ASSOCIATION OF MORPHOLOGICAL CHARACTERS AND FUSARIUM WILT RESISTANCE WITH SEED YIELD IN A KABULI × DESI CHICKPEA (*Cicer arietinum* L.) CROSS

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CERTIFICATE

Mr. Fekadu Tefera Tesfaye has satisfactorily prosecuted the course of research and that thesis entitled, "ASSOCIATION OF MORPHOLOGICAL CHARACTERS AND FUSARIUM WILT RESISTANCE WITH SEED YIELD IN A KABULI X DESI CHICKPEA (*Cicer arietinum* L.) CROSS" 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.

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CERTIFICATE

This is to certify that the thesis entitled, "ASSOCIATION OF MORPHOLOGICAL CHARACTERS AND FUSARIUM WILT RESISTANCE WITH SEED YIELD IN A KABULI X DESI CHICKPEA (*Cicer arietinum* L.) CROSS" submitted in partial fulfilment of the requirements for the degree of "MASTER OF SCIENCE IN AGRICULTURE" in Genetics and Plant Breeding of the Acharya N.G. Ranga Agricultural University, Hyderabad, is a record of the bonafide research work carried out by Mr. Fekadu Tefera Tesfaye 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. All the assistance and help received during the course of investigations have been duly acknowledged by the author of the thesis.

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FEKADU TEFERA

DECLARATION

I, FEKADU TEFERA TESFAYE, hereby declare that the thesis entitled, **ASSOCIATION OF MORPHOLOGICAL CHARACTERS AND FUSARIUM WILT RESISTANCE WITH SEED YIELD IN A KABULI × DESI CHICKPEA (*Cicer arietinum* L.) CROSS**, submitted to Acharya N.G. Ranga Agricultural University for the Degree of MASTER OF SCIENCE IN AGRICULTURE is the result of the original research work done by me. It is further declared that the thesis or any part thereof has not been published earlier in any manner.

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Place : HYDERABAD

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ABSTRACT

Studies were taken up to ascertain the inheritance of morphological characters and to determine their association among themselves and with seed yield and fusarium wilt resistance in chickpea cross, ICCV2 x JG62. ICCV2 is a kabuli type with fusarium wilt resistance and medium bold seed weight of 26 g 100^{-1} seeds. JG62 is a typical desi type with 16 g 100^{-1} seed weight. However, it is susceptible to fusarium wilt. F_2 from this cross was grown in a healthy plot as well as in a fusarium wilt-sick plot. Random recombinant inbred lines (RILs) in F_{10} were also grown in healthy and sick plots. This work was done during the postrainy season 1997/98 on the research farm at the International Crops Research

Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Andhra Pradesh 502 324, India.

Inheritance studies were made for seven morphological characters; flower colour, stem colour, double pod trait, seed shape, seed colour, seed weight and fusarium wilt resistance and association studies for six of these and four quantitative characters; seed yield, number of pods per plant, number of seeds per plant and number of seeds per pod on the 120 plants in F_2 population and 76 F_{10} RILs. The former was grown in a completely randomized design and the latter in an incomplete block design in the three replications. Both parents were used as controls.

Mongoenic inheritance was confirmed for three morphological characters, pink vs. white flowers, pigmented vs. non-pigmented stem colours, and single podded vs. double podded characters. The flower colour genotype of ICCV2 was determined as PPbbCC (or PPBBcc) and of JG62 as PPBBCC. This gene was found to have pleiotropic effect as it also controlled the stem colour. Seed type was governed by two pairs of genes which act in an additive manner in which dominant alleles had cumulative effects. All plants with 3 or 4 dominant alleles had desi seed type, 1 or 2 dominant alleles were expressed as intermediate seed type and those with all recessive alleles had kabuli seed type. Coloured seed coat was dominant over salman white seeded coat and was probably controlled by three pairs of genes. There was some association between the genes for flower colour, seed colour and seed shape. Seed size was polygenically controlled but with the influence of major genes. Since correlations of 100-seed weight with all qualitative characters were nonsignificant, it appears possible to produce desi qualitative characters with increased kabuli seed weight. Two RILs were actually noted which exceeded kabuli seed size with desi seed shape and brown colour. Genotypic correlations showed that number of pods per plant can be taken as an important selection criterion. Resistance to fusarium wilt was governed by homozygous recessive condition for two genes and though very strongly linked with lesser number of the seeds per pod and seed type, the linkage is not absolute and therefore, recombinations are possible to obtain, if desired, in large inbred population of the hybrid.

These and other studies on qualitative traits in chickpea may be useful in saturating the rather 'preliminary' map of chickpea genome, which at present has only 9 morphological markers. The use of these RILs for developing molecular marker map can help in identifying quantitative trait loci and thus help enrich the genome map and improvement of this crop in future. Unlike F_2, the genotypes of the RILs are not ephemeral therefore, small bits of information gathered over time could result in a quantum jump in our knowledge about the chickpea genome.

LIST OF ABBREVIATIONS

Abbreviation(s)	Description(s)
B/Bco	Gene for blue corolla
Blsc/Bsc	Black seed coat
Brt	Brown testa
cm	Centimeter
cm^2	Square centimeter
et al.	and others
FAO	Food and Agriculture Organization
Fig.	Figure
F_1	First filial generation
F_2	Second filial generation
F_{10}	Tenth filial generation
FOC	*Fusarium oxysporum* f.sp.*ceceri*
g	gram
kg/ha	Kilogram per hectare
Lvco	Gene for violet corolla
m	meter
m^2	Square meter
No.	number
P/Pco	Gene for pink corolla
P_1	Parent 1

contd...2..

Abbreviation(s)	Description(s)
P_2	Parent 2
%	percent
RADPs	Random amplified polymorphic DNAs
RFLP	Restriction fragment length polymorphism
RILs	Recombinant inbred lines
S/Sf1	Gene for single flowered (podded) trait
Sco	Gene for salmon corolla colour
T	Gene for testa colour
tpc	Gene for K 850 polycarpy
vs.	versus
wco	Gene for white corolla

INTRODUCTION

CHAPTER I

INTRODUCTION

The cultivated chickpea (*Cicer arietinum* L.), is a self-pollinated (2n=2x=16) crop of the tribe *Cicereae* Alef. and family Leguminosae. It is the third most important food legume in the world after dry bean (*Phaseolus vulgaris* L.) and dry pea (*Pisum sativum* L.). It is grown annually on about 10 million ha and produces on an average 750 kg/ha (FAO, 1996). It is a good source of inexpensive protein for many people, particularly in the Indian subcontinent which accounts for about 80% of the global chickpea production (FAO, 1996). In these countries a large proportion of the population relies on legume proteins due to economic, social and/or religious reasons. No other pulse is used in as many ways as chickpea. The leaves may be eaten as a vegetable, a refreshing drink can be prepared from the plant exudates, the seeds may be consumed green, raw, soaked, germinated, roasted, fried, or boiled, and can be used to prepare an amazing array of different dishes. The chickpea flour is used to prepare variety of snacks, sweets, breakfast foods, chapatis and for preparing beauty aids.

The cultivated chickpea originated in south-eastern Turkey and has been under domestication for over 7000 years (van der Maesen, 1984). C. *reticulatum* Lad. and C. *echinospermum* produce fertile hybrids with the cultivated chickpea. The former has been proposed as the progenitor of the cultivated chickpea. C. *reticulatum*, C. *echinospermum* and C. *arietinum* constitute the primary gene pool for the cultivated chickpea (Muehlbauer *et al.* 1994).

In cultivated chickpea, there are two distinct types — desi and kabuli, mainly based on their seed colour and shape. The desi type is considered to be primitive and the kabuli type to be of recent origin. Both types had been geographically isolated for many years.

Desi chickpea is usually small seeded, angular in shape, with seed colours ranging from white to black, and seed surface is smooth or rough. The aerial plant parts usually have anthocyanin pigmentation and the plants usually have pink or purple flowers. They are mostly distributed in south Asia; although desi types are also cultivated in Ethiopia, Tanzania and to some extent in Mexico, and Iran. They are adapted to winter sowing in the subtropics and hilly areas of tropics.

The kabulis, on the other hand, are usually large seeded with owl's head shape and white or light pinkish seed coat. The plants are green, lack anthocyanin pigmentation and the flowers are white. The kabuli chickpea is distributed mainly in the Middle East and Mediterranean region, Spain, Chile and Mexico and are adapted to spring sowing at higher altitudes. In recent years these are also grown in the United States of America.

Having been separated geographically (Gowda *et al.*, 1987), these two types differ for various morphological characters and important yield components. Hence some of these characters stand together as kabuli characters and others as desi. Therefore, it may be possible to improve yield by introgressive hybridization.

Inheritance of various morphological characters such as flower colour, stem colour, double pod trait, seed type, seed colour and seed size has been studied in different crosses. In the F_2 generation resulting from the kabuli and desi parents, it is important to find if these characters segregate independently of each other. If independent, it means that there is no linkage involved and it is easy to obtain the desired character combinations. One of the important characters is fusarium wilt resistance which usually lacks in kabuli types. This disease causes an annual yield loss of about 10% as reported by Mandal, 1989 and as high as 60-70% as reported by Jalali *et al.* (1992). At ICRISAT and in Mexico, the desirable combinations of kabuli types with fusarium resistance have already been achieved (Kumar and Haware, 1983).

The objectives of this study were:

1. To ascertain the inheritance of flower colour, stem colour, twin pod trait, seed colour, seed size, seed shape and fusarium wilt resistance in F_2 population and F_{10} random recombinant inbred lines (RILs) of the chickpea cross ICCV2 x JG62, and

2. To determine the association of these and important quantitative characters.

REVIEW OF LITERATURE

CHAPTER II

REVIEW OF LITERATURE

2.1. The Nature of Sub-specific Variation in Cultivated Chickpea

Chickpea has wide genetic variation for qualitative and quantitative traits, in many ways similar to that of related genera such as *Pisum* and *Lens* (Muehlbauer and Singh, 1987). Some of the variation was described by Ayyar and Balasubramanian (1936). Studies since have considered variation in plant habit, leaf form and colour, flower colour, podding habit, seed coat colour, disease resistance, and many quantitative traits. The extensive variation available in chickpea forms a basis for breeding efforts and is vitally important to its improvement. With this variation, improved genotypes that will be productive and have quality attributes acceptable to producers and consumers can be developed.

Chickpea is often divided into two major groupings (Auckland and van der Maesen, 1980) that correspond to differences in size, shape and colouration of the seeds. The types that produce large owl's head shaped smooth seeds, that are white or pale-cream are referred to as kabuli types. Flowers of these kabuli types are white.

The types that produce small seeds, that have an angular appearance with sharp edges, and are variously pigmented, are referred to as desi types. These generally have pink or other colour flowers, and pigmented stems and leaves. Even though these groups have been separated for centuries, there are no barriers to hybridization between them (Auckland and van der Maesen, 1980). The desi type is grown principally in the Indian subcontinent, Iran, East Africa and to some extent Mexico, and the kabuli type is grown primarily in the Mediterranean region, and in Central and South America. Hybridization between the two groups may provide genetic diversity for chickpea crop improvement and also reveal genetic traits that could be useful to the study of gene systems in *Cicer*.

2.2. Inheritance of Morphological Characters in Chickpea

2.2.1. Flower colour

The colour of chickpea flower may be white, greenish white or with various shades of pink or blue. The pink flowers fade to blue as they wither. Various types of gene actions were reported to control flower colour in chickpea. Pimplikar (1943) and Khan *et al.* (1950) reported that a single locus is responsible for pink and white flower colours in chickpea. However, Khan and Akhtar (1934) earlier found that two pairs of genes, P and B control flower colour in chickpea. The genotypes P-B-, ppB-, P-bb, and ppbb produce pink, blue, white, and white flowers, respectively. Ayyar and Balasubramanian (1936) and Balasubramanian (1950) suggested one additional locus C affecting flower. Thus, pink flowers are produced when all three genes (P, B and C) are present in the dominant condition, blue when P is homozygous recessive and white when all the three genes are in homozygous recessive condition or either B or C is homozygous recessive.

More and D'Cruz (1970, 1976a) and Patil and Deshmukh (1975) suggested that flower colour in chickpea is controlled by two loci, Sco and Bco. The genotypes Sco-Bco-, Sco-bco bco, sco sco Bco — and sco sco bco bco produced pink, salmon, blue and white flowers respectively. Two loci Lvco and Wco were proposed for flower colour by Deshmukh *et al.* (1972). It was suggested that the genotypes Lvco-Wco-, lvco lvco Wco-, Lvco-wco wco and lvco lvco wco wco produced pink, violet, white and white flowers, respectively. Reddy and Chopde (1977) reported that two complementary genes, designated Pco_a and Pco_b, controlled flower colour with pink dominant to violet. Kumar (unpublished data) showed that the two chickpea varieties, namely ICCV2 and JG62 produce pink flower, when crossed to a blue flowered line the genotype of which was determined as ppBBCC. Thus the genotype of ICCV2 is PPbbCC or PPBBcc and that of JG62 is PPBBCC.

2.2.2. Twin pod character

Normally chickpeas have one flower or pod on each peduncle. Mutants with two flowers or pods on each peduncle have been identified. Khan and Akhtar (1934) suggested that number of flowers per peduncle was governed by a single locus (S) with one flower dominant to two. This finding has been confirmed by many researchers (Ahmad, 1964; Singh, 1965; Patil, 1966; D'Cruz and Tendulkar, 1970; More and D'Cruz, 1976b; Yadav *et al.* 1978; Pawar and Patil, 1983; Rao and Pundir, 1983). D'Cruz and Tendulkar (1970) suggested the symbol Sfl for the dominant single flowered (podded) trait.

A second double podded mutant was reported by Pundir *et al.* (1988). This mutant had twin flowers on each peduncle with the two pods jointed at their bases. This mutant was isolated from the cultivar K 850 and was named 'K 850 polycarpy'. Genetic analysis indicated that a single recessive gene, designated tpc, was responsible for K 850 polycarpy.

Singh and van Rheenen (1994) studied contribution of the multi-seeded and double-podded characters to grain yield found that double-poddedness was inherited as monogenic recessive trait and contributed positively to higher productivity in chickpea. Sheldrake *et al.* (1978) have also reported, its significant advantage in yield under the conditions in which it is well expressed.

2.2.3. Seed traits/characters

2.2.3.1. Seed type

Chickpea seeds generally classified into three types based on their shape. Desi with angular seed shape, kabuli with owl's head seed shape and an intermediate (or) pea (nearly spherical) seeds shape (Knights, 1979). Of the world production, about 85% are of desi types and the remaining being kabuli (Singh *et al.*, 1985). Almost two-third of the chickpea growing countries cultivate only the Kabuli type, and one-third mostly the desi type. Inheritance studies on seed type in chickpea indicate that pea type is dominant to both desi and kabuli and desi is dominant to kabuli type (Knights, 1979). The colour of the testa shows great variation with many hues. Pea type has the drawback of having very thin testa which results in poor storage quality, and germination is impaired during storage. Moreover this type has the least consumer preference. Salmon cream colour is the major acceptable colour in the kabuli types and bright yellow to brown yellow is most acceptable among desi types depending on the local preference (Gill, 1980). In the F_2 generation from desi x kabuli crosses, recovery of desi types has ranged from 2.3 to 53.3% and that of kabuli types from 0 to 9.8% depending on the parental lines used (Knights, 1979).

2.2.3.2. Seed coat colour

Seed coat (testa) colour in chickpea is a highly variable and complex character and may be governed by several genes. Sometimes 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. Inconsistency in gene symbols makes it difficult to compare different reports. Balasubramanian (1937) suggested that two genes T_1 and T_2 darken testa colour. Later, Balasubramanian (1952) suggested two additional genes, T_3 and T_4, such that T_3 in the presence of P (flower colour) produces dark brown testa, whereas T_4 produces black testa irrespective of the presence of P. Four pairs of genes governed colour variations in chickpea according to Alam, 1935.

Brar and Athwal (1970) suggested five genes, P_1, S_1, S_2, S_3 and S_4 for testa colour. The dominant allele P is essential for the production of fawn and darker colours, while the recessive allele P is epistatic over other loci influencing testa colour. S_1 produces reddish brown testa, whereas its recessive allele s_1 produces fawn testa. The recessive allele s_2 produces seal-brown testa and is epistatic over S_1, and s_3 produces green testa and is epistatic over alleles at the S_1 and S_2 loci. S_4 produces dark grey testa in the presence of S_2 and black testa in presence of s_2 and is epistatic to all alleles of S_1 and S_3.

D'Cruz and Tendulkar (1970) reported that a single locus, Brsc, is responsible for the control of brown and white seed coat (testa), brown being dominant over white. More and D'Cruz (1970, 1976b) reported that brown seed coat colour is dominant over yellow and governed by a single dominant gene Brt. Reddy and Chopde (1977) suggested two complementary loci, $Blsc_a$ and $Blsc_b$ for black seed coat colour. $Blsc_a$ and $Blsc_b$ alone produce yellow and brown seed coat respectively. Since relationship between different studies has not been established the inheritance of seed coat colour is not clear.

2.2.3.3. Seed size

A great amount of genetic variability exists for seed size within desi and kabuli types, some desi types being as large, as kabulis, and some kabuli types are as small as desi.

Balasubrahmanyan (1950) concluded that seed size in chickpeas was controlled by two pairs of genes with gene interaction. Argikar (1956) observed that large seed was recessive to small seed and controlled by a single gene. Patil and D'Cruze (1964) reported that two genes were responsible for seed size in chickpea. Athwal and Sandha, 1967; Smithson *et al.*, 1985; and Kumar and Singh (1995) independently reported that small seed size was partially dominant over large seed size. Niknejad *et al.* (1971), however, found the reverse to be true. Heritability estimates for seed size were reported to be low by Sandha and Chandra (1969) and high by Niknejad *et al.* 1971; Ram *et al.* 1978; Agarwal, 1985; Samal and Jagadev, 1989. Additive gene effects in determining 100-seed weight was reported by Malhotra and Singh (1989).

2.2.4. Fusarium wilt resistance

Diseases are the major impediment to chickpea production. More than 50 pathogens have been reported so far from different countries growing chickpea (Nene and Reddy, 1987). The two most important diseases of chickpea are fusarium wilt (*Fusarium oxysporum* Schlecht. emd.: Fr. f. sp. *ciceris* (Padwick) Matuo and K. Sato (FOC), and Ascochyta blight (*Ascochyta rabiei* (Pass. Lab).

Fusarium wilt is caused by *Fusarium oxysporum* f.sp.*ciceri*. Several studies reported that resistance of chickpea to fusarium wilt is due to a single recessive gene (Pathak *et al.*, 1975; Tiwari *et al.*, 1981; Kumar and Haware, 1982; Sindhu *et al.*, 1983; Phillips, 1983. However, Kumar and Haware (1982) also reported that segregation for JG62 ×WR315 cross did not fit 3(S):1(R) ratio and that probably more genes were involved.

Sindhu *et al.* (1983) assigned the gene symbol rfo to this recessive gene. However, the studies of Lopez (1974) and Upadhyaya *et al.* (1983a, 1983b) suggest that two pairs of recessive genes are needed for resistance. Resistance in chickpeas to race 1 of FOC is known to be controlled by at least three independent loci: two incompletely recessive and one dominant gene, individually delaying wilting and any two in combination confer complete resistance (Smithson *et al.*, 1983). In other studies, Gumber *et al.* (1995) found that resistance to race 2 of fusarium wilt is controlled by two genes one of which (A) must be present in the homozygous recessive form, and the other (B) in the dominant form, whether homozygous or heterozygous, for complete resistance. Early wilting results if the plant is homozygous recessive for bb. Late wilting occurs if both loci are dominant.

Harjit Singh *et al.* (1987) studied the reactions of parents and F_1 and F_2 generations of crosses of chickpea cultivars K-850 with C-104 and JG-62 and F_3 progenies of K-850 x C-104 to race 1 of FOC and confirmed that K-850 carries a recessive allele for resistance at a locus different from and independent of that carried by C-104 and that the recessive alleles at both loci together confer complete resistance.

Mandal (1989) reported simple nature of genetics of inheritance to wilt in chickpea in a cross involving two resistant and one susceptible parents in F_1 and F_2 generations. It is not clear whether this is one strong gene or the other gene(s) were not segregating between the parents use in the study.

2.3. Association of Morphological Characters

2.3.1. Qualitative characters

The existence of wide morphological diversity in chickpea (*Cicer arietinum* L.) offers ample opportunity for genetic studies. Qualitative characters being less influenced by environmental variations are used as markers for quantitative traits in soybean (Raut *et al.*, 1994).

The association of genes for economically important traits with easily identified markers, can improve the efficiency of breeding and hasten the development of improved cultivars. There are numerous reports of associations of traits in chickpea. Most of these are on the association of foliage, corolla, and seed coat colouration; and stem, pedicel and corolla colour and fusarium wilt resistance. Seed coat colour can have overriding importance in determining market class of chickpea and acceptance of improved cultivars, breeders need a thorough understanding of its inheritance and its relationship to plant pigmentation in general.

Ayyar and Balasubramanian (1936) found that five factors are involved in seed colour determination, two of which also affect flower colour. Another studies, Singh and Ekbote (1936), Pimplikar (1943) and Kadam *et al.* (1945) reported that flower colour, seed colour and seed shape are inherited together monogenically where pink flower, yellowish-brown testa and irregular shape of the seed were dominant to the white flower and orange-yellow coloured round seed. Further they indicated that the seed and flower colours were completely linked. Balasubramanian (1950) demonstrated the pleiotropic effects of one factor on the petal, seed coat colour and seed size. Aziz *et al.* (1960) in their character association studies on gram found that the locus (corolla colour) was linked with the loci W (smooth vs. wrinkled) and R (seed coat colour). Argikar and D'Cruz (1962) and Bhapkar and Patil (1962) reported that seed coat colour is controlled by two complementary genes of which one was linked to the flower colour gene. They also determined the relationship of seed colour inheritance to flower colour in chickpea and suggested that four factors are involved in seed colour determination one of which simultaneously affects flower colour.

The relationships among morphological traits and fusarium wilt resistance have not been adequately described; and few studies claim that there is virtually no correlation between plant traits and resistance to either of the two major disease of chickpea, ascochyta blight or fusarium wilt. Kumar and Haware (1983) from their studies, identified a number of segregants with kabuli characteristics and resistance to fusarium wilt, from kabuli x desi crosses. Harjit Singh *et al.* (1988) from their character association studies among genotypes differing in resistance to *F. oxysporum* f.sp.*ciceri*; showed that the wilt reactions of F_3 progenies segregated independently of the flower colour and flower number/peduncle in the F_2 generation.

Simon and Muehlbauer (1997) published a map of a chickpea genome which has 91 markers. These include 9 morphological, 27 isozyme, 10 RFLP and 45 RAPDs. Thus the map has little value unless more morphological markers are added.

2.3.2. Quantitative characters

Breeding projects aimed exclusively at increased yield may not achieve fast results because yield is a complex quantitative character which is governed by several other contributing characters. So that the study of associations among various traits such as seed yield, number of pods/plant, number of seeds/pod, number of seeds/plant, and 100 seed weight is useful to breeders in selecting genotypes possessing groups of desired characteristics. However, degree of emphasis on a particular character will be governed by extent of its effect on yield.

It is known that correlation coefficients for a given trait vary with the type of genotypes studied and the environment where the test is carried out. Moreover correlation coefficients show patterns of association among yield components and growth attributes, indicating what complexities determine yield. Most of the studies on associations between yield and yield components have been carried out on homozygous populations. The conclusions drawn from such studies may not be useful in the selection of F_2 progeny.

2.3.2.1. Relationship among generations based on the characters studied

The use of early generation yield data and statistics for the association of plant characters with yield have received much attention. Early generation yield testing may help a breeder to identify and eliminate poorly performing populations at an early stage and therefore, can save time and other resources. Prediction of the performance of crosses from early-generation yield testing (F_2 and F_3) of chickpea was reported by Auckland and Singh, 1977.

Correlations between the yields of the F_2 and F_3, F_2 and F_4, and F_3 and F_4 generations in chickpea were reported to be significant and positive (Dahiya *et al.*, 1983b). Significant yield increase in chickpea was also realised from early-generation yield tests, compared with both visual and random selections (Dahiya *et al.*, 1984). However, poor intergeneration associations were reported for pods per plant and grain yield in chickpea by Rahman and Bahl (1986). Conflicting results have been reported in other crops. The use of later generations was suggested for yield tests in wheat, since it attains a reasonable degree of homogeneity (Knott and Kumar, 1975). In cowpea, nonsignificant correlations were noted among different generations (Virupakshappa, 1984). Inconsistent associations among generations were found in soybean (Weiss *et al.*, 1947) and in chickpea (Geletu *et al.*, 1991). Virupakshappa (1984) estimated inter-generation correlations in two crosses of cowpea in F_2-F_3, F_3-F_4 and F_5-F_6 generations and found nonsignificant inter-generation correlations in any of the cases for yield. On the other hand, Ntare *et al.* (1984) reported that the differences in yielding ability of F_3 lines of two cowpea crosses persisted over generations indicating that selection was effective. This was further confirmed by the highly significant correlations between F_3 yields and those of later generations which ranged from r=0.51** to 0.85**.

In wheat, Whan *et al.* (1981) planted all the generations from F_2 to F_5 together in one season so that the results were not influenced by seasonal differences. The correlations ranged from r=0.51** for the F_2 plant/F_3 line mean comparison to r=0.68** for the F_3 line/F_4 mean to r=0.78* for the F_4 line/F_5 mean. Their observations revealed that the absence of replications, where single lines were grown as single plots, reduced the accuracy in the determination of the yield and could have lowered the correlations.

Geletu (1987) in his correlation studies between yield and yield components separately in F_2, F_3, F_4 and F_6 revealed that all the characters studied except days to 50% flowering and maturity had significant positive associations with seed yield per plant. The correlation values between these characters and seed yield per plant increased with advanced generations upto F_5 and then stabilized.

2.3.2.1.1. Correlations in F_2 generation

Many experiments have been conducted in field crops to obtain information on inter-relationship between plant characters and yield. Dahiya *et al.* (1986) compared the effectiveness of different selection criterion using the number of top yielding lines superior to the check. The results of this study in two crosses showed that selection based on pod number and seed weight was as effective as yield per se selection for obtaining superior yielding progenies.

Salimath and Bahl (1983) and Agrawal (1986) studied the relationships among yield and yield components. In most of the cases the seed yield was positively correlated with the number of pods per plant and the number of seeds per plant.

Ram *et al.* (1980) studied six yield components in F_2's and F_3's of three crosses of chickpea and the results suggested that during selection, attention must be given to the number of pods and seeds per plant. They reported that pods per plant and seeds per plant were effective measures of yield in chickpea. These two characters were also reported to have the maximum direct effect consistently in all the crosses used.

Among the seven characters assessed in the F_1 and F_2 of 45 crosses, a negative correlation between seeds per pod and 250-seed weight and positive correlation between pods per plant with seed yield were detected in both generations (Katiyar, 1979). Similarly, Singh *et al.* (1976) reported a negative correlation between 100-seed weight and number of seeds per pod. Seed number per plant was found to be negatively correlated with 100-seed weight (Mishra *et al.*, 1974). Tomar *et al.* (1982) observed positive associations between yield and number of pods per plant, number of seeds per pod, both in F_1 and F_2 generations of several crosses. But Khan and Chaudhary (1975) reported a negative association between yield and number of seeds per pod in the F_3 generation of two crosses and their reciprocals. Geletu *et al.* (1991) in their character association studies among the F_2 to F_6 generations of 9 chickpea crosses found inconsistency in association among the generations for six characters except for days to 50% flowering, number of days to maturity and seed weight which showed consistent result over the generations. The number of pods per plant was significantly and positively correlated with all the morphological traits studied but seed yield showed a negative correlation with both number of seeds per pod and seed size. The number of seeds per pod and 100-seed weight had a negative correlation in a study by Singh *et al.*, 1976. The results of the study of F_2 chickpea populations of crosses of small x small and large x large seeded parents showed that the number of pods per plant in all crosses and the seed number per pod in association with the number of pods per plant in all small x small and the 100-seed weight in large x large seeded crosses were suitable characters for selecting high yielding varieties.

Jatasra *et al.* (1978) observed in F_2 generation that there was a positive association between number of pods per plant and number of seeds per plant while the number of pods per plant had a negative correlation with the number of seeds per pod. This shows that the number of pods per plant and the number of seeds can be simultaneously improved, but this is very difficult to achieve for the number of pods per plant and the number of seeds per pod. On the other hand, seeds/pod was positively correlated with seed yield in segregating generations (Singh and van Rheenen, 1994).

Waldia *et al.* (1988) studied association for 100-seed weight and seed yield in F_2 of various crosses made between 4 parents in chickpea and found that 100-seed weight was highly associated with yield in plants with 100-seed weight between 10-13.5 g class; their values decreased with increase in seed mass.

Kharrat *et al.* (1991) in their study aimed at genetics of grain yield components in three desi x kabuli chickpea crosses reported that yield/plant was significantly and positively correlated with pods/plant, seeds/plant and seed size. There was no correlation of seed size (100-seed weight) with seeds/plant.

In summary, most of the results obtained by Salimath and Bahl (1983), Agrawal (1986), Ram *et al.* (1980), Mishra *et al.* (1974) and Tomar *et al.* (1982) revealed that number of pods per plant and the number of seed per plant are the most important traits for selection to improve yield in chickpea.

2.3.2.1.2. Correlations among homozygous lines

The associations studied in nine chickpea lines among eight different characters and found positive correlation between number of pods per plant and seed yield and between seed size and seed yield (Baluch and Soomro, 1968).

Sharma *et al.* (1969) carried out studies on relation between yield and other characters in chickpea and found out that yield was positively correlated with eight morphological characters in the 44 lines studied. It was highly correlated genotypically, phenotypically and environmentally with number of pods, number of seeds per pod, 100-seed weight and number of branches.

Important traits registered by Gill and Brar (1980) include plant height, days from flowering to maturity, primary branches, pods per plant, seeds per pod, seed size, 100-seed weight, seed yield, protein and ascorbic acid content of the seed.

Yield and six components of yield were studied by Sandhu and Singh (1970) on sixty lines from thirteen countries and the results obtained revealed that the expected genetic advance for 100-seed weight and pod number per plant was high.

Hundred seed weight was found to be positively correlated with number of seeds per pod and secondary branches per plant (Chowdhry and Khan, 1974). On the other hand, Dobholkar (1973) and Raju *et al.* (1978) obtained results which exhibited a negative correlation between seed yield and 100-seed weight, but a positive correlation between yield and number of pods per plant and seeds per pod. The results obtained by Dahiya *et al.* (1983a) were not in favour of using 100-seed weight as a selection criterion since the varieties used were unstable for this character.

The analysis of data collected on thirteen traits in 132 lines of chickpea showed that pods per plant and seeds per pod were among the important components (Rang *et al.*, 1980). Tyagi *et al.* (1982) and Shahi *et al.* (1984) stressed the importance of pods per plant since it was significantly and positively correlated with seed yield per plant. Dobholkar (1973) observed that number of pods per plant was positively correlated with number of seeds per pod. Among the components studied by Adhikari and Pandey (1982a), hundred seed weight was found to have a significant and negative correlation with seeds per pod. Singh *et al.* (1980) proposed to increase the number of pods per plant, seed size, the number of seeds per pod and the number of plants per unit area in tall plant types of chickpea.

Dahiya *et al.* (1976) conducted an experiment to identify physiologically efficient genotypes in chickpea found that in large-seeded types, the 100-seed weight contributed to an improved harvest index, whereas in small-seeded types the number of seeds per pod was important. The major characters contributing to yield in chickpea, according to Govil *et al.* (1980) were; vigorous growth, erect habit, early flowering but late maturing, increase in pods per secondary branch and per plant, numerous seeds per pod, resistance to *Fusarium oxyporium* f.sp. *ciceri* and small and less wrinkled seeds. The number of pods per plant, flower colour and seed colour, which were positively correlated with seed yield, were negatively correlated with leaf characters, height, days to flowering, pod size, seed size and degree of seed wrinkling (Govil *et al.*, 1980).

Khan *et al.* (1983) studied the variability, inter-relationships and path coefficients for some characters in chickpea and found out high heritability values of 96% for number of pods per plant, 57% for 100-seed weight and 53% for seed yield per plant. The results indicated that these characters are not much affected by the environment. According to these results, number of pods per plant was positively and significantly associated with seed yield; so that this character is ideal for effective selection for seed yield.

Singh *et al.* (1984) on the basis of review of 74 studies on correlations among different traits in chickpea covering the period 1915-1983, reported wide variation in the nature and magnitude of correlation coefficients, except for number of pods/plant and 1000-seed weight, which were, in most cases, positively correlated with seed yield. However, Hadjichristodovlou (1987) reported nonsignificant and negative correlation of number of pods/plant and 1000-seed mass with seed yield and significant negative correlation between themselves.

Causation and association analysis in 30 *Cicer arietinum* strains revealed that seed yield was positively and significantly correlated with 100-seed weight, pods/plant, and seeds/pod (Sindhu and Prasad, 1987). A similar association was reported by Jivani and Yadavendra (1988) and Haq (1990). Thus these three characters are ideal for effective selection for seed yield.

Among the components studied by Salimath and Bahl (1986) number of pods/per plant was positively and significantly correlated with seed yield genotypically. They also noted high genotypic variability for 100-seed weight, pods/plant, and seed yield/plant, indicating scope for improvement by selection. The effectiveness of number of pods/plant for indirect selection of yield was further stressed by Singh and Singh (1989), Mishra *et al.* (1988), Rahman and Path (1988) and Singh *et al.* (1992).

Mishra *et al.* (1988) studied genetic variability, correlations and their implication in selection of high yielding genotypes of chickpea and found that high heritability coupled with high genetic advance was observed for pods/plant, seed yield/plant and 100-seed weight and grain yield was positively and significantly correlated with these characters. This was further supported by the report of Mishra *et al.* (1988) and Misra (1991).

Choudhury *et al.* (1988) studied variability, character association and path analysis in 13 genetically diverse chickpea lines for different characters and found significant and positive genotypic and phenotypic correlations among seed yield, pod/plant, and 100-seed weight. The result also indicated that selection for them would be effective. The importance of selection for seeds/pod to improve yield was emphasized by Sandhu *et al.* (1988), for seeds/pod and pods/plant by Paliwal *et al.* (1987), Shukla (1988) and Govil and Kumar (1989). Their findings further showed positive and significant correlation between pods/plant and number of seeds/pod. Seeds/pod was positively correlated with 100-seed weight (reported by Sandhu and Mandal, 1989), on the other hand, Tagore and Singh (1990) observed a negative and significant correlation between the two characters. Khorgade *et al.* (1995) in their character association and path analysis conducted on 9 characters in 30 chickpea genotypes reported positive and significant correlations of seed yield with pods/plant, and 100-seed weight and negative correlation with seeds/pod. In the same type of studies Bhambota *et al.* (1994) emphasized the importance of pods/plant, as it was significantly and positively correlated with seed yield at both genotypic and phenotypic levels. Estimates of genotypic correlation coefficients were similar in sign but higher in magnitude than the ones observed at phenotypic level for most of the traits (Bhambota *et al.*, 1994 and Pooran, 1997).

In summary, most of the results reported on correlations between yield and yield components have shown that yield is positively associated with number of pods per plant. Selection based on this character was suggested to be very important and reliable in improving the yield.

MATERIALS AND METHODS

CHAPTER III

MATERIALS AND METHODS

The present investigations were carried out with the objective of determining the inheritance of and association between morphological traits and fusarium wilt resistance with seed yield in a chickpea cross. The studies were carried out during postrainy season 1997/98 at the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, A.P. 502 324, India.

3.1. Materials

The materials for the present investigation consisted of parents, F_2 population and 76 F_{10} generation recombinant inbred lines (RILs) of kabuli x desi cross ICCV2 × JG62. The F_1 and F_9 seeds of the cross were obtained from the Chickpea Breeding Section, ICRISAT for advancing to F_2 and F_{10} generations. Parental and F_1 characters are given in Table 1.

3.2. Methods

3.2.1. Evaluation of cross

The cross was made in 1993 and F_1 and further generations were grown in a glasshouse through rapid generation turnover at ICRISAT. The seed harvested from F_1 was planted on October 15, 1997, while the seed obtained from F_9 generation RILs was planted on November 3, 1997. Both the parents were planted along with each generation.

3.2.1.1. Experimental layout

The 76 F_{10} RILs and the parental seeds were planted in incomplete block design with three replications. Each replication consists of 12 blocks and 6-8 treatments (lines) appeared in each block. The size of the plot was 2.4 m^2 (4 m x 0.6 m) with one row per plot. Spacing of 20 cm between plants in a row was used. ICCV2 was planted along the fringes of the plots to eliminate border effects. The same materials were planted in a wilt-sick plot without replication to evaluate their wilt reaction.

The F_2 seeds of the same cross with their parents were planted unreplicated with spacing of 60 cm between rows and 10 cm between plants. The F_2 population had 120 plants. The 640 F_2 seeds of the same cross with their parents were planted in a wilt-sick plot to observe their wilt reaction.

3.2.1.2. Pest control and other cultural practices

Plots were sown rainfed. Rain occurred on 30 October, second week of November, first, second and third week of December, 1997 and, second and fourth week of January, 1998. Usual cultural practices were adopted to maintain a good crop, free of weeds.

Endosulfan 35% emulsifiable concentrate at the rate of 2 liters per hectare was sprayed to control pod borer (*H. armigera*) as and when needed

Table 1. Characters of parents and their F_1.

Character	ICCV2	JG62	F_1
Varietal status	Released	Released	-
Flower colour	White	Pink	Pink
Seed type	Kabuli	Desi	Intermediate
Seed colour	White	Brown	Brown
Seed size	Medium (26g/100)	Small (16g/100)	Intermediate
Seed surface	Smooth	Rough	NA
Seed fibre	Low	High	NA
Anthocyamin pigment	Absent	Present	Present
Fusarium wilt	Resistant	Susceptible	Susceptible
Flowering	Very early	Medium	NA
Maturity	Early	Medium	NA
No. of pods/peduncle	One	Two	One
No. of pods/plant	Medium	High	NA
Pod size	Bold	Small	NA
No. of branches	Low	Medium	NA
Primary	3	5	NA
Secondary	6	14	NA
Tertiary	33	51	NA
Branches	Long	Short	NA
Canopy	Wide	Narrow	NA
Drought	Escape	Tolerant	NA
Internode length	Long	Short	NA
Leaf size	Big	Small	NA
Sugar content	High	Low	NA
Plant height	Moderate	Moderate	NA
Seed yield	Medium	High	NA
Malic acid	Low	High	NA

Source: Chickpea Breeding, ICRISAT.

NA = Information was not available.

3.3. Characters Studied

In the present investigation, data on the following characters were recorded for both F_2 and F_{10} RILs.

1. Flower colour
2. Stem colour (anthocyanin pigmentation)
3. Seed colour
4. Seed type
5. Podding trait
6. Fusarium wilt resistance
7. Number of pods/plant
8. Number of seeds/plant
9. Number of seeds/pod
10. 100-seed weight (g)
11. Single plant seed yield (g)

3.3.1. Observational procedures

Observations for each characters were recorded in five competitive random plants per plot in each of the 76 RILs in the F_{10} generation RILs and parents, and 120 single plants in the F_2 population.

The particulars of characters studied are as follows:

Flower and stem colours:

Observations on flower and stem colours were made on individual plant basis at the time of flowering and for stem colour, observations were made at two times, once at flowering and again at maturity when the stem pigmentation was much more clear. Since most of the material planted in wilt-sick plots were killed before their flowering stage; so that indirect evaluation were made on these characters from those for the same material planted in normal fields. Flower colour was recorded as white and pink, while stem colour (anthocyanin pigmentation) was recorded as present or absent.

Seed type and seed colour:

The seeds were classified for type (based on their seed shape) and colour in the laboratory. Seed type was recorded as angular, owl's head and intermediate (roundish). Seed colour was classified to parental colour, i.e., coloured (non-white) and salman white. In addition other colour segregrants also occurred. It was found to be difficult to classify F_2 seeds into subclasses for seed colour due to continuous variation.

Podding character:

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

Fusarium wilt resistance:

Each of 76 F_{10} RILs in single row and 640 F_2 seeds and the two parents were planted in a wilt-sick plot which was uniformly infested with *F. oxysporum* f.sp.*ciceri*. The numbers of wilted and healthy plants were recorded near maturity and classified as resistant or susceptible. Percentages of wilted plants were also determined and used in correlation of susceptibility with other characters. Absolute resistance was regarded as resistance in arriving at the segregating ratio.

Number of pods per plant:

The total number of matured pods per plant was counted at harvest.

Number of seeds per plant:

The total number of seeds per plant was recorded after threshing.

Number of seeds per pod:

The number of seeds per pod were obtained using the overall number of pods and seeds per plant, i.e.,

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

100-seed weight (g):

The weight of 100-seed was calculated from the relation of number of seeds per plant and single plant seed yield (g), i.e.,

$$\frac{\text{Seed yield per plant}}{\text{Number of seeds per plant}} \times 100$$

Single plant seed yield (g)

The weight of the total seed of a plant to the fraction of 0.1 g was recorded on an electronic balance.

3.4. Statistical Analysis

3.4.1. χ^2-test

The inheritance of flower colour, stem colour, seed type, seed colour, pod character and fusarium wilt resistance were determined by χ^2 test for goodness of fit to expected ratio and for independent assortment, based on data for F_2 population further results were confirmed with F_{10} generation RILs. Frequency distribution was used to determine the inheritance of seed size.

3.4.2. Correlations

Simple correlations between number of pods per plant, number of seeds per pod, seed yield per plant, 100-seed weight, flower colour, stem colour, seed type, seed colour and fusarium wilt reaction in both RILs, and except fusarium wilt, all the rest of the character correlations in F_2 generations were worked out utilising the following formula suggested by Snedecor and Cochran (1967).

$$r\,(X_i\,.\,X_j) = \frac{\text{COv.}\,(X_i\,.\,X_j)}{(\text{Var}\,X_i\,.\,\text{Var}\,X_j)^{½}}$$

where,

$r(X_i . X_j)$ = Correlation coefficient between i^{th} and j^{th} characters.

$COv. (X_i . X_j)$ = Covariance between i^{th} and j^{th} characters.

$Var X_i$ and $Var X_j$ = Variance of i^{th} and j^{th} characters.

3.4.3. Phenotypic and genotypic correlations

The phenotypic and genotypic correlation coefficients were calculated for 5 quantitative characters by working out the variance components for each character and the covariance components for each pair of characters using the formulae suggested by Al-jibouri *et al.* (1958).

$$\text{Genotypic } r = \frac{\text{COv . XY (genotypic)}}{\text{Var (X) . Var (Y) (genotypic)}}$$

Genotypic variance was calculated as:

$$= \frac{\text{Treatments MS - Error MS}}{\text{Number of replications}}$$

Similarly:

$$\text{Genotypic COv.} = \frac{\text{Treatment COv - Error COv.}}{\text{Number of replications}}$$

$$\text{Phenotypic } r = \frac{\text{COv . XY (phenotypic)}}{\text{Var (X) . Var (Y) (phenotypic)}}$$

The value of genotypic correlations exceeding unity should be considered as unity only (of the same sign). To test the significance of the correlation coefficients at phenotypic level, the estimated values were compared with the table values of correlation coefficients (Fisher and Yates, 1963) at 5 percent and 1 percent levels of significance with (n-2) degree of freedom.

RESULTS

CHAPTER IV

RESULTS

4.1. Inheritance of Morphological Characters

4.1.1. Flower colour

In this study, inheritance of pink and white flower colour (Plate 1) was studied. The observed ratio of 87 pink:33 white flowered plants in F_2 population indicates segregation for one gene. This corresponds with the expected 3:1 ratio (P=0.40) (Table 2).

Similarly, the inheritance of flower colour was studied in the 76 recombinant inbred lines (RILs). Here also the segregation of pink and white flower colour gave a good fit to the expected 1:1 ratio in this cross (Table 3).

4.1.2. Stem Colour (anthocyanin pigmentation)

Inheritance of anthocyanin pigmentation (stem colour) (Plate 2) was studied in ICCV2 x JG62, kabuli x desi chickpea cross. F_2 segregation of pigmented and non-pigmented gave a good fit to the expected 3:1 ratio (Table 2).

In the RILs also the inheritance of stem colour was studied. The pigmented and non-pigmented stem colour gave a good fit to the expected 1:1 ratio (Table 3).

Plate 1. Flower of the parents JG62 and ICCV2.

Plate 2. Stem colour of the parents non-pigmented (ICCV2) and pigmented (JG62).

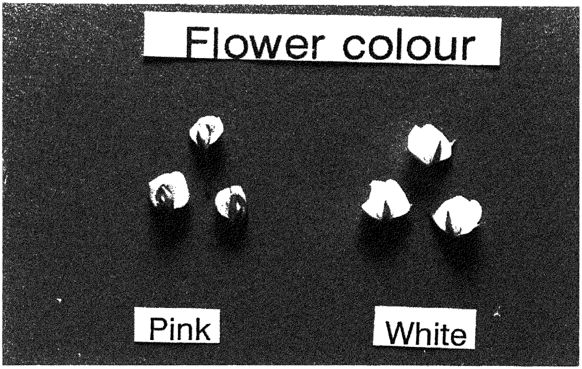

Flower colour
Pink
White

Table 2. Segregation data for F_2 generation of kabuli x desi cross of chickpea.

Cross	Character	F_2 phenotype	Observed number	Appropriate ratio	χ^2	P
ICCV2 × JG62	Flower colour	Pink	87	3:1	0.4	0.60-0.50
		White	33			
	Stem colour	Pigmented	87	3:1	0.4	0.60-0.50
		Non-pigmented	33			
	Twin pod trait	Single pod	102	3:1	6.4	0.05-0.01
		Double pod	18			
	Seed shape	Desi (angular shape)	54	5:10:1	11.88	0.01-0.001
		Intermediate (round shape)	63			
		Kabuli (owl's shape)	3			
	Seed colour	Coloured (non-white)	116	63:1	2.29	0.20-0.10
		Salman white	4			
	Fusarium wilt	Susceptible	598	15:1	0.107	0.75-0.50
		Resistant	42			

Table 3. Segregation data for RILs of a kabuli x desi cross of chickpea.

Cross	Character	RIL phenotype	Observed number	Appropriate ratio	χ^2	P
ICCV2 × JG62	Flower colour	Pink	45	1:1	2.59	0.20-0.10
		White	31			
	Stem colour	Pigmented	45	1:1	2.59	0.20-0.10
		Non-pigmented	31			
	Twin pod trait	Single pod	42	1:1	0.84	0.50-0.30
		Double pod	34			
	Seed shape	Desi (angular shape)	17	1:2:1	0.50	0.90-0.70
		Intermediate (round shape)	41			
		Kabuli (owl's shape)	18			
	Seed colour	Dark brown	13	1:1:1:1:1:1:1:1	8.63	0.30-0.20
		Brown	11			
		Yellow brown	2			
		Orange brown	11			
		Light brown	10			
		Light orange	9			
		Light yellow	8			
		Salman white	12			
	Fusarium wilt	Susceptible	57	3:1	0	1.00-0.95
		Resistant	19			

4.1.3. Twin pod character

In the present study, the cross was obtained from combination of single podded variety ICCV2 and double podded parent JG62 (Plate 3). F_2 segregation for single and double pods per node did not give a good fit to the expected 3:1 ratio (Table 2), probably due to lack of penetrance and inadequate population size.

Inheritance of podding characters was also observed in RILs. The 76 RILs had 42 single podded and 34 double podded which corresponds with the expected 1:1 ratio (Table 2). This indicates that the larger population of RILs have made possible, the correct conclusion. In addition, variation in the expression was found within the double podded lines, which confirmed lack of penetrance.

4.1.4. Seed shape

JG62 has desi seed type with angular shape and ICCV2 had kabuli seed type with owl's head shape (Plate 4). The F_1 was intermediate (Kumar, 1998). The inheritance of seed shape was studied in F_2 population. The seeds of F_2 plants segregated in three phenotypic classes. The segregation for angular, pea and owl's head shape. They could not fit to expected 5:10:1 ratio based on two gene segregation, probably due to limited population size (Table 2).

However, inheritance of seed shape in F_{10} RILs showed segregation for the three seed shapes and showed a good fit to the expected 1:2:1 ratio

(Table 3). This indicated that additive gene action is operating.

4.1.5. Seed colour

The parental line ICCV2 has Salman white (cream) and JG62 has brown seed coat colour at maturity (Plate 4). The seed of F_2 population segregated into various seed coat colours. Due to difficulty in classifying F_2 seed into distinct sub-classes; in this study, classification was made into two major classes, i.e., coloured or non-white (brown or various degree of brownish colour) and Salman white seed colours. The segregation result of coloured and Salman white seed was good fit to the appropriate ratio of 63:1 for three gene segregation (Table 2). However, for the inheritance study of seed coat colour, the RILs were further classified into various colour classes. These appeared to segregate dark brown, brown, yellow brown, orange brown, light brown, light orange, light yellow, and Salman white colours which gave a good fit to the expected 1:1:1:1:1:1:1:1 ratio (Table 3).

4.1.6. Seed size

Inheritance of seed size was determined by measuring 100-seed weight from individual plants of parents, RILs and F_2 populations. ICCV2 (P_1) has large seeds with a seed weight of 26 g per 100 seeds and JG62 (P_2) has small seeds with a seed weight of 16 g per 100 seeds. The F_2 generations of the cross did not segregate into discrete classes of seed size; the frequency distribution of 100-seed weight in the F_2 population was continuous with no distinct modes. However, the frequency distribution of RILs suggested the presence of major genes (Fig. 1). The

Plate 3. Podding trait of the parental lines. Single podded (left side), and double podded (right side).

Plate 4. Seed colour and shape of the parental lines. ICCV2 Salman white, smooth owl's head, and JG62 brown and angular.

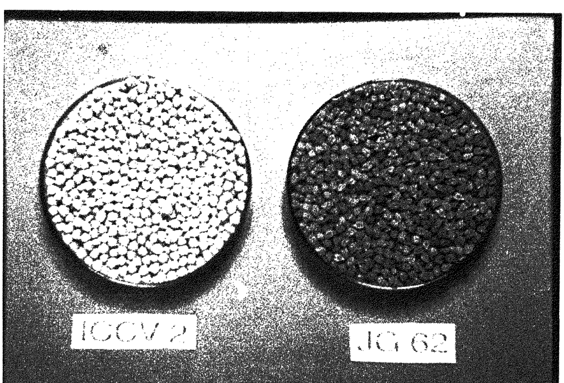
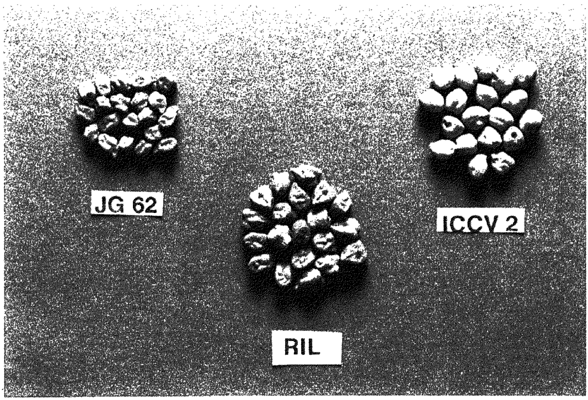

ICCV 2
JG 62

Plate 5. A large seeded desi RIL (middle) selected from ICCV2 × JG62 cross.


JG 62
RIL
ICCV 2

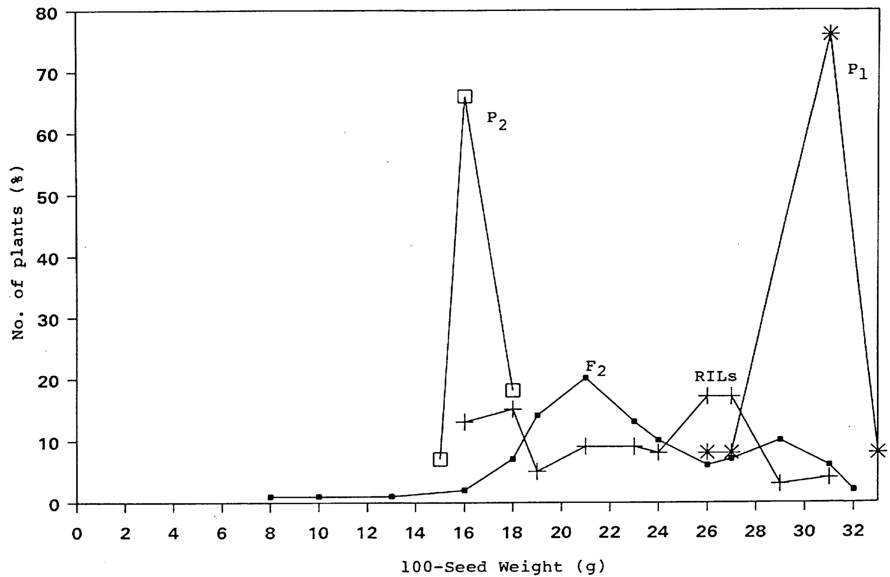


Fig.1: FREQUENCY DISTRIBUTION OF SEED SIZE FOR PARENTS, F_2 POPULATION AND RILs OF ICCV2 (P_1) x JG62 (P_2) CHICKPEA CROSS

figure shows that some segregants were much smaller than the smaller seed sized parent. However, no segregants exceeding the seed size of ICCV2 were obtained in the small F_2 population indicating the dominance of smaller seed size. The segregants for larger seed size may be obtained in succeeding generations from large inbred populations of large seeded selections in F_2. The RILs, however, extended within the parental seed sizes only as they are progeny of random selections and have not been selected on the basis of seed size. Two lines were found exceeding the kabuli seed size (more than 26 g/100) having desi seed type (Plate 5). These can be utilized to develop bold seeded desi.

4.1.7. Fusarium wilt resistance

Inheritance study of fusarium wilt resistance was made on these RILs planted separately in wilt-sick plots. Both F_2 and F_{10} generations were used to determine the inheritance. F_2 segregation of susceptible and resistance plants gave a good fit to the expected 15(S):1(R) ratio (Table 2) indicating that resistance was controlled by two recessive genes. Similarly, the 76 F_{10} generation recombinant inbred lines gave a good fit to the expected 3(S):1(R) ratio based on two recessive genes for resistance (Table 3).

4.1.8. Linkage between flower colour and seed shape, and flower colour and seed colour

In the F_2 population of ICCV2 ×JG62, the χ^2 values for flower colour and seed shape at two degree of freedom, as well as for flower colour and seed coat colour at one degree of freedom were found to be highly significant (Table 4), showing lack of independence (presence of linkage). It appears that white flower colour allele is linked to gene(s) for owl's head shape and pink flower allele is linked to allele(s) for angular seed shape. Similarly white flower allele is linked to salman white coloured seeds (Table 4).

4.2. Correlations Among Characters in F_2 Generation and RILs

In this study, the relationship of qualitative characters, flower colour, stem colour, seed colour and seed shape, among themselves and with quantitative characters were determined by assigning values for parental phenotypes. For instance, lesser value for ICCV2 and higher value for JG62 parental phenotypes and inbetween values for intermediate classes were given accordingly to compute correlation analysis.

The magnitude and direction of association among morphological traits in F_2 and F_{10} generations are presented in Table 5. Similar association trends with positive and significant values were obtained for both the generations for pods per plant with seeds per plant and seed yield per plant; seed yield per plant with seeds per plant; and flower and stem colours with seed colour; while 100-seed weight and seeds per pod showed significant and negative association in both generations. On the other hand, only positive and nonsignificant relationships for pods per plant and seeds per pod, seed yield with flower and stem colours; and seeds per pod and seed type were obtained. Positive significant associations for

Table 4. Test of independence of seed shape and seed colour with flower colour, in the F_2 population of the chickpea cross ICCV2 × JG62.

	Flower colours (3:1)				
	Observed		Expected ratio		
Seed shape	Pink	White	Pink	White	χ^2
		Seed shape (5:10:1)			
Angular	49	11	15	5)	
Round	38	19	30	10)	27.98**
Owl's head	0	3	3	1)	
Total	87	33	3	1	0.40
		Seed coat colour (63:1)			
Coloured	87	29	189	63)	
Salman white	0	4	3	1)	27.96**
Total	87	33	3	1	0.40

* Significant at 0.05
** Significant at 0.01

4.2.1. F_2 generation

Number of pods per plant: Number of pods per plant was positively correlated with number of seeds per plant (r=0.963**) and seed yield per plant (r=0.939*). It showed only non-significant correlations with other characters.

Number of seeds per plant: Number of seeds per plant was positively correlated with number of pods per plant (r=0.963**), seed yield per plant (r=0.941**) and seeds per pod (r=0.305**). It had non-significant association with other characters.

Seed yield per plant: The correlation values estimated in F_2 generation showed that seed yield per plant had positive association with number of pods per plant (r=0.939**), number of seeds per plant (r=0.941**) and number of seeds per pod (r=0.192*). It showed no association with 100-seed weight, flower and stem colours, seed type and seed colour.

Number of seeds per pod: Number of seeds per pod was positively associated with number of seeds per plant (r=0.305**) and seed yield (r=0.192*). It showed no correlation with number of pods per plant, flower and stem colours, seed type, and seed colour. Negative and significant association was, however, observed with 100-seed weight (r=-0.344**).

100-seed weight: 100-seed weight showed no significant positive associations with seed yield per plant and other characters. It had however a significant negative

Table 5. Correlation coefficient values among various morphological characters in F_2 generation and F_{10} RILs in ICCV2 × JG62 chickpea cross.

			Pods per plant	Seeds per plant	Seed yield per plant (g)	Seeds per pod	100-seed weight (g)	Flower colour	Stem colour	Seed shape	Seed colour
Pods per plant	1.	F_2	1.000								
		F_{10}	1.000								
Seeds per plant	2.	F_2	0.963**	1.000							
		F_{10}	0.873**	1.000							
Seed yield per plant (g)	3.	F_2	0.939**	0.941**	1.000						
		F_{10}	0.524**	0.360**	1.000						
Seeds per pod	4.	F_2	0.077	0.305**	0.192*	1.000					
		F_{10}	0.005	0.485**	-0.162	1.000					
100-seed weight (g)	5.	F_2	-0.094	-0.173	0.119	-0.344**	1.000				
		F_{10}	-0.544**	-0.768**	0.296**	-0.588**	1.000				
Flower colour	6.	F_2	0.096	0.092	0.061	-0.097	-0.064	1.000			
		F_{10}	-0.084	-0.021	0.068	0.118	0.072	1.000			
Stem colour	7.	F_2	0.096	0.092	0.061	-0.097	-0.064	1.000**	1.000		
		F_{10}	-0.084	-0.021	0.068	0.118	0.072	1.000**	1.000		
Seed shape	8.	F_2	-0.084	-0.038	-0.053	0.121	-0.042	-0.067	-0.067	1.000	
		F_{10}	-0.099	-0.082	-0.052	0.012	0.062	0.311**	0.311**	1.000	
Seed colour	9.	F_2	0.004	0.003	-0.005	-0.059	-0.008	0.733**	0.733**	0.172	1.000
		F_{10}	-0.102	-0.052	0.096	0.083	0.140	0.820**	0.820**	0.526**	1.000

* Significant at 0.05
** Significant at 0.01

d.f. for		0.05	0.01
F_2 = 118		0.185	0.241
F_{10} = 74		0.225	0.293

seed yield per plant and 100-seed weight was obtained for the RILs. Seed colour with seed type was positively significant in RILs only.

To compute correlation analysis among qualitative characters and with quantitative characters (in Tables 5 and 6) values were assigned as follows:

S.No.	Characters	Phenotypes	Values	Generations
1.	Flower colour	White	1	
		Pink	2	F_2 & RILs
2.	Stem colour	Non-pigmented	1	
		Pigmented	2	F_2 & RILs
3.	Seed shape	Kabuli (owl's shape)	1	
		Intermediate (round shape)	2	F_2 & RILs
		Desi (angular shape)	3	
4.	Seed colour	Salman white	1	F_2
		Coloured (non-white)	2	
5.	Seed colour	Salman white	1	
		Light yellow	2	
		Light orange	3	
		Light brown	4	RILs
		Orange brown	5	
		Yellow brown	6	
		Brown	7	
		Dark brown	8	

association with number of seeds per pod (r=-0.344**).

Flower colour and stem colour: The results of this study showed that flower and stem colour had absolute association with each other (r=1.00**) and showed positively strong association with seed colour (r=0.733**).

Seed shape: All the characters showed non-significant association with seed shape.

Seed colour: High and same correlation values of 0.733** were obtained between seed colour and flower colour and seed colour and stem colour.

4.2.2. Recombinant inbred lines

Simple correlation analysis was made to determine association of nine morphological traits in recombinant inbred lines (Table 5).

Number of pods per plant: In this generation number of pods per plant had positive correlation with seeds per plant (r=0.873**) and seed yield per plant (r=0.524**) only. Number of pods per plant showed negative significant relationship with 100-seed weight (r=-0.544**).

Number of seeds per plant: Number of seeds per plant had positive significant correlation with number of pods per plant (r=0.873**), seed yield per plant (r=0.360**) and number of seeds per pod (r=0.485**). On the other hand, number of seeds per plant had strong negative association with 100-seed weight (r=-0.768**).

Seed yield per plant: The seed yield per plant was found to have positive associations with number of pods per plant (r=0.524**), number of seeds per plant (r=0.360**) and 100-seed weight (r=0.296**). The other characters showed no associations with seed yield per plant.

Seeds per pod: Seeds per pod had significant positive associations with seeds per plant (r=0.485**) and significant negative association with 100-seed weight (r=-0.588**). Seeds per pod showed no relationship with all other characters.

100-seed weight: 100-seed weight had negative association with number of seeds per plant (r=-0.768**), number of seeds per pod (r=-0.588**) and number of pods per plant (r=-0.544**) and positive association with seed yield per plant (r=0.296**). 100-seed weight showed no relationship with other characters.

Flower and stem colours: Flower and stem colours had strong positive association with seed colour (r=0.820**) and seed shape (r=0.311**). Flower colour is absolutely associated with stem colour. They had no association with other characters.

Seed shape and seed colours: Seed shape and seed colours showed positive association (r=0.526**) and both had strong positive association with flower colour and stem colour.

4.2.2.1. Correlation between fusarium wilt susceptibility and other morphological characters in RILs

In the RILs, association studies were made on the data obtained from percent of plants attacked by fusarium wilt disease. Fusarium wilt susceptibility had strong positive association with greater number of seeds per pod and desi seed shape. It had strong negative association with seed yield per plant, seeds per plant and seed colour. Fusarium wilt susceptibility had no significant association with other characters (Table 6).

4.2.2.2. Phenotypic and genotypic correlations among major yield components in RILs

Phenotypic and genotypic correlation coefficients for yield and four major yield components are presented in Table 7. Phenotypic association values were more than genotypic values in case of seed yield with number of pods per plant and number of seeds per plant and number of pods per plant with number of seeds per plant. In other associations, genotypic values are found to be more than phenotypic values.

Table 6. Correlation coefficient values between fusarium wilt susceptibility (%) and other morphological characters in F_{10} RILs of ICCV2 × JG62 chickpea cross.

	Pods per plant	Seeds per plant	Seed yield per plant (g)	Seeds per pod	100-seed weight (g)	Flower colour	Stem colour	Seed shape	Seed colour
Fusarium wilt susceptibility	-0.024	-0.360**	-0.606**	0.999**	-0.127	0.131	0.131	0.980**	-0.253*

* Significant at 0.05 — 74 d.f.
** Significant at 0.01 — 74 d.f.

Number of pods per plant: Number of pods per plant showed positive phenotypic correlation coefficients with number of seeds per plant (r=0.905**) and seed yield per plant (r=0.697**) while it had negative correlation with 100-seed weight (r=-0.455**) and no correlation with number of seeds/pod. It also exhibited highly significant and positive genotypic correlation with number of seeds per plant (r=0.874**) and seed yield/plant (r=0.347**). The number of pods per plant had negative genotypic correlation with 100-seed weight (r=-0.658**) and no significant genotypic correlation with number of seeds per pod.

Number of seeds per plant: Phenotypically, this character exhibited high positive correlations with number of pods per plant (r=0.905**), seed yield per plant (r=0.593**) and number of seeds per pods (r=0.407**) and negative correlation with 100-seed weight (r=-0.652**). This character expressed high positive genotypic correlation with number of pods per plant (r=0.874**) and number of seeds per pod (r=0.487**) and no correlation with seed yield per plant. Negative genotypic correlation was obtained between number of seeds per plant and 100-seed weight (r=-0.866**).

Seed yield per plant: The phenotypic correlation coefficients were high positive and significant with number of pods per plant (r=0.697**) and number of seeds per plant (r=0.593**) and no correlation with 100-seed weight and number of seeds per pods.

Seed yield per plant also expressed positive genotypic correlations with number of pods per plant (r=0.347**) and 100-seed weight (r=0.346**) and no correlation with number of seeds per plant. It had however significant negative genotypic correlation with number of seeds per pod (r=-0.288**).

Number of seeds per pod: This characters exhibited positive phenotypic correlation only with number of seeds per plant (r=0.407**). It showed significant negative correlation with 100-seed weight (r=-0.553**) and no correlation with number of pods and seed yield per plant.

Number of seeds per pod exhibited positive genotypic correlation only with number of seeds per plant (r=0.487**). It had no association with number of pods per plant, while it had negative association with seed yield (r=-0.288*) and 100-seed weight (r=-0.589**).

100-seed weight: 100-seed weight showed positive association only with seed yield per plant genotypically (r=0.346**). Negative phenotypic relationships were obtained with number of pods per plant (r=-0.455**), number of seeds per plant (r=-0.652**) and number of seeds per pod (r=-0.553**). It also showed negative genotypic correlation with number of pods per plant (r=-0.658**), number of seeds per plant (r=-0.866**) and number of seeds per pod (r=-0.589**).

Table 7. Phenotypic (P) and genotypic (G) correlation coefficients for five quantitative characters in 76 RILs of ICCV2 x JG62 chickpea cross.

			Pods per plant	Seeds per plant	Seed yield per plant (g)	Seeds per pod	100-seed weight (g)
Pods per plant	1.	P	1.000	0.905**	0.697**	-0.005	-0.455**
		G	1.000	0.874**	0.347**	0.005	-0.658**
Seeds per plant	2.	P		1.000	0.593**	0.407**	-0.652**
		G		1.000	0.144	0.487**	-0.866**
Seed yield per plant (g)	3.	P			1.000	-0.068	0.191
		G			1.000	-0.288*	0.346**
Seeds per pod	4.	P				1.000	-0.553**
		G				1.000	-0.589**
100-seed weight (g)	5.	P					1.000
		G					1.000

* Significant at 0.05 74 d.f.
** Significant at 0.01

4.3. Mean Performance of F_2 Population and F_{10} RILs

The mean value and C.V in Table 8 reveal that the higher mean value and less coefficient of variation for RILs was recorded for most quantitative characters and lesser mean value and higher coefficient of variation for F_2 population. This variations were attributed to F_2 population was planted at close spacing of 60 cm x 10 cm. Moreover the data of F_2 was recorded on single plant basis and the data of RILs were taken from plot mean basis which resulted in lesser error of variation for the latter. The average fusarium wilt susceptibility for RILs was 65.4% and for F_2 population 93.4%. This wilt susceptibility result was in close agreement with the expected 75.0% and 93.8% susceptibility of the two generations based on two recessive genes controlling complete resistance to race 1 of fusarium wilt.

Table 8. Mean value, Standard deviation (S.D), Coefficient of variation (C.V), of F_{10} RILs and F_2 population for quantitative characters.

Generations		No. of pods per plant	No. of seeds per plant (g)	Seed yield per plant (g)	No. of seeds per pod	100-seed weight (g)	Wilt susceptibility count (%)
RILs	Minimum	68.40	64.20	18.44	0.81	14.26	0
	Mean	131.50	144.10	30.36	1.10	21.96	65.40
	Maximum	258.40	298.8	57.88	1.55	31.09	100
	S.D						
	Minimum	18.48	20.75	4.26	0.04	0.90	-
	Average	19.84	22.40	4.62	0.05	0.99	35.76
	Maximum	22.18	25.07	5.17	0.06	1.12	-
	C.V%	15.09	15.54	15.20	4.80	4.52	54.70
F_2 population							
	Minimum	10.00	8.00	1.70	0.61	8.00	-
	Mean	79.51	69.65	15.13	0.87	22.20	93.40
	Maximum	199.00	200.00	39.40	1.32	31.67	-
	S.D	45.65	43.68	9.25	0.14	4.48	-
	C.V%	57.41	62.71	61.14	16.09	20.18	-

DISCUSSION

CHAPTER V

DISCUSSION AND CONCLUSIONS

5.1. Inheritance of Morphological Characters

This study was conducted to determine the inheritance of morphological characters like flower colour, stem colour, twin podded character, seed shape, seed colour, and seed size, and fusarium wilt resistance in F_2 population and F_{10} random recombinant inbred lines (RILs) of the chickpea cross ICCV2 x JG62.

Generally the segregation pattern obtained for each character for F_2 generation (Table 2) was confirmed in the F_{10} RILs (Table 3).

The inheritance of flower and stem colours was studied in ICCV2 x JG62 chickpea cross. Genetics of flower colour is important as it has profound effect on seed colour. The results suggest that pink vs. white flower colour and pigmented vs. non-pigmented stem colour are each controlled monogenically; where pink is dominant over white and pigmented stem colour is dominant over non-pigmented colour. Similarly, Pimplikar (1943) and Khan *et al.* (1950) reported that pink flower colour was dominant to white and controlled by a single gene. However, Khan and Akhtar (1934) had previously reported that two pairs of genes, P and B, control flower colour in chickpea. Further they suggested that the dominant B gene is responsible for blue flowers, while P in the presence of B produces pink flowers. White flowers occur when B is recessive, irrespective of the dominant condition of P. Ayyar and Balasubramanian (1936) suggested a third factor, C, was involved. According to them pink flowers are produced when all the three genes, P, B and C are present in the dominant condition, blue when P is homozygous recessive and white when either B or C is homozygous recessive. If this is the proper explanation then either C or B was segregating in the present study and in the studies of Pimplikar (1943) and Khan *et al.* (1950). Kumar (unpublished data) showed that both ICCV2 and JG62 produce pink flower when crossed to a blue flowered line the genotype of which was determined as ppBBCC. Thus the genotype of ICCV2 is PPBBcc or PPbbCC (more likely) and that of JG62 is PPBBCC.

Most cultivars of chickpea produce single flower at each flowering node, but some produce two flowers and have the potential to form two pods per node. However, two pods are produced at only a minority of pod bearing nodes and can confer a small but significant advantage in yield under the conditions in which it is well expressed (Sheldrake *et al.*, 1978). The occurrence of double flowered types is well documented in desi types but in kabuli types it is scanty. Khan and Akhtar (1934) suggested that number of flowers per peduncle was governed by a single locus with one flower dominant to two. This finding has been confirmed by many researchers (Ahmad, 1964; Singh, 1965; Patil, 1966; D'Cruz and Tendulkar, 1970; More and D'Cruz, 1976b; Yadav *et al.*, 1978; Pawar and Patil, 1983; Rao and Pundir, 1983; Pundir *et al.*, 1988). However, in the present study, double poddeness was not well expressed, which is shown by a high chi-square value F_2's (Table 2). Lack of penetrance of the gene in the limited F_2 population could not confirm the report of monogenic inheritance of earlier workers. However, the results from larger RILs populations confirmed the monogenic inheritance (Table 3).

Chickpea is cultivated over a wide range of agroclimatic conditions that affect the performance of varieties with different seed sizes. This crop is mainly of two types, the desi type and kabuli type. Desi types are characterized by small seed size, angular shape, and coloured seeds with a high percentage of fiber; whereas, kabuli types with large seed size, owl's head shape and Salman white coloured seeds possessing low percentage of fiber. A third type, i.e., intermediate has pea shape and light pink coloured (gulabi) seeds. Of the world production, about 85% are of desi type and the remaining being kabuli (Singh *et al.*, 1985). Gulabi types are cultivated in small pockets in Central India, mainly for parching chickpea market. Almost two-third of the chickpea growing countries cultivate only the kabuli type, and one-third mostly the desi type.

Inheritance studies on seed shape in chickpea indicated that pea seed shape is dominant to both desi and kabuli, and desi is dominant to kabuli shape (Knights, 1979). The F_2 segregation from desi x kabuli crosses generally produce up to five classes — pea, desi, kabuli and two intermediate forms (pea-desi and pea-kabuli). Frequencies of these types are variable and dependent on the parental lines used. There is further segregation of desi and kabuli from pea (intermediate types) on inbreeding. Small number of segregation classes suggest that the seed shape is controlled by a few major genes. The variable frequencies of segregation classes together with the instability of desi and kabuli types in early generations, suggested epistatic interaction (Knights, 1979). From Table 3, it can be seen that the inheritance of seed shape in ICCV2 x JG62 chickpea cross was governed by two major pairs of genes which are acting in an additive manner in which dominant alleles had a cumulative effects (1:2:1). Plants with 3 or 4 dominant alleles had desi seed type, 1 or 2 dominant alleles had intermediate seed type and those with all recessive alleles had kabuli seed shape.

The present results thus differ from those of Knights (1979) where angular seed shape is not dominant to owl's head shape or intermediate shape. In this study the F_1 seed was intermediate type (Kumar, 1998). Thus heterozygote intermediate seed type can produce all the three seed shapes and heterozygote desi type may segregate to produce desi and intermediate types. Owl's head shape seed accordingly should be stable. This has important implications to breeding. Thus the intermediate seed shape may not be rejected in early generations as it may produce desi and kabuli types.

Seed coat colour in chickpea is a highly variable character. Sometimes even the coat of a single seed develops patches in which more than one colour or shade gets intermixed, making gradation of seed coat colour extremely difficult. Age of seed also tends to affect seed coat colour. Different results were reported by various researchers about inheritance of seed coat colour in chickpea. Thus, inconsistency in gene symbols makes it difficult to compare different reports. The number of genes governing colour variations in chickpea were reported as five by Balasubramanian (1952), Phadnis (1978) and Brar and Athwal (1970); as four by Alam (1935); as one by D'Cruz and Tendulkar (1970), More and D'Cruz (1970, 1976b), and Pawar and Patil (1983). In the present study the F_2 plant seeds could be classified as coloured or non-white vs. Salman white seed colour, which gave a good fit to 63:1 ratio (Table 2), indicating three gene segregation. This was further confirmed by the eight phenotypic classes for RILs (Table 3) for seed coat colour. Thus the present parents may differ only for three genes. However, which of the earlier genes are involved could not be determined. Further studies are needed involving parents used in different studies.

The extensive variation for seed size available forms a basis for studying genetics of seed size and is important to chickpea improvement. Within this variation, genotypes with different seed sizes coupled with desirable attributes of quality and yield acceptable to producers and consumers can be developed.

Inheritance of seed size has been reported to be partial dominance of smaller seeds over the larger ones (Athwal and Sandhu, 1967; Smithson *et al.*, 1985; Kumar and Singh, 1995); while Niknejad *et al.* (1971) reported that large seeds are partially dominant to small seeds. Additive gene effects were largely involved in determining 100-seed weight (Malhotra and Singh, 1989). These studies on inheritance indicated that seed size is a predictable trait that is relatively uninfluenced by environment. Selection, therefore, for this character in segregating populations has excellent chance of success. However, in the present study it is evident from Fig. 1 that frequency distribution of 100-seed weight in the F_2 population was continuous with no distinct modes. This suggests polygenic inheritance for seed size. Similar observation was also made by Kumar and Singh (1995). On the other hand, in the present investigation, frequency distribution of RILs apparently suggests a major gene controlling much variation and thus, selection for this trait should bring quick improvement. It may be possible to breed larger seeded chickpeas as relatively few genes may be involved.

Wilt, caused by *Fusarium oxysporum* f.sp.*ciceri* is a serious disease of chickpea. It causes an annual yield loss of about 10 per cent (Mandal, 1989) to as high as 60-70% (Jalali *et al.*, 1992). It is evident from the earlier reports that the inheritance of resistance is simple to complex in nature. From Tables 1 and 2, it is evident that the digenic duplicate ratios (15:1 and 3:1) were observed for F_2 and RILs showing high probabilities of goodness of fit. The results indicate that fusarium wilt resistance was conditioned by two pairs of recessive genes. Homozygous recessive condition for both is necessary for resistance. This observation was in close agreement with the study made by Lopez (1974) and Upadhyaya *et al.* (1983a, 1983b).

5.2. Association Studies

To improve the inherent ability of a crop plant, the selection criterion may be yield, one or more of the components of yield and quality traits. Therefore, an understanding of the nature of association among them and between each component and yield is of great significance in proper planning of selection programmes.

The magnitude and direction of association among morphological traits in F_2 population and F_{10} generation RILs were determined for different characters (Table 5). Similar association trends with positive and significant values were obtained for both generations for seed yield with number of pods per plant indicating that selection can be made in the F_2 generation to identify segregants with higher seed yield. Significant relationship among the F_2 to F_4 generations in chickpea for yield were reported by Dahiya *et al.* 1983b. On the contrary, poor intergeneration association was reported for pods per plant and grain yield in chickpea by Rahman and Bahl (1986). Inconsistent association among generations for important characters were reported by Weiss *et al.* (1947) for soybean and Geletu *et al.* (1991) for chickpea.

Correlations estimated among yield components in each of F_2 generation and RILs separately indicated that number of pods per plant had significant positive correlation with number of seeds per plant in F_2 (0.963**), and F_{10} (0.873**) and with seed yield per plant in F_2 (0.939**), and F_{10} (0.524**) generations

(Table 5). Such association between number of pods per plant with number of seeds per plant and seed yield per plant were reported by Sandhu and Singh (1970), Dobholkar (1973), Jatasra (1983), Shahi *et al.* (1984), Salimath and Bahl (1986) and Kharrat *et al.* (1991). The effectiveness of number of pods/plant for indirect selection for yield was further stressed by Mishra *et al.* (1988), Rahman and Bahl (1986), Singh and Singh (1989), and Singh *et al.* (1992). In the present study number of pods per plant had negative correlation with 100-seed weight (-0.544**) in RILs. It had weak associations with the remaining five characters. Similar observation was also reported by Hadjchristodovlou (1987).

Number of seeds per plant had significant positive association with number of pods per plant in F_2 (0.963**) and in F_{10} (0.873**), with seed yield per plant in F_2 (0.941**) and in F_{10} (0.360**) and with number of seeds per pod in F_2 (0.305**) and F_{10} (0.485**) generations. The highest correlation values were obtained in both generations between number of seeds per plant and seed yield per plant indicating that the number of seeds per plant is the most effective selection criterion in this cross of chickpea.

Number of seeds per pod has shown significant positive association with number of seeds per plant in F_2 and F_{10} generations and with seed yield per plant in F_2 generation. Such associations between number of seeds per pod and seed yield per plant were reported by Rang *et al.* (1980), Paliwal *et al.* (1987), Sindhu and Prasad (1987), Sandhu *et al.* (1988), Shukla (1988), Jivani and Yadavendra

(1988), Govil and Kumar (1989) and Haq (1990). On the contrary, Khan and Chaudhary (1975) and Khoragade *et al.* (1995) reported a negative correlation between number of seeds per pod and seed yield per plant.

Among the yield components that determine seed yield in chickpea, 100-seed weight was positively and significantly associated with seed yield in RILs, but it was negatively correlated with number of pods per plant, seeds per plant and number of seeds per pod. Similar to the present studies negative association between number of seeds per pod and seed weight were reported by Singh *et al.* (1976), Katiyar (1979), Adikari and Pandey (1982a) and Tagore and Singh (1990). Contrary results were, however, reported by Sandhu and Mandal (1989). They reported a positive correlation between number of seeds per pod and seed weight. In close agreement with the present finding, 100-seed weight was found to be positively correlated with seed yield by Singh *et al.* (1984), Dahiya *et al.* (1986), Sindhu and Prasad (1987), Mishra *et al.* (1988), Waldia *et al.* (1988), Misra (1991) and Khoragade *et al.* (1995). On the contrary, Dobholkar (1973), Singh *et al.* (1976), Raju *et al.* (1978) and Hadjchristodovlou (1987) reported a negative correlation between 100-seed weight and seed yield. Thus this association may depend on the genetic constitution of the parents used.

The association of genes for economically important traits with easily identified markers can improve the efficiency of selection and hasten the development of improved cultivars. It is evident that qualitative characters being less influenced by environmental variations are used as markers (Raut *et al.*, 1994). However, in the present investigation, no associations were observed among any one of qualitative characters with quantitative characters indicating that the genes controlling these characters were segregating independently. The flower colour and seed colour were reported to be positively correlated with seed yield (Govil *et al.*, 1980). It appears that the gene for flower colour is pleiotropic and totally affects the stem colour. In this study there were no pink flowered plants with non-pigmented stem and no white flowered plants with pigemented stem. Interestingly there were strong associations among qualitative characters. Flower colour was absolutely associated with stem colour in F_2 (1.000**) and F_{10} (1.000**) generations and strongly associated with seed colour in F_2 (0.733**) and F_{10} (0.820**) generations. White flower was associated with non-pigmented stem colour and Salman white seed colour, while pink flower was associated with pigmented stem colour and coloured (non-salman white) seed coat. Singh and Ekbote (1936), Pimplikar (1943) and Kadam *et al.* (1945) reported that flower colour, seed colour and seed shape are inherited together mongenically where pink flower, yellowish-brown testa and irregular shape of the seed were dominant to the white flower, orange-yellow coloured testa and round seed; further they indicated that the seed and flower colours were completely linked. This finding was further supported by Argikar and D'Cruz (1962) and Bhapkar and Patil (1962). In the present work, association between seed shape with flower and stem colours (0.311**) and with seed colour (0.526**) in F_{10} generation (Table 5); though strong, were not absolute, indicating the possibility of obtaining recombinants.

This indicated that other gene(s) than the flower colour gene segregating in this study also influence the shape and colour of the seeds. Kabuli seed type was associated with white flower colour and non-pigmented stem, while desi type was associated with pink flower and pigmented stem. A test of independence between flower colour segregation and seed shape, flower colour and seed colour, also confirmed lack of independence and consequent indication of linkage (Table 4). However, no association was found between 100-seed weight and seed type indicating that recombination is possible between greater 100-seed weight and desi seed type.

The relationships among morphological traits and fusarium wilt resistance have not been adequately described; few studies reported that there is any useful correlation between plant traits and resistance to fusarium wilt disease. In this work, fusarium wilt susceptibility had no association with number of pods per plant, flower colour and stem colour (Table 6). Similarly, Harjit Singh *et al.* (1988) found that the wilt reactions of F_3 progenies segregated independently of flower colour.

From Table 6, it can be clearly seen that fusarium wilt susceptibility was positively correlated with number of seeds per pod (0.999**) and angular seed shape (0.980**) indicating that susceptibility is with JG62 characteristics of more seeds per pod and angular seed type and resistance is with ICCV2 characteristics of fewer seeds per pod and owl's head seed type. Kumar and Haware (1983) found the same relationships from their studies aimed at identifying a number of segregants with kabuli characteristics and resistance to fusarium wilt from kabuli x desi crosses. On the contrary the association between fusarium wilt susceptibility and seed colour was negative. Interestingly, fusarium wilt susceptibility was negatively correlated with seed yield per plant (-0.606**) and number of seeds per plant (-0.360**) indicating that it may be possible to find the segregants that combine high yielding characteristics with fusarium wilt resistance.

The partitioning of correlation coefficients into genotypic and phenotypic level is important for effective selections. A positive and high genetic correlation with positive low/high phenotypic correlation will be useful for selection programme.

Phenotypic and genotypic correlation coefficients for yield and four major yield components in Table 7 reveal that the estimates of genotypic correlation coefficients were similar in sign but lesser in magnitude than the ones observed at phenotypic level for seed yield with number of pods per plant and number of seeds per plant and number of pods per plant with number of seeds per plant. In other associations, genotypic values are found to be more than phenotypic values which in turn indicate a strong inherent association between the characters under study. Seed yield had positive and significant association with number of pods per plant, at genotypic and phenotypic levels and with 100-seed weight at genotypic level. Choudhury and Khalegue (1988), Bhambota *et al.* (1994) have also reported similar positive association between number of pods per plant and seed yield. Pooran (1997) recommended seeds per plant and pods per plant to be a reliable criteria for selection in chickpea. The present investigation showed that pods per plant can be used as a selection criteria as its phenotypic and genotypic correlations with seed yield per plant was significant. This study did not show any significant genotypic correlation of seeds per plant with seed yield per plant. Therefore it may not be used as selection criterion for yield. Since 100-seed weight has positive significant genotypic correlation with seed yield but without significant phenotypic correlation, it will also be difficult to use it as selection criterion for yield.

In the present study the results on genetic and correlation studies were obtained independently on two generations, F_2 and F_{10}. Therefore, these can be relied upon with a relatively greater degree of confidence. To our knowledge this is the first time that inheritance results in chickpea were reported on the RILs. Future studies should add data for more qualitative and quantitative traits and study genetic interactions. Such data will be additive as the RIL genotypes are not ephemeral, unlike those for segregating generations. The recently published map of chickpea genome traits (Simon and Muehlbauer, 1997) has only 9 genes for morphological traits out of 91 total markers. Therefore, studies on these and other RIL populations can be of great value for resolving the genetics of various traits and hopefully map them on chickpea genome with the help of molecular markers.

Even location of quantitative trait loci can be possible if studies on the RILs are conducted even in different years and locations. Above all identification of a few lines with useful traits may eventually lead to development of high yielding varieties.

SUMMARY

CHAPTER VI

SUMMARY

The study was aimed at (1) ascertaining the inheritance of flower colour, stem colour, twin pod character, seed shape, seed colour, seed size and fusarium wilt resistance and (2) determining the association of these and other important morphological characters among themselves and with seed yield in F_2 population and F_{10} random recombinant inbred lines (RILs) of the chickpea cross ICCV2 x JG62. The studies were carried out during the postrainy season 1997/98 at the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, A.P. 502 324, India. The seeds harvested from F_1 and F_9 generations of the cross were obtained from the Chickpea Breeding Section, ICRISAT for evaluation of F_2 and F_{10} generations. The 76 F_{10} RILs with their parents were laid out in an incomplete block design with three replications. The F_2 population was evaluated in a normal field and both generations and the parents were also tested separately in fusarium wilt-sick plots to determine their wilt reactions. The experiments were planted on 15 October (F_2) and 3 November (F_{10}), 1997.

Data were recorded for six qualitative and five quantitative characters. The inheritance of these characters was determined by using chi-square test and frequency distributions and their associations were determined by correlation analysis. The following results were obtained.

Monogenic inheritance was confirmed for three morphological characters, pink vs. white flower, pigmented vs. non-pigmented stem colour, and single podded vs. double podded characters. Seed shape was governed by two pairs of genes which act in additive manner in which dominant alleles had a cumulative effect. All plants with 3 or 4 dominant alleles had angular seed, 1 or 2 dominant alleles were expressed as intermediate seed and those with no dominant alleles had owl's head seed type. Coloured seed coat was dominant over salman white seed coat and probably controlled by at least three pairs of genes. Seed size was polygenically controlled but with the influence of major gene(s). Resistance to fusarium wilt was confirmed to be due to two pairs of recessive genes; only homozygous recessive condition for both gives resistance. Same results were obtained for the RILs.

The magnitude and direction of associations among all morphological characters in F_2 generation and RILs revealed that in both generations similar association trends with positive and significant values were obtained for seed yield with number of pods per plant and number of seeds per plant. This shows that selection for these characters can be made in the F_2 generation to identify segregants with higher seed yield and seed characters.

Correlations estimated among yield components for F_2 generation and RILs separately indicated that number of pods per plant had significant positive correlation with number of seeds per plant and with seed yield per plant. It was negatively correlated with 100-seed weight in RILs. It had weak associations with the remaining five characters.

Number of seeds per pod was positively correlated with number of seeds per plant in both generations and with seed yield in F_2 generation. It was negatively correlated with 100-seed weight. It showed no relationship with remaining characters.

100-seed weight was positively associated with seed yield in RILs. It was negatively correlated with number of pods per plant, number of seeds per plant and number of seeds per pod in RILs. It had no association with other characters.

Computation of genotypic and phenotypic correlations emphasised the merit of selection for seed yield based on number of pods per plant, as it alone had highly significant genotypic and phenotypic correlations with seed yield, which makes it a good selection criterion.

In the present investigation, no associations were observed among any one of qualitative characters with quantitative characters indicating that the genes controlling these characters were segregating independently.

Flower colour was absolutely and strongly associated with stem colour and seed colour, respectively. It appears that the flower colour gene is pleiotropic and fully determines the stem colour as no crossovers were observed. The associations of seed shape with flower, stem and seed colours for F_{10} generation, though strong were not absolute, indicating the possibility of obtaining recombinants. However, these linkages have important implications in chickpea breeding. Also in this work, no association was found between 100-seed weight and seed shape indicating that recombination is possible between larger 100-seed weight and angular seed shape. Actually two lines were noted among the RILs having larger than ICCV2 seed size with angular seed type, which may be evaluated as bold seeded desi lines for possible release as varieties.

Fusarium wilt susceptibility was positively correlated with greater number of seeds per pod and angular seed type. It was negatively correlated with seed colour, seed yield per plant and number of seeds per plant. This negative association may be helpful in selecting the resistant high yielding lines.

These genetic results were obtained indepdently for F_2 generation and on the RILs in this study and therefore, can be relied upon with relatively greater confidence. To our knowledge this is the first use of RILs for genetic studies in chickpea. It is hoped that the results of this and future studies on these RILs will help saturate the genetic and molecular map for chickpea. As further recording of the data on these RILs will be additive, genetic studies will help resolve the relationship of common genes named in different studies. In this study important ones are genes for flower, stem and seed colour, seed shape, double pod trait and resistance for fusarium wilt race 1. Future molecular studies may help place these on the chickpea map.

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