Breeding Chickpea for Improved Adaptation to the Semi-Arid Tropical Environments

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INTRODUCTION

Chickpea (*Cicer arietinum* L.), also known as Garbanzo bean or Bengal gram, is the second most cultivated grain legume grown globally after dry bean (FAOSTAT data, 2007). It is cultivated annually on an area of about 10 million hectares over 50 countries. Over 80% of its area is in the semi-arid tropics (SAT) that encompass most of south Asia, parts of southeast Asia, a swathe across sub-Saharan Africa, much of southern and eastern Africa, and parts of Latin America. These regions are characterized by high atmospheric water demand, a high mean annual temperature, limited and erratic monsoonal rainfall, and nutrient poor soils. The major constraints to chickpea production in SAT include terminal drought and heat stresses, fusarium wilt and *Helicoverpa* pod borer. Soil salinity is also a major constraint to adaptation of chickpea in some areas, particularly in India, Pakistan, Bangladesh, Iran and Australia. High instances of dry root rot are reported from Sub-Saharan Africa and India.

India is the largest chickpea producing country with 64% of global chickpea production (FAOSTAT data, 2007). Chickpea is grown on 6.7 m ha from latitude 32°N in northern India with cooler, long-season environment to 10°N in southern India with warmer, short-season environment. There has been a large shift in chickpea area from north to central and southern India, mainly because of expansion in area under irrigation and wheat cultivation in northern India. During the past four decades, chickpea area declined by about 4.2 m ha in northern and north-eastern sates (Punjab, Haryana, Uttar Pradesh and Bihar) and increased by 2.6 m ha in central and southern states (Madhya Pradesh, Maharashtra, Karnataka and Andhra Pradesh). This drastic shift in chickpea cultivation from cooler, long-season environments to warmer, short-season environments resulted in

chickpeas being more prone to abiotic and biotic stresses that are prevalent in warm short-season environments (e.g. terminal drought and heat stresses).

The crop improvement efforts at ICRISAT and National Agricultural Research System (NARS) in SAT countries have largely focused on improving adaptation of chickpea to SAT environments by enhancing resistance/tolerance to biotic and abiotic stresses prevalent in SAT environments. This paper reviews recent progress in breeding chickpea for improved adaptation to the SAT environments.

Terminal Drought

Terminal or end-of-season drought is the most critical constraint to chickpea production throughout the SAT regions, where the crop is largely grown rainfed during the post-rainy season on residual soil moisture. The crop has to survive through to harvest on progressively declining residual soil moisture and often experiences moisture stress at the reproductive stage, which is the most critical phase of the crop growth. The crop plants are known to have different mechanisms to adjust to water stress conditions. These are generally classified into three categories – (1) drought escape, (2) drought avoidance, and (3) drought tolerance.

Terminal drought escape: Early phenology (early flowering, early podding and early maturity) is the most important mechanism to escape terminal drought and heat stresses. Chickpea improvement program at ICRISAT emphasizes on development of early maturing varieties for enhancing adaptation of chickpea to environments prone to terminal drought and heat stresses (Gaur *et al.,* 2007a). The collaborative efforts of ICRISAT and national agricultural research systems (NARS) in several SAT countries, including India, Myanmar, Bangladesh, Ethiopia and Sudan, have led to the development of several high yielding, early-maturing and fusarium wilt resistant cultivars. Some of the popular varieties developed in India through ICRISAT-NARS partnership include ICCC 37, JG 11, JG 130 and JAKI 9218 in desi type; and ICCV 2, KAK 2, JGK 1, JGK 2, Vihar and Virat in kabuli type. These varieties cover large area in central and southern India. Further, ICRISAT has developed super-early chickpea breeding lines (ICCV 96029 and ICCV 96030) that mature in 75 to 80 days in southern India (Kumar and Rao, 1996). The super-early lines provide opportunities for cultivation of chickpea in new niches, such as a short-duration catch crop for vegetable purpose following a rice crop and preceding a wheat crop in northern India (Sandhu *et al.,* 2007). Efforts are being made to improve super-early lines for fusarium wilt resistance and seed size.

Historically kabuli chickpea area in SAT was negligible, as the available kabuli cultivars were late maturing and more suited to cooler long-season environments. Availability of early maturing cultivars has made production of kabuli chickpea profitable in the SAT environments. The kabuli chickpea area has expanded rapidly in Myanmar, southern and central India, and Ethiopia. It is interesting to note that Myanmar, which has a short-growing season similar to southern India, now has about 60% of chickpea area under kabuli type (Than *et al.,* 2007). This change was brought about by the extra-early cultivar ICCV 2 (released as Yezin 3 in Myanmar), which has witnessed very high rate of adoption and is now grown in 55% of chickpea area (Than *et al.,* 2007).

Adoption of early maturing desi and kabuli chickpea cultivars along with suitable crop production packages has led to enhancement of chickpea production in some SAT regions.

For example, in Myanmar during the past decade (1995/96 to 2004/05), the chickpea area has increased by 23% (from 166,000 to 205,000 ha), yields have almost doubled (from 588 to 1171 kg ha^{-1}), and production has increased 2.6 times (from 92,000 to 239,000 t) (Than *et al.,* 2007). Similarly in Andhra Pradesh state in southern India, the chickpea area has increased from 106,000 ha in 1996/97 to 384,000 ha in 2005/06 and the yield has increased from 853 to 1,596 kg ha^{-1} during this period. Increase in area and yield levels has led to 7-fold increase in chickpea production (90,000 to 629,000 t). Andhra Pradesh was once considered a low productive state for chickpea due to warmer and short-season environments, but now has the highest average chickpea yield in India.

Though the early maturing varieties provide more stable yields than the late maturing varieties in short-season environments, the early maturing varieties may not give higher yield in more favorable seasons as these can not accumulate enough total plant biomass due to reduced total photosynthetic period compared to the relatively longer duration varieties. Thus, there is a need to match the crop duration with the available length of the crop season for realizing high yield.

Drought avoidance: Plants can avoid drought through dehydration postponement by maintaining high water potential or turgor pressure under soil water deficit conditions (Turner, 2003). This can be achieved by water uptake by the roots from deeper soil layers, by reducing water loss or by osmotic adjustment (Turner and Jones, 1980; Turner, 1986).

Drought avoidance through continuing water uptake: The role of root traits, such as root depth and root vigor, in extraction of water from deeper soil layers under depleting soil moisture conditions is well recognized. ICRISAT scientist identified a high root biomass line ICC 4958 that showed tolerance to drought not only at Patancheru but also at several other locations in India and in the Mediterranean type climate (Saxena *et al.,* 1993; Krishnamurthy *et al.,* 1996; Ali *et al.,* 2005). Subsequently, in a field experiment at ICRISAT-Patancheru with 12 diverse chickpea germplasm, including ICC 4958, it was shown that a prolific root system, especially in the 15-30 cm soil depth, had positive contribution to the seed yield under moderate terminal drought intensity and a deeper root system was shown to contribute to improved yield under severe terminal drought conditions (Kashiwagi *et al.,* 2006).

Conducting research on root systems in field condition is very laborious, expensive and time-consuming. ICRISAT has established a modified monolith method (Serraj *et al.,* 2004). Though this method is fairly reliable, it can not be employed for large scale screening of genotypes. The pot-culture method is less cumbersome but rooting profile can not be estimated in shallow pot-grown plants. Thus, extensive research efforts were made at ICRISAT-Patancheru to optimize a PVC cylinder culture system as an alternative method that allows screening of large number of genotypes (Kashiwagi *et al.,* 2006). With this system, the sampling efficiency could be improved dramatically.

Genetic variability for root traits was assessed in a mini-core collection of chickpea germplasm using the cylinder culture system at Patancheru. Large and significant genotypic variation was found for root length density (RLD), root dry weight (RDW), rooting depth (RDp) and root to total plant weight ratio (R/T) (Kashiwagi *et al.,* 2005). Accession ICC 4958, earlier identified to have large root system, was among the top ranking genotypes for prolific root system. In addition, ICC 8261 was identified to have the most prolific and deeper root system among the chickpea mini-core collection.

A study was conducted to estimate gene effects for root traits using generation mean analysis. The parents (P1, P2) and the F1, F2, BC1, and BC2 generations from two crosses, ICC 283 (smaller roots) × ICC 8261 (larger roots) and ICC 4958 (larger roots) × ICC 1882 (smaller roots), were used. In both the crosses, the additive and additive × additive interaction effects played important role in governing the root length density and root dry weight. The direction of the additive gene effects was consistent and towards increasing the root growth. Generating larger populations and delaying selections to later generations were proposed to exploit additive × additive gene interaction for improving root systems of chickpea (Kashiwagi *et al.,* 2008).

Despite the importance of root traits in drought avoidance and availability of germplasm with prolific root systems, breeding efforts on improvement of root traits have been negligible. This is because of the laborious, time-consuming and destructive methods involved in root studies. Molecular markers linked to major quantitative trait loci (QTLs) for root traits can greatly facilitate marker-assisted selection (MAS) for root traits in segregating generations. A simple sequence repeat (SSR) marker, TAA 170, was identified for a major QTL that accounted for one-third of the variation for root weight and root length in recombinant inbred lines (RILs) of the cross Annigeri × ICC 4958 (Chandra *et al.,* 2004). New RIL mapping populations have been developed from the two crosses used above in generation mean analysis for root traits. These are being studied to identify additional QTLs for root traits. We expect that marker-assisted breeding for root traits will begin soon and accelerate progress in breeding chickpea cultivars with improved root traits.

Drought avoidance through reducing water loss: The water loss can be reduced through stomata conductance or by reduction in leaf area due to leaf shedding or change in leaf morphology (e.g. few leaflets, tiny leaves). Though differences in stomatal conductance of chickpea leaf in response to water potential have been reported (Lawn, 1982; Muchow, 1985), no evidence is available on use of this trait in chickpea improvement.

Reduction in leaf area is expected to reduce water loss. Two chickpea accessions (ICC 5680 and ICC 10448), with smaller leaf area were described by Saxena (2003). ICC 5680 has fewer leaflets, while ICC 10448 has narrow leaflets. The fewer leaflet trait in ICC 5680 reduced transpiration loss of water by 30% compared to ICC 4958 in experiments conducted under controlled environmental facilities at ICRISAT. Breeding lines were developed that combined large root traits of ICC 4958 and few leaflet trait of ICC 5680 (Saxena, 2003).

Drought avoidance through osmotic adjustment: In osmotic adjustment (OA), solutes are accumulated in the cell in response to water deficit to maintain cell turgor. This accumulation of solutes in the cell reduces its water potential leading to movement of water into the cell leading to greater extraction of water from the soil, as observed in wheat (Morgan, 1983), sorghum (Basnayake *et al.,* 1996) and barley (Gonzalez *et al.,*1999). Though OA has been reported to be an important trait for drought tolerance in some cereal crops, e.g. wheat (Morgan *et al.,* 1986) and sorghum (Tangpremsri *et al.,* 1995), there are variable reports on association of OA with grain yield in chickpea. Some studies have shown an association between OA and seed yield under water stress conditions (Morgan *et al.,* 1991; Moinuddin and Khanna Chopra, 2004), while some studies found inconsistent or no relationship (Singh *et al.,* 1990; Leport *et al.,* 1999). A

recent study conducted at multiple locations in India and Australia concluded that phenotypic expression of OA is not stable and it can not be considered as a selectable drought tolerance trait in chickpea breeding programs (Turner *et al.,* 2007)

Drought tolerance: Drought tolerance, also known as dehydration tolerance, refers to the ability of cells to continue metabolism at low leaf water status (Turner *et al.,* 2003). Membrane injury occurs when dehydration reaches a critical point. Though electrolyte leakage from the cell is a measure of cell injury (Nayyar *et al.,* 2005), the relationship between electrolyte leakage and crop performance under water-limited conditions has not been demonstrated (Blum and Ebercorn, 1981; Blum, 1988).

Proline accumulation in the cytosol has been reported to occur in many legumes, including soybean, faba bean, field pea, and common bean, as a response to water deficits (Hanson and Nelson, 1980). However, selection for lines with high proline accumulation suggested that proline was not a selection criterion for improved drought tolerance (Hanson *et al.,* 1979 and Hanson and Hitz, 1982). Transgenic chickpea plants over-expressing the gene encoding delta 1-Pyrroline-5-Carboxylate Synthetase (P5CS), the enzyme involved in proline biosynthesis, have been produced (ICRISAT, 2005). The transgenic plants besides producing 2 to 3-fold higher proline did not differ significantly from the wild type in transpiration efficiency. However, wide differences were observed for total transpirable soil water and stomatal conductance, which need further investigation.

ICRISAT has also been involved in generating transgenic plants of chickpea by using the transcription factors such as *DREB1A* from *Arabidopsis thaliana* driven by a stress-inducible promoter from the *A. thaliana rd29A gene.* The DREB1A protein binds to several abiotic stress responsive genes that are native to the plant species and thereby inducing them in response to the stress. Several transgenic events now in T5 generation are being evaluated for various physiological, molecular and biochemical studies under a typical dry down set-up for water deficits. Some of these transgenic events performed superior to the parental cultivar C235 for transpiration efficiency, photosynthetic activity, stomatal conductance and total transpiration under water-limited conditions. A few transgenic lines with contrasting responses have been selected for further detailed studies on the leaf gas exchange characteristics and further characterization under both contained greenhouse and field conditions.

Heat (High Temperature) Stress

In addition to terminal drought stress, heat stress has become a major constraint to chickpea production in SAT environments because of increasing chickpea area in warm short season environments and in various late sown conditions and reduction in winter period due to global climate changes.

Reproductive growth stage (flowering and podding) is known to be very sensitive to changes in external environment and heat stress at this stage leads to reduction in seed yield (Summerfield *et al.,* 1984). Drastic reduction in chickpea seed yields was observed when plants at 50% flowering were exposed to hot days (35°C) (Summerfield *et al.,* 1984). In chickpea, heat stress adversely affects pollen viability, fertilization and seed development, therefore reducing harvest index. Thus, cultivars that can tolerate heat stress during the reproductive phase are very much needed in chickpea for enhancing and

stabilizing its production in SAT environments and expanding its cultivation to new niches.

The major limitation in breeding for heat tolerance in chickpea has been the lack of effective screening techniques and lack of information on genetic variability for heat tolerance. Some of the methods used to measure heat tolerance in legumes include pollen viability test, cell membrane thermostability analysis and chlorophyll fluorescence analysis. Chickpea was found to be more sensitive in terms of membrane stability and PS II function at high temperatures than groundnut, pigeonpea and soybean (Srinivasan *et al.* 1996). However, Malhotra and Saxena (1993) found higher critical temperatures for heat tolerance in chickpea than lentil, pea and faba bean. Limited efforts have been made to screen chickpea germplasm for heat tolerance. Two genotypes, ICCV 88512 and ICCV 88513, have been reported to have heat tolerance at reproductive stage (Dua, 2001).

We often take two crops of chickpea in field for rapid generation advancement. It is possible at ICRISAT-Patancheru because of short growing season. The first crop is sown during end of September to first week of October and harvested by mid or end of January (winter crop or main season crop). The second crop is sown during mid-January to first week of February, immediately after the harvest of the first crop and harvested by the end of April (spring crop). The spring crop faces relatively high temperatures, low relative humidity, high evaporation and high solar radiation, particularly at the reproductive stage, compared to the winter crop. Thus, spring crop provides an opportunity to screen germplasm for heat tolerance. Preliminary results on the performance of nine desi type and nine kabuli type genotypes in the winter and the spring season indicated that the kabuli types are more tolerant to high temperature than the desi types (Gaur *et al.,* 2007b). The seed yield reduction in the spring crop as compared to the winter crop was less in kabuli type (30.6%) than in desi type (51.4%) due to less reduction in number of pods per plant in kabuli type (23%) than the desi type (43.4%). The reduction in seed size was almost similar (13.2 to 13.6%) in both types. There are genotypic variations for relative performance in winter and spring seasons, giving opportunity for selecting high temperature tolerant genotypes.

There is a need to develop simple and effective screening techniques for screening germplasm for reproductive stage heat tolerance. A large number of germplasm accessions, including the wild species, need to be screened to identify lines with high levels of heat tolerance. The information on genetics of heat tolerance is needed to develop an effective breeding strategy for improving heat tolerance. Direct selection for heat tolerance may be difficult and thus marker-assisted selection (MAS) could be used to enhance the efficiency of breeding programs.

Soil Salinity

Salinity is another major limiting constraint to chickpea production in many parts of SAT. Saline soils contain sufficient neutral soluble salts (mainly sodium chloride and sodium sulphate) to adversely affect the growth of plants. It is estimated that about 36.0 m ha land is saline in South Asia (23.2 m ha in India, 10.5 m ha in Pakistan, 2.5 m ha in Bangladesh), 36.8 m ha in South-east and East Asia (36.2 m ha in China, 0.6 m ha in Myanmar) and 30.0 m ha in Central Asia (26.4 m ha in Iran, 3.1 m ha in Afghanistan) (Abrol *et al.,* 1988).

Chickpea, like many other legumes, is sensitive to soil salinity. Limited earlier efforts to identify salinity tolerance in chickpea indicated low genotypic variation (Saxena, 1984). A desi chickpea variety Karnal Chana 1 (CSG 8963), which can be grown in saline soils with ECe up to 6 dS/m, was released in India. In Australia, the ICRISAT breeding line ICCV 96836 (released as *Genesis 836*) was among the most salt tolerant lines identified in pot trials (Maliro *et al.,* 2004).

A recent screening of 263 diverse chickpea genotypes (including the mini-core collection, breeding lines, wild relatives and some earlier reported salinity tolerant lines) at ICRISAT-Patancheru showed a six-fold range of variation for seed yield under salinity, with several genotypes yielding 20% more than the salinity tolerant cultivar Karnal Chana 1 (Vadez *et al.,* 2006). No significant relation was found between biomass at the late vegetative stage and final seed yield under salinity. Performance of seed yield under salinity was explained in part by the yield potential under control conditions, and a salinity tolerance component. The parents of ICCV 2 x JG 62 RIL mapping population showed good contrast for salinity tolerance and this population is being used to identify markers for salinity tolerance QTLs. Preliminary data from association mapping revealed some association between marker data and seed yield under salinity and/or seed yield under control (Vadez *et al.,* 2007)

Fusarium Wilt

Fusarium wilt (FW) caused by *Fusarium oxysporum* f. sp. *ciceri* is the most devastating disease of chickpea in the SAT regions as the warm and dry chickpea growing season of SAT is favorable for occurrence of this disease. FW is prevalent in at least 33 countries (Nene and Reddy, 1987) encompassing the SAT regions of Asian, African and the South American countries. The disease is highly devastating and can cause yield losses up to more than 90% in susceptible cultivars (Haware and Nene 1980).

Till date eight races (0, 1A, 1B/C, 2, 3, 4 5 and 6) of FW pathogen with distinct geographical distributions have been documented. Races 2, 3 and 4 were found in India (Haware and Nene, 1982), whereas races 0, 1B/C, 5 and 6 were found in the Mediterranean region and in the USA (California) (Jiménez-Díaz *et al.,* 1993; Halila and Strange, 1996). Race 1 earlier identified from India (Haware and Nene, 1982) was later designated 1A and was also found in the USA and the Mediterranean region (Jiménez-Díaz *et al.,* 1993). In susceptible chickpea cultivars, races 0 and 1B/C induce the yellowing syndrome (yellowing pathotype), whereas races 1A, 2, 3, 4, 5 and 6 induce the wilting syndrome (wilting pathotype) (Trapero-Casas and Jiménez-Díaz, 1985; Jiménez-Díaz *et al.,* 1993).

Several studies have been conducted on genetics of resistance to fusarium wilt and molecular mapping of fusarium wilt resistance genes. Information available on genetics of resistance to six races (0, 1A, 2, 3, 4 and 5) of the pathogen suggest that the resistance to each of these races is controlled by one to three genes. Molecular markers have been identified for at least one resistance gene for each of these six races. These resistance genes formed two clusters on two different chickpea linkage groups (reviewed by Millan *et al.,* 2006 and Sharma and Muehlbauer, 2007).

Several sources with high resistance to FW have been identified in chickpea and most of these are available in desi type. A world collection of over 13,500 germplasm accessions

was evaluated for race 1 of FW at ICRISAT-Patancheru and 160 accessions (150 desi and 10 kabuli type) were identified resistant (Haware *et al.,* 1992). Desi × kabuli crosses have been widely used at ICRISAT for enhancing FW resistance of kabuli chickpea. Recently, two accessions (ICC 14194 and ICC 17109) of extra large seeded (100 seed weight > 50 g) kabuli chickpea with high resistance to FW have been identified (Gaur *et al.,* 2006) and are being used in kabuli chickpea breeding.

Excellent progress has been made in development of cultivars with high resistance to fusarium wilt in both desi and kabuli types. This has been possible mainly because effective field screening technique for resistance to FW and germplasm with high resistance to FW are available. Some accessions are resistant to more than one race of FW pathogen. For example WR 315 is resistant to race 0, 1A, 2, 4, 5 and 6, while JG 74 is resistant to race 0, 1A, 3, 4, and 6 (Haware, 1997). Most cultivars have shown stable resistance over the years.

MAS for FW resistance has not been initiated probably because of the availability of effective field screening technique. However, MAS will certainly be useful in pyramiding of resistance genes for various races of fusarium wilt and improving fusarium wilt resistance along with other traits (e.g. resistance to other biotic and abiotic stresses).

Dry Root Rot

Dry root rot (DRR), caused by *Rhizoctonia bataticola,* is an important disease of chickpea in dry areas whenever the crop is exposed to temperature above 30°C. The disease generally appears around flowering and podding time. Dry soil conditions promote the disease. Many accessions with moderate levels of resistance to DRR have been identified. Pundir *et al.* (1988) provided a list of 47 such accessions available in the ICRISAT's genebnk. Some accessions have combined resistance to DRR and FW. There have been limited efforts to breed specifically for DRR resistance. At ICRISAT-Patancheru, the breeding lines are usually screened for FW and DRR simultaneously in a multiple root disease nursery. There is a need to screen more germplasm to identify sources with higher levels of resistance and use these in breeding programs to enhance levels of DRR resistance in cultivars targeted for SAT.

Pod Borer

Pod borer, *Helicoverpa armigera* Hübner (Lepidoptera: Noctuidae) is a devastating polyphagous pest, with amazing degree of genotypic plasticity causing heavy damage to the crop. Yield loss in chickpea due to pod borer is estimated between 18 and 24% equivalent to loss of over $542 million annually (Ryan, 1997).

Sources of high level of resistance to pod borer are not available in cultivated chickpea germplasm. However, many germplasm accessions/breeding lines/cultivars with low level of resistance have been identified (see Sharma *et al.,* 2003 for a review). Because of the predominance of fixable (additive) genetic variance and high heritability, pedigree selection was expected to enhance pod borer resistance in early maturity desi types. On the other hand, both additive and dominance variance are important for pod borer resistance in medium and long-duration desi and kabuli chickpea. Hence, it was suggested

that selection for pod borer resistance should be delayed until F5 generation (Gowda *et al.,* 2005)

Over 160 accessions of annual wild *Cicer* species have been screened at ICRISAT for *Helicoverpa* resistance. Larval growth was slow on 21 of these accessions and this phenomenon of antibiosis was unique to the wild species (Sharma *et al.,* 2005). Efforts are being made to combine the non-preference (antixenosis) mechanism of resistance identified in the cultigen (e.g. ICC 506 EB) and antibiosis mechanism of resistance identified in *C. reticulatum*. The preliminary screening of some of perennial wild *Cicer* species revealed that *C. microphyllum* and *C. canariense* had pod borer rating as low as 1.0, while *C. judaicum*, reported earlier as a source of resistance, had a damage rating of 4.0, and cultivated chickpea genotypes had leaf and pod damage rating of 8.5 and 9.0 (Sharma *et al.,* 2006). Thus, these two species offer the best source of *Helicoverpa* resistance in chickpea. However, these are not accessible currently due to crossability barriers with the cultigen.

Development of transgenics has the most potential for enhancing resistance to *Helicoverpa*. At ICRISAT efficient protocols for the development of chickpea transgenics have been developed (Sharma *et al.,* 2006) and we have generated a large number of transgenic events with *Bacillus thuringiensis* (Bt) *cry1Ab* or *cry1Ac* genes driven by the CaMV 35S promoter. These transgenics have been bio-assayed for resistance to *H. armigera*. Though there was approximately 30-40% reduction in the *H. armigera* larvae weight on transgenics plants as compared to the control plants, none of the transgenic events was very effective in controlling pod damage. Efforts are now being made to generate additional transgenic events using better gene constructs to identify the events with high expression of the *Bt* genes that can result in high mortality rates of the pod borer larvae.

CONCLUSION

Though there is no appreciable change in global chickpea area, the geographic distribution of chickpea area has changed drastically. Most of the chickpea area is in the SAT where terminal drought and heat continue to be major abiotic stresses. The large shift in chickpea area from cooler, long-season environments to warmer, short-season environments has made chickpea more prone to these stresses. Despite these odds, there has been continuous improvement in chickpea productivity. Development of short duration varieties with resistance to fusarium wilt has helped in expansion of area and productivity of chickpea in warm, short-season environments.

Recent advances in research on root traits have been encouraging and the techniques for study of root traits have been refined. MAS for root traits is likely to begin soon and will facilitate breeding for improving drought avoidance in chickpea. There are still challenges in improving drought tolerance *per se* because of inadequate information on the mechanisms and component traits. Transgenics have been developed in chickpea for improvement of various traits, including drought tolerance and *Helicoverpa* pod borer resistance. The efforts in past were mainly devoted on development of technology and transgenic events. We expect increased emphasis on new gene constructs (with better expression of resistance) and field evaluation of these in the coming years. Similar to transgenic technology, the research in chickpea genomics in the past has largely focused

on development of tools and techniques for molecular breeding. Molecular markers are now available for many traits and MAS is expected to be an integrated component of breeding process in the coming years. With the tools and techniques of transgenic and molecular research, we look forward to beginning of an era of precision breeding for chickpea.

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