



## **Breeding for Early Flowering in Chickpea (*Cicer arietinum* L.) – A Key Strategy to Accelerate Chickpea Productivity: 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. Authors KGKM and VH managed the literature searches and all authors read and approved the final manuscript.*

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### **ABSTRACT**

Chickpea is one of the most important pulse crop cultivated across the globe which is conventionally a low-input crop that is being cultivated mostly in moisture deficient rainfed environments during post-rainy season. The crop is being severely affected with various biotic and abiotic stresses among which, drought and heat stress are considered as serious constraints limiting chickpea productivity in sub-tropical regions. Several strategies were adopted to enhance the productivity under drought and heat stress environments among which, the development of early flowering varieties is one of the key strategies gaining importance in recent past. Some of the early / super early varieties like ICCV 2, JG 11, JG 14, KAK 2, JAKI 9218, ICCV 96029 and ICCV 96030 were developed during the last three decades. One of the most significant milestones in breeding for early varieties is the identification of four genes *efl-1*, *efl-2*, *efl-3* and *efl-4* governing early flowering by using various lines viz., ICCV 2, ICCV 96029, ICC 5810, BGD 132 and ICC 16641. Several QTLs controlling time of flowering were also mapped on linkage groups LG1, LG2,

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LG3, LG4, LG5, LG6 and LG8. The information on inheritance of time of flowering, correlation between early flowering with other yield attributing traits like number of pods per plant, number of seeds per pod, seed size, 100-seed weight, identified QTLs for early flowering and abiotic and biotic stresses tolerance may be useful for developing early maturing varieties that possess tolerance to various abiotic stresses by using different conventional and biotechnological approaches.

**Keywords:** Chickpea; early flowering; genetics of early flowering; correlation; mapping.

## ABBREVIATIONS

**BLAST** :Basic Local Alignment Search Tool  
**DES** :Directorate of Economics and Statistics  
**ICRISAT** :International Crops Research Institute for the Semi-Arid Tropics  
**LG** :Linkage Group  
**LOD** :Logarithm of Odds  
**PVE** :Phenotypic Variance Explained  
**QTL** :Quantitative Trait Locus  
**QTLs** :Quantitative Trait Loci  
**RIL** :Recombinant Inbred line  
**RILs** :Recombinant Inbred lines

## 1. INTRODUCTION

Chickpea (*Cicer arietinum* L.), is a cool season annual legume with a diploid set of chromosomes ( $2n=2x=16$ ), which is one of the foremost food legumes across globe and highest produced pulse crop in India with an estimated genome size of 738 Mb [1]. Chickpea is conventionally a low-input crop and is grown widely in the moisture deficient rainfed environments during post-rainy season [2,3]. The key limitations in its production include various biotic and abiotic stresses across worldwide, among which terminal drought is one of the soil moisture stress that occurs at the pod filling and seed development stages of the crop with increasing severity towards the end of the season, is considered as main restriction to its production in over 80% of the global area and in addition heat stress that occurs at reproductive stage. Thus, the duration of crop play a vital role in its adaptation, yield and productivity under such restricted stress environments. Therefore, time of flowering is an important element of chickpea adaptation, predominantly in the areas characterized by terminal drought and heat stress. Photoperiod and temperature influence the time of flowering in chickpea [4-6]. In addition season, date of sowing, altitude and latitude also causes the variation in time of flowering [7]. Photoperiod and temperature both have impact on flowering time in some genotypes whereas, in

others it is resolute exclusively by photoperiod. In semi-arid regions where the growth is limited by water deficiency and seasonal temperature, flowering time is an important for crop adaptation [8]. Early flowering helps in overcoming loss of yield by escaping from drought [9].

During the recent past, there is large shift in cultivated area of chickpea from cooler long season to warmer short season, as such early flowering and early maturity plays an important role under such environments to enhance and stabilize the chickpea productivity [10]. Thus, to enhance chick pea productivity one of the strategies is to develop early flowering and early maturing cultivars that can minimize overall agronomic practices, fertilizers, cost of labour, time of raising crop and by overcoming the effects of abiotic and biotic stress [11-14] more specifically the terminal drought and heat stress which are becoming major constraints for chickpea production as a consequence of climate change.

## 2. CURRENT STATUS OF CHICKPEA IN INDIA

India is the largest chickpea producing country with 10.09 million tons of output and 1043 kg/ha of productivity cultivated in an area of 9.67 m ha (DES 2018-19) (Fig. 1a, 1b and 1c). While there are no precise data showing global chickpea production disaggregated into desi and kabuli types, some estimates showed that Kabuli types account for 15 to 30% of world chickpea production while the desi type accounts for the remaining proportion [15-17]. Globally chickpea ranks 3<sup>rd</sup> after bean with an area of 14.56 M ha, with 11.5 MT mean annual production [18].

During the last three decades the production of chickpea is stagnated despite considerable increase in variability. In addition, it was also observed that yield contributed positively and area contributed negatively chickpea production [19]. In spite of long history of cultivation and being an important crop for small and marginal

farmers, the productivity has remained very low and more or less stagnated at about 800 Kg/ha [20]. It is considered as a valuable source of protein and livelihood for small and marginal farmers in developing countries. The low production witnessed during the recent years is a cause of concern and requires urgent attention [21] for enhancing productivity through developing early maturing varieties that can perform well under adverse environmental conditions.

### 3. MAJOR CONSTRAINTS LIMITING CHICKPEA PRODUCTION

Globally, the main constraints restricting chickpea development include specific abiotic and biotic stresses. Among the abiotic stresses, terminal drought is considered to be a major constraint limiting chickpea production in over 80 percent of the global area mainly due to its' cultivation in rainfed conditions during post-rainy season [2,3] and the crop also suffers due to heat stress during reproductive phase.

Apart from abiotic stresses, chickpea production is hampered by a number of biotic stresses. Under biotic stress, over 50 pathogens were reported to affect chickpea but only a few devastate the crop [22]. The soil borne diseases such as fusarium wilt (*Fusarium oxysporum f. sp. ciceris*), dry root rot (*Rhizoctonia bataticola*), collar rot (*Sclerotium rolfsii*) and black root rot (*Fusarium solani*) are considered as major biotic stresses in chickpea production [23,24].

Fusarium wilt, dry root rot and collar rot are the chickpea's major root diseases in areas where the chickpea is grown in dry and warm seasons e.g., Southern and Eastern Asia (Central and Southern India) and East Africa whereas ascochyta blight (*Ascochyta rabiei*) and botrytis grey mould (*Botrytis cineria*) are the major foliar diseases in cool and humid conditions [25,26]. The pod borer [*Helicoverpa armigera* H. (Lepidoptera: Noctuidae)] is responsible for causing severe damage due to its polyphagous nature and can feed on various plant parts such as leaves, tender shoots, flower buds, and immature seeds [27,28].

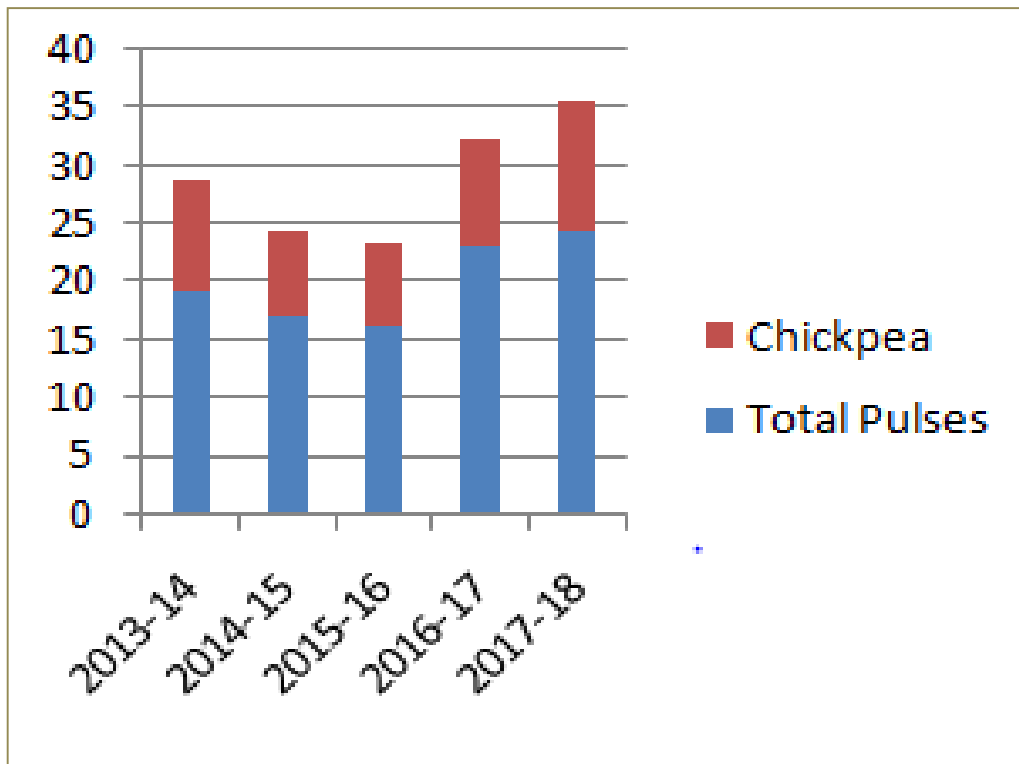
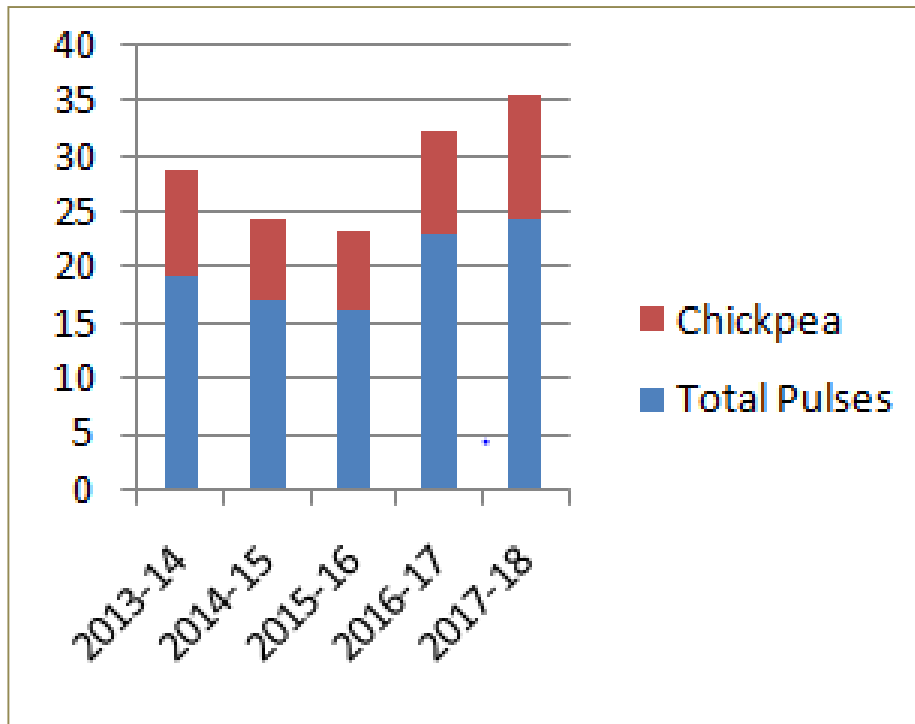
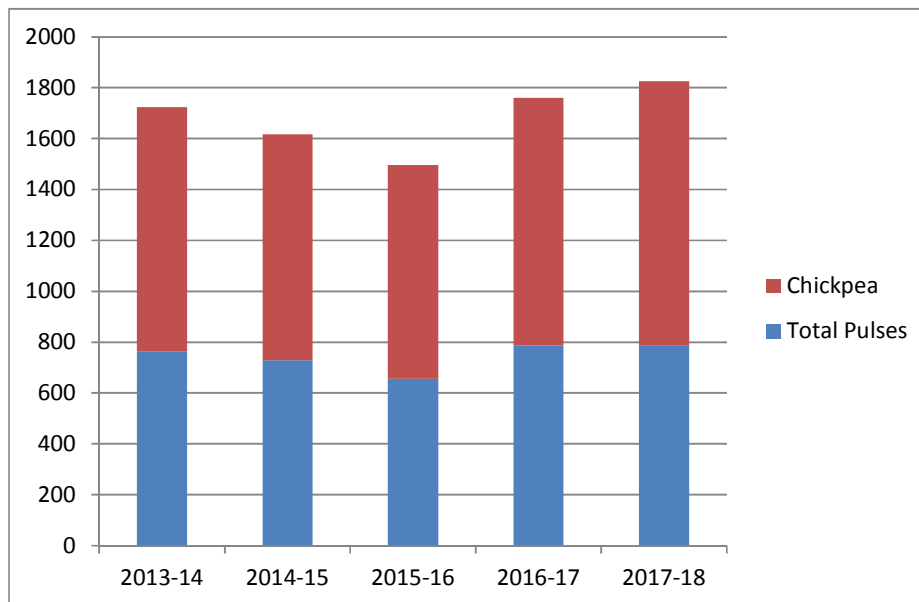


Fig. 1a. Area (m.ha) of total pulses and chickpea



**Fig. 1b. Production (Million tonnes) of total pulses and chickpea**



**Fig. 1c. Productivity (Kg ha<sup>-1</sup>) of total pulses and chickpea**

Among all the major constraints, because of climate change terminal dry spell and heat are considered as major constraints limiting chickpea production. So as to escape these anxieties breeding for early blooming is an important

strategy to increase efficiency of chickpea in such situations. Keeping in view of importance of developing varieties with early flowering, the research work carried out on development of early maturity varieties is reviewed hereunder

focussing mainly on inheritance of time of flowering, correlation of time of flowering with agro-morphological traits, biotic and abiotic stress tolerance etc.,

#### 4. INHERITANCE AND GENETICS OF TIME OF FLOWERING

The knowledge on inheritance of traits (monogenic, oligogenic and polygenic) may be helpful in designing breeding strategies for improvement of the characters under consideration. The genetics of flowering timing needs to be understood before cultivars can be fine-tuned to the demands of a specific environment. Chickpea provides some advantages for the study genetics of flowering time due to the presence of large genetic variation for flowering time in chickpea as reported by Pundir et al. [29], who recorded a time range from 33 to 107 for days to 50 % flowering through the study on a set of 12,018 accessions. Such a large variation in time for flowering in chickpea germplasm provides opportunities for development of cultivars with desirable period of maturity. The available information on inheritance of flowering time in chickpea varies depending on the genotypes used as parents and the environment. The study of inheritance of flowering time in new & diverse earliness sources will promote breeding of chickpea cultivars better adapted to terminal stress environments.

Since the early decades of the twentieth century, genetic methods were used to analyze the flowering variations between varieties of the same species which was usually done by making crosses between two varieties that exhibit different flowering timings and then following the segregation of flowering time between the progeny of the cross in various crops. [26] stated that the chickpea flowering period is governed by at least two distinct loci. [30]. conducted preliminary genetic studies of flowering time and revealed that early blooming was triggered by two duplicate genes in the homozygous recessive state. In chickpea, oligogenic inheritance for flowering-time was also documented [30-32].

[33] identified twenty eight early maturing chickpea germplasm lines representing wide geographical diversity using core collection approach and evaluated by using four checks under five different environments for seven qualitative and sixteen quantitative traits. The

study revealed that the lines ICC 16641, ICC 16644, ICC 11040, ICC 11180, and ICC 12424 were found to be early when compared with Harigantars and ICCV 2 check varieties.

Kumar and van Rheenen [34] revealed that a single gene controls the difference of flowering time in chickpea by studying the recombinant inbred lines (RILs) obtained from a cross between extra short duration cultivar ICCV 2, and a medium duration cultivar JG 62 and also reported a major gene "*efl-1*" for early flowering.

Kumar and Rao [35] selected a super early chickpea segregant ICCV 96029 from F<sub>6</sub> generation of a cross between two extra-early variants ICCV 2 and ICCV 93929. It was also reported that ICCV 96029 had shown inheritance of *efl-1* from ICCV 2 and at least one additional gene affecting an early flowering from other parent ICCV 93929, flowered around a week earlier than either parent. The study further revealed that the flowering period was affected by more than one gene. Anbessa et al. [31] made crosses between two early flowering lines, 272-2 and 298T-9 derived from ICCV 96029 as one of the parents with late-flowering Canadian cultivars 'CDC Anna' and 'CDC Frontier' and the resulting hybrids were tested for flowering time in temperate short season climate of western Canada. The results of the study revealed that the crosses were segregated for two major genes with duplicate recessive epistasis and indicated the presence of additive x additive interaction. The study suggested the presence of two major flowering time genes in ICCV 96029.

Or et al. [36] postulated that a single major gene called '*ppd*' (photoperiod dependent) regulates the flowering time in chickpea as a part of study conducted by using an early flowering line ICC 5810 (Harigantars), a black-seeded landrace from central India. The accession is comparatively day length or photoperiod-insensitive as reported by Roberts et al. [4], and flowered about two months earlier than the cultivar Hadas (days to bloom 115 to 140) at Rehovot, Israel. The direct and reciprocal crosses exhibited bimodal pattern of inheritance.

Kumar and Abbo [37,38] reported that recessive early-flowering genes '*ppd*' and '*efl-1*' identified from ICC 5810 and ICCV 2 respectively could be alleles of the same locus. However, Hegde [32] studied the allelic relationship between ICCV 2 (*efl-1*) and ICC 5810 (*ppd*) early flowering genes by crossing them and observed that F<sub>2</sub> plants of

this cross, differentiated into 9 (late): 6 (early): 1 (super-early) which indicated the involvement of two duplicate dominant genes which interact with a combined but unequal effect on flowering time. Therefore, it was concluded that ICCV 2 (*efl-1*) and ICC 5810 (*ppd*) early flowering genes were non-allelic. The gene "*ppd*" present in ICC 5810 was renamed as "*efl-2*". These findings were also supported by allelic relationship studies conducted by Gaur et al. [39] at ICRISAT.

Hegde [32] identified another source of early flowering kabuli line BGD 132, derived from the cross ICCV 2 × ICCV 5. He generated all the F<sub>1</sub>s of crosses involving early × early parents such as ICCV 2 × ICC 5810, BGD 132 × ICC 5810, BGD 132 × BGD 9812, BGD 132 × ICCV 2 and BGD 132 × SBD 377 and suggested that the late flowering was dominant over early flowering as all the F<sub>1</sub>s were late. He also postulated that genes for flowering time are non-allelic in all the genotypes under study. The F<sub>2</sub> plants of this cross segregated into 110 late: 73 early: 11 super-early. The pattern of segregation from F<sub>2</sub> was verified by observing the breeding pattern of 82 F<sub>3</sub> families and provided confirmatory evidence on the presence of several duplicate dominant genes for chickpea flowering time. Further, monogenic segregation for days to flowering in the cross BG 362 × BGD132 was observed and concluded that BGD 132 has a dominant gene in one of the loci that is distinct from ICCV 2 (*efl-1*) and ICCV 5810 (*efl-2*) and named the gene as "*efl-3*".

Gaur et al. [39] conducted a study to establish the allelic relationships of ICC 16641, ICC 16644 and ICCV 96029 early flowering genes with three existing early flowering genes viz., *efl-1* (ICCV 2), *ppd* or *efl-2* (ICC 5810), and *efl-3* (BGD 132). They used six early flowering genotypes, comprising three landraces (ICC 5810, ICC 16641, ICC 16644), two breeding lines (ICCV 96029 and BGD 132), and one released cultivar (ICCV 2) as parents for 19 crosses. Results indicated that ICC 16641/ICC 16644's major early flowering gene was not an allelic to any of the earlier reported early flowering genes and the latest gene was named as *efl-4*. Similarly, between ICCV 2 and ICCV 96029 the major gene for earliness was the same. It had already been predicted because ICCV 2 was used as one of the parents in ICCV 96029 development [37,38]. The study also revealed that *efl-1* (ICCV 96029, ICCV 2), *efl-2* (ICC 5810), *efl-3* (BGD 132) and *efl-4* (ICC 16641, ICC 16644) were non-allelic.

Thus, so far four genes governing inheritance of flowering time was reported in chickpea such as *efl-1* in ICCV 2 [34] and in ICCV 96029 [39], *efl-2* in ICC 5810 [36], *efl-3* in BGD 132 [32] and *efl-4* in ICC 16641 [39] as shown in Table 1 and Fig. 2.

#### 4.1 Correlation of Early Flowering with Other Agro-morphological Traits Associated with Yield

The studies on correlation between early flowering and other yield attributes may be useful for planning of selective breeding methods for simultaneous improvement of the traits in desired direction. Significant positive correlation between flowering and early maturity in chickpea was reported by Anbessa et al. [40]; Varshney et al. [41] and Das et al. [42,43]. Whereas positive correlation between time of flowering and 100-seed weight was reported by Hovav et al.[44] while the studies conducted by Gaur et al. [39]; Ali et al. [45]; Jivani et al. [46]; and Gaur et al. [47] revealed lack of correlation or negative correlation between flowering time and 100-seed weight. The results from the experiments conducted by Wallace et al. [48] and Anbessa et al. [4] revealed that early flowering and early maturity are correlated with high harvest index. The positive correlation for the days to flowering with days to maturity, number of pods per plant, number of seeds per plant and seed yield per plant was reported by Gaur et al. [47] and open the scope to breed early flowering genotypes with large seed size with higher yield

#### 4.2 Early Flowering in Escaping Abiotic Stresses Such as Terminal Drought, Heat and Frost Stress

Chickpea majorly grown under rainfed environments which coincides with summer terminal drought and heat stress due to rapid rise in temperature at maturity period resulting huge yield loss in mediterranean and semi-arid regions (Zhang et al. [49]; Turner et al., 2001; Kumar et al. [37,38]; Siddique et al. [50]; Berger and Turne [12,13]; Kumar et al. [35]; Singh et al.[51,52]; Than et al. [53] and Gaur et al. [2,3].

Frost damage coincides with the sensitive pod development stage in higher- latitude regions like western Canada due to the cultivation of late maturity cultivars (Croser et al. [50]; Berger et al.[54]; Clarke and Siddique [55]; Anbessa et al [40]. The importance of early flowering trait in escaping from various abiotic stresses such as

drought (Siddique et al. [50]; Berger et al. [54]; Berger et al. [8]; Subbarao et al. [9]; Kumar and Abbo [37,38]; Miller et al. [56]; Johansen et al. [52], heat stress [10]. and frost [57]; Gaur et al. [39]. There is large shift in area from cooler long season to warmer short season in chick pea cultivation, therefore, early flowering and early maturity plays important role under such environments to enhance and stabilize the chickpea productivity [41].

#### 4.3 Early Flowering in Relation to Biotic Stresses Such as Aschochyta Blight

Earlier studies revealed that there is a significant negative genetic correlation between days to flowering and aschochyta blight resistance (Lichtenzveig et al. [58]; Lichtenzveig et al. [11]; Aryamanesh et al. [59] and Daba et al. [60]. Kumar and Abbo [37,38] showed that aschochyta blight tolerant lines were late flowering and aschochyta blight susceptible lines were early flowering which is undesirable and further need to be analysed to find out that the negative correlation is due to linkage or pleiotropy. There is scope for identification of gene (s) for earliness which are not linked to blight resistance, to overcome negative correlation [15]; Gaur et al. [39] and the gene(s) can be combined with other gene(s) resistant to aschochyta blight from the different genomic backgrounds (Bhardwaj et al. [61]; Pande et al. [62]; Stephens et al. [63] lead to development of early maturing and aschochyta blight resistant cultivars (Warkentin et al. [57]. Further chickpea productivity can be enhanced by the use of markers linked to QTL as suggested by Varshney et al. [41] and Daba et al. [60].

#### 4.4 Factors Influencing the Expression of Time of Flowering

The information on factors affecting the expression of time of flowering will enable the researchers to develop varieties suitable for a specific environment. The studies of Summerfield and Roberts [7] revealed that the time of flowering is influenced by sowing date, latitude, altitude and season whereas the affect of temperature and photoperiod on time of flowering was reported by Roberts et al. [4]; Khanna-Chopra and Sinha [20]. Ellis et al. [5,6] reported that the time of flowering was influenced in some genotypes by both photoperiod and temperature while in other genotypes it was due to photoperiod alone. Correct timing of flowering is a critical component of crop environmental adaptation, especially when climatic factors such

as drought and high temperature restrict the growing season [9]. Kumar and Abbo [37,38] observed the involvement of several genetic systems that respond to the chickpea's day length and temperature, causing a typical continuous frequency distribution of flowering time. While chickpea is a quantitatively long day in its response, there are also some relatively photoperiod-insensitive genotypes [4].

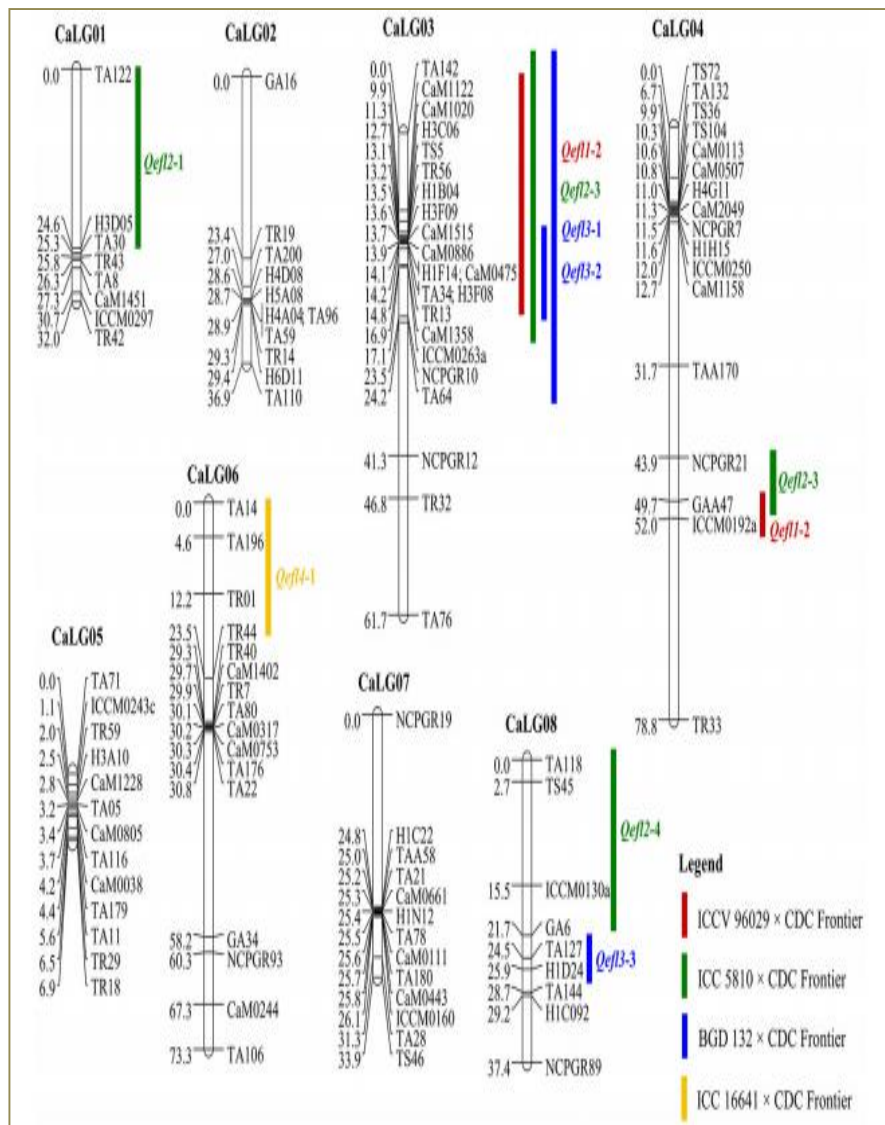
#### 4.5 Mapping Gene(s) / QTLs Governing Time of Flowering

Studies on molecular mapping of genes / quantitative trait loci (QTLs) controlling flowering time in chickpea have been performed. The major gene, *efl-1* from ICCV 2 was mapped on LG03 Mallikarjuna et al. [64] and the same was also reported by Cho et al. [65], Jamalabadi et al. [66] and Daba et al. [60]. Another QTL / Gene *efl-2* was mapped by Mallikarjuna et al. [64] recently on LG04, which is considered as same QTL as earlier mapped QTL by Cobos et al. [67] and Daba et al. [60]. The major QTLs from ICC 5810 were mapped on LG01, LG02 and LG08 [11]. Daba et al. [60] identified QTLs on LG03, LG04, LG05 and LG08 for days to flowering using ICCV 96029. Recently a study was conducted on molecular mapping of genes / quantitative trait loci (QTLs) controlling flowering time in chickpea using F<sub>2</sub> populations derived from four crosses (ICCV 96029 x CDC Frontier, ICC 5810 x CDC Frontier, BGD 132 x CDC Frontier and ICC 16641 x CDC Frontier) and a consensus map was drawn up by combining these four genetic maps. A total of 10 genomic regions for flowering time are distributed across CaLG01, CaLG03, CaLG04, CaLG06 and CaLG08 of the genetic map of chickpea and major QTLs corresponding to flowering time genes *efl-1* from ICCV 96029, *efl-3* from BGD 132 and *efl-4* from ICC 16641 were mapped on CaLG04, CaLG08 and CaLG06, respectively [64]. So the studies shown that all genes previously reported are mapped. Several other studies also reported QTLs for flowering time on LG01 [68]; Mallikarjuna et al. [64], LG02 [69], LG03 [70]; Aryamanesh et al. [59]; Hossain et al. [71]; Rehman et al., [68]; Karami et al., [69]; Upadhyaya et al. [43]; Daba et al. [60]; Mallikarjuna et al. [64] LG04 [67]; Upadhyaya et al., 2015; Daba et al. 2016; Mallikarjuna et al., 2017), LG05 (Upadhyaya et al. [42,43]; Daba et al. [60] LG06 (Mallikarjuna et al. [64] and LG08 [68,60] Mallikarjuna et al. [64] using different parental lines in chickpea. Detection of QTLs on various linkage groups showed that

chickpea may have several genes controlling flowering time. Till date, the QTLs / gene(s) mapped for early flowering are listed in the Table 2 along with respective linkage group

**Table 1. The list of early flowering genes reported in chickpea along with their sources**

S. No.	Early flowering gene	Source(s)	Reference(s)
1.	<i>efl-1</i>	ICCV2 ICCV 96029	[34] [39]
2.	<i>efl-2</i>	ICC 5810	[36]
3.	<i>efl-3</i>	BGD 132	[32]
4.	<i>efl-4</i>	ICC 16641	[39]



**Fig. 2. QTLs mapped for early flowering in Chickpea [64]**



**Table 2. QTLs / gene(s) mapped for the trait time of flowering in chickpea**

<b>Cross/Source</b>	<b>QTL/Gene</b>	<b>LG</b>	<b>LOD</b>	<b>PVE (%)</b>	<b>Closest marker</b>	<b>Reference</b>
ICCV 2 × JG-62	QTL	3	3.03	11	TS57-Ta127	Cho et al. [65]
Hadas × ICC5810	QTL1	1	9	56	H1F022-GAA40	Lichtenveig et al. [11]
Hadas × ICC5810	QTL2	2	4.4	22	H4B09-H1B06	Lichtenveig et al. [11]
Hadas × ICC5810	QTL8	8	3.9	17	H1C092-H3C110	Lichtenveig et al. [11]
CA2156 × JG62	QTL <sub>DF1</sub>	4	4.4	20	STMS GAA47	Cobos et al. [67]
ICCL81001 × Cr5-9	QTLDF3	3	1.3	26	TA142	Cobos et al. [70]
ICC 3996 × ILWC 184	QTL 3[10]	3	32.4	90.2	TAA142-TA64	Aryamanesh et al. [59]
ICC 3996 × ILWC 184	QTL 3[13]	3	32.4	90.2	TS29-TA76	Aryamanesh et al. [59]
ICC3996 × S95362 and S95362 × Howzat	QTL1	3	6.2	23	TS19-TR56	Hossain et al. [71]
ILC 588 × ILC 3279	Q1-1	1	7.8	15	H5A08-TA8	Rehman et al. [68]
ILC 588 × ILC 3279	Q3-1	3	10.9	22	TA6-NCPGR12	Rehman et al. [68]
ILC 588 × ILC 3279	Q4-2	4	2.9	5	TA132-GA137	Rehman et al. [68]
ILC 588 × ILC 3279	Q8-2	8	3.7	8	TA159-GA6	Rehman et al. [68]
ILC3279 × ICCV2	QTLDF	3	5.6	33	TA117	Jamalabadi et al. [66]
ILC 3279 × ILC 588	QTL-2	2	3.1	23	URP6f2-TA37	Karami et al. [69]
ILC 3279 × ILC 588	QTL-3	2	3.4	35	CaSTMS22-TA76	Karami et al. [69]
ICC 16374 × ICC 762	<i>CaqDF3.1</i>	3	6.3	11.3	CakSNP4307 CakSNP4313	Upadhyaya et al [43].
ICC 16374 × ICC 762	<i>CaqDF3.2</i>	3	8.9	15.4	CakSNP4801 CakSNP4805	Upadhyaya et al. [43]
ICC 16374 × ICC 762	<i>CaqDF4.1</i>	4	11.7	25.2	CakSNP6695 CakSNP6699 CakSNP6704	Upadhyaya et al., [43]
ICC 16374 × ICC 762	<i>CaqDF4.2</i>	4	10.8	22.4	CakSNP5894 CakSNP5900 CakSNP5910	Upadhyaya et al. [43]
ICC 16374 × ICC 762	<i>CaqDF5.1</i>	5	9.5	19.5	CakSNP8449 CakSNP10106	Upadhyaya et al. [43]
ICCV 96029 × CDC Frontier	qtlDTf-3.1	3	5.3	9	CAV1SC48.1P396061	Daba et al. [60]
ICCV 96029 × CDC Frontier	qtlDTf-4.1	4	3.1	11	scaffold205p25023	Daba et al. [60]
ICCV 96029 × CDC Frontier	qtlDTf-4.2	4	5.7	10	scaffold360p479554	Daba et al. [60]

<b>Cross/Source</b>	<b>QTL/Gene</b>	<b>LG</b>	<b>LOD</b>	<b>PVE (%)</b>	<b>Closest marker</b>	<b>Reference</b>
ICCV 96029 × CDC Frontier	qtlDTf-4.3	4	3.8	13	CAV1SC2.1P566504	Daba et al. [60]
ICCV 96029 × CDC Frontier	qtlDTf-4.4	4	5.7	14	scaffold34p1977386	Daba et al. [60]
ICCV 96029 × CDC Frontier	qtlDTf-5.1	5	18	44	CAV1SC.1P4940145	Daba et al. [60]
ICCV 96029 × CDC Frontier	qtlDTf-8.1	8	4.3	17	scaffold937p67148	Daba et al. [60]
ICC96029 x CDC Frontier	<i>Qef1-1</i>	3	3.45	5.6	CaM1122-TR13	Mallikarjuna et al. [64]
ICC96029 x CDC Frontier	<i>Qef1-2</i>	4	5.6	11.7	GAA47-ICCM0192a	Mallikarjuna et al. [64]
ICC5810 x CDC Frontier	<i>Qef2-1</i>	1	12.8	20.2	TA122-TA30	Mallikarjuna et al. [64]
ICC5810 x CDC Frontier	<i>Qef2-2</i>	3	16.7	24.9	CaM1358-TA142	Mallikarjuna et al. [64]
ICC5810 x CDC Frontier	<i>Qef2-3</i>	4	9.1	10.5	NCPGR21-GAA47	Mallikarjuna et al. [64]
ICC5810 x CDC Frontier	<i>Qef2-4</i>	8	17.7	25.7	GA6-TA118	Mallikarjuna et al. [64]
BDG132 x CDC Frontier	<i>Qef3-1</i>	3	5.2	4.3	CaM1515-TR13	Mallikarjuna et al. [64]
BDG132 x CDC Frontier	<i>Qef3-2</i>	3	4.2	4.0	TA142-TA64	Mallikarjuna et al. [64]
BDG132 x CDC Frontier	<i>Qef3-3</i>	8	44.3	64.9	TA127-H1D24	Mallikarjuna et al. [64]
ICC16641 x CDC Frontier	<i>Qef4-1</i>	6	55.6	88.1	TA14-TR44	Mallikarjuna et al. [64]

## 5. SIGNIFICANT ACHIEVEMENTS

The collaborative research efforts of National Agricultural Research System (NARS) institutes in Asia and Africa and ICRISAT have developed one extra early variety, ICCV 2 and several early varieties such as JG 11, JG 14, KAK 2, JAKI 9218 etc. During a period of 10 years from 1995/96 to 2004/05, Yezin 3 (ICCV 2) an extra early chickpea variety area increased from 166,000 to 205,000 ha (about 23.5 % area), 2.6 times increased production from 92,000 to 239,000 t (about 2.6 times) and almost doubled yield from 588 to 1171 kg ha<sup>-1</sup> in Myanmar [53]. JG 11 one of the early maturing varieties had occupied large area (70% during 2008/09) from 102,000 to 602,000 ha (3.8-times) during period of 10 years i.e., from 1999/2000 to 2008/09, and production was raised from 95,000 to 884,000 t (9.3 times) and doubled yield levels from 583 to 1,407 kg ha<sup>-1</sup> (2.4 times) in southern Indian state of Andhra Pradesh [72,73].

Thus, early flowering varieties / genotypes play pivotal role in minimizing major hurdles such as abiotic and biotic stresses and minimizes cost of production by consuming low inputs, which enhance the chickpea stability and productivity and hence, accelerate the genetic gain.

## 6. CONCLUSION

- There is a need to develop early maturing varieties in chickpea by exploiting the available sources of early flowering genes to combat most important abiotic stresses viz., terminal drought and heat stress.
- The future breeding strategies need to be focused on the studies on inheritance of time flowering, correlation between time of flowering and other yield attributing traits, biotic and abiotic stress tolerance, identification of gene(s) for early flowering, mapping of QTLs and their validation.
- Genotype x environment interaction may sharpen the hands of the breeders to develop early flowering varieties with wider adaptability and resistance to various biotic and abiotic stresses.
- The modern approaches like marker assisted breeding, genomic selection and speed breeding may also be used for developing early maturing cultivars to overcome major constraints in chickpea cultivation to meet ever increase in

demand for food, especially under short season environments.

## FUTURE PROSPECTS

1. Need to understand the value of other time of flowering genes in maximizing genetic variation and genetic gains from selection for earliness.
2. Further fine mapping of all mapped QTLs/gene(s) governing the time of flowering
3. Need to validate the reported QTLs/gene(s) after fine mapping
4. Marker assisted introgression of validated QTLs / gene(s) to develop early maturing cultivars
5. BLAST techniques are needed to validate the germplasm at genetic level
6. Map based cloning and functional validation of early flowering genes
7. Need to study the molecular mechanism underlying the large variation for early flowering.
8. Need to search for earliness from different germplasm with different genetic background.

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## COMPETING INTERESTS

Authors have declared that no competing interests exist.

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