



# **Current Status of Mapping Quantitative Trait Loci (QTL) for Different Traits and Marker Assisted Breeding in Chickpea (*Cicer arietinum* L.) – A Review**

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## **Authors' contributions**

*This work was carried out in collaboration among all authors. Author AN wrote the first draft of the manuscript. Author VH and Author KGKP managed the literature searches. All authors read and approved the final manuscript.*

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## **ABSTRACT**

Chickpea is one of the most important pulse crops having estimated genome size of 738 Mb. The crop is affected by various biotic and abiotic stresses causing significant yield reduction. During the recent past, some biotic stresses like fusarium wilt, ascochyta blight, botrytis grey mould and abiotic stresses like drought, heat and salinity were found to reduce the productivity, thereafter, these demands for development of high yielding early maturing chickpea varieties with resistance to various biotic and abiotic stresses. Due to the advent of molecular techniques and availability of highly polymorphic and co-dominant microsatellite and other molecular markers, development of genetic maps for chickpea has progressed significantly. Molecular markers are now considered better than morphological and physiological characters for being stable, unaffected by

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environmental influences and easily detectable irrespective of their growth and development stages. The mapping of genes / QTLs for various traits like flowering time, yield and yield related traits, resistance to fusarium wilt, ascochyta blight, BGM, drought, salinity, heat may be useful in developing improved varieties of chickpea besides deeper understanding of genetics underlying the inheritance of the characters. The knowledge on mapped genes / QTLs for various traits of interest could help in integration of genomics-assisted breeding through various approaches like Marker Assisted Back Crossing, introgression of superior alleles from wild species through Advanced Backcross QTL, Marker Assisted Recurrent Selection and Genome Wide Selection for improving chickpea.

**Keywords:** Chickpea; mapping; quantitative trait loci.

## ABBREVIATIONS

**AFLP** : Amplified Fragment Length Polymorphisms  
**ALP** : Amplicon Length Polymorphisms  
**BGM** : Botrytis Grey Mould  
**CAPS** : Cleaved Amplified Polymorphic Sequences  
**DES** : Directorate of Economics and Statistics  
**DNA** : Deoxyribonucleic acid  
**FAO** : Food and Agriculture Organization  
**FW** : Fusarium Wilt  
**ISSR** : Inter Simple Sequence Repeats  
**MAS** : Marker Assisted selection  
**PCR** : Polymerase Chain Reaction  
**QTL** : Quantitative Trait Locus  
**QTLs** : Quantitative Trait Loci  
**RAPD** : Random Amplified Polymorphic DNA  
**RFLP** : Restriction Fragment Length Polymorphisms  
**RIL** : Recombinant Inbred line  
**SCAR** : Sequence Characterized Amplified Region  
**SNP** : Single Nucleotide Polymorphism  
**SSR** : Simple Sequence Repeats  
**STS** : Sequence Tagged Sites

## 1. INTRODUCTION

Chickpea (*Cicer arietinum* L.) is an autogamous, diploid (2n=2x=16) annual grain legume (2n=2x=16) with an estimated genome size of 738 Mb [1]. It belongs to the family Fabaceae, sub-family Papilionaceae, tribe Cicereae, and the genus *Cicer*. Chickpea is believed to be originated from Turkey in the South East [2]. With a share of approximately 66 percent (11.38 million tonnes) of its global production, India is found to be the largest producer of chickpeas [3]. In the last three and a half decades, the world chickpea area has increased by 40 percent while total production has more than doubled over the same period. Due to its low cost of production, wider adaptation, ability to fix atmospheric

nitrogen, able to fit in different crop rotations and the existence of a prolific tap root system, it is one of the most essential food legume plants in a sustainable agriculture system ([4]. It is cultivated in almost all parts of the world covering India, Australia, Turkey, Myanmar, Pakistan and Ethiopia, Mexico, and USA and in India, major chickpea producing states are Madhya Pradesh, followed by Maharashtra, Rajasthan, Uttar Pradesh; Andhra Pradesh and Karnataka. It is a highly nutritious grain legume crop and offers several health benefits by reducing the risk of several diseases.

Globally, various abiotic and biotic stresses have been established to restrict the chickpea production and its further improvement. Among the abiotic stresses, terminal drought and heat stress are considered to be the most promising factors limiting chickpea productivity. Under biotic stress, Fusarium wilt (FW) [caused by *Fusariumoxysporum f. sp. ciceri*] shows its severity under dry and warm conditions, while ascochyta blight (AB), [caused by *Ascochyta rabiei* (Pass.) Labr.] and botrytis grey mould (BGM) [caused by *Botrytis cineria* Pres.] shows their effect under cool and humid conditions. Ascochyta blight (AB), [caused by *Ascochytarabiei* (Pass.) Labr.] and botrytis grey mould (BGM) are the important foliar diseases of chickpea. A polyphagous pest, pod borer (*Helicoverpa armigera* Hubner.) is regarded as the most important and destructive pest of chickpea. Increase in yield can be achieved by developing varieties resistant to biotic and abiotic stresses besides improving yield attributing traits. Chickpea breeding therefore focuses on increasing yield by pyramiding genes for resistance/tolerance to the drought, cold, salinity, fungi, and pod borer into elite germplasm. It has been aptly illustrated that from the primary gene pool comprising progenitor species, tolerance to major biotic and abiotic stresses can be successfully introgressed. However, by using

special techniques to tackle pre and post fertilization barriers, many beneficial characteristics, including a high degree of tolerance/resistance to multiple stresses present in species belonging to secondary and tertiary gene pools, can also be exploited. In addition, identification of QTLs related to biotic and abiotic stresses and yield QTLs from wild species can also be introgressed. For this introgression, marker assisted breeding helps in knowing those QTLs and provides deeper understanding of the genetics underlying these traits, which is very much important for getting success in breeding of varieties with higher yield and resistance to various biotic and abiotic stresses.

Marker-assisted selection (MAS) will allow the desired genes to be better targeted. The genetic mapping in chickpea which was hindered for a long time by the less diversity in the genome is allowed now a days due to the availability of highly polymorphic, co-dominant microsatellite-based markers. Their application for genetic mapping of traits resulted in development of comparable inter-laboratory maps. Agronomic character inheritance information is a fundamental prerequisite for the detection and incorporation of interesting genes in linkage maps and marker-assisted selection (MAS) of these characters helps to speed up the process in developing new varieties [5].

Nowadays marker-assisted breeding has fastened and become a very useful tool in developing new varieties in all the major crops. It has brought a drastic change in modern genetics era, reduced time gradually and helped breeders to do new improvements. Marker-assisted breeding combines conventional plant breeding and molecular biotechnology, especially using the newly developed markers. The markers are helping in knowing the genetic constitution of plants in contrast to classical breeding where one cannot notice the genetic constitution of a plant only by its physical appearance. Markers have also exhibited their importance in improving the effectiveness of selection and developing new cultivars. MAS would be useful for improving those traits which are difficult or inconvenient to select directly (e.g. root traits for preventing drought, antinutritional factors, consistency traits, etc.), for pyramiding resistance genes from different sources when the resistance is polygenically mediated (e.g. ascochyta blight resistance), to assemble genes that impart different resistance mechanisms (e.g. antixenosis, antibiosis and tolerance for pod

borer) and to combine resistance to two or more stresses (e.g., fusarium wilt resistance and pod borer resistance). MAS will also be used to monitor the introgression of transgenic resistance genes to cultivars / elite breeding lines.

Molecular markers are now considered better than morphological and physiological characters for being stable, unaffected by environmental influences and easily detectable irrespective of their growth and development stages. Molecular markers are suitable for the study of genetic diversity, QTL recognition, fingerprinting, gene tagging, genetic and physical map creation, useful gene location cloning, evolutionary studies and marker-assisted selection [6,7,8] and also for germplasm characterization, genetic diagnostics, characterization of transformants, study of genome organization, phylogenetic analysis, etc. [9]. Molecular markers are approaching a stage where they can be used in breeding programs cost-effectively.

Several attempts have been made to map quantitative trait loci (QTLs) and their flanking regions for different agronomic traits even though the cultivated chickpea exhibited limited polymorphism for the molecular markers developed during the early phase resulted in use of inter-crosses in construction of linkage maps by the researchers [1]. Gaur and Slinkard [10,11] developed first linkage map of chickpea by using isozyme markers and inter-specific crosses of *Cicer arietinum* with *Cicer reticulatum* and *Cicer echinospermum*. Cho et al., [12] developed an intra-specific genetic linkage map and determined map positions of genes that confer double podding and seed traits using a population of 76 F<sub>10</sub> derived RILs from the cross ICCV 2 (large seeds and single pods) x JG 62 (small seeds and double podded), while Cho et al., [12] developed first intra-specific linkage map by using RILs derived from a cross between ICCV 2 x JG 62. Simon and Muehlbauer [13] integrated DNA based markers RAPD and RFLP into chickpea linkage maps. Consensus genetic mapping by using both inter-specific and intra-specific populations was also developed in chickpea [14]. Several other linkage maps were also developed by using different mapping populations with different morphological and molecular markers [12,15,16,17,18].

Further, several molecular studies has been reported for agronomic traits [19,20,21,22,23,24, 25,26,27]. These maps have allowed for a range of genes and QTL to be linked to markers because these maps are based on different

mapping population, traits, location and years [28,19,29]. However, no single population would segregate for all the economic traits of interest, genes for those traits need to be mapped on linkage maps developed from different segregating populations. As the map becomes saturated with more markers, complex traits could be dissected and utilized efficiently in breeding programs [30].

The present review is briefly going to discuss the status of molecular mapping for various traits in chickpea which is pre-requisite to exploit mapped genes for improvement of chickpea through genomics assisted breeding. The trait-wise QTLs / genes mapped in chickpea are presented below

## 2. FLOWERING TIME

Breeding for early flowering and developing early maturing cultivars helps in escaping terminal drought and heat stress which led to a significant increase in the productivity of chickpea. A key yield contributing characteristic that determines the rate of pod setting and thus seed/pod yield in chickpea under rainfed cropping patterns facing terminal drought conditions, especially in the semi-arid tropical regions, is the number of days to flowering [31,32,33]. Time to flowering, time of podding and early maturity plays a crucial role in the adaptation of chickpea varieties to distinct environments [34,35,36,37].

The development of the linkage map in chickpea was based on the commencement of morphological markers and isozyme loci. However, their small numbers and the fact that the environment often influences the expression of these markers, make them unsuitable for routine use. The interspecific RIL population of the cross *C. arietinum* (ICC 4958) × *C. reticulatum* (PI 489777) has been considered as a basic mapping population and substantially utilized for genome mapping [38,39,40,41] and [42].

Several studies were conducted on the molecular mapping of flowering time genes in chickpea and so far all the reported four genes governing the time of flowering are mapped. Reported QTLs for the flowering time were located on LG01 ([43]; [44]), LG02 [26], LG03 ([21,32,22,43,26,45,44], LG04 [46,47,45,44], LG05 [45], LG06 [44] and LG08 [43,47,44] using different parental lines in chickpea. The detection of QTLs on various linkage groups indicate that chickpea may have several genes controlling flowering time and these QTLs / genes could be used for developing

early maturity varieties through marker assisted selection. The QTLs / genes mapped for time of flowering are given in Table 1.

### 2.1 Yield Related Traits

According to Cho et al., [12] conducted study to construct an intraspecific genetic linkage map using a population of 76 F<sub>10</sub> derived RILs obtained from a cross ICCV 2 × JG 62 through the of 55 sequence-tagged microsatellite sites (STMS), 20 random amplified polymorphic DNAs (RAPDs), 3 intersimple sequence repeats (ISSR) and 2 phenotypic markers. The study revealed that, the gene for double podding was located on LG6 and linked to Tr44 and Tr35 markers while the gene for pigmentation was mapped on LG8 and was found linked to Tr33. The study further identified four QTLs for 100 seed weight (located on LG4 and LG9), seed number plant<sup>-1</sup> (LG4) and days to 50% flower (LG3).

Lal and Ravikumar [30] identified five QTLs for productivity related traits, out of which one QTL (qPods 13-2-1) and four QTLs respectively for number of pods per plant during the years 2013 and 2014, whereas two QTLs (qFlowering 14-1-1 and qFlowering 14-1-2) for days taken to 50% flowering and two QTLs (qTW 14-1-1 and qTW 14-2-1) for 100 seed weight through the studies on 125 RILs derived from a cross between JG 62 and WR315 over two seasons by using 60 polymorphic markers.

According to Jingade and Ravikumar [48] reported nine QTLs for three traits viz., seed yield plant<sup>-1</sup>, plant height and 100-seed weight through the studies on 141 RILs obtained from a cross between K850 and WR 315. Further, the study revealed that, out of nine mapped QTLs, two QTLs one each for seed yield plant<sup>-1</sup> (GSSR 50-TA 72) and 100 seed weight (TA 72-GSSR 41) were identified.

According to Verma et al., [49] reported seven QTLs (qSW1 – qSW7) for seed weight on linkage groups 1,2,5,6 and 7; four QTLs for seed number per plant (qSN1 – qSN4) on linkage groups 4, 6, 7 and 8; five QTLs for number of seeds per pod (qSP1 – qSP5) on LGs 1, 2, 5 and while four QTLs for number of pods per plant (qPP1 – qPP5) on LGs 1, 2, 6 and 8.

### 2.2 Fusarium Wilt

Chickpea is found to be affected by more than 50 pathogens, but only a few devastate the crop. Among the biotic stresses, Fusarium wilt (FW) limits chickpea production and it is caused by

*Fusarium oxysporum f. sp. ciceri*. It mostly occurs under dry and warm conditions and can cause annual yield losses up to 10-15%, under epidemics it may cause 100% yield loss [48,50,51]. It is characterized by having pathogenic variability, i.e., consists of eight different pathogenic races and pathotypes [51]. Races are differentiated based on their ability to incite new symptoms. Yellowing and drying of plants are the main characters under fusarium wilt disease. Early wilting causes significant losses and further increases the cost of production. Pathogen shows its effect by creating a disturbance in the vascular system of the plant and make the plants to become dry. It is important for the breeding programme and for the efficient use of available sources of resistance to recognize different races of the pathogen in a given area of chickpea production but the determination of races of this pathogen is a tedious process.

Breeding efforts were taken effectively to reduce the fusarium wilt effect on the chickpea crop. Mapping has been done in the past few years regarding resistance to different Foc races of fusarium wilt. Genetic resistance to Foc races was reviewed by Sharma et al., [52] and some genes resistant to races 0, 1, 2, 3, 4 and 5 (*foc0<sub>2</sub>*, *foc-1*, *foc-2*, *foc-3*, *foc-4* and *foc-5*) were found to be located on LG2 of the chickpea map [52]; [53,54,55,21,56]. However, one of the two resistance genes for race 0 (*foc0<sub>1</sub>*) was found in LG5 [57]. Garg [58] reported that, the fusarium wilt resistant gene against race 1 and 3 was

located on LG02 flanked by the markers *TR19*, *H2B061* and *TA27*.

Garg et al., [59] constructed a genetic map by using 84 SSR and 27 SNP markers on 188 RILs obtained from a cross between JG 62 x ICCV 05530 and reported five QTLs for resistance to fusarium wilt with phenotypic variance explained from 6.63 to 31.55%. Out of five QTLs identified three QTLs on CaLG02 and a minor QTL each on CaLG04 and CaLG06 were mapped for race 1. A major QTL each on CaLG02 and CaLG04 was identified for race 3. The genes / QTLs mapped for resistance against fusarium wilt were presented in Table 2.

### 2.3 Ascochyta Blight

Ascochyta blight is one of the major diseases in Chickpea and it is caused by *Ascochyta rabiei*. It is recognized as important disease under cool, humid weather conditions capable of causing 100% yield losses if the conditions are favourable [60,61]. Occurrence of serious loss has been observed in the earlier reports in various chickpea growing countries. It generally affects the above ground portions and produce lesions on leaflets, stem, petioles and on green pods, etc. As the disease progresses, patches of diseased plants become prevalent in the field and propagate gradually, covering the entire field. The section above the point of attack easily dies as lesions girdle the stem and the entire plant dies if the primary stem is girdled in the collar region.

**Table 1. QTLs / genes mapped for flowering time in Chickpea**

Cross	QTL/Genes	Reference
ICCV 2 × JG-62	QTL	Cho et al. [12]
Hadas × ICC5810	QTLs	Lichtenveig et al. [20]
CA2156 × JG62	QTLDF1	Cobos et al. [46]
ICCL81001 × Cr5-9	QTLDF3	Cobos et al. [21]
ICC 3996 × ILWC 184	QTL 3	Aryamanesh et al. [32]
ICC3996 × S95362 and S95362 × Howzat	QTL1	Hossain et al. [22]
ILC 588 × ILC 3279	Q1-1, Q3-1, Q4-2, Q8-2	Rehman et al. [43]
ICCV 2 × JG-62	QTL	Vadez et al. [75]
ILC3279 × ICCV2	QTLDF	Jamalabadi et al. [24]
ICC96029 x CDC Frontier	<i>Qef1-2</i>	Mallikarjuna et al. [44]
ICC5810 x CDC Frontier	<i>Qef2-1</i> <i>Qef2-3</i> <i>Qef2-4</i>	
BDG132 x CDC Frontier	<i>Qef3-1</i> <i>Qef3-2</i> <i>Qef3-3</i>	
ICC16641 x CDC Frontier	<i>Qef4-1</i>	

According to Garg [58] conducted an experiment to identify the QTLs associated with resistance to three major diseases of chickpea viz., ascochyta blight, botrytis grey mould and fusarium wilt by using 125 molecular markers and one phenotypic marker on 188 RILs ( $F_8$ ) obtained by crossing JG 62 and ICCV 05530 and reported that, the major QTL associated with ascochyta blight resistance at adult and seedling stages against the isolate 8 of race 6 (3968) was present on LG01B, while QTL associated with pathotype I at adult plant stage reported on LG01B whereas the QTL for Hissar race at seedling stage was reported on LG04B [59]. The QTLs identified for ascochyta blight resistance were presented in Table 3.

## 2.4 Botrytis Grey Mould (BGM)

BGM is one of major disease in chickpea, which is caused by *Botrytis cinerea* Pers. ex. Fr., and mostly occurs under cool and humid conditions. The occurrence of BGM has been reported in many countries, including Argentina, Australia, Canada, Columbia, Bangladesh, Nepal, Pakistan, India, Spain and the United States of America [62]. Arise in chickpea epidemics have been observed due to this disease and have been discovered in previous studies. Resistance to this pathogen has been identified in wild *Cicer* species, because of its wide host range the

**Table 2. Mapping of genes for different races of Foc**

Cross	Genes	Reference
CA2139 X JG 62	<i>Foc0<sub>2</sub>/foc0<sub>2</sub></i>	Halila et al., [54]
WR 315 X C-104	<i>foc-1</i>	Mayer et al., [56]
JG 62 X Vijay	<i>foc-1</i>	Gowda et al., [53]
JG 62 X Vijay	<i>foc-2</i>	Gowda et al., [53]
WR 315 X C-104	<i>foc-3</i>	Sharma et al., [80]
ICC 4958 X PI 498777	<i>foc-4</i>	Winter et al., [28]
ICC 4958 X PI 498777	<i>foc-4</i>	Benko-Iseppon et al., [81]
ICCL 81001 X Cr 5-9	<i>foc-5</i>	Cobos et al., [21]
ICC 4958 X PI 498777	<i>foc-5</i>	Winter et al., [28]
CA 2156 X JG 62 and CA 2139 X JG 62	<i>Foc0<sub>1</sub>/foc0<sub>1</sub></i>	Cobos et al., [57]

**Table 3. QTLs / markers linked to Ascochyta blight resistance in Chickpea**

Cross	QTL/Marker	Reference
FLIP84-92C X PI 599072	UBC733b, UBC181a, Dia4	Santra et al., [16]
ICC1 2004 X Lasseter	TS45, TA146, TA130	Flandez-Galvez et al., [15]
ILC 1272 X ILC 3279	Ta20, TA72, ar1	Udupa and Baum [82]
PI 359075 X FLIP84-92C	GA16, GA24, GAA47, Ta46	Cho et al., [17]
Hadas X ICC5810	H3C041, TA2 H1A12/H1H13, H1G20 H1C092, TA3/H3C11a	Lichtenzweig et al., [20]
ILC72 X Cr5-10	OPAI09746, UBC881621	Cobos et al., [29]
ILC3279-WR315	TA194	Iruela et al., [83]
ICCV96029 X CDC Frontier	TA64, TS54, TA176	Tar'an et al., [84]
CDC Frontier X ICCV 96029	TR19, TS54	Antbesa et al., [85]
CDC Luna X ICCV 96029	TA132, TS45	
CDC Corinne X ICCV 96029	TA64	
Amit X ICCV 96029		
ICC 12004 X Bivanij	TA125, TA72, GA26	Kanouni et al., [86]
ICC 3996 X ILWC 184	TA34, TA142 STMS11, TAA170 H3D09, H1A12	Aryamanesh et al., [32]
C 214 X WR 315	STMS11, Ta106, CaM0244	Sabbavarapu et al., [87]
C214 X ILC 3279		
Lasseter X ICC3996	SNP_40000185	Stephens et al., [88]
S95362 X Howzat	TA146, TA72	
ILC3279 xWR315	CaETR, GAA47	Castro et al., [89]

disease may occur at any stage of chickpea development. Garg [58] revealed that, the QTL for BGM resistance was located on LG06 for isolate 4 of race 3.

According to Anuradha et al., [63] constructed an intraspecific linkage map by using 144 markers on recombinant inbred lines (RILs) derived from cross JG 62 x ICCV 2. The study revealed that, the resistant QTLs like QTL1 was mapped on LG 6A and was found tightly linked to markers *SA14* and *TS71/ts36r*. QTL2 and QTL3 were mapped on LG 3. QTL 2 was flanked by markers *TA25* and *TA144* whereas QTL3 was flanked by *TA159* at 12 cM distance on one side and *TA118* at 4 cM distance on the other side.

According to Sachdeva et al., [64] screened 371 chickpea lines by using 300 SSR markers and under field conditions. The study reported that the markers namely *TA144*, *GA102*, *TA194*, *TA140* and *TR2* were strongly correlated with resistant bulks for botrytis grey mould disease.

According to Ranjana et al., [65] validated two primers *TA144* and *TR29* for botrytis grey mould disease resistance by using twenty genotypes and reported that, there is a correlation between the primers *TA144* and *TA29* for BGM disease resistance.

## 2.5 Drought Tolerance

Drought is considered as one of most important abiotic stresses, particularly the terminal drought is a major constraint limiting chickpea production globally in over 80% of the area. Drought accounts for 40-50% of yield loss annually worldwide [66]. Breeding efforts for development of drought tolerant varieties in the past is not encouraging because of quantitative and temporal variability of moisture stress across years, low genotypic variance, inherent methodologies, difficulty in evaluation of component traits besides using yield as an selection criteria [67,68]. In the recent past due to the availability of large scale genomic resources and high throughput phenotyping facilitated for genetic analysis of drought tolerance in chickpea [69]. As such, identification of genomic regions contributing for drought tolerance can help to develop better chickpea varieties through pyramiding of favourable alleles by marker-assisted breeding [70]. One of the challenges of marker-assisted selection is the pyramiding of genes (having small effects) related to complex traits like drought and yield.

The information on the identified QTLs for drought tolerance would enable the breeders to develop varieties with improved drought tolerance genomics-assisted breeding / marker assisted selection.

Initially, attempts were made to understand the tolerance of drought in improving the efficiency of agronomic or physiological traits [43,71]. Rehman et al. [43] reported that the presence of two QTLs on LG03 and LG01 are related to drought whereas Hamwieh et al., [71] found four QTLs on LG03 and LG04. A comprehensive understanding of drought tolerance in chickpea was given by Varshney et al. [47] and they found a genomic region spanning in 29cM on LG04 constitutes 12 QTLs governing drought tolerance and referred to that region as "QTL-hotspot". The study revealed that out of twelve markers, seven SSR markers viz., *ICCM0249*, *NCPGR127*, *TAA170*, *NCPGR21*, *TR11*, *GA24* and *STMS11* were found to be important for marker assisted introgression in new genetic backgrounds for improving the drought tolerance in chickpea. There are several hundreds of QTLs for drought tolerance [47] that have been mapped.

## 2.6 Salinity Tolerance

Salinity stress is considered to be the second major abiotic stress after drought in chickpea, which limits its productivity and reduces total production globally by 10 percent approximately [72]. Most of the arable land in the world is vulnerable to salinity tension. It has become one of the major threats to the productivity of chickpea in the last few decades, since it affects plant growth at various stages of production. It also showed its effect by hampering the germination, growth, reproduction, and the ability to biologically fix nitrogen besides affecting essential physiological functions, hormonal control and nutritional balance, decreases carbon fixation, causes flower abortion, reduces flower numbers and pod setting, and ultimately limits crop yield. Unlike cereals, chickpea shows sensitivity to salt stress and hinders its growth, development, reproduction, grain composition and yield. Salinity also promoted leaf necrosis and chlorosis, which subsequently lead to leaf senescence in grain legumes and reduces photosynthesis. Till date very limited number of QTLs were reported for salinity tolerance.

According to Pushpavalli et al. [73] constructed a genetic map by using 28 SSR and 28 SNP

markers on 188 RILs derived from a cross ICCV 2 x JG 11. The study revealed two key genomic regions on CaLG05 (28.6 cM) and on CaLG07 (19.4 cM), that harboured QTLs for six and five different salinity tolerance traits, respectively, and imparting either higher plant vigour (on CaLG05) or higher reproductive success (on CaLG07). Two major QTLs for yield in the salinity treatment (explaining 12 and 17% of the phenotypic variation) were also identified within the two key genomic regions.

According to Soren et al., [74] carried out a study by using RIL population developed from a cross between parental lines ICCV 10 (salt-tolerant) and DCP 92-3 (salt-sensitive) and constructed a linkage map comprising of 1856 SNP markers to develop salinity tolerant chickpeas. The study revealed that 28 quantitative trait loci explained up to 28.40% of the phenotypic variance in the population and identified QTL clusters on CaLG03 and CaLG06, each harbouring major QTLs for yield and yield component traits under salinity stress.

According to Vadez et al., [75] first reported mapping of QTL for salinity stress on the linkage groups LG 1, 2, 3, 4, 5, 6 and 7 in chickpea in a recombinant inbred line population derived from a cross between JG 62 (tolerant) and ICCV 2 (sensitive).

## 2.7 Heat Stress Tolerance

In the context of changes in global climate and cropping systems, heat stress is more prominent that severely affects chickpea at reproductive stage. Identification and exploitation of QTLs linked with heat stress tolerance may facilitate breeding varieties for heat stress. Pranob et al., [76] reported four major QTLs for heat stress by using 396 polymorphic SNPs on 292 F<sub>8-9</sub> RIL populations developed from a cross between ICC 4567 (heat sensitive) × ICC 15614 (heat tolerant). Four major QTLs for number of filled pods per plot (*qfpod*), total number of seeds per plot (*qts*), grain yield per plot (*qgy*) and % pod setting (*q%podset*) were reported to be located in the CaLG05 genomic region, whereas four QTLs for visual score (*qvs*), number of filled pods per plot (*qfpod*), grain yield per plot (*qgy*) and % pod setting (*q%podset*) were reported to be located in the CaLG06 region. The study also reported that 25 putative candidate genes for heat-stress were identified in the two major genomic regions.

## 2.8 Stem Growth Habit

Morphologically chickpea plants are classified as determinate, semi-determinate and indeterminate types depending on their terminal meristem behaviour. Predominantly chickpea is considered as an indeterminate crop and is used to show its vegetative growth if the surrounding environment is favourable. It leads to an increase in its crop duration and found competition between the vegetative and reproductive parts [77]. Genetic improvement through change in the plant architecture is the need of the hour, as it has major agronomic importance that determines the adaptability of a plant for cultivation and potential grain yield [78]. Some studies were conducted to determine the genetics of semi-determinate growth habit in chickpea.

According to Harshavardhana et al., [79] given the first report on the identification of markers linked to Dt1 locus in chickpea. *TA42* and *TR29* are the two markers found associated with the Dt1 locus and subsequently validated in different indeterminate, semi-determinate and determinate genotypes as well.

## 3. CONCLUSION

Chickpea is affected with various abiotic and biotic stresses which includes drought, heat, salinity, fusarium wilt, ascochyta blight, BGM and pod borer that adversely influence the yield. Conventional breeding had played a major role in chickpea improvement and contributed for improved productivity, stability of yield and adaptation of chickpea to new niches. Initially, chickpea exhibited limited polymorphism for available markers, but due to the remarkable progress in the recent years in respect of developing novel genetic tools like molecular markers, genetic maps, genome profiling techniques to identify quantitative trait loci for various traits, genomic regions and candidate genes governing various traits of interest have opened up new and exciting opportunities for researchers to develop chickpea varieties with resistance / tolerance to various biotic and abiotic stress. The identified QTLs for various traits may be exploited through genomics-assisted breeding by employing the recent approaches viz., Marker Assisted Back Crossing, introgression of superior alleles from wild species through Advanced Backcross QTL, Marker Assisted Recurrent Selection, Genome Wide Selection for improving chickpea.



#### 4. FUTURE PROSPECTS

1. Further fine mapping of all mapped QTLs/gene(s) of concerned traits are needed.
2. Validation of mapped QTLs is essential in new populations.
3. Marker assisted introgression of validated QTLs / gene(s) to develop varieties with resistance/tolerance to respective traits.
4. Map based cloning and functional validation of various genes.
5. It provides to know the distinct molecular mechanisms underlying distinct traits.

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#### COMPETING INTERESTS

Authors have declared that no competing interests exist.

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