene in one or two loci have high growth vigour (Gv_1Gv_2, Gv_1gv_2 or gv_1Gv_2) and recessive alleles in both the loci produce low growth vigour (gv_1gv_2). This character had significant negative correlation with days to first flower, days to 50% flowering, days to first pod and days to maturity. This shows that with the selection of high growth vigour genotypes may increase options of escaping terminal drought stress where the growing season is short and terminal drought stress predominates. Seed coat colour was controlled by at least three gene pairs (Ysc, Bsc, Rsc). If the three loci are present in dominant condition, the seed coat colour is yellow brown. The genotypes with two loci in dominant condition are brown, reddish

brown or light brown. If dominant gene is present at one locus, the seed coat colour is yellow beige, dark beige and dark brown. Three recessive genes result in light yellow seed coat colour. Comparison single and double podded in F_2 and RILs showed that double pod character did not effect significantly on seed size and seed yield.

The study of interrelationship between two pairs of characters: flower colour, stem colour, seed coat colour, seed type and seed surface showed that gene 'b' controlling the white flower colour had pleiotropic effect on non-pigmentation (stem colour). One of the genes for flower colour (B) was linked with one of the genes for seed type (St_1, St_2) and distance between two genes was about 29 cM. Investigation of joint segregation between number of pods per peduncle and seed coat colour indicated that all the colours were inherited independently of the locus for number of pods per peduncle. Also there was no linkage between number of pods per peduncle and flower colour, stem colour, seed type and seed surface. One of the genes for flower colour was linked with one of the genes for seed coat colour (Ysc, Bsc, Rsc). The genes responsible for seed surface was independent from the genes controlling flower colour, stem colour, seed type and seed coat colour. There was linkage between one of the genes governing seed coat colour and one of the genes governing seed type and distance between two genes was 35 cM. Also there was linkage between gene controlling stem colour and one of the genes governing seed type and seed coat colour. Distance between one of the gene governing stem colour and seed type was 29 cM.

Narrow sense heritability and genetic advance percentage as mean for quantitative characters indicated 100-seed weight, leaf weight and specific leaf weight had very high heritability and genetic advance. High narrow sense heritability along with high genetic advance indicated that substantial contribution of additive genetic effect in the expression of these characters. Therefore, selection for these traits can be effective in early generations. Seed yield per plant had moderate narrow sense heritability coupled with moderate genetic advance. Thus, the results indicated the presence of both additive and nonadditive gene action for this character. The gene action for days to first flower, days to first pod and days to maturity suggest non additive genetic effects and it would be desirable to carry earlier generations of population derived from crosses by bulk method and postpone selection to later generation till maximum homozygosity is attained by the populations when the gene complexes are fixed. The highest heritability value by regression in this study was for days to first pod followed by days to first flower and 100-seed weight.

The number of pods per plant followed by number of seeds per plant and number of secondary branches per plant had high correlated response with seed yield per plant. Number of secondary branches per plant, number of pods per plant and number of seeds per plant exhibited high correlated response to selection with seed yield per plot. These show that through selection for number of pods per plant, number of secondary branches per plant and number of seeds per plant improved seed yield per plant and per plot could be achieved in chickpea.

The coheritability estimates of different characters with yield per plant revealed yield per plot had high coheritability with yield per plant. Days to maturity, number of seeds per pods, number of secondary branches per plant and number of primary branches per plant had moderate coheritability with seed yield per plant. Number of pods per plant had high coheritability with 100-seed weight. Seed yield per plot exhibited high coheritability with days to first pod, number of pods per plant, number of seeds per plant, number of primary branches per plant and seed yield per plant. The coheritability value of yield per plot with days to maturity and number of secondary branches per plant were moderate. The results of the present study indicate that simultaneous selection for days to first pod, number of pods per plant and number of seeds per plant can improve seed yield of chickpea.

In the present study high values for heterosis over mid parent and better parent were observed for number of pods per plant followed by seed yield per plant, number of seeds per plant, days to first flower, number of seeds per pod, days to first pod, plant width and days to maturity.

Among the 126 RILs 4 RILs (#s 8, 49, 67 and 108) were superior to ICCV2 for most of yield component characters. RILs number 8, 78 showed 13 and 14 out of 19 characters superior than ICCV2. Also 11 RILs (#s13, 41, 48, 67, 69, 73, 85, 96, 99, 109 and 116) were superior to JG62 for most characters. RIl numbers 13, 73, 85 and 109 were superior to JG62 for 13, 14, 13 and 14 out of 19 characters studied.

Future strategy

Many quantitative characters of economic value are under polygenic control. Direct selection of these traits is quite often ineffective, because the genes controlling these traits have small individual effects and are influenced markedly by environment. Therefore, it should be necessary to know linkage between quantitative traits and to know major marker gene. However study on 18 quantitative characters in this investigation in F_2 and RILs and future studies in markers it become possible to identify map quantitative traits loci (QTL) in chickpea.

Future investigations should include complementation studies for effect of double podded nature per peduncle on seed yield. Comparisons should be made between single and double podded lines along with parents having significant difference in seed yield.

A uniform recording system for seed surface and seed coat colour in chickpea is needed to overcome the difficulties.

Selection for desi type segregants with low fibre content would help in maximum recovery of *dhal*. Transfer of high fibre content to kabuli seeds may offer better resistance against bruchids and root disease. But it may not be a suitable character for consumer.

The future studies should be taken up with use of RILs number 8 with high growth vigor and early maturity and 67 with large seed, high growth vigour and early maturity in breeding programme. By crossing these two RILs new variety with good agronomic desirable traits coupled with high yielding lines can be realised.

Literature cited

LITERATURE CITED

Ahmad Nazir 1964 Inheritance of pod character in *Cicer* species and its economic importance. West Pakistan Journal of Agricultural Research 2: 58-61.

Alam M 1935 A genetical analysis for *Cicer arietinum* L. Proceeding Indian Science Congress., 22 : 369-370.

Allard R W 1960 Principles of plant breeding. John Wiley and Sons, Inc., New York.

Argikar G P 1955 Two cases of pleiotropy in *Cicer arietinum*. Indian Journal of Genetics and Plant Breeding 15: 50-52.

Argikar G P 1956 Some qualitative and quantitative servations on the genetic improvement of green seed strains of *Cicer arietinum*. Indian Journal of Genetics and Plant Breeding 16: 52-56.

Argikar G P and D'Cruz R D 1962 Inheritance of Foliage, Cotyledon and Testa colour in *Cicer*. Indian Journal of Genetic and Plant Breeding, 22: 241-243.

Argikar G P and D'Cruz R 1963 Genetic studies in gram. Journal of the Indian Botanical Society 42: 401-405.

Arora P P and Pandya B P 1987 Heterosis in chickpea. International chickpea Newsletter. ICRISAT. 16: 3-4.

Athwal D S and Sandhu G S 1967 Inheritance of seed size and seed number per pod in *Cicer*; Indian Journal of Genetics and Plant Breeding 27: 21-33.

Auckland A K and Singh K B 1977 The Exploitation of Natural Genetic Variability for the Improvement of Chickpea (*Cicer arietinum* L.). pp. 83-95. In; International Symposium on Genetic Control of Diversity in Plants. Eds. A Muhammed, R. Askel and R.C. von Borstel, Lahore.

Ayyar V R and Balasubramanyan R 1936 Inheritance of certain colour characters in gram (*Cicer arietinum*). Proceedings of the Indian Academy of Science 4: 1-26.

Ayyar V R and Balasubramanian R 1937 Inheritance of branching habit in gram (*Cicer arietinum*). Madras Agricultural Journal 25: 105- 106.

Aziz M A, Shah S and Asghar, M 1960 Association of qualitative characters in gram (*Cicer arietinum*) Proceedings of Pakistan Science Conference 12: 74.

Bahl P N and Kumar J 1989 Evaluation and utilization of high yielding hybrids of chickpea. Indian Journal of Genetics and Plant Breeding 49(1): 53-58.

Balasubrahmanyan R 1937 Inheritance of characters in gram (*Cicer arietinum* L.) Foliage colour and rough seed coat. Madras Agricultural Journal 25: 207-208.

Balasubramanian R 1950a The association of size and colour in gram (*Cicer arietinum* L.). Current Science 19: 246-247.

Balasubramanian R 1950b Inheritance of seed-coat colour in gram. Madras Agricultural Journal 37: 379-384.

Baradat P 1976 Use of juvenile-mature relationships and information from relatives in combined multitrait selection. IUFRO, Advanced Generation Breeding, Bordeax-June 14 18,1976,pp, 121-138. INRA, Lab. d'Amelioration des Coniferes, 33610 CESTAS, France.

Bhapkar D G and Patil J A 1962 Inheritance of foliage and seed-coat colour in gram. Science and Culture 28 (9): 441-442.

Bhapkar D G and Patil J A 1963 Inheritance of Foliage, Flower, and Seed-coat colour in gram. Crop Science 3: 361.

Bhat N R and Argikar G 1951 A genetic linkage in *Cicer arietinum* L. Heredity 5: 143-146.

Bhatt D D and Singh D P 1980 Heterosis in *Cicer arietinum* L. International Chickpea Newsletter. 3: 4-5.

Bhatt D .D and Singh D P 1980 Combining ability in chickpea. Indian Journal of Genetics and Plant Breeding 40: 456-460.

Biswas P K and Sasmal B 1989 A study of coheritable variation in white tossa and interspecific Jute hybrids. Phytobreedon, 5(1): 42-45.

Black J N 1959 Seed size in herbage legumes. Herbage Abstracs (29): 235-41.

Brar H S and Athwal D S 1970 Identification of Gene Controlling Seed Colour in *Cicer arietinum* L. Indian Journal of Genetics and Plant Breeding. 30 (3): 690-703.

Chand H Srivastva L S and Trehan K B 1975 Estimates of genetic parameters, and path coefficient analysis in gram *(Cicer arietinum* L.). Madras Agricultural Journal 62: 178-181.

Chandra S 1968 Variability in gram. Indian Journal of Genetics and Plant Breeding 28: 205-210.

Chauhan Y S, Saxena N P and Johansen C 1992 Abiotic factors limiting chickpea and pigeonpea production. Pages: 111-213 in Proceedings of the National Symposium

on New Frontier in Pulses Research and Development. Directorate of Pulses Research, Kanpur, Uttar Pradesh, India: Directorate of pulses Research.

Chavan V W, Patil H S and Rasal P N 1994 Genetic variability, correlation studies and their implications in selection of high yielding genotypes of chickpea. Madras Agricultural Journal 81(9): 463-465.

Cubero J I 1987 Morphology of Chickpea. Pages 35-56 in the chickpea (Saxena, M.C. and Singh, K. B.,eds.). Wallingford, Oxon, U: CAB International.

Dahiya B S, Solanki I S and Kumar R 1985 Germination rate and its genetics in chickpea. International Chickpea Newsletters, 13: 6-8.

Davis T M 1991 Linkage relationships of genes for leaf morphology, flower colour, and root nodulation in chickpea. Euphytica 54: 117-123.

Davis D R, Berry G J, Heath M C and Dawkins T C K 1985 Pea (*Pisum sativum* L.). Grain Legume crops. Collin, 8 Grafton Street, London W.I. U K. 147-198.

D'Cruz R and Tendulkar A V 1970 Genetics studies in Bengal gram (*Cicer arietinum* L.) I. Double pod x White flower gram. II. Research Journal of Mahatma Phule Krishi Vidyapeeth, Rahuri, India 1: 121-127.

Deshmukh R B 1972 Inheritance in Bengal Gram. Kolhapur Agricultural College Magazine 6 (1 and 2): 1-5.

Deshmukh R B and Bhapkar D G 1982 Heterosis and inbreeding depression in chickpea. Indian Journal of Genetics and Plant Breeding 42: 208-212.

Deshmukh R B, Patil J A and Deokar AB 1972 Genetic studies in Bengal gram V. Chikodi V.V. x Wh. Fl. Wh. Gr. II. Research Journal of Mahatma Phule Krishi Vidyapeeth, Rahuri, India 3: 96-105.

Dixit P D 1932a Studies in Indian pulses, a note in gigatism in gram (*Cicer arietinum* L.). Indian Journal Agriculture Science 2(4): 391-406.

Dixit P W 1932b Studies in Indian Pulses (a note on the cytology of "Kabuli" and "Desi" gram types). Indian Journal Agriculture Science 2(4): 385-390.

Dombrowsky- Sudsky L 1927 Introduction to the Botany of field crops. Johanesburg, South Africa Central News Agency Ltd.

Dudley J W 1997 Quantitative genetic and plant breeding. pp 1-23 In Advance in Agronomy, Academic Press, Inc.

Falconer D S 1989 Introduction to quantitative Genetics. John Wiley and sons, Inc., New York.

FAO 1999 Quarterly bulletin of statistics. Food and Agriculture Organization of the United Nation, Rome. Vol. 12 (3/4) 25-25.

Fehr W R 1987 Principles of cultivar development. Macmillan, New York.

Frey K .J and Horner T 1957 Heritability in Standard Units. Agronomy Journal, 49(2): 59-62.

Ghatge R D, Kolhe A K and D'Cruz R 1985 Inheritance of corolla and seed coat colour in gram. Journal of Maharashtra Agricultural Universities 10: 164-166.

Ghatge R D 1992 Genic relationship of leaf/leaflet shape inheritance with leaf/leaflet size in chickpea (*Cicer arietinum* L.) Annals of Agriculture Research 13(3) : 228-234.

Ghatge R D 1993 Inheritance of seed size in chickpea (*Cicer arietinum* L.) J. Soils and Crops, 3(1): 56-59.

Ghatge R D 1994 Genetics of stem and corolla colour in chickpea (*Cicer arietinum* L.). Crop Research (3): 431-436.

Gil J and Cubero I 1993 Inheritance of Seed Coat Thickness in Chickpea (*Cicer arietinum* L.). Plant breeding 111: 257-260.

Gowda C L L and Bahl P N 1978 Combining ability in chickpea. Indian Journal of Genetics and Plant Breeding 38: 245-251.

Godawat S L and Choudhary B R 1990 Correlated response of grain yield in proso millet (*Panicum miliaceum*). Indian Journal of Agricultural Sciences. 60 (11): 758-759.

Gumber R K Sandhu T S and Singh S 1992 Genetic distance, heterosis and choice of parents in chickpea. Programme and Abstracts, Second International Food Legume Research Conference, Cario, Egypt, 12-16 April 1992. International Food Legume Research Conference Organising Committee pp 56.

Gupta S N 1985 Studies on genetic variability for drought resistance in chickpea (*Cicer arietinum* L.). Ph.D. Thesis submitted to Haryana Agricultural University, Hisar (India).

Gupta P K 1997 Genetics. Rekesh Kumar Rastogi. New Delhi, India.

Gupta S P, Luthra R C Gill AS and Phull P S 1972 Variability and correlation studies on yield and its components in gram. Journal Research Punjab Agricultural University, Ludhiana, 9: 405-409.

Hall A E and Grantz D A 1981 Drought resistance of Cowpea improved by selecting for early appearance of mature pods. Crop Science 21: 461 464.

Hall A E and Patel P N 1985 Breeding for resistance to drought and heat. Pages 137-151 in Cowpea Research, Production, and Utilization (Singh, S.R., and Rachie, K.O., eds). Wiley , England.

Haskins F A and Gorz H J 1975 Influence of seed size, planting depth and companion crop on emergence and vigour of seedlings in sweetclover. Agronomy Journal (67) 562-564.

Hawtin G C.and Singh K B 1980 Kabuli-Desi Introgression: Problems and Prospects. *In* Proc. International Workshop on Chickpea Improvement. ICRISAT, Hyderabad pp 51-60.

Jagtap D R, Deokar A B, Sonone H N and D'Cruz R 1973 Genetic studies in Bengal gram VI. A triangular cross. Research Journal of Mahatma Phule Krishi Vidyapeeth, Rahuri, India 4(1): 7-22.

Jain P K, Ramgiry S K and Singh C B 1998 Genotype and environment interaction of seedling character in chickpea. Crop Research 16(3): 321-324.

Jahagirdar J E Patil R A and Khare P R 1994 Genetic variability and its relevance in chickpea improvement. Indian Journal of Pulses Research 7(2): 179-180.

Jambunathan R, Blain H L, Dhindsa K S, Hussein L A, Kogure K, Li-Juan L and Youssef M M 1994 Diversifying use of cool season food legumes through processing. pp. 98-112. In: F.J. Muehlbauer and W.J. Kaiser (eds.), Expanding the Academic Publishers, the Netherlands.

Jambunathan R and Singh U 1979 Studies on desi and kabuli chickpea (*Cicer arietinum* L.) cultivars. I. Chemical composition. Proceedings of International Workshop on Chickpea Improvement, ICRISAT, Hyderabad, India (Eds J. M. Green, Y. L., Nene and J. B. Smithson), pp. 61-66.

Jambunathan R and Singh U 1980 Studies on desi and kabuli chickpea (*Cicer arietinum* L.) cultivars. I. Chemical composition. Pages 61-66 in Proceedings of the International Workshop on Chickpea Improvement, 28 Feb to 2 Mar 1979, ICRISAT, Hyderabad, India. Patancheru, A.P. 502 324, India : International Crops Research Institute for the semi-Arid Tropics.

Janssens M J J 1979 Co-heritability: its relation to correlation response, linkage, and pleiotropy in cases of polygenic inheritance. Euphytica 28: 601-608.

Jha S K, Jaiswal H K and Saha A K 1997 Genetic analysis of some quantitative characters in chickpea (*Cicer arietinum* L.) Annals Agricultural Research 18(4): 420-426.

Jinks JL, Pooni H S and Chowdhury M K U 1985 Detection of linkage and pleiotropy between characters of *Nicotiana tabacum* using inbred lines produced by dihaploidy and single seed descent. Heredity, 55 : 327-333.

Jivani L L and Yadavendra J P 1988 Genetic variability in chickpea. Indian Journal of Pulses Research 1(1): 62-63.

Johansen C, Baldev B, Brower J B, Erskine W, Jermym W A, Li-Juang L, Malik B A, Ahmad Mia and Silim S N 1994a Biotic and abiotic stresses constraining productivity of cool season food legumes in Asia, Africa and Oceania. In: Expanding the Production and Use of Cool Season Food Legumes. (pp.175-194), Muehlbauer, F. J. and W. J. Kaiser, Eds., Kluwer, Academic Publishers, Dordrecht, The Netherlands.

Johansen C, Singh D N, Krishnamurthy L, Saxena N P, Chauhan Y S and Kumar Rao J V D K 1997 Options For Alleviating Moisture Stress in Pulse Crops. In : Recent advances in pulses Research. A.N. Asthana and Masood Ali (Eds), Indian Society of Pulses Research and development. IIPR. Kanpur India.

Johansen C, Singh D N, Krishnamurthy L, Saxena N P and Sethi S C 1994b Genotypic variation in moisture response of chickpea grown under line-source sprinklers in a semi-arid tropical environment. Field Crops Research (37): 103-112.

Johnson S K, Helsel D B and Frey K J 1983 Direct and indirect selection for grain yield in oats (*Avena Sativa* L.) Euphytica 32: 407-413.

Kadam B S, Patel SM and Patankar V R 1941 Two new genes for corolla colour in *Cicer arietinum*. Current Science 10: 78-79.

Kamatar M Y, Biradar B D and Hiremath S M 1996 Heterosis studied in chickpea (*Cicer arietinum* L.). Crop Research 11 (2): 174-178.

Katiyar R P and Katiyar P K 1993 Heterosis and combining effects in chickpea. Indian Journal Pulses Research 6(2) : 127-131.

Katiyar P K and Katiyar R P 1994 Correlated response for physiological, quality and yield attributes in chickpea. Indian Journal of Pulses research. 7(2): 119-122.

Kempthorne O and Tandon O B 1953 The estimation of heritability by regression of offspring on parent. Biometrics 9 : 90-100.

Khan A R and Akhtar A R 1934 The inheritance of petal colour in gram. Agriculture and Livestock in India 4: 127-155.

Khan Imtiaz Ahmed, Imtiaz Seema and Malik Bashir Ahmed 1991 Selection of diverse parents of chickpea (*Cicer arietinum* L.) by multivariate analysis and the degree of heterosis of their F_1 hybrids. Euphytica 51: 227-233.

Khan S, Khan A R and Khan M N 1950 Some breeding investigations on gram in the Punjab. The Linkage of Factors. Proceeding Pakistan Science Conference 2: 11-12.

Khosh- Khui M and Niknejad M 1971a Flower colour inheritance in reciprocal crosses of white and black chickpea (*Cicer arietinum* L.). Israel Journal of Agricultural Research 21: 81-82.

Khosh-Khui M and Niknejad M 1972b Heritability and number of genes responsible for seed yield per plant in reciprocal crosses of chickpea: (*Cicer arietinum* L.). Current Science 41: 296-297.

Kneebone W R and Cramer C L 1955 The relationship of seed size to seedling vigour in some grass species. Agronomy Journal (47) 472-477.

Knights E J 1987 The double podded gene in chickpea improvement. International Chickpea Newsletter 17: 6-7.

Knights E J 1980 Kabuli-Desi Introgression: The Experience in Australia: In Proc. International Workshop on Chickpea Improvement. ICRISAT, Hyderabad. PP 70-74.

Knights E J and Maller R J 1989 Association of seed type and colour with establishment, yield and seed quality in chickpea (*Cicer arietinum* L.) Journal of Agricultural Science, Cambridge. 113, 325-330.

Kumar J 1997 Complementation for flower colour in two chickpea crosses. . Indian Journal Pulses Research 10: 227-228.

Kumar J 1998 Heritability estimates as computed by different methods in chickpea. . Indian Journal Pulses Research 11(1): 77-78.

Kumar J, Kaiser W J and Hanna R M 1991 Damping-off resistance in chickpea. Plant Disease 75 (12): 1244-1245.

Kumar J Sethi S C Johansen C Kelley T G Rahman M M and Van Rheenen H A 1996 Potential of short-duration chickpea varieties. Indian Journal of Dryland Agricultural Research and Development 11 (1): 28-32.

Kumar J, Srivastava R K and Ganesh M T 2000 Penetrance and Expressivity of the Gene for Double Podding in Chickpea. The Journal of Heredity 91(3): 234-236.

Kumar J, Vijayalakshmi N V S and Nageshwar Rao T 2000 Inheritance of Flower Colour in Chickpea. The Journal of Heredity 91 (5): 416-417.

Kumar S and Singh O 1995 Inheritance of seed size in chickpea. Journal of Genetics and Breeding 49: 99-103.

Kunadia B A and Singh D P 1980 Heterosis and Inbreeding depression in kabuli gram (*Cicer arietinum* L.). International Chickpea Newsletter. ICRISAT. 3: 3-4.

Ladizinsky G 1975 A new Cicer from Turkey. Notes from the Royal Botanic Gardens, Edinburgh 34: 201-202.

Lather V S, Waldia R S and Mehla I S 1997 Early Vigour Spontaneous Mutant in Chickpea. International Chickpea Newsletter 4 : 11-12.

Laxman Singh, Gupta S C and Faris D G 1990 Pigeonpea : Breeding. Pages 375-399 in The Pigeon pea (Nene, Y. L., Hall, S.D., and Sheila, V.K.eds.). Wallingford, UK: CAB International.

Luciano A, Kinman M L and Smith J D 1965 Heritability of Self-Incompatibility in the Sunflower (*Helianthus annuus*). Crop Science. 5: 529-532.

Lush J L 1940 Intra-sire correlations or regressions of offspring on dam as a method of estimating heritability of characteristics. Proceeding American Society Animal Production 293-301.

Malhotra R S, Geletu Bejiga and Singh, K.B 1997 Inheritance of seed size in chickpea. Journal of Genetics and Breeding 51: 45-50.

Mandal A K 1992 Pattern of variation of harvest index in chickpea crosses. Indian Journal of Genetics and Plant Breeding 52 (2): 164-168.

Mandal A K and Bahl P N 1980 Estimates of variability and genetic correlations in chickpea. Annals of Agricultural Research 1: 136-140.

Mandal A K and Bahl P N 1983 Genetic variability and correlation of harvest index in chickpea. International Chickpea Newsletter, 8: 11- 12.

Mandal A K and Bahl P N 1984 Heterosis in diverse crosses of chickpea. Indian Journal of Genetics and Plant Breeding 44 (1): 173-176.

Mathur D S 1989 Light- dependent Purple Pigmentation in Chickpea Plant. International Chickpea Newsletter, Dec 1989, ICRISAT.

Mathur D S 1998 Inheritance of light dependent purple pigmentation in chickpea. Indian Journal of Genetics and Plant Breeding 58 (2): 149-152.

Mather K and Jinks J L 1982 Biometrical Genetics. Chapman and Hall, London.

Mathur R and Mathur M L 1996 Estimation of genetic parameters and interrelationship of quantitative traits in chickpea. Madras Agricultural Journal 83(1): 9-11.

Matthews S, Powell A S and Spaeth S C 1988 Seedling vigour and susceptibility to diseases and pests: *In* World crop: Cool season legumes. Summerfield- R.J (ed) Reading University UK. Dept of Agriculture. Dordrecht (Netherlands). Kluwer Academic Publishers. 619-625.

Mc Blain B A and Hume D J 1980 Physiological studies of higher yield in new early maturing soybean cultivars. Canadian Journal of Plant Science 60: 1315-1326.

Mehan D K, Singh G and Saini S S 1982 Coheritable variation in rice. Indian Journal of Genetics and Plant Breeding 42: 296-301.

Menendez Cristina M and Hall Anthony E 1995 Heritability of Carbon Isotope Discrimination and correlations with Earliness in Cowpea. Crop Science 35: 673-678.

Mian M A 1971 Inheritance of flower colour in gram (*Cicer arietinum* L.). Agriculture Pakistan 22: 457-463.

Mian M A and Bahl P N 1989 Genetic divergence and hybrid performance in chickpea. Indian Journal of Genetics and Plant Breeding 49(1): 119-124.

Misra R C 1991 Stability of Heritability, Genetic Advance, and Character Association Estimates in chickpea. International Chickpea Newsletter, ICRISAT. 25: 10-11

Mishra A K, Raghu J S, Pathak K N, Ali S A and Ghurraya R S 1994 Genetic parameters and interrelationship analysis in chickpea (*Cicer arietinum* L.). Crop Research 8(1): 109-111.

Mishra R, Rao S K and Koutu G.K 1988 Genetic variability, correlation studies and their implication in selection of high yielding genotypes of chickpea. Indian Journal of Agricultural Research 22(1): 51-57.

Mishra R, Rao S K, Koutu G K and Bilaiya S K 1992 Correlated response in chickpea (*Cicer arietinum* L.) Agricultural Science Digest, 12 (2): 69-72.

More D C 1976 Genetic studies in gram. M.Sc. (Agri.) Thesis, University of Poona, Poona.

More D C and D'Cruz R 1970 Genetics studies in Bengal gram (*Cicer arietinum* L.). Poona Agriculture College Magazine 60 : 27-32.

More D C and D'Cruz R 1976a Genetic Studies in Bengal Gram (*Cicer arietinum* L). Journal of Maharashtra Agricultural Universities (1): 15-17.

More D C and D'Cruz R 1976b Genetic studies in Bengal Gram (*Cicer arietinum* L.) V: D-70-10 x White Flowered White Grained- II. Journal of Maharashtra Agricultural Universities 1(1): 11-14.

More D C and D'Cruz R 1976c Inheritance of cotyledon, testa, foliage and corolla colour in Bengal gram (*Cicer arietinum* L.) Botanique 7: 37-40.

Moreno M T and Cubero J I 1978 Variation in *Cicer arietinum* L. Euphytica 27, 465-468.

Muehlbauer F J and Singh K B 1987 Genetics of Chickpea. *In*: The chickpea. Eds. M.C. Saxena and K.B. Singh. Walling Ford, Oxon, U. K., CAB Intl., 99-125.

Narayanan A, Saxena N P and Sheldarke A K 1981 Varietal differences in seed size and seedling growth of pigeonpea and chickpea. Indian Journal of Agricultural Science. 51 (6): 389-393.

Nayeem K A, Kolhe A K and D'Cruz 1977 Inheritance of colour, seed surface and spinate seed in 'P 4-14-1' x 'D 70-10' gram. Indian Journal of Agricultural Science 47 (12): 608-611.

Niknejad M, Kosh-khui M and Ghorashy 1971 Inheritance of seed size in chickpea. Crop Science 51 (5): 768-769.

Or E, Hovav R and Abbo S 1999 A major gene for flowering time in chickpea. Crop Science 39: 315-322.

Oudhia P, Kolhe S S and Tripathi R S 1997 Allelopathic effect of *Blumea lacera* L. on wheet. Abstracts Seventh Biennial Conference. Ludhiana, Punjab, India: Indian Society of Weed Science. 109 pp.

Pal B P 1945 Studies in hybrid vigour, notes on the manifestation of hybrid vigour in gram, sesamum, chili, and maize. Indian Journal of Genetics and Plant Breeding 5: 106-121.

Panchbhai K M, Thote S G, Patil A J and Wanjari KB 1992 Study of genetic variation in bulk populations of chickpea (*Cicer arietinum* L.) developed through different breeding methods. Annals of Plant Physiology 6 (1): 73-76.

Pandey R L and Tiwari A S 1983 Heritability and genetic gain. International Chickpea Newsletter, 9: 5-6.

Pandey R L and Tiwari A S 1989 Estimation of gene effects and heterosis in chickpea. . Indian Journal of Agricultural Research 23 (4): 191-199.

Pandey R L Tiwari A S and Thakur S K 1990 Genetic variance and heritability under different genetic backgrounds of chickpea. Indian Journal Pulses Research 3(2): 117-120.

Panse VG and Sukhatme P V 1989 Statistical Methods for Agricultural Workers. Indian Council of Agricultural Research. New Delhi. pp 359.

Parthasarathy V A and Medhi R P 1983 Coheritability, path coefficient and discriminate functions in radish. Indian Journal of Agricultural Science 53(2): 111-114.

Patil A B, Salimath P M, Chetti M B and Patil S A 1996 Exploitation of D x K crosses for breaking yield bariers in chickpea. International Crop Science Congress, Second : Crop Productivity and Sustainability- Shaping the Future, National Academy of Agricultural Science : Indian Council of Agricultural Research, New Delhi. pp 225.

Patil J A and D'Cruz R 1964 Inheritance of seed size in gram (*Cicer arietinum*), Poona Agricultural College Magazine 54: 21-22.

Patil J A and Deshmukh R B 1975 Inheritance and linkage studies in Bengal gram (*Cicer arietinum* L.) T-54-A x D-70-10 chickpeas. Research Journal of Mahatma Phule Krishi Vidyapeeth, Rahuri, India. 6: 88-95.

Patil V N and Phadnis B A 1977 Genotypic variability and its implication in selection of gram (*Cicer arietinum* L.). Journal of Maharashtra Agricultural Universities 2: 121-123.

Pawar A .M and Patil J A 1979 Genetic Studies in Bengal Gram (*Cicer arietinum* L.) Journal of Maharashtra Agricultural Universities 4(1): 61-64.

Phadnis B A 1976 Genetics of flower colour in Bengal gram. Indian Journal of Genetics and Plant Breeding 36: 54-58.

Phundan Singh and Narayanan S S 1997 Biometrical Techniques in Plant Breeding. Kalyani Publishers New Delhi pp 187.

Pimplikar E D 1943 The inheritance of some characters in grams (*Cicer arietinum*). Nagpur. Agricultural College Magazine 18: 27-40.

Pundir R P S and Reddy G V 1998 Two new traits – open flower and small leaf in chickpea (*Cicer arietinum* L.) Euphytica 102: 357-361.

Pundir R P S, Reddy K N and Mengesha M H 1988 ICRISAT Chickpea Germplasm Catalogue; Evaluation and Analysis. ICRISAT. Patancheru A.P. 502 324. Indian International; Crops Research Institute for the Semi Arid Tropic, pp 94.

Pundir R P S, Reddy K N and Mengesha M H 1991 Genetics of some physio-morphic and yield traits of chickpea (*Cicer arietinum* L.).Legume Research, 14(4): 157-161.

Pundir R P S and vander Maesen L J G 1983 Interspecific hybridization in Cicer International Chickpea Newsletter 8: 4 -5.

Radford P J 1967 Growth analysis formulae-their use and abuse. Crop Science 8: 171-175.

Raje R S 1992 Evaluation of chickpea genotypes of varying seed size for germination, seedling vigour and seed yield components. M. Sc (Ag.) Thesis, JNKVV, Jabalpur.

Raju DB, Mehra R B and Bahl P N 1978 Genetic variability and correlations in chickpea. Tropical Grain Legume Bulletin, 13-14 : 35-39.

Ramanujam S, Rohewal S S and Singh S P 1964 Potentialities of heterosis in *Cicer*. Indian Journal of Genetics and Plant Breeding. 24 (2): 122-129.

Ram C, Chandra S, Chaudhary M S and Jatasra D S 1978 Heritability of some quantitative characters in crosses of desi and kabuli varieties of chickpea (*Cicer arietinum* L.). Indian Journal of Agricultural Research 12: 187-190.

Rana O P S, Maherchandani N and Singh KP 1995 Studies on nodulation and its association with seed yield and its components in chickpea (*Cicer arietinum* L.). Crop Research 9(2): 324-329.

Rao B G and Chopra V L 1989 Heterosis and heterobeltiosis in diverse crosses of chickpea. Legume Research 12 (3): 136-138.

Rao N K and Pundir R P S 1983 Inheritance and linkage relationships of a new lobed vexillum mutant in chickpea. Journal of Heredity 74: 300.

Rao S S, Singh R and Das G K 1994 Genetic variability, heritability, expected genetic advance and correlation studies in chickpea. Indian Journal of Pulses Research 7(1): 25-27.

Rastogi K B 1979 Genetic analysis of seed size in chickpea. Indian Journal of Agricultural Science 49 (1): 42-44.

Rastogi K B and Singh L 1977 Heritability, phenotypic and genotypic correlation coefficients of some of the characters in the F_2 population of gram. Crop Improvement, 4: 191-197.

Reddy V G and Chopde P R 1977 Genetic Studies in Bengal Gram (*Cicer arietinum* L.) Chikodi V.V. x Chrysanthefolia. Journal of Maharashtra Agricultural Universities 2(3): 224-226.

Roberts E H 1986 In Physiology of Seed Deterioration, pp. 102-123 (Eds M. B. McDonald, Jr and C.J. Nelson). Madison: Crop Science Society of America.

Roberts E H and Osei- Bonsu K 1988 Seed and seedling vigour *In*: World crop cool season legumes; Summerfield- R.J. Reading University UK. Dept of Agriculture. Dordrecht (Netherlands). Kluwer Academic Publishers 619-625.

Rose I A, K S Mc Whirter and R A Spurway 1992 Identification of drought tolerance in early maturing indeterminate soybeans *(Glycine max L.* Merr.). Australian Journal Agricultural Research 43: 645-657.

Rubio J, Moreno MT, Cubero J I and Gil J 1998 Effect of the gene for double pod in chickpea on yield, yield components and stability of yield. Plant Breeding 117: 585-587.

Sadhu S K and Mandal A K 1987 An analyses of heterosis in chickpea. Phytobreedon 3: 115-117.

Saini H.S and Knights E J 1984 Chemical constitution of starch and oligosaccharide components of 'desi' and 'kabuli' chickpea (*Cicer arietinum* L.) seed types. Journal of Agricultural and Food Chemistry 32: 940-944.

Salimath P M, Bahl P N and Mehra R B 1984 Genetic diversity in chickpea (*Cicer arietinum* L.). Z. Pflanzenziichtg. 92: 52-60.

Salimath P M and Patil S S 1990 Genetic study in F_3 and F_4 generations of chickpea. Indian Journal of Genetics and Plant Breeding 50 (4): 378-381.

Sandhu J S, Verma M M and Brar H S 1993 Inheritance of Foliage Colour in Chickpea. International Chickpea Newsletter, ICRISAT 28: 8.

Sandhu S S, Keim W F Hodges H F and Nyquist W E 1974 Inheritance of protein and sulphur content in seeds of chickpea. Crop Science 14: 649-652.

Sandha G S and Chandra S 1969 Heritability of some quantitative characters in two crosses of Bengal gram. Indian Journal of Genetics and Plant Breeding 29: 216-219.

Sandhu T S, Gumber R K and Bhullar B S 1991 Correlated response of grain yield and protein content in chickpea (*Cicer arietinum* L.). Legume Research 14(1): 45-49.

Sandhu T S and Singh N B 1970 Genetic variability, correlation and regression studies in gram (*Cicer arietinum* L.), Journal of Research Punjab Agricultural University Ludhiana, 7: 423-427.

Saxena N P 1987 Screening for adaptation to drought: case studies with chickpea and pigeonpea. Pages 63-76 in Adaptation of Chickpea and pigeonpea to abiotic stresses. Proceedings of the Consultants Workshop, 19-21 Dec, 1984, ICRISAT Asia Center. India. Patancheru 502-324, A.P., India: ICRISAT.

Setty A N, Patil M S and Hiremath K G 1977 Genetic variability and correlation studies in *Cicer arietinum* L. Mysore Journal Agricultural Science 11: 131-134.

Sharma B D, Sood B C and Malhotra V V 1990 Studies on Variability, heritability and genetic advance in chickpea. . Indian Journal Pulses Research 3 (1): 1-6.

Shaw F L F 1932 Scientific report of the Agril, Research, Station, Pusa, New Delhi.

Sheldrake AR, Saxena NP and Krishnamurthy L 1978. The expression and influence of the 'double-podded' character in chickpea (*Cicer arietinum* L.). Field Crops Research 1:243-253.

Shinde NV and Deshmukh R B 1990 Heterosis and inbreeding depression for yield and its components in chickpea. . Indian Journal Pulses Research 3(2): 121-126.

Simmonds N W 1979 Principles of Crop Improvement. Longman Group, London.

Singh B 1965 Genetics of double-podded mutant in gram *(Cicer arietinum* L.). Science and Culture 31: 145-146.

Singh B D 1997 Plant breeding. Kalyani, New Delhi. pp 702.

Singh H and Ekbote R B 1936. The inheritance of seed characters in gram (*Cicer arietinum* L.) Indian Journal of Agricultural Science 6: 1087-1104.

Singh Harbans and Singh K B 1976 Heterosis in Bengal Gram. Indian Journal of Genetics and Plant Breeding 36 (1): 6-9.

Singh K B 1987 Chickpea Breeding. In: M.C. Saxena and K.B. Singh eds., The Chickpea. CAB International, Wallingford, pp. 127-162.

Singh K B 1993 Problems and prospects of stress resistance breeding in chickpea. In: K.B. Singh and M.C Saxena (eds), Breeding for stress tolerance in cool-season food legumes, pp.17-36. John Wiley & Sons, Chichester, UK

Singh K B and Jain R P 1970 Heterosis in mungbean. Indian Journal of Genetics and Plant Breeding 30: 251-260.

Singh K B, Omar M, Saxena M C and Johansen C 1997 Screening for drought resistance in spring chickpea in the Mediterranean region. Journal of Agronomy and Crop Science 178: 227-235.

Singh K B, Pundir R P S, Robertson L D, van Rheenen H A, Singh U, Kelly T J, Parthasarathy Rao P, Johansen C and Saxena N P 1997 Chickpea. *In* Biodiversity in trust, Edited by D. Fuccillo., L. Sears., P. Stapleton. Cambrige, UK.pp 101-113.

Singh K B, Reddy M V and Malhotra R S 1985 Breeding Kabuli Chickpea for high yield, Stability and adaptation. pp. 71-90. In: M.C. Saxena. And S. Verma (eds.), proceedings of International workshop on Faba Bean, Kabuli chickpea and Lentil in the 1980s . May 1983, ICARDA, Aleppo, Syria.

Singh K B, Saxena N P, Singh Onkar, Saccardo F, Acikgoz N7, and Knights E J 1990 Breeding chickpeas for new applications. Pages 245-253 *in* Chickpea in the Nineties: Proceedings of the Second International Workshop on Chickpea Improvement, 4-8 Dec 1989, ICRISAT Center, India: ICRISAT.

Singh O and Paroda R S 1986 Association analysis of grain yield and its components in chickpea following hybridization and a combination of hybridization and mutagenesis. Indian Journal of Agricultural Science 56: 139-141.

Singh Onkar and van Rheenen H A 1989 A possible role of the double-podded character in stabilizing the grain yield of chickpea. Indian Journal of Pulses Research 2: 97-101.

Singh Onkar and van Rheenen H A 1994 Genetics and contributions of the multiseeded and double- podded characters to grain yield of chickpea.. (En). Indian Journal of Pulses Research 7 (2): 97- 102.g

Singh R K and Chaudhary B D 1996 Biometrical methods in quantitative genetic analysis. Kalyan; publishers, New Delhi pp 318.

Singh R P and Subba Reddy G 1986 Identifying crops and cropping systems with greater production stability in water deficit environments. In: Drought Research Priorities for the Dryland Tropics. (pp. 77-85), Bidinger, F. R. and C. Johansen, Eds., ICRISAT, Patancheru, India.

Singh S P and Mehra R B 1980 Genetic analysis of yield and yield components in Bengal gram. Indian Journal of Genetics and Plant Breeding 40: 482-489.

Singh S P and Ramanujum S 1981 Genetic divergence and hybrid performance in *Cicer arietinum* L. Indian Journal of Genetics and Plant Breeding 4: 268-276.

Singh U 1984 Dietary fibre and its constituent in desi and kabuli chickpea (*Cicer arietinum* L.) cultivars. Nutrition Reports International 29 (2): 419-426.

Smith J D and Kinman M L 1965 The use of parent-offspring regression as an estimator of heritability. Crop Science 5: 595-596.

Smithson J B, Thompson JA and Summerfield R J1985 Chickpea. *In* : Grain legume crops, Edited by R.J. Summerfield and E.H. Roberts. Collins, UK.

Srivastava A N and Jain J K 1994 Variability and coheritability estimates for physiological and economic attributes in soybean. Indian Journal of Genetics and Plant Breeding 54(2): 179-183.

Srivastava R K 1998 Penetrance and expressivity of the Gene for double podding and genetic study of some important yield contributing traits in chickpea (*Cicer arietinum* L.) M.Sc.(Agric) Thesis. Acharya N.G. Ranga Agricultural University Rajendrana, Hyderabad -500 030, Andhra Pradesh, India.

Subbarao G V Johansen C Slinkard A E Nageswara Rao R C Saxena N P and Chauhan Y S 1995. Strategies for improving drought resistance in grain legumes. Critical Reviews in Plant Sciences, 14 (6): 469-523.

Sumathi R and Ramanathan T 1995 Heritability estimated by parent-offspring regression method in groundnut. Madras Agricultural Journal 82(4): 324-325.

Smith H F 1936 A discriminant function for plant selection. Annual Egencies 7: 240-250.

Tefera F 1998 Association of morphological characters and fusarium wilt resistance with seed yield in a Kabuli x Desi chickpea (*Cicer arietinum* L.) cross. M. Sc. (Agric) Thesis. Acharya N.G. Ranga Agricultural University Rajendrana, Hyderabad -500 030, Andhra Pradesh, India.

TendulkarA V 1965 Genetic studies in gram. M.Sc. (agri.) Thesis, Univ. Of Poona, Poona.

Tewari S K and Pandey M.P 1987 Heterosis and inbreeding in chickpea. Indian Journal of Genetics and Plant Breeding 47(3): 261-264.

Tullu A 1996 Genetics of fusarium wilt resistance in chickpea. Ph.D Thesis, Crop and Soil Science Department, Washington State University Pullman, Wash. USA.

Tuner N C 1886a Adaptations to water deficits: a changing perspective. Australian Journal of Plant Physiology (13): 175-190.

Tuner N C 1986b Crop water deficits: a decade of progress. Advance in Agronomy (39): 1-51.

Uddin M .J, Hamid H A, Rahman A R M S and Newaz M A 1990 Variability, correlation and path analysis in chickpea (*Cicer arietinum* L.) Bangladesh Journal of plant Breeding and Genetics 3(1,2) : 51-55.

Ugale S D 1980 Incorporation of Germplasm from kabuli to desi and vice versa in Chickpea (*Cicer arietinum* L.). Ph. D. Thesis. IARI, New Delhi.

vander Maesen L J G 1972 Cicer L., Monograph of the Genus, with Special Reference to Chickpea (*Cicer arietinum* L.): its Ecology and Cultivation, Veenman, H. and Zonen, N.V., Wageningen.

van Rheenen H A, Saxena N P, Singh K B, Sethi C and Acosta-Gallegos 1990 Breeding chickpea for resistance to abiotic stresses: what are the problems and how can we solve them? *In*: H. A. Van Rheenen and M.C. Saxena (eds.), Chickpea in the Nineties: Proceedings of the Second International Workshop on Chickpea Improvement, pp. 239-244, 4-8 December 1989. ICRISAT, Patancheru, A.P., India.

Vijyalakshmi Satya N V 1998 Genetic studies of flower colour, protein content and some important qualitative and quantitative characters in two crosses of chickpea (*Cicer arietinum* L.) M Sc (Agric) Thesis. Acharya N.G. Ranga Agricultural University Rajendrana, Hyderabad -500 030, Andhra Pradesh, India.

Virmani S M and Singh P 1986 Agroclimatological characteristics of the groundnut growing regions in the semi-arid tropics. In: Agrometeorology of Groundnut. (pp. 35-46), Sivakumar, M. V. K. and S. M. Virmani, Eds., ICRISAT, Patancheru, India.

Waldia R S, Chhabra A K, Solanki I S and Tomer R P S 1992 Inheritance studies of plumule emergence in chickpea. Journal of Genetics and Breeding 46: 209-214.

Warner J N 1952 A method for estimating heritability. Agronomy Journal 44: 427- 430.

Yadav L N, Mahadik C N and Dixit S S 1978 Inheritance of double podded character and petal colour in gram (*Cicer arietinum* L.). Science and Culture 44: 537.