

Global Scenario of Chickpea Research - Present Status and Future Thrusts

C.L.L. Gowda and P.M. Gaur

International Crops Research Institute for the Semi-Arid Tropics, Patancheru 502 324, AP

Abstract

Globally, chickpea (*Cicer arietinum* L.) is an important cool season food legume. The importance has further increased after its spread in Oceania and North America. There has been 4-fold increase in the global trade of chickpea in the past two decades. Extensive breeding efforts in many countries and at the two CG centers (ICRISAT and ICARDA) have led to development of over 300 improved varieties. However, a breakthrough in its productivity is still awaited. Though the potential yield of chickpea is estimated at 5.0 tons ha⁻¹, its global average yield is around 0.8 tons ha⁻¹, mainly because chickpea is generally grown under rainfed conditions and a number of biotic and abiotic stresses constrain productivity. Thus, research efforts in chickpea have mainly focused on resistance breeding. Excellent progress has been made in development of short-duration varieties that are able to escape terminal drought, resistance to fusarium wilt, and development of varieties suitable for winter sowing in West Asia and North Africa regions. Breeding for resistance to other stresses still remains a challenge due to non-availability of sources of high level of resistance in the cultigen and cross-compatible wild species. The success in transfer of resistance to cyst nematodes from *C. reticulatum* and ascochyta blight from *C. echinospermum* is encouraging. This will encourage researchers to utilize other wild *Cicer* species to introgress useful genes to the cultigen. There has been good progress in development of integrated pest management strategies for ascochyta blight, botrytis gray mold and pod borer. However, efforts are still needed to promote their adoption by the farmers. Extensive efforts have been made in the recent past on biotechnological approaches to chickpea improvement. Several advanced research centers are engaged in development of molecular map of chickpea and identification of markers for resistance to important biotic and abiotic stresses. The recently formed International Chickpea Genomics Consortium will further strengthen efforts in this area. Excellent progress has been made in development of protocols for efficient *in vitro* regeneration of chickpea and development of transgenics for resistance to pod borer by incorporating insecticidal protein gene from *Bacillus thuringiensis*. It is expected that support of biotechnological methods to conventional breeding will catalyse rapid progress in chickpea improvement in the near future.

1. Introduction

Chickpea (*Cicer arietinum* L.) is grown in over 40 countries across five continents. However, 95% of its area is in developing countries. The farmers have long known that chickpea is a hardy crop and can be grown in marginal lands where the high-input crops fail to give economic returns. They also realize that still higher economic returns

from chickpea are possible by good crop management, including need-based irrigations. Canada, Mexico and Australia have obtained an average yield of more than 1.2 tons ha⁻¹ for many years, while the global average yield never exceeded 0.8 tons ha⁻¹. Similar gain in chickpea yield is possible in other countries provided the crop receives good management.

The demand for chickpea in 2010 is estimated at 11.1 million tons (Joshi *et al.*, 2001). This is a major challenge to the chickpea scientific community, policy makers and extension agencies. A combination of productivity enhancement (yield potential and agronomic management) and area expansion can help achieve this target. The vast rice-fallows in south Asia offer an opportunity for expansion of area under chickpea.

Considerable progress has been made in chickpea research globally during the past three decades. An attempt has been made in this paper to review the recent advancement and to suggest future thrust for chickpea research.

2. Production and Trade

The past two decades have witnessed considerable change in global scenario of chickpea production and trade. The global chickpea area increased from 9.7 to 11 million ha, production from 6.4 to 8.4 million tons and yield from 658 to 765 kg ha⁻¹ during 1981-85 to 1996-2000 (Table 1). However, the severe drought during the past three years in many parts of two major chickpea producing countries, India and Pakistan, has reduced the global area and production of chickpea substantially. Drastic changes in chickpea area have occurred in many countries. Chickpea area has increased from 304,000 to 648,000 ha in Turkey, 185,000 to 746,000 ha in Iran, and 12,000 to 222,000 ha in Australia during 1981-85 to 2001-02. Canada has emerged as an important chickpea growing country where chickpea area increased from 3,000 ha in 1996 to 340,000 ha in 2001.

There has been 4-fold increase in the global trade of chickpea during the past two decades, export increased from 250,000 tons during 1981-85 to 1.0 million tons during 2001 (Table 2). Chickpea import by India has increased considerably and in 2001 India accounted for 48% of the global chickpea import. Other importing countries were Pakistan (9.8%), Spain (6.3%), Saudi Arabia (2.3%), Italy (2.1%), Jordan (2.0%) and Tunisia (1.8%). Turkey was the major exporter of chickpea during 1981-85, accounting for 70% of global chickpea export. Australia, Canada, and Mexico emerged as important exporters of chickpea during the past decade. Thus, during 2001, the major exporters of chickpea were Australia (26.8%), Mexico (20.8%), Turkey (15.5%) and Canada (15.0%).

Table 1: Trends in area (000 ha), production (000 tons) and yield (kg ha⁻¹) of chickpea in major chickpea growing countries

	Period	India	Pakistan	Mexico	Turkey	Iran	Australia	Canada	World
Area	1981-85	7183	914	141	304	185	12	-	9746
	1986-90	6767	990	133	727	242	92	-	9902
	1991-95	6691	1041	106	797	654	195	1	10421
	1996-00	7210	1074	146	659	680	233	95	11043
	2001-02	5796	905	172	648	746	222	339	9740
Production	1981-85	4714	433	156	308	113	15	-	6407
	1986-90	4658	512	163	735	115	100	-	6943
	1991-95	5062	472	160	749	306	189	2	7549
	1996-00	5694	661	211	620	254	196	131	8435
	2001-02	4421	397	283	563	260	257	450	7355
Yield	1981-85	657	472	1107	1033	618	1154	-	658
	1986-90	685	514	1214	1026	481	1086	-	700
	1991-95	754	453	1500	938	468	1004	1396	723
	1996-00	791	615	1495	939	372	848	1344	765
	2001-02	757	439	1639	869	348	1178	1327	753

Source: FAOSTAT (<http://apps.fao.org/>)**Table 2: Global chickpea trade (in tons)**

		1981-85	1986-90	1991-95	1996-00	2001
Import	India	7754	138069	79547	137612	516819
	Iraq	15849	30383	9560	6007	3000
	Italy	0	11670	23862	20033	22743
	Jordan	8449	11877	14028	15438	21942
	Lebanon	11200	5560	4820	8194	17382
	Pakistan	5169	11751	75956	59507	106123
	Saudi Arabia	6413	9938	12823	17531	25384
	Spain	34612	39157	48149	56334	68734
	Tunisia	1741	2110	4254	17907	19967
	World	159343	378655	457800	552091	1087859
Export	Australia	0	41049	143702	238987	266519
	Canada	0	91	1269	33420	149212
	Mexico	49143	59666	52829	131815	207093
	Turkey	168116	320273	212639	153119	153953
	World	249676	456852	464320	663002	996519

Source: FAOSTAT (<http://apps.fao.org/>)

3. Genetic Enhancement - Present Status

3.1 Tolerance to Abiotic Stresses

The important abiotic stresses affecting chickpea productivity are drought, heat, cold and salinity. The total yield losses to chickpea by abiotic stresses exceed those caused by biotic stresses. The value of annual yield losses caused by abiotic stresses in chickpea yield is estimated to be \$ 4.4 billion, that includes \$ 1.3 billion by drought and heat, \$ 186 million by cold and \$ 354 million by salinity (Ryan, 1997).

3.1.1 Drought tolerance: Drought, particularly terminal drought, is the most important abiotic stress for chickpea as it is grown rainfed, in post-rainy season on residual soil moisture. The crop often experiences progressively increasing drought stress during the reproductive phase, resulting in early senescence and reduction in pod and seed development. Two genetic options being employed in chickpea for drought management are escape and tolerance.

Developing early maturing cultivars to escape terminal drought is the most effective strategy as it enables crop to complete its life cycle before onset of severe drought. ICRISAT has paid high emphasis on development of short duration chickpea varieties. A breakthrough in *kabuli* chickpeas was the development of extra-early variety ICCV 2 that matures in 85 days in southern India. This variety also demonstrated that short-duration varieties of *kabuli* chickpea could be successfully grown in tropical environments. Cultivation of *kabuli* chickpea was earlier confined to cooler areas with long growing season. ICCV 2 was first released in India (1989) and then in Sudan (1998) and Myanmar (2000). It is cultivated in large areas in these countries. ICCV 2 has replaced other chickpea varieties in more than 50% of area in Myanmar within a short period. Success of ICCV 2 has led to development of several short-duration, large-seeded *kabuli* varieties in India, such as ICCV 3, KAK 2, JGK 1 and Vihar. A large number of short-duration varieties of *desi* chickpea (e.g. ICCV 37, JG 11) have also been released in India. The short-duration *desi* and *kabuli* varieties have helped expansion of chickpea area in southern India and the total chickpea area in two southern states (Karnataka and Andhra Pradesh) has increased from 189,000 ha to 532,000 ha in the past two decades.

Desi chickpea lines that mature in only 75 days have been developed at ICRISAT. Two such lines, ICCV 96029 and ICCV 96030, were found to set pods during the cooler winter months in northern India (Sandhu *et al.*, 2002). These super-early, cold tolerant lines have opened new niches for chickpea cultivation.

Efforts have been made to identify drought tolerant germplasm and the traits contributing to drought tolerance. Some promising drought tolerant lines are ICC 4958,

ICC 5680 and ICC 10448. High root mass was found responsible for drought tolerance in ICC 4958, while smaller leaf area was the most important drought trait in ICC 5680 and ICC 10448 (Saxena, 2003). The large root trait helps in greater extraction of water available in soil, and the smaller leaf area reduces transpiration loss of water. ICC 4958 was found to have 30% more root volume than the popular variety Annigeri (Saxena *et al.*, 1993). Lines with greater degree of drought tolerance have been developed by combining large root traits of ICC 4958 with fewer pinnules trait of ICC 5680 (Saxena, 2003). A recent screening of the mini-core collection has identified several other lines with large root traits (Krishnamurthy *et al.*, 2003).

3.1.2 Cold tolerance: Chickpea has been traditionally grown in spring season in West Asia and North Africa (WANA) region. As the crop is grown on residual moisture under rainfed conditions, it is often exposed to high temperature and moisture stress during the pod filling stage. Advancement of sowing to winter can help escape these stresses, and prolong crop duration. Resistance to ascochyta blight and cold tolerance both at seedling and flowering stages are needed in the cultivars for winter sowing in WANA.

Over 6000 germplasm and breeding lines were screened for cold tolerance at ICARDA and 11 *kabuli* germplasm lines and 121 breeding lines were found tolerant. The best sources of tolerance in the cultigen were ILC 8262, ILC 8617 and FLIP 8-82C with a consistent score of 3 (on 1 to 9 scale, where 1= no damage and 9 = all plants killed) over years and locations (Singh *et al.*, 1995). Several accessions with higher level of cold tolerance (score 2) have been identified in the wild species (Table 3). A number of varieties suitable for winter sowing have been released in WANA from the breeding material supplied by ICARDA. The cold tolerant lines produced nearly 4 tons ha⁻¹, which corresponded to 4-fold increase over spring sowing (Singh *et al.*, 1993).

Chickpea is particularly sensitive to chilling temperature (mean daily temperature <15° C) during reproductive growth phase as chilling temperatures adversely affect pollen germination, fertilization and pod setting. Considerable yield losses in chickpea can occur due to cold temperature stress in northern India, Canada and some parts of Australia. ICRISAT has developed a number of cold tolerant lines, such as ICCV 88502, ICCV 88503, ICCV 88506, ICCV 88510 and ICCV 88516 which are able to set pod at low temperatures. A pollen selection method has been successfully used for transfer of cold tolerance from ICCV 88516 to a susceptible chickpea cultivar 'Amethyst' in Australia (Clarke and Siddique, 2003).

3.1.3 Salinity tolerance: Chickpea is very sensitive to salinity and the extent of yield losses depends on the level of soil salinity. Yield losses occur due to reduction in

germination, plant growth (biomass) and seed size. In chickpea growing areas, saline soils are common in west and central Asia and Australia. Some salinity tolerant lines have been identified in India (Singh and Singh, 1984, Dua and Sharma, 1995) and Pakistan (Asharf and Waheed, 1992). A salt tolerant variety Karnal Chana 1 (CSG 8963) has been released in India that can be grown in saline soils with electrical conductivity up to 6 dS/m (Dua *et al.*, 2001).

3.2 Resistance to Biotic Stresses

3.2.1 Diseases

Ascochyta blight (AB), caused by *Ascochyta rabiei* (Pass) Labr., is a highly devastating foliar disease of chickpea in West and central Asia, North Africa, North America and Australia. It occurs in some areas of northwest India and Pakistan where cool, cloudy, and humid weather occurs during the crop season.

Studies on pathogenic variability in different countries indicate existence of numerous pathotypes. A standard set of well characterized chickpea genotypes as differentials and a common disease screening and scoring procedure are needed for determining the extent and distribution of pathotypes of *A. rabiei* in different geographic regions. The earlier studies on inheritance of resistance to AB suggested that resistance is controlled monogenically, by a dominant gene in some genotypes and by a recessive gene in other genotypes. Recent studies, however, indicate involvement of many genes, *e.g.*, two complementary dominant genes (Dey and Singh, 1993), three recessive and complementary major genes with several modifiers (Tekeoglu *et al.*, 2000a), three major quantitative trait loci (QTLs) (Santra *et al.*, 2000), and seven major and minor QTLs (Taylor *et al.*, 2002).

Extensive efforts have been made at ICARDA and ICRISAT to identify sources of AB resistance. Over 13,000 germplasm accessions were evaluated and 11 *kabuli* and 6 *desi* accessions were identified as resistant (Reddy and Singh, 1984). Four lines (ILC 72, ILC 191, ILC 3279, ILC 3856) were resistant in eight countries (Singh *et al.*, 1984b). Three *desi* accessions (ICC 4475, ICC 6328 and ICC 12004) and two *kabuli* accessions (ILC 200 and ILC 6482) showed resistance to six races during repeated greenhouse and field screening during 1979-1991 (Singh and Reddy, 1993). Over 3000 AB resistant high yielding lines have been developed by ICARDA during 1978-2002 and made available to National Agricultural Research System (NARS) globally (Malhotra *et al.*, 2003). Many AB resistant varieties have been released in countries where AB is a major disease of chickpea.

Botrytis gray mold (BGM), caused by *Botrytis cinerea* Pres., is an important disease of chickpea in Bangladesh, Nepal, Pakistan, northern India and Australia. The

chickpea area has decreased drastically in Bangladesh and Nepal due to this disease. No systematic studies have been undertaken to characterize the pathogenic variability, though reports on existence of pathogenic variability are available. Two dominant genes with epistatic interaction have been identified for resistance (Chaturvedi *et al.*, 1995). Some accessions with erect plant type, such as ICCL 87322 and ICCV 88510 were found to be less affected by the disease (Haware and McDonald, 1993).

Stunt has been reported to cause significant yield losses occasionally in some pockets. A number of viruses, transmitted by a number of aphids can cause stunt. Chickpea chlorotic dwarf monogeminivirus (CCDV) and chickpea luteovirus (CPLV) are important in India and Pakistan; fababean necrotic yellows nanvirus (FBNYV) in Syria, Turkey and Lebanon; and bean leaf roll luteovirus in Algeria. Chalam *et al.* (1986) identified two accessions (ICC 1781, ICC 8203) resistant to cucumber mosaic virus (CMV) and nine accessions (ICC 607, ICC 1468, ICC 2162, ICC 2342, ICC 3440, ICC 3508, ICC 4045, ICC 6999, ICC 11550) resistant to bean yellow mosaic virus (BYMV). Of the 10,000 germplasm accessions and breeding lines screened by ICRISAT at Hisar in northern India, which is hot spot of chickpea chlorotic dwarf monogeminivirus (CCDV), two lines (GG 669, ICC 10) showed field resistance. However, these lines were susceptible to luteovirus when screened at Junagarh in Gujarat state of India (Haware, 1997). Several varieties released in India (*eg.*, Pusa 244, Girnar, Valai, SAKI 9516) have some level of resistance to stunt (Dua *et al.*, 2001).

Fusarium wilt (FW) caused by *Fusarium oxysporum* f sp. *ciceri*, is the most important root disease of chickpea. It is more important between the latitudes 30° N and 30° S where the chickpea-growing season is dry and warm. Seven races of the fungus of FW are known. Races 1, 2, 3, and 4 were identified from India (Haware and Nene, 1982), races 0 and 5 from Spain (Jimenez-Diaz *et al.*, 1989) and race 6 from California (Phillips, 1988). Three loci have been identified each for resistance to race 1 (Singh *et al.*, 1987) and race 2 (Kumar, 1998), two loci for resistance to race 4 (Tullu *et al.*, 1998, 1999) and one locus each for resistance to race 0 and race 5 (Tekeoglu *et al.*, 2000b).

Effective field, greenhouse and laboratory screening methods for FW have been established (Nene *et al.*, 1981) and large number of good sources of resistance have been identified (Pundir *et al.*, 1988; Haware *et al.*, 1992; Dua *et al.*, 2001). Two most important sources of resistance are the germplasm line WR 315 (ICC 8933) and the cultivar JG 74. The former is resistant to all races except race 3, while the latter is resistant to all races except race 2 (Haware, 1997). A twin-podded variety JG 62 is highly susceptible to all races, except race 0, and widely used as susceptible check for races 1 to 4 in India. The availability of good sources of resistance to FW and

the availability of easy and effective field screening methods have made breeding for resistance to FW an easy task.

Dry root rot (DRR), caused by *Rhizoctonia bataticola*, is an important chickpea disease that occurs during reproductive growth phase when the crop is exposed to high temperature ($>30^{\circ}\text{C}$) and there is moisture stress in the soil. There is limited research on characterization of pathogenic variability and the single report available on genetics of its resistance suggests a dominant gene for resistance (Rao and Haware, 1987). Many germplasm accessions with moderate level of resistance have been identified and some of the accessions, such as ICC 2867, ICC 9023, ICC 1003, ICC 11550 and ICC 1151 have combined resistance to DRR and FW (Nene *et al.*, 1989). A number of moderately resistant varieties (ICCC 37, ICCV 10, JG 130, WCG 1) have been released in India (Dua *et al.*, 2001).

Collar rot (CR) caused by *Sclerotium rolfsii* is an important disease in areas where seedling is exposed to high temperature and high moisture in the soil. No report is available on races or inheritance of resistance to CR. Germplasm accessions ICC 1696, ICC 4709, and ICC 14391 (S.D. Singh, Personal communication), breeding lines RSG 130, 132 and 191 (Chitale *et al.*, 1990), and cultivar SAKI 9516 (Dua *et al.*, 2001) have shown low incidence of CR.

Phytophthora root rot (PRR), caused by *Phytophthora medicaginis* Hansen, is the major disease of chickpea in some parts of Australia. The level of resistance identified in the cultivated species is low, and therefore, resistance has been introgressed from *C. echinospermum* (Knights *et al.*, 2002).

Root nematodes, particularly root knot nematodes (*Meloidogyne* spp.), cyst forming nematodes (*Heterodera* spp.) and lesion nematodes (*Pratylenchus* spp.) are the major root nematodes affecting chickpea yield. The root knot nematodes are important in the Indian sub-continent and the Mediterranean region, whereas cyst nematodes and lesion nematodes cause marked yield losses in Syria. Many germplasm lines with low to moderate levels of resistance have been identified for root knot nematodes but only limited progress has been made on development of root knot nematode resistant varieties. Sources of resistance to cyst nematode have been identified only in the wild species (Table 3) and good progress has been made in introgression of resistance to the cultigen (Malhotra *et al.*, 2002).

3.2.2 Insect-pests

Pod borer (*Helicoverpa armigera* Hübner) is the most devastating insect-pest of chickpea and annual global losses are estimated at \$500 million (Ryan, 1997). Considerable progress has been made on development of screening methods (Sharma

Table 3: Wild *Cicer* species and their accessions with high level of resistance to biotic and abiotic stresses

Stress and level of resistance	<i>C. reticulatum</i>	<i>C. echinospermum</i>	<i>C. bijugum</i>	<i>C. judaicum</i>	<i>C. pinnatifidum</i>	<i>C. chorrasonicum</i>	<i>C. cuneatum</i>
Ascochyta blight Score 2*	-	ILWC 245	ILWC 42, 260	ILWC 255, 256	ILWC 248 to 251	-	-
Fusarium wilt Score 1	ILWC 109, 112, 115 to 117, 123, 124, 129, 140, 142, 237	ILWC 39, 179 to 181	ILWC 7, 32, 34, 42, 62 to 65, 67, 70 to 83, 177, 178, 194, 195, 220, 228, 243	ILWC 46, 58, 59, 61, 94 to 99, 101, 102, 148, 152, 161, 166 to 204, 251 168, 174, 176, 188 to 191, 197, 199 to 201	ILWC 144, 149, 150, 171,	-	-
Leaf minor Score 2	-	ILWC 35	ILWC 227	ILWC 4, 31, 38, 41, 43, 44, 46 to 48, 50, 56, 58, 103, 206, 207, 210, 211, 223	ILWC 9, 97, 226, 252	ILWC 147	ILWC 40, 185, 187, 232
Bruchids Score 1	ILWC 104	ILWC 39, 179, 181	ILWC 65, 67, 68, 70, 73 to 75, 83, 177	ILWC 46, 54, 173, 174, 176, 189,	-	-	ILWC 187
Cyst nematode Score 1	-	-	ILWC 64, 67, 68, 70, 73 to 75, 83, 177	-	ILWC 236	-	-
Cold Score 2	ILWC 182, 233	-	ILWC 32, 62 to 69, 71, 73 to 79, 84, 209, 220, 228, 240	-	-	-	-
Phytophthora root rot Score 2	-	ILWC 246, L204	ILWC 195, 70	ILWC 6	-	-	-

* on 1 to 9 scale, where 1 = free from any damage and 9 = highly susceptible

References: Knights *et al.* (2003) for Phytophthora root rot and Robertson *et al.* (1995) for other stresses

et al., 2003) and to identify sources of resistance in the cultivated and wild *Cicer* species. A large number of germplasm accessions, breeding lines and cultivars have been identified with low to moderate levels of resistance (Sharma *et al.*, 2003). ICC 506 appears to be the best source of resistance available in the cultivated species. Over six years, ICC 506 showed a mean of 9% pod damage as against 30% in the popular variety Annigeri (Lateef and Pimbert, 1990). ICC 506 is highly susceptible to fusarium wilt. Development of breeding material with high level of wilt resistance and level of *Helicoverpa* resistance similar to ICC 506 has been a challenging task. Sharma *et al.* (2002) screened 164 accessions of annual wild *Cicer* species and found that the larval growth was slow in 21 accessions. Efforts are being made at ICRISAT to combine various mechanisms of resistance.

Leaf miner (*Liriomyza ciceriana* Rondani) is an important insect-pest of chickpea in west Asia, northern Africa, and southern Europe. Four promising sources of resistance (ILC 726, ILC 1776, ILC 3350, ILC 5901), all with small leaflets have been identified at ICARDA (Malhotra *et al.*, 1996). Higher levels of resistance have been identified in the wild species (Table 3). Not much progress has been made in breeding for leaf miner resistance.

Seed beetle or bruchid (*Callosobruchus* spp.) is the most important storage-pest of chickpea. Sources of resistance have been identified only in the wild species (Table 3). No report is available on introgression of resistance from wild species to the cultigen.

3.3 Exploitation of Wild Gene Pool

The wild species of *Cicer* include 8 annual and 34 perennial species and constitute valuable genetic resources for the cultigen. However, they have largely remained unutilized due to crossability barriers. Most studies on wild *Cicer* species have concentrated on annual species because of various difficulties associated with propagation of perennial species.

Phylogenetic relationships among annual *Cicer* species and a few perennial species have been studied using data on karyotype, protein banding patterns, isozyme and allozyme polymorphisms, DNA-based markers or crossability (Ahmad, 1999 and references therein). In almost all studies, *C. reticulatum* Lad., the proposed wild progenitor of chickpea, has been found to be the most closely related wild species and together with *C. echinospermum* have been placed in one group. *C. bijugum*, *C. judaicum* and *C. pinnatifidum* have been generally grouped together and are closer to the group that contains the cultigen. *C. chorassanicum* and *C. yamashitae* were generally grouped together, while *C. cuneatum* did not group with any other species.

The current status of the success in intercrossing of *Cicer* species is summarized in Table 4. The cultivated species can be easily crossed with *C. reticulatum* and the hybrids are as fertile as the intraspecific hybrids of the cultivated species. It is also easy to make crosses between the cultigen and *C. echinospermum* but the hybrids show various levels of sterility depending on the accessions involved in crossing. Crosses of *C. arietinum* with the remaining species have been difficult and often needed application of growth hormones during pollination or embryo rescue. There are few reports on successful crosses of *C. arietinum* with *C. bijugum*, *C. judaicum* and *C. pinnatifidum* and the hybrids obtained had very low fertility. It has not been possible to cross the cultigen with *C. chorassanicum* and the hybrids obtained from the crosses of cultigen with *C. yamashitae* and *C. cuneatum* through embryo rescue were sterile.

The annual wild *Cicer* species have been evaluated for useful agronomic traits including resistance to various abiotic and biotic stresses. Wild *Cicer* species are so far the only source of resistance identified for resistance to cyst nematodes and they have higher levels of resistance than the cultivated species for botrytis gray mold,

Table 4: Current status of the success of interspecific crosses in chickpea

	<i>C. arietinum</i>	<i>C. reticulatum</i>	<i>C. echinospermum</i>	<i>C. bijugum</i>	<i>C. judaicum</i>	<i>C. pinnatifidum</i>	<i>C. yamashitae</i>	<i>C. chorassanicum</i>	<i>C. cuneatum</i>
<i>C. arietinum</i>		F* [1]**	PF [1]	PF [1, 6]	PF [1, 6]	PF [1, 6]	S [8]	-	S [5]
<i>C. reticulatum</i>	F [7]		S [1]	-	-	-	-	-	-
<i>C. echinospermum</i>	PF [7]	PF [7]		-	-	-	-	-	-
<i>C. bijugum</i>	S [9]	-	-		PF [1]	PF [1]	-	-	-
<i>C. judaicum</i>	PF [9]	-	-	PF [1]		PF [1, 2]	-	PF [3,9]	S [2]
<i>C. pinnatifidum</i>	-	-	-	PF [1]	PF [1]		-	-	-
<i>C. yamashitae</i>	-	-	-	-	-	-		-	-
<i>C. chorassanicum</i>	-	-	-	-	-	Albino [4]	-		-
<i>C. cuneatum</i>	S [9]	-	-	-	-	-	-	-	

* F = Fertile, PF = Partially fertile, S = sterile

**Reference(s): 1 = Ladizinsky and Adler (1976), 2 = Pundir and van der Maesen (1983), 3 = Ahmad *et al.* (1987), 4 = Ahmad (1988), 5 = Singh and Singh (1989), 6 = Verma *et al.* (1990), 7 = Singh and Ocampo (1993), 8 = Singh *et al.* (1989)

phytophthora root rot, leaf miner and cold. The accessions of wild species identified to be good sources of resistance/tolerance to various biotic and abiotic stresses are listed in Table 3.

Though successful crosses of the cultivated species have been reported with several annual wild species, introgression of genes into the cultivated species has been reported only from two species, *C. reticulatum* and *C. echinospermum*. At ICARDA, resistance to cyst nematode has been successfully introgressed from *C. reticulatum* to the cultigen. Two lines with high level of resistance to cyst nematode and relatively good agronomic traits (ILC 10765 and ILC 10766) have been registered (Malhotra *et al.*, 2002). Promising high yielding lines with good agronomic and seed traits have been obtained from crosses of *C. arietinum* with *C. reticulatum* and *C. echinospermum*. The yield levels of top 10 lines ranged between 4.5 and 5.7 tons ha⁻¹ (Malhotra *et al.*, 2003). Transgressive segregants for early flowering were obtained from *C. arietinum* x *C. reticulatum* crosses. Some segregants flowered in 37 to 39 days as compared 70 to 90 days in wild and cultivated parent, respectively (Singh *et al.*, 1984a). These lines were cold tolerant and useful for development of early and cold tolerant cultivars (Malhotra *et al.*, 2003). Lines with high level of cold tolerance, high yield and high biomass have also been obtained from crosses of *C. arietinum* with *C. echinospermum* (ICARDA, 1995). Transfer of phytophthora root rot resistance from *C. echinospermum* to the cultigen has been successful (Knights *et al.*, 2002).

3.4 Mutation Breeding

The cultivated species has exhibited limited variability for most molecular markers, except for the SSR (simple sequence repeats) markers, which reveal DNA polymorphism of microsatellite regions. On the other hand, large variability is seen in the cultivated species for morphological traits. It has been suggested that the high level of phenotypic variability seen for morphological traits could be the expression of limited number of mutant loci, as a single mutation can have marked influence on the plant traits (Gaur and Gour, 2003).

Several mutants with agronomically useful traits have been induced in chickpea. These include mutants for high yield, high protein content, early maturity, root nodulation, erect plant type, determinate growth, compact growth habit, and resistance to ascochyta blight, fusarium wilt, root rots, nematodes, stunt, and leaf miner. Many of these mutants have been used in breeding programmes. At least 11 cultivars have been developed through mutation breeding. These include four ascochyta blight resistant varieties (CM 72, CM 88, CM 98, CM 2000) released in Pakistan (www.niab.org.pk), six varieties (Pusa 408, Pusa 413, Pusa 417, RS 11, RSG 2, WCG 2) released in India (Kharkwal *et al.*, 1988; Micke 1988; Dua *et al.*, 2001), and one high protein variety (Hyprosola) released in Bangladesh (Oram *et al.*, 1987).

3.5 Transgenics

The development of an efficient plant regeneration system was a challenging task in chickpea, as many researchers experienced difficulties in getting rooting or establishment of plants in the soil. Recently, a novel rooting protocol that gives rooting frequency of 90%, and efficient hardening and transplantation procedures have been reported (Jayanand *et al.*, 2003). The first transgenic chickpea plant was reported by Kar *et al.*, (1997). They introduced *Bt Cry IA* gene from the bacterium *Bacillus thuringiensis* (Bt) for development of *Helicoverpa* pod borer resistant chickpeas. The transformation was confirmed through molecular analysis. Insect feeding assay indicated inhibition of development of feeding larvae. There is no further report available on field-testing of these transgenics. However, more recently, transgenic chickpea plants incorporating *Bt Cry IAB* and *SbTi* (Soybean trypsin inhibitor) genes have been developed at ICRISAT. The molecular characterization and insect bioassays are currently ongoing (Kiran K. Sharma, pers. communication). Efforts are also being made to transfer anti-fungal genes, such as PGIP (polygalacturonase inhibitory protein), chitinases and glucanases for development of transgenics resistant to ascochyta blight, botrytis gray mold and collar rot; and drought responsive elements and osmoregulation genes for tolerance to drought, salinity and cold (Kiran K. Sharma, pers. Communication).

Like in other legumes, sulfur-containing amino acids, methionine and cystine, are the primary limiting amino acids in chickpea protein. This imbalance in amino acids reduces biological value of protein, despite good digestibility. Improvement in sulfur-containing amino acids could not be achieved by conventional breeding so far. It has been possible to enhance methionine content of some grain legumes, *e.g.*, soybean, narban bean and lupins by introducing foreign genes encoding methionine rich proteins, such as Brazil nut 2S albumin (BNA) and sunflower seed albumin (SSA) (Muntz *et al.*, 1998). Similar progress is possible in chickpea through transgenic technology.

3.6 Genome Mapping and Marker-Assisted Breeding

A high-density genome map of a crop can facilitate mapping, maker-assisted selection and map based cloning of agronomically important genes. The progress in genome mapping of chickpea has been slow due to low level of polymorphism in the cultivated chickpea and limited number of markers available for mapping. Almost all earlier studies (1990-2000) on genome mapping in chickpea have used interspecific cross mapping populations (*C. arietinum* x *C. reticulatum* and/or *C. arietinum* x *C. echinospermum*) (Table 5), as most markers were monomorphic in the cultivated chickpea.

Table 5 : Chronological development of the genome map of chickpea

Year	Traits/markers mapped	Mapping population	Reference
1990	26 isozymes, 3 morphological traits	F ₂ of <i>C. arietinum</i> x <i>C. reticulatum</i> , <i>C. arietinum</i> x <i>C. echinospermum</i> and <i>C. reticulatum</i> x <i>C. reticulatum</i>	Gaur and Slinkard (1990b)
1993	11 isozymes, 5 morphological traits, 1 seed storage protein	F ₂ of <i>C. arietinum</i> x <i>C. reticulatum</i> and <i>C. arietinum</i> x <i>C. echinospermum</i>	Kazan <i>et al.</i> (1993)
1997	45 RAPDs, 27 isozymes, 10 RFLPs, 9 morphological traits (map length 550 cM)	F ₂ and F ₃ of <i>C. arietinum</i> x <i>C. reticulatum</i>	Simon and Muehlbauer (1997)
1999	112 STMSs (map length 613 cM)	RILs of <i>C. arietinum</i> x <i>C. reticulatum</i>	Winter <i>et al.</i> (1999)
2000	118 STMSs, 96 DAFs, 70 AFLPs, 37 ISSRs, 17 RAPDs, 8 isozymes, 3 cDNAs, 2 SCARs (map length 2077.9 cM, average distance between markers = 6.8 cM)	RILs of <i>C. arietinum</i> x <i>C. reticulatum</i>	Winter <i>et al.</i> (2000)
2000	89 RAPDs, 17 ISSRs, 9 isozymes, 1 morphological trait (map length 981.6 cM, average distance between markers = 8.4 cM)	RILs of <i>C. arietinum</i> x <i>C. reticulatum</i>	Santra <i>et al.</i> (2000)
2002	55 STMSs, 20 RAPDs, 3 ISSRs, 2 morphological traits (map length 297.5 cM, distance between markers = 3.7 cM)	RILs of an intraspecific cross of <i>C. arietinum</i>	Cho <i>et al.</i> (2002)
2003	51 STMSs, 3 ISSRs, 12 RGAs (map length 534.5 cM, distance between markers = 8.1 cM)	F ₂ of an intraspecific cross of <i>C. arietinum</i>	Flandez – Galvez <i>et al.</i> (2003)

The first linkage map of chickpea, consisting of 26 isozyme and three morphological trait loci, was published from University of Saskatchewan in 1990 (Gaur and Slinkard, 1990a, b). Only two major reports on genome mapping of chickpea appeared during 1991-1998, and both were from Washington State University (Kazan *et al.*, 1993; Simon and Muehlbauer, 1997). Though a preliminary chickpea map based on DNA

markers was first published in 1997 (Simon and Muehlbauer, 1997), a rapid progress in genome mapping of chickpea has taken place only in recent years after the availability of highly polymorphic microsatellite-based markers. Over 200 STMS (sequence-tagged microsatellite sites) markers were developed at University of Frankfurt (Huttel *et al.*, 1999; Winter *et al.*, 1999), which have been extensively used in many laboratories. The most comprehensive integrated molecular map of chickpea, consisting of 354 markers, was published in 2000 (Winter *et al.*, 2000). The availability of highly polymorphic microsatellite-based markers also made it possible to use intraspecific mapping populations for development of a genome map of chickpea. Two recently published maps are based on intraspecific mapping populations of *C. arietinum* (Cho *et al.*, 2002, Flandez-Galvez *et al.*, 2003). Such maps will be more useful than the interspecific maps as most breeding programmes use only intraspecific crosses.

Marker-assisted selection can hasten crop improvement for traits that are difficult or inconvenient to score directly. Intensive efforts have been made to identify markers for fusarium wilt resistance in chickpea. Linkage analyses indicated that one of the three genes for resistance to race 1, one of the two genes for resistance to race 4 and the gene for resistance to race 5 were in the same linkage group, while gene for resistance to race 0 was not linked to these genes (Ratnaparkhe *et al.*, 1998, Tekeoglu *et al.*, 2000b). These linked fusarium wilt resistance genes have been assigned to linkage group VI of *Cicer* genome (Ratnaparkhe *et al.*, 1998). A distance of 5 cM was estimated between the genes for resistance to race 1 and race 4 (Tullu *et al.*, 1998) and 11 cM between the genes for resistance to race 4 and 5 (Winter *et al.*, 1999). Two RAPD markers (CS 27700 and UBC-170550) were mapped at the distance of 9 cM and one ISSR markers (UBC 855500) at a distance of 5 cM from the gene for resistance to race 4. An allele specific associated primer (ASAP) product, developed from the C 27 primer of RAPD marker CS 27700, was located between the genes for resistance to race 4 and race 5, with a distance of 7 and 4 cM, respectively (Winter *et al.*, 1999). Recently, one resistance gene analogue (RGA) has also been mapped to this linkage group (Huttel *et al.*, 2002).

Markers have also been identified for some quantitative trait loci (QTLs) for resistance to ascochyta blight. Santra *et al.* (2000) identified two major QTLs (QTL-1 and QTL-2), which accounted for > 45% of the estimated phenotypic variation for resistance in the mapping population used by them. Two RAPD markers flanking QTL-1 (10.9 cM apart), and one ISSR and one isozyme markers flanking QTL-2 (5.9 cM apart) were identified. Later, Tekeoglu *et al.* (2002) identified 6 STMS markers associated with these loci. In another study, Taylor *et al.* (2002) mapped 7 QTLs using intraspecific mapping population of *C. arietinum* and 4 QTLs using interspecific mapping population of *C. arietinum* x *C. echinospermum*. RGA and STMS markers

closely flanking major QTLs were identified, two markers were located 0.1 cM from the largest QTL peak (QTL 3).

4. Future Thrusts

The global average yield of chickpea ($0.75 \text{ tons ha}^{-1}$) is very low compared to other legumes. Concerted efforts are needed to enhance the production potential through participatory technology development with farmers. There is need to further refine the integrated crop management strategies for different agro-ecosystems. The models for prediction of abiotic and biotic stresses responsible for yield reduction need to be developed and validated. The integrated pest management options already established for ascochyta blight, botrytis gray mold, and pod borer need to be further refined and popularized among farmers. A vast opportunity exists for expansion of chickpea area in the rice-fallow areas (about $14 \text{ m}^2 \text{ ha}$) of south Asia. However, techniques for sowing in rice-fallow still need to be refined to get good plant establishment in such conditions.

The non-availability of strong sources of resistance for many stresses (drought, ascochyta blight, botrytis gray mold and pod borer) has been the major constraint in development of resistant varieties. Efforts need to be strengthened to identify new sources of resistance in the cultivated and wild *Cicer* germplasm, pyramid resistance genes from diverse sources, and develop varieties with multiple resistances. The wild *Cicer* species should be exploited for enhancing the genetic base of the cultigen and for introgression of genes for resistance/tolerance to stresses.

Rapid genetic enhancement can be achieved by using a combination of conventional breeding and biotechnological approaches. Some of the areas of great potential are embryo rescue for interspecific hybridization, double haploid technology for achieving homozygosity, marker-assisted selection and transgenics for traits, which can not be improved through conventional methods. Challenges are many, but chickpea scientists should convert these challenges into sustained opportunities for research effort to enhance science and production of chickpea.

References

- Ahmad, F. 1988. Interspecific hybridization and genetic relationships among the annual *Cicer* L. species. Ph. D. thesis, University of Saskatchewan, Canada.
- Ahmad, F. 1999. Random amplified polymorphic DNA (RAPD) analysis reveals genetic relationships among the annual *Cicer* species. *Theoretical & Applied Genetics* **98**: 657-663.
- Ahmad F., Slinkard A.E. and Scoles, G.J. 1987. The cytogenetic relationship between *Cicer judaicum* Bioss. and *Cicer chorassanicum* (Bge.) M. Pop. *Genome* **29**: 883-886.
- Asharf, M. and Waheed, A. 1992. Screening chickpea (*Cicer arietinum* L.) for salt tolerance. *Tropenlandwirt* **93**: 45-55.

- Chalam, T.V., Reddy, M.V., Subbayya, J., Nene, Y.L. and Beniwal, S.P.S. 1986. Screening of chickpea for resistance to cucumber mosaic and bean yellow mosaic viruses. *International Chickpea Newsletter* **14**: 25-26.
- Chaturvedi, R., Singh, I. S. and Gupta, A. K. 1995. Inheritance of resistance to Botrytis gray mould in chickpea (*Cicer arietinum* L.). *Legume Research* **18**: 1-4.
- Chitale, K., Tyagi, R.N.S. and Singh, R.D. 1990. Reaction of chickpea cultivars to collar rot disease induced by *Sclerotium rolfsii*. *Indian Journal of Mycology & Plant Pathology* **20**: 262-263.
- Cho, S., Jagdish Kumar, Shultz, J., Anupama, K., Tefera, F. and Muehlbauer, F.J. 2002. Mapping genes for double podding and other morphological traits in chickpea. *Euphytica* **128**: 285-292.
- Clarke, H. and Siddique, K. 2003. Chilling tolerance in chickpea – Novel methods for crop improvement. Pages 5-12 In: *Chickpea Research for the Millennium: Proceedings of the International Chickpea Conference* (Eds., R. N. Sharma, G. K. Shrivastava, A. L. Rathore, M. L. Sharma, and M. A. Khan), 20-22 January 2003, Indira Gandhi Agricultural University Raipur, Chhattisgarh, India.
- Dey, S.K. and Singh, G. 1993. Resistance to Ascochyta blight in chickpea – Genetic basis. *Euphytica* **68**: 147-153.
- Dua, R.P. and Sharma, P.C. 1995. Salinity tolerance of kabuli and desi chickpea genotypes. *International Chickpea & Pigeonpea Newsletter* **2**: 19-22.
- Dua, R.P., Chaturvedi, S.K. and Shiv Sewak. 2001. *Reference Varieties of Chickpea for IPR Regime*. Indian Institute of Pulses Research, Kanpur, India. 34 pp.
- Flandez-Galvez, H., Ford, R., Pang, E.C.K. and Taylor, P.W.J. 2003. An intraspecific linkage map of the chickpea (*Cicer arietinum* L.) genome based on sequence tagged microsatellite site and resistance gene analog markers. *Theoretical & Applied Genetics* **106**: 1447-1456.
- Gaur, P.M. and Gour, V.K. 2003. Broad-few-leaflets and outwardly curved wings: two new mutants of chickpea. *Plant Breeding* **122**: 192-194.
- Gaur, P.M. and Slinkard, A.E. 1990a. Inheritance and linkage of isozyme coding genes in chickpea. *Journal of Heredity* **81**: 455-461.
- Gaur, P.M. and Slinkard, A.E. 1990b. Genetic control and linkage relations of additional isozyme markers in chickpea. *Theoretical & Applied Genetics* **80**: 648-656.
- Haware, M.P. 1997. Diseases of Chickpea. Pages 473-516 In: *The Pathology of Food and Pasture Legumes* (Eds., D.J. Allen and J.M. Lenne), International Crops Research Institute for the Semi-Arid Tropics, ICRISAT Asia Center, Patancheru, Andhra Pradesh, India.
- Haware, M.P. and McDonald, D. 1993. Botrytis gray mold of chickpea. Pages 3-6 In: *Recent Advances in Research on Botrytis Gray Mold of Chickpea : Summary Proceedings of the Second Working Group Meeting* (Eds., M.P. Haware, C.L.L. Gowda, and D. McDonald), ICRISAT, Patancheru, Andhra Pradesh, India.
- Haware, M.P. and Nene, Y.L. 1982. Races of *Fusarium oxysporum* f. sp. *ciceri*. *Plant Disease* **66**: 809-810.

- Haware, M.P., Nene, Y.L., Pundir, R.P.S. and Narayana Rao, J. 1992. Screening of world chickpea germplasm for resistance to fusarium wilt. *Field Crops Research* **30**: 147-154.
- Huttel, B., Santra, D., Muehlbauer, F. J. and Kahl, G. 2002. Resistance gene analogues of chickpea (*Cicer arietinum* L.): isolation, genetic mapping and association with a *Fusarium* resistance gene cluster. *Theoretical & Applied Genetics* **105**: 479-490.
- Huttel, B., Winter, P., Weising, K., Choumane, W., Weigand, F. and Kahl, G. 1999. Sequence-tagged microsatellite site markers for chickpea (*Cicer arietinum* L.). *Genome* **42**: 210-217.
- ICARDA. Annual Report for 1995. Germplasm Program Legumes. ICARDA, Aleppo, Syria. 210 pp.
- Jayanand, B., Sudarsanam, G. and Sharma, K.K. 2003. An efficient protocol for the regeneration of whole plants of chickpea (*Cicer arietinum* L.) by using axillary meristem explants derived from in vitro-germinated seedlings. *In Vitro Cellular & Developmental Biology-Plant* **39**: 171-179.
- Jimenez-Diaz, R. M., Trapero-Casea, A., and Cabrera de la Colina, J. 1989. Races of *Fusarium oxysporum* f. sp. *Ciceri* infecting chickpea in southern Spain. Pages 515-520 In: *Vascular Wilt of Plants* (Eds., E.C. Tjamos and C. Beckman), NATO ASI Series, Berlin, Germany.
- Joshi, P.K., Parthasarathy Rao, P., Gowda, C.L.L., Jones, R.B., Silim, S.N., Saxena, K.B., and Jagdish Kumar. 2001. The world chickpea and pigeonpea economies: facts, trends, and outlook. ICRISAT, Patancheru, Andhra Pradesh, India. 68 pp.
- Kar, S., Basu, D., Das, S., Ramakrishnan, N.A., Mukherjee, P., Nayak, P. and Sen, S.K. 1997. Expression of cryIA(C) gene of *Bacillus thuringiensis* in transgenic chickpea plants inhibits development of pod borer (*Heliothis armigera*) larvae. *Transgenic Research* **6**:177-185.
- Kazan, K., Muehlbauer, F.J., Weeden, N.F. and Ladizinsky, G. 1993. Inheritance and linkage relationships of morphological and isozyme loci in chickpea (*Cicer arietinum* L.). *Theoretical & Applied Genetics* **86**: 417-426.
- Knights, E. J., Southwell, R. J. and Schwinghamer, M. W. 2003. Evaluation of wild *Cicer* species for resistance to phytophthora root rot. Pages 54-57 In: *Chickpea Research for the Millennium: Proceedings of the International Chickpea Conference* (Eds., R.N. Sharma, G. K. Shrivastava, A. L. Rathore, M. L. Sharma and M. A. Khan), 20-22 January 2003, Indira Gandhi Agricultural University, Raipur, Chhattisgarh, India.
- Knights, E.J., Brinsmead, R.B., Fordyce, M., Wood, J.A., Kelly, A. and Harden, S. 2002. Use of the wild relative *Cicer echinospermum* in chickpea improvement. Pages 145-149 In: *Plant Breeding for the 11th Millennium: Proceedings of the 12th Australian Plant Breeding Conference* (Eds., J. A. McComb), 15-20th September 2002, Australian Plant Breeding Assoc. Inc., Perth, Western Australia.
- Krishnamurthy, L., Kashiwagi, J., Upadhyaya, H.D. and Serraj, R. 2003. Genetic diversity of drought-avoidance root traits in the mini-core germplasm collection of chickpea. *International Chickpea & Pigeonpea Newsletter* **10**: 21-24.
- Kharkwal, M.C., Jain, H.K. and Sharma, B. 1988. Induced mutations for improvement of chickpea, lentil, pea and cowpea. Pages 89-109 In: *Improvement of grain legume production using*

- induced mutations: Proceedings of a workshop on the improvement of grain legume production using induced mutations*, 1-5 July 1988, Pullman, Washington. International Atomic Energy Agency, Vienna.
- Kumar, S. 1998. Inheritance of resistance to *Fusarium* wilt (race 2) in chickpea. *Plant Breeding* **117**: 139-142.
- Ladizinsky, G. and Adler, A. 1976. Genetic relationships among the annual species of *Cicer* L. *Theoretical & Applied Genetics* **48**: 197-203.
- Lateef, S.S. and Pimbert, M.P. 1990. The search for host resistance to *Helicoverpa armigera* in chickpea and pigeonpea at ICRISAT. In: *Summary Proceedings, First Consultative Group Meeting on Host Selection Behaviour of Helicoverpa armigera*, ICRISAT, Patancheru, Andhra Pradesh, India.
- Malhotra, R. S., Singh, K. B., Vito, M. Di, Greco, N. and Saxena, M. C. 2002. Registration of ILC 10765 and ILC 10766 chickpea germplasm lines resistant to cyst nematode. *Crop Science* **42**: 1756.
- Malhotra, R.S., Singh, K.B., van Rheenen, H.A. and Pala, M. 1996. Genetic improvement and agronomic management of chickpea with emphasis on the Mediterranean region. Pages 217-232 In: *Adaptation of Chickpea in the West Asia and North Africa Region* (Eds., N.P. Saxena, M. C. Saxena, C. Johansen, S. M. Virmani and H. Harris), ICRISAT, Patancheru, Andhra Pradesh, India and ICARDA, Aleppo, Syria.
- Malhotra, R.S., Baum, M., Udupa, S.M., Bayaa, B., Kabbabe, S. and Khalaf, G. 2003. Ascochyta blight resistance in chickpea: Present status and future prospects. Pages 108-117 In: *Chickpea Research for the Millennium: Proceedings of the International Chickpea Conference* (Eds., R. N. Sharma, G. K. Shrivastava, A. L. Rathore, M. L. Sharma and M. A. Khan), 20-22 January 2003, Indira Gandhi Agricultural University Raipur, Chhattisgarh, India.
- Micke, A. 1988. Genetic improvement of food legumes in developing countries by mutation induction. Pages 1031-1047 In: *World Crops: Cool Season Food Legumes*, (Eds., R. J. Summerfield), Kluwer Academic Publisher, Dordrecht, The Netherlands.
- Muntz, K., Christov, V., Saalbach, G., Saalbach, I., Waddell, D., Pickardt, T., Schieder, O. and Wustenhagen, T. 1998. Genetic engineering for high methionine grain legumes. *Nahrung* **42**: 125-127.
- Nene, Y.L., Haware, M.P. and Reddy, M.V. 1981. Chickpea diseases: resistance-screening techniques, Information Bulletin No. 10, International Crops Research for the Semi-Arid Tropics. Patancheru, Andhra Pradesh, India.
- Nene, Y.L., Haware, M.P., Reddy, M.V., Phillips, J.C., Castro, E.L., Kotasthane, S.R., Gupta, O., Singh, G., Shukla, P. and Sah, R.P. 1989. Identification of broad-based and stable resistance to wilt and root-rots of chickpea. *Indian Phytopathology* **42**: 499-505.
- Oram, R. N., Shaikh, M. A. Q., Zaman, K. M. S. and Brown, A. H. D. 1987. Isozyme similarity and genetic difference in morphology between Hyprosola, a high yielding, high protein mutant of chickpea (*Cicer arietinum* L.) and its parental cultivar. *Environment & Experimental Botany* **27**: 455-462.

- Phillips, J.C. 1988. A distinct race of chickpea wilt in California. *International Chickpea Newsletter* **18**:19-21.
- Pundir, R.P.S., Reddy, K.N. and Mangesha, M.H. 1988. *ICRISAT Chickpea Germplasm Catalog: Evaluation and Analysis*. International Crops Research Institute for the Semi-Arid Tropics, Patancheru, Andhra Pradesh, India.
- Pundir, R.P.S. and van der Maesen L.J.G. 1983. Interspecific hybridization in *Cicer*. *International Chickpea Newsletter* **8**: 4-5.
- Rao, P.K.A. and Haware, M.P. 1987. Inheritance of dry root rot (*Rhizoctonia bataticola*) resistance in chickpea (*Cicer arietinum*). *Plant Breeding* **98**: 349-352.
- Ratnaparkhe, M., Santra, D. K., Tullu, A. and Muehlbauer, F. J. 1998. Inheritance of inter-simple-sequence-repeat polymorphism and linkage with a fusarium wilt resistance gene in chickpea. *Theoretical & Applied Genetics* **96**: 348-353.
- Reddy, M.V. and Singh, K.B. 1984. Evaluation of a world collection of chickpea germplasm accessions for resistance to Ascochyta blight. *Plant Disease* **68**: 900-901.
- Robertson, L.D., Singh, K.B. and Ocampo, B. 1995. *A Catalogue of Annual Wild Cicer Species*. ICARDA, Aleppo, Syria. 171 pp.
- Ryan, J.G. 1997. A global perspective on pigeonpea and chickpea sustainable production systems: present status and future potential. Pages 1-31 *In: Recent Advances in Pulses Research* (Eds., A.N. Asthana and M. Ali), Indian Institute of Pulses Research, Kanpur, India.
- Sandhu, J.S., Bains, T.S. and Sidhu, P.S. 2002. Evaluation of super early chickpea genotypes for vegetable purpose as a catch crop. *International Chickpea & Pigeonpea Newsletter* **9**: 10-12.
- Santra, D.K., Tekeoglu, M., Ratnaparkhe, M.L., Kaiser, W.J. and Muehlbauer, F.J. 2000. Identification and mapping of QTLs conferring resistance to ascochyta blight in chickpea. *Crop Science* **40**: 1606-1612.
- Saxena, N.P. 2003. Management of drought in chickpea – a holistic approach. Pages 103-122 *In: Management of Agricultural Drought - Agronomic and Genetic Options* (Ed., N.P. Saxena), Oxford & IBH Publishing Co. Pvt. Ltd., New Delhi, India.
- Saxena, N.P., Krishnamurthy, L. and Johansen, C. 1993. Registration of a drought-resistance chickpea germplasm. *Crop Science* **33**:1424.
- Sharma, H.C., Gowda, C.L.L., Sharma, K.K., Gaur, P.M., Mallikarjuna, N., Buhariwalla, H.K. and Crouch, J.H. 2003. Host plant resistance to pod borer, *Helicoverpa armigera* in chickpea. Pages 118-137 *In: Chickpea Research for the Millennium: Proceedings of the International Chickpea Conference* (Eds., R. N. Sharma, G. K. Shrivastava, A. L. Rathore, M. L. Sharma and M. A. Khan), 20-22 Januray 2003, Indira Gandhi Agricultural University., Raipur, Chhattisgarh, India.
- Sharma, H.C., Mann, K., Kashyap, S.L., Pampapathy, G. and Ridsdill-Smith, J. 2002. Identification of *Helicoverpa* resistance in wild species of chickpea. Pages 277-280 *In: Plant Breeding for the 11th Millennium: Proceedings of the 12th Australian Plant Breeding Conference* (Ed., J. A. McComb) 15-20 September 2002, Australian Plant Breeding Assoc. Inc, Perth, Western Australia.

- Simon C.J. and Muehlbauer F.J. 1997. Construction of a chickpea linkage map and its comparison with maps of pea and lentil. *Journal of Heredity* **88**: 115-119.
- Singh, H., Kumar, J., Smithson, J.B. and Haware, M.P. 1987. Complementation between genes for resistance to race 1 of *Fusarium oxysporum* f. sp. *ciceri* in chickpea. *Plant Pathology* **36**: 539-543.
- Singh, K.B. and Ocampo, B. 1993. Interspecific hybridization in annual *Cicer* species. *Journal of Genetics & Breeding* **47**: 199-204.
- Singh, K.B. and Reddy, M.V. 1993. Resistance to six races of *Ascochyta rabiei* in the world germplasm collection of chickpea. *Crop Science* **33**: 186-189.
- Singh, K.B., Di Vito, M., Greco, N. and Saxena, M.C. 1989. Reaction of wild *Cicer* spp. lines to *Heterodera ciceri*. *Nematology Mediterranean* **17**: 113-114.
- Singh, K.B., Malhotra, R.S. and Saxena, M.C. 1995. Additional sources of tolerance to cold in cultivated and wild *Cicer* species. *Crop Science* **35**: 1491-1497.
- Singh, K.B., Reddy, M.V. and Nene, Y.L. 1984b. International testing of chickpeas for resistance to ascochyta blight. *Plant disease* **68**: 782-784.
- Singh, N.B. and Singh, R.A. 1984. Screening for alkalinity and salinity tolerance in chickpea. *International Chickpea Newsletter* **11**: 25-26.
- Singh, K.B., Malhotra, R.S. and Saxena, M. C. 1993. Relationship between cold severity and yield loss in chickpea (*Cicer arietinum* L.). *Journal of Agronomy* **170**(2): 121-127.
- Singh, R.P. and Singh, B.D. 1989. Recovery of rare interspecific hybrids of gram *Cicer arietinum* x *C. cuneatum* L. through tissue culture. *Current Science* **58**: 874-876.
- Taylor, P., Phan, H., Galvez, H., Collard, B., Ades, P., Pang, E. and Ford, R. 2002. Mapping ascochyta blight resistance genes in chickpea. Pages 355-361 In: *Plant Breeding for the 11th Millennium: Proceedings of the 12th Australian Plant Breeding Conference* (Ed., J. A. McComb), 15-20 September 2002, Australian Plant Breeding Assoc. Inc., Perth, Western Australia.
- Tekeoglu, M., Rajesh, P.N. and Muehlbauer, F.J. 2002. Integration of sequence tagged microsatellite sites to the chickpea genetic map. *Theoretical & Applied Genetics* **105**: 847-854.
- Tekeoglu, M., Santra, D.K., Kaiser, W.J. and Muehlbauer, F.J. 2000a. Ascochyta blight resistance inheritance in three chickpea recombinant inbred line populations. *Crop Science* **40**: 1251-1256.
- Tekeoglu, M., Tullu, A., Kaiser, W.J. and Muehlbauer, F.J. 2000b. Inheritance and linkage of two genes that confer resistance to fusarium wilt in chickpea. *Crop Science* **40**: 1247-1251.
- Tullu, A., Kaiser, W.J., Kraft, J.M. and Muehlbauer, F.J. 1999. A second gene for resistance to race 4 of *Fusarium* wilt in chickpea and linkage with a RAPD marker. *Euphytica* **109**: 43-50.
- Tullu, A., Muehlbauer, F.J., Simon, C.J., Mayer, M.S., Kumar, J., Kaiser, W.J. and Kraft, J. M. 1998. Inheritance and linkage of a gene for resistance to race 4 of fusarium wilt and RAPD markers in chickpea. *Euphytica* **102**: 227-232.
- Verma, M.M., Sandhu, J.S., Brar, H.S. and Brar, J.S. 1990. Crossability studies in different species of *Cicer* (L.). *Crop Improvement* **17**: 179-181.

- Winter, P., Benko-Iseppon, A.M., Huttel, B., Ratnaparkhe, M., Tullu, A., Sonnante G., Pfaff, T., Tekeoglu, M., Santra, D., Sant, V.J., Rajesh, P.N., Kahl, G. and Muehlbauer, F.J. 2000. A linkage map of chickpea (*Cicer arietinum* L.) genome based on recombinant inbred lines from a *C. arietinum* x *C. reticulatum* cross: localization of resistance genes for Fusarium wilt races 4 and 5. *Theoretical & Applied Genetics* **101**: 1155-1163.
- Winter, P., Pfaff, T., Udupa, S. M., Huttel, B., Sharma, P. C., Sahi, S., Arreguin-Espinoza, R., Weigand, F., Muehlbauer, F. J. and Kahl, G. 1999. Characterization and mapping of sequence-tagged microsatellite sites in the chickpea (*Cicer arietinum* L.). *Genome* **262**: 90-101.