



Altered Expression of an *FT* Cluster Underlies a Major Locus Controlling Domestication-Related Changes to Chickpea Phenology and Growth Habit

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Ortega R, Hecht VFG, Freeman JS, Rubio J, Carrasquilla-Garcia N, Mir RR, Penmetsa RV, Cook DR, Millan T and Weller JL (2019) Altered Expression of an FT Cluster Underlies a Major Locus Controlling Domestication-Related Changes to Chickpea Phenology and Growth Habit. Front. Plant Sci. 10:824. doi: 10.3389/fpls.2019.00824 Flowering time is a key trait in breeding and crop evolution, due to its importance for adaptation to different environments and for yield. In the particular case of chickpea, selection for early phenology was essential for the successful transition of this species from a winter to a summer crop. Here, we used genetic and expression analyses in two different inbred populations to examine the genetic control of domestication-related differences in flowering time and growth habit between domesticated chickpea and its wild progenitor *Cicer reticulatum*. A single major quantitative trait locus for flowering time under short-day conditions [*Days To Flower* (*DTF*)3A] was mapped to a 59-gene interval on chromosome three containing a cluster of three *FT* genes, which collectively showed upregulated expression in domesticated relative to wild parent lines. An equally strong association with growth habit suggests a pleiotropic effect of the region on both traits. These results indicate the likely molecular explanation for the characteristic early flowering of domesticated chickpea, and the previously described growth habit locus *Hg*. More generally, they point to de-repression of this specific gene cluster as a conserved mechanism for achieving adaptive early phenology in temperate legumes.

Keywords: chickpea, domestication, florigen, flowering, growth habit, legume, photoperiod, QTL

INTRODUCTION

The timing of flowering is a critical trait for crop adaptation, and as such has significant implications for yield and economic output (Jung and Muller, 2009; Nelson et al., 2010). The wild forms of many crops have a strong environmental requirements for flowering, ensuring that seed development occurs under favorable conditions. However, such requirements often constitute a physiological barrier for adaptation to wider agro-ecological ranges, and in general, domestication and subsequent diversification has involved selection of variants in which these requirements have been modified. A well-known example is wheat (*Triticum aestivum* L.), where relaxation of

photoperiod and vernalization responses has allowed the development of spring cultivars (Trevaskis et al., 2003; Yan et al., 2003; Fu et al., 2005; Beales et al., 2007; Díaz et al., 2012; Kippes et al., 2015, 2016). Similar adaptations have been reported in many other species (Nakamichi, 2015), including legumes, where a loss-of-function mutation in the circadian clock gene *ELF3* overcame the obligate LD requirement of pea (*Pisum sativum* L.), permitting its conversion from a winter to a spring crop at higher latitudes (Weller et al., 2012). Similarly, a mutation at the *Ppd* locus in the short-day species common bean (*Phaseolus vulgaris* L.) enabled summer cropping and broad global adaptation of this crop (Wallace et al., 1993; Weller et al., 2019).

Chickpea (Cicer arietinum L.) is a major grain legume, ranking third in global production after bean and pea (FAO, 2016). It is more drought-tolerant than other cool season legumes, and its relative importance is projected to increase in future due to global population growth and climate change (Bar-El Dadon et al., 2017; Muehlbauer and Sarker, 2017). Despite being domesticated in parallel with other long day vernalization-responsive legumes (pea, lentil) and cereals (wheat, barley) (Zohary and Hopf, 2000), the domestication history of chickpea is distinct from these other species (Abbo et al., 2003a). One key difference is the decline of chickpea in the archeological record between the Neolithic period, approximately 9000 years before present (ybp) and the early Bronze Age (approximately 5000 ybp) (Abbo et al., 2003b). A second key difference is that across its center of origin, chickpea has traditionally been grown as a summer crop (Abbo et al., 2003b), and varieties with the winter annual habit typical of wild chickpea are notably absent. This contrasts with other species domesticated in the Fertile Crescent region over the same period, such as barley and pea, in which a significant proportion of the domesticated germplasm retains the ancestral, wild phenology (Saisho et al., 2011; Weller et al., 2012).

The reasons for these two differences are not known, but it is thought that chickpea was neglected as a winter crop in favor of other pulses, as a result of its inherently greater susceptibility to Ascochyta blight, a fungal disease caused by Ascochyta rabiei. This disease can cause total crop failure, particularly during humid Mediterranean winter conditions (Siddique et al., 2000; Millan et al., 2003; Sharma and Ghosh, 2016) and its impact would likely have intensified as planting densities increased with cultivation. This pressure may have motivated attempts by early farmers to shift cultivation from autumn sown, over-winter crop (when most precipitation occurs in this region) to a springsown summer crop that matures in the predominantly dryer summer season. In such a scenario the selection of earlierflowering genotypes able to complete their life cycle prior to the onset of summer drought would likely have been essential (Kumar and Abbo, 2001), and the increase in the frequency of archaeobotanical remains of chickpea in the Bronze Age is suggested to reflect the success of this transition (Kumar and Abbo, 2001; Abbo et al., 2003a).

Early phenology continues to be important in presentday chickpea cultivation, as a large proportion of the global chickpea crop is grown in short season environments exposed to end-of season stresses that reduce their productivity (Kumar and Abbo, 2001; Muehlbauer and Sarker, 2017). In Mediterranean and semi-arid environments, where chickpea is grown under rain-fed conditions and matures into summer, terminal drought is the most common cause of yield loss (Zhang et al., 2000; Turner et al., 2001; Siddique et al., 2003; Berger and Turner, 2007). In higher-latitude continental temperate environments like western Canada, the short growing season is instead limited by declining temperatures, delayed maturity and increased potential for frost damage at the sensitive phase of pod development (Croser et al., 2003; Berger J.D. et al., 2004; Clarke and Siddique, 2004; Anbessa et al., 2007). In both situations, early flowering and maturity is thus an important primary escape strategy (Siddique et al., 2003; Berger J.D. et al., 2004; Berger et al., 2006) Hence, genetic control of this trait has been a topic of increasing interest (e.g., Gaur et al., 2008; Ridge et al., 2017).

Several flowering time loci have been reported in chickpea from both classical and quantitative trait locus (QTL) analyses. These include four major loci; *Photoperiod* (Or et al., 1999), *Early flowering* 1 (*Efl*1), *Efl*3, and *Efl4* (Kumar and Van Rheenen, 2000; Hegde, 2010; Gaur et al., 2014), and several QTL that appear recurrent in different populations. One prominent example is a "hot-spot" on linkage group (LG) four (Cobos et al., 2007; Varshney et al., 2014; Daba et al., 2016; Mallikarjuna et al., 2017). Another important genomic region is the central portion of chromosome 3 between markers TA6 and TA64, in which flowering time QTL have been reported from all wide crosses investigated for this trait (Cobos et al., 2009; Aryamanesh et al., 2010; Das et al., 2015; Samineni et al., 2015), as well as in several other intraspecific populations (Hossain et al., 2010; Hamwieh et al., 2013; Daba et al., 2016; Mallikarjuna et al., 2017).

In this study we aimed to elucidate the genetic basis of changes in flowering time that occurred early in chickpea crop evolution, through QTL analysis and candidate gene evaluation in two recombinant inbred populations between *Cicer arietinum* and its wild progenitor *C. reticulatum*. Our results point to a strong genetic association between the early flowering and erect growth habit typical of domesticated chickpea, and the elevated expression of a cluster of *FT* genes on chromosome 3. We conclude that a *cis*-acting genetic change leading to deregulated expression of this gene cluster may have played a key role in the prehistoric shift in phenology and farming practice integral to chickpea evolution under domestication.

MATERIALS AND METHODS

Plant Material

CRIL2 is a recombinant inbred line (RIL) population developed from an interspecific cross between *C. arietinum* (accession ICC4958) and *C. reticulatum* (PI489777) by Tekeoglu et al. (2000), Winter et al. (2000), Muehlbauer and Sarker (2017) at the United States Department of Agriculture (USDA), Agricultural Research Service and Washington State University, United States. ICC4958 is an early-flowering desi chickpea type with an erect growth habit, while the wild parent PI489777 is a Turkish accession with prostrate growth habit and late flowering typical of wild chickpea. Three other recombinant inbred populations were used in this study, developed by the chickpea breeding group in IFAPA (Institute of Agricultural and Fisheries Research and Training, Centro Alameda del Obispo, Cordoba, Spain) and University of Córdoba, Spain. RIP12 is an interspecific population consisting of 88 $F_{6:7}$ RILs derived from a cross between the kabuli cultivar ICCL81001 and a *C. reticulatum* accession, as described in Cobos et al. (2009). RIP5 (102 RILs) and RIP8 (113 RILs) are two $F_{6:8}$ RIL populations derived from reciprocal crosses between the early flowering desi landrace WR315 and the late kabuli accession ILC3279 (Iruela et al., 2007; Ali et al., 2015).

Growing Conditions and Phenotypic Evaluation

Four plants of each of the CRIL2 parents and 124 RILs were grown under long day (LD) or short day (SD) conditions in an automated phytotron at the University of Tasmania between December 2015 and April 2016. Plants under SD received 8 h (8 AM-4 PM) of natural daylight and were then moved to complete darkness inside the phytotron. Plants under LD received natural daylight, extended throughout the growing season with artificial light from high-pressure sodium lamps (50 μ molm⁻² s⁻¹) to provide a total photoperiod of 18 h. Night temperature inside the phytotron was maintained at 16°C. Flowering time was recorded as the number of days from seedling emergence to opening of the first flower (DTF) on each individual plant. Lines remaining vegetative at 130 days were assigned a nominal DTF value of 130 in subsequent analyses. Branching tendency was quantified at 3 weeks after emergence and expressed as the ratio of total branch length to main shoot length (branching index, BI) to normalize for differences in general vigor and stem elongation. Growth habit (GH) was scored using a four-category scale (values from 1 to 4), according to the angle of the branches from the vertical axis at harvest stage, as follows: (1) prostrate (branches $0-10^{\circ}$ above horizontal), (2) semi-prostrate (10-45°), (3) semi-erect (45-70°), and (4) erect $(>70^{\circ})$. For all three traits, the mean value from the four replicate plants was used for analysis.

RIP12 was sown in March in the field at the IFAPA site in Cordoba (latitude/longitude/altitude: 37°53'N/4°47'W/117 m) over four different seasons (2001, 2004, 2008, and 2014). Plots consisted of 2 m-long rows set 0.5 m apart, each sown with 20 plants of each RIL. Every fifth row was sown with one of the parent lines as a check. In 2001, a greenhouse trial was also conducted to assess flowering time under natural short day conditions (Cobos et al., 2009). RIP5 was sown in the field in March 2003 at two different sites: the IFAPA site in Cordoba and the IFAPA Venta del Llano site (Mengibar, Jaen, Spain; latitude/longitude/altitude: 37°57'N/3°48'W/280 m). In this trial, RILs were randomly distributed in four blocks and parents were included as reference in each trial. The unit plot was two rows of 2 m, with 10 seeds/m and 0.7 m between rows (Ali et al., 2015). RIP8 was sown in the field in February 2003 at the IFAPA site in Cordoba with two replications, in which RILs were distributed randomly into four blocks with 20 lines per block. Four check lines were included in each block following a Latin square design to verify environmental homogeneity. The plot unit was three rows, 4 m long, with 0.5 m between rows and a density of 20 plants m^{-2} . For these three populations, days from sowing to 50% flower was recorded (DTF). The data obtained from each of the two trials of RIP8 were analyzed separately. Information about the photoperiod experienced by RIP12, RIP5, and RIP8 during the different growing seasons can be found in **Supplementary Table 5**.

Molecular Markers

Both markers from previous linkage maps and new markers developed specifically for this study were used for map construction and QTL analysis. Polymorphisms in target genes across chickpea LG3 and LG4 were identified by sequencing of the parental accessions or from information available in previous reports (Saxena et al., 2014), and used to design 27 highresolution melt (HRM) markers (Supplementary Table 1) that were added to the markers previously genotyped in the RIP12, RIP5, and RIP8 populations previously described in Iruela et al. (2007), Cobos et al. (2009), Ali et al. (2015), respectively. In the case of CRIL2, the HRM markers were combined with a subset of 210 molecular markers selected from a dense map incorporating 2956 markers (Supplementary Figure 1; von Wettberg et al., 2018), to provide an even distribution [approximately 1 marker/5 centiMorgan (cM)] of high-quality (minimal missing data) markers (Supplementary Table 1).

Genetic Mapping and QTL Analysis

Linkage analysis in each population was performed using JoinMap v4.0 (Van Ooijen, 2006). Markers were grouped with a minimum logarithm of odds (LOD) value of 3.0, and the regression algorithm was used for mapping, using default options and the Kosambi function for the estimation of genetic distances (Kosambi, 1943). The initial maps were reviewed and problematic markers were removed where necessary based on the following criteria: Chi-square goodness-of-fit threshold (>1); nearest neighbor fit; genotype probability function; and the level of segregation distortion compared to surrounding markers. Following the removal of problematic markers, the maps were recalculated and the process repeated where necessary, until maps with robust order were produced.

The numbering of the LGs followed the chickpea consensus genetic map (Millan et al., 2010), based on the presence of markers in common with the consensus map itself or others marker of known position, using the Cool Season Food Legume Database¹.

Quantitative trait locus analysis was performed using MapQTL6.0 software (Van Ooijen, 2009). First, interval mapping was carried out to detect putative QTL associated with the variation in each trait. For each putative QTL, the marker closest to the LOD peak and two markers either side of this were used in Automatic Cofactor Selection (ACS) to select the best cofactor for subsequent Multiple QTL Mapping (MQM) analysis. The MQM function was employed iteratively with each new cofactor selection until all QTLs for a specific trait were determined. In both interval and MQM mapping, putative QTL were declared at

¹https://www.coolseasonfoodlegume.org

a chromosome-wide threshold (p < 0.05) based on permutation testing with 1000 permutations.

RNA Extraction and qPCR

For the expression study, the six parental lines of the four populations (RIP5 and RIP8 share the same parental accessions, and therefore were represented only once) were grown in an automated phytotron at the University of Tasmania under SD (8 h) and LD (16 h) conditions. For quantitative reverse-transcriptase PCR (qRT-PCR), dissected apical buds and the uppermost fully expanded leaflets were harvested. Each sample consisted of pooled material from two plants, harvested at midday at 2–4 weeks after seedling emergence. RNA extraction, cDNA synthesis and gene expression determination were performed as described in Sussmilch et al. (2015) using the primers indicated in **Supplementary Table 2**. The expression level of tested genes was normalized against *ACTIN* using the $\Delta\Delta$ Ct method.

Statistical Analysis

Statistical analysis was conducted using IBM SPSS Statistics (version 22), including box-plot and frequency distribution graphs. Correlation between traits was measured using Spearman's rank correlation coefficient, and statistical significance was tested by paired or independent *t*-test, according to the nature of the data.

RESULTS

A Major Locus Controls Flowering in the CRIL2 Interspecific Reference Population

We initially characterized flowering time in the CRIL2 reference population under controlled 8-h SD and 18-h LD conditions in an automated phytotron. Phenotypic values obtained are summarized in **Supplementary Figure 2**. Under LD, the difference in flowering time between the parental lines was not significant, with both flowering between 30 and 33 days after emergence. In contrast, under SD, ICC4958 flowered at around 60 days while PI489777 remained vegetative until the experiment was terminated 130 days after sowing. Thus, under these conditions, ICC4958 shows a moderate, quantitative response to photoperiod, whereas the wild line shows an obligate requirement for LD.

Among the RILs, the mean DTF under LD conditions was intermediate between the two parents while the range was substantially wider, with 12 days difference between the minimum and maximum values. Under SD, flowering time in the CRIL2 population showed a clear bimodal distribution, with a significant proportion of lines (68 out of 124) failing to initiate flowering by 130 days after sowing, like the wild parent. All RILs flowered considerably later under SD than under LD (p < 0.001) but, interestingly, phenotypic values for DTF in the two conditions were significantly correlated (with only 56 RILs able to flower in both LD and SD considered; rs[56] = 0.500, p < 0.001), indicating that part

of the variation is independent of photoperiod. Transgressive segregation, particularly toward earliness, was observed under both photoperiods (**Supplementary Figure 2**), suggesting that alleles associated with early flowering have been contributed from both parents.

Consistent with the phenotypic homogeneity observed for flowering time in CRIL2 under LD, QTL analysis under these conditions revealed only one minor QTL, *DTF3C* (**Table 1**), located at the top of LG3 (**Figure 1**). In contrast, under SD conditions, a major effect QTL, *DTF3A*, was found in the middle of LG3 (LOD 50.2, PVE 85). As the peak markers for these loci are separated by only around 10 cM, and the effective population size for the LD analysis is relatively small, the possibility that the loci may be the same cannot be excluded. However, as it is also not trivial to prove, we have adopted a conservative interpretation and assigned them distinct names.

Quantitative trait locus analysis was also performed using a subset of the population formed by those 56 RILs that were able to flower under both SD and LD. Interestingly, no significant QTL were found in this case, supporting the idea that only QTL *DTF3A* is acting in CRIL2 grown under SD. However, these results should be interpreted with caution, considering the small population size.

Mapping Identifies the *FT* Cluster as Strong Positional Candidates for *DTF*3A

Several previous studies have reported major flowering QTLs in the central region of chromosome 3 between markers TA6 and TA64 (summarized in Supplementary Figure 3), indicating this as a particularly important genomic region (Weller and Ortega, 2015). We scanned this region for genes similar to known flowering time genes in other species and added 18 additional markers to the CRIL2 linkage map, including 13 within the TA6-TA64 interval (Supplementary Figure 3 and **Supplementary Table 1**). This confirmed the presence of *DTF3A* within this interval and narrowed its location to a smaller interval flanked by markers SUVH4 and CDF2d (Figure 1), that corresponds to a physical distance of 1.4 Mbp and contains 124 annotated genes, according to the reference genome. Many of the flowering-related genes annotated in this region lie outside of this interval and were thus considered to be unlikely candidates, including SOC1a (SUPPRESSOR OF CONSTANS OVEREXPRESSION 1), COLh (CONSTANS-LIKE h), AG (AGAMOUS)-like, LUX (LUX ARRHYTHMO)-like, CDF (CYCLING DOF FACTOR), and WRKY (Supplementary Figure 3). However, the analysis confirmed the presence of a cluster of FT genes directly under the QTL peak, and a marker for one of these, FTa1, showed the strongest association with SD flowering time among all the markers tested (Table 1).

The dramatic delay in flowering of the PI489777 parent line and the bimodal distribution of the flowering phenotypes in CRIL2 under SD suggested that the QTL could also be analyzed as a single Mendelian locus, to refine its position. **Figure 2** illustrates all recombinants identified in the CRIL2 population across the LG3A region, and shows that *DTF3A* can be further delimited to a region of 0.8 Mb between markers *SUVH4* and *GATA9/ING2*

Traita Condb ΟΤΙ **PVE**^d Marker^e I G^f Thrh Population Place Year Earlv^g I ate⁹ CRIL2 DTF3C S1202p50545 Hobart 2016 DTF LD. P 2.9 9.6 3 29 30.3 2.8 DTF3A SD P 50.2 85.2 FTa1 3 66.2 128.6 26 2016 GH SD, P GH3 34 66.6 FTa1 3 34 1.6 26 GH4 4 28 22 55 5.9 S360p1277380 31 2016 BI SD, P BIЗ 10.6 33.1 FTa1 З 0.4 0.9 2.6 LD. P BIЗ 5.4 18.4 FTa1 3 0.2 0.5 2.5 RIP12 Cordoba 2001 DTF GLH DTF3A 10.8 46.9 FTa1 3 14.1 39.6 3.1 DTF3A 4.5 22 FTa1 З 60.4 68.6 2.9 Field 3 2004 DTF Field DTF3A 14.8 51.1 FTa1 8.9ⁱ 21.7ⁱ 2.9 DTF4B 3.6 9.2 STMS11 4 17.9ⁱ 12.6ⁱ 3.3 2008 DTF Field DTF3B 6.3 29.6 COLh 3 70.3 76.8 2.9 2014 DTF Field DTF3A 84 29.8 FTa1 3 58.3 64.2 3 DTF4A GAA47 4 63.5 59 2.8 5.3 17.3 RIP5 Cordoba 2003 DTF Field DTF3D 9.6 38.7 WRKY 3 60.4 64.8 2.7 Cordoba DTF3A 3 87 FTa1/2 З 61.3 63.9 27 Mengibar DTF3A 5.7 26.9 FTa1/2 З 64.2 66.7 2.8 RIP8 Rep1 2003 DTE Field DTE3D 75 29.2 TA125 3 84.3 87.3 26 DTF3D Rep2 6.8 29.0 TA125 3 84.6 87.3 2.7

TABLE 1 | Quantitative trait loci (QTL) identified by multiple QTL mapping for flowering time, growth habit and branching index in four populations grown in different environments.

^a Trait analyzed: DTF, flowering time; GH, growth habit; BI, branching index. ^bCondition: LD, long days; SD, short days; P, phytotron; GLH, glasshouse. ^cThe LOD scores for each QTL. ^dPVE, Phenotypic variation explained. ^eMarker nearest to the peak LOD score. ^fLG, linkage group harboring the QTL. ^gMarker genotype class means for early (C. arietinum accessions ICC4958, ICCL81001 and WR315 for CRIL2, RIP12, and RIP5/8, respectively) and late (C. reticulatum accessions Pl489777 and Cr5-9 in CRIL2 and RIP12 and C. arietinum ILC3279 in the case of RIP5/8) parents, calculated for the marker with higher LOD. ^hThreshold LOD for a 0.995 confidence value, calculated through permutation test for each trait and linkage group. ⁱFlowering time in 2004 is a relative value, as specified in **Supplementary Figure 2**.

(**Supplementary Table 3**). This region contains only 59 genes, but still includes the *FT* cluster.

Comparison of the DTF3A Region in Other Crosses

The segregation of a major flowering time locus in CRIL2 and several other interspecific populations suggests a potential role for this locus in early crop evolution. However, a lack of common markers has made it difficult to compare the position of QTL between studies and clearly demonstrate their co-location. To investigate the position of DTF3A relative to previously described OTLs, and assess the possible relevance of this region at the intraspecific level, we selected three additional populations for parallel analysis through mapping of common markers. RIP12 is another interspecific population, for which a major flowering QTL has been reported in the TA6-TA64 region (Cobos et al., 2009). The intraspecific populations RIP5 and RIP8 were also examined, as preliminary evidence indicated an association of markers in the 3A region with flowering time in this cross (Castro, 2011). Where polymorphisms were available, the genes targeted in CRIL2 were also genotyped and added to the linkage maps in these additional populations (Supplementary Table 1) by recalculation of the linkage maps with markers for these genes and previously mapped markers (Supplementary Figures 4-7). These maps were then used for QTL analysis of flowering data for the three populations across different locations, years, and environments (**Supplementary Figure 2**), revealing a total of 12 significant flowering QTL (**Table 1**).

In the RIP12 population, analysis over several years, in glasshouse and field environments, yielded seven QTL; five on LG3 and two on LG4 (**Table 1**). The QTL on LG3 were defined by the same interval 3A described above for CRIL2 (**Figure 1**), and the *FTa1* marker again explained the highest proportion of variation (up to 51%). During 2008, a flowering QTL *DTF3B* was detected in a second region of LG3 between markers *FTa1* and Q05₁₈₂₈. Since both the position of the interval (**Figure 1**) and the significance of the QTL (~30% PVE) are very close to those obtained for *DTF3A* (**Table 1**), it seems highly probable that these two QTL are equivalent.

In the intraspecific populations, two regions on chromosome 3 influenced flowering time. One of these was region 3*A*, which was detected in the RIP8 population, with a variable effect on flowering time depending on location, with a strong effect when grown in Mengibar, and a weaker influence in Cordoba (26.9 vs. 8.7% variance explained, respectively). An additional highly significant QTL (*DTF3D*) was detected on LG3, between markers LOB189 and PRT6, in both intraspecific populations (**Figure 1**). Although this QTL was not detected in RIP5 at Mengibar, in situations where it was detected it had a greater effect than *DTF3A* (**Table 1**).



FT Genes in Chickpea

In view of the central location of an *FT* gene cluster under the *DTF3A* QTL, we characterized the entire chickpea phosphatidylethanolamine-binding protein (PEBP) family, which includes *FT* genes and the related *TFL1* (*TERMINAL FLOWER 1*) family of flowering repressors (Wickland and Hanzawa, 2015; **Supplementary Figures 8A, 9** and **Supplementary Table 4**). Five chickpea *FT*-like genes were identified in the three previously described legume *FT* subclades; *FTa, FTb,* and *FTc* (**Supplementary Figure 10**; Hecht et al., 2011). This analysis confirmed that chickpea, like Medicago, possesses three *FTa* genes, with two of these (*FTa1* and *FTa2*) located together with the single *FTc* gene on chromosome 3 in a tandem arrangement (Hecht et al., 2011; Laurie et al., 2011). Only one other PEBP gene was found on this chromosome (*TFL1a*), while the remaining genes were located on chromosomes 1 (*TFL1b*), 2 (*FTb* and *FTa3*), 6 (*MOTHER OF FT*, *MFT*), and 8 (*TFL1c*) (**Supplementary Figure 8B**). The only difference in the chickpea *FT* family compared to other related legume species is the apparent presence of only a single *FTb* gene, where Medicago and pea each have two highly similar paralogs located in tandem in a conserved genomic location on chromosome 7 and LG5, respectively (Hecht et al., 2011; Laurie et al., 2011). In the broader PEBP family, chickpea possesses single-copy orthologs of the *BFT* (*BROTHER OF FT*) and *MFT* genes, and also of two of the three *TFL1* genes previously described



recombinant inbred lines from the CRIL2 population showing recombination breakpoints across a 7.14 Mb region of chromosome 3 spanning the *DTF3A* locus. Numbers over the markers correspond to their physical position (in Mb) in the CDC Frontier genome assembly in NCBI (ASM33114v1; Varshney et al., 2013). Alleles from the domesticated parent ICC4958 are shown in white and those from the wild parent Pl489777 in gray. Flowering phenotype is shown in the column headed SD and indicates whether the indicated lines flowered (Y) or remained vegetative (N) under an 8h photoperiod. This phenotype showed no recombination between markers *FTa1* and GATA9.

in pea and Medicago, *TFL1a* and *TFL1b*. The third gene, *TFL1c*, was represented by three gene models in the CDC Frontier genome assembly (**Supplementary Table 4**), but was not represented at all in the other available chickpea genome (from ICC4958, assembly ASM34727v3); a discrepancy that will require clarification in future.

Genes in the *FT*a1-*FT*a2-*FT*c Cluster Are Upregulated in Early Accessions

FT genes are well-known as important positive regulators of flowering. This is also true in legumes, where several FT genes have been identified and most are capable of promoting flowering when overexpressed in Arabidopsis (Kong et al., 2010; Hecht et al., 2011; Laurie et al., 2011; Sun et al., 2011). Therefore, if one of the FT genes in the cluster was the basis for the effect of the DTF3A locus, increased activity or expression of one or more of these genes would be expected in the early-flowering parent. To evaluate this possibility, we examined the expression of FT genes in the parent lines of the mapping populations. In view of previous reports indicating tissue- and photoperiodspecific expression of FT genes in pea and Medicago, we collected samples from leaf and apex tissue under both LD and SD conditions at two timepoints. Expression of the AP1 homolog PROLIFERATING INFLORESCENCE MERISTEM (PIM) was used as an indicator of flowering commitment, as previously

described for other legumes including chickpea (Hecht et al., 2011; Ridge et al., 2016).

Figure 3 shows that 2 weeks after emergence PIM expression in shoot apices was not detectable in any of the accessions. By 4 weeks, PIM was expressed significantly above background in all three late parents under LD but not in SD, whereas it was strongly expressed under both LD and SD in the early parents. In parallel, the expression of all three genes in the chromosome 3 FT cluster (FTa1, FTa2, and FTc) was elevated in the early parents at 4 weeks under SD and LD. In ICC4958, expression of all three genes was higher than the wild parent even by week 2; i.e., before detectable expression of PIM. Similarly, expression of FTa2 and FTc was also elevated in the early parent of RIP12 (ICCL81001) at week 2. However, FTa2 transcript could not be detected in the early parent of RIP5/8 (WR315), reflecting a complete deletion of the gene (Supplementary Figure 11). This result suggests that the elevated expression of FTa2 seen in the domesticated parents of CRIL2 and RIP12 is unlikely to be solely responsible for the effect of DTF3A in these populations. As in pea and Medicago, FTa1 and FTc in chickpea differed in the tissuespecificity of their expression, with FTa1 expressed strongly in leaves and weakly at the shoot apex, and FTc expressed only weakly at the shoot apex. Despite these differences, both genes showed similar expression profiles, with an early upregulation in the domesticated/early flowering parents that preceded PIM induction, and they therefore represent good candidates to underlie the QTL.

Significant expression of the single FTb gene was seen in 2-week-old plants, but only under LD, and at a similar level in both early and late parents. This is similar to the strongly photoperiod-dependent expression of FTb genes previously reported in pea and Medicago (Hecht et al., 2011; Laurie et al., 2011), and indicates that FTb misexpression is not a factor in the effect of DTF3A under SD. The expression of FTa3 was restricted to leaf tissue, and only detected at a late developmental phase after commencement of flowering (Supplementary Figure 12), suggesting it is unlikely to make a major contribution to the observed differences in flowering time. The expression of TFL1b and TFL1c was also tested in apical tissue. Whereas expression of TFL1c in this tissue did not change significantly, TFL1b expression was higher in the wild line under non-inductive conditions and gradually decreased in cultivated and wild accession grown in long photoperiod, consistent with a possible role as a floral repressor. However, the level of expression observed in both genes was very low and the biological significance of these changes is therefore uncertain (Supplementary Figure 12).

The DTF3A Locus Coincides With QTL for Plant Architecture

The late-flowering phenotype of wild chickpea is also associated with a prostrate growth habit (GH), reduced apical dominance and an increased number of branches (Singh and Shyam, 1959; Aryamanesh et al., 2010; Ali et al., 2015). Consistent with these reports, we also observed major differences in growth habit between CRIL2 parents and in the CRIL2



population in SD, which we quantified for genetic analysis using a four step scale (Supplementary Figures 13A-D). We also recorded branching propensity in young plants (prior to visible flower initiation) under both SD and LD. Late flowering RILs also showed a shoot architecture that resembled the wild parent, so we investigated the correlation between these three traits (Supplementary Figure 13). A highly significant difference (p < 0.001) was found between the flowering dates of erect/semierect RILs compared to those with a prostrate/semiprostrate growth habit (Supplementary Figure 13E), confirming that in the segregating population, prostrate growth habit is associated with late flowering, as expected. Inspection of individual RILs showed a nearly perfect correlation, with flowering observed in all 53 erect or semi-erect RILs but in only three out of 71 lines categorized as prostrate or semi-prostrate. A strong negative correlation (r = -0.504, p < 0.001) was found between growth habit and branching index (Supplementary Figure 13F), indicating that erect and semi-erect plants in general also had a lower branching index (BI).

BI of the population was generally higher in SD than in LD, as might be expected in view of the longer vegetative growth phase. However, across the population, a strong positive correlation (r = 0.679, p < 0.001) was found in the BI between photoperiods, suggesting that at this stage (3 weeks old plants) a genetic

component of this trait is unrelated to photoperiod. QTL analysis revealed two QTLs for growth habit; a major QTL on LG3 that explained 66% of the variation for this trait, and a minor QTL on LG4. For BI, a single QTL in a similar location was identified under both photoperiods (**Table 1**). Interestingly, the QTL for both GH and BI in chromosome 3 were closely co-located with the *DTF3A* flowering time QTL described above (**Figure 4**). In addition, the physiology of these three QTL is similar with respect to their strong effect under SD and their absence, or minor effect, under LD, as seen in the genotype means for the *FTa1* peak marker shown in **Table 1**.

DISCUSSION

One of the critical events in chickpea evolutionary history is thought to have been its conversion from a winter to a summer crop, likely achieved by Neolithic farmers in an attempt to reduce the incidence of Ascochyta blight, whose onset is favored by the cool, wet conditions that typify Mediterranean winters (Kumar and Abbo, 2001; Abbo et al., 2003a,b). For this shift in the chickpea farming system to succeed, a major modification of phenology toward earliness would have been required in order to match the considerably shorter growing season. This selective pressure is evident today in the typically early flowering



phenotype of the domesticated *C. arietinum* relative to wild *Cicer* species (Berger J. et al., 2004).

Our analyses identify a central region of chromosome 3 (referred to as region 3A) that makes a major contribution to this difference in flowering time between domesticated chickpea and its wild progenitor, *C. reticulatum*, in two populations utilizing different *C. arietinum* parents and grown in different conditions. This result is consistent with several previous reports. Das et al. (2015) found a recurrent major QTL on chromosome 3 in an interspecific cross using ICC4958 as the domesticated parent. Aryamanesh et al. (2010) found a major QTL on chromosome 3 defined by the same interval as that reported initially in RIP12 by Cobos et al. (2009) and narrowed in the present study. The fact that these studies use different and unrelated *C. arietinum* accessions suggests that the presence of early alleles at this locus may be a defining feature of domesticated chickpea.

Another interpretation is that the apparent importance of this locus could reflect the fact that the wild parents used in all of these studies are closely related and could conceivably carry a unique variant at this locus that is not representative of the wider *C. reticulatum* germplasm. However, this is discounted by the recent finding of von Wettberg et al. (2018), who examined crosses between a common domesticated parent and 29 newly

collected wild accessions representing a much wider diversity, and found that all progenies shared a common major QTL in a 3.55 Mb interval of chromosome 3 encompassing the LG3A region. Interestingly, this region also appears to have a significant effect within domesticated chickpea, as revealed by our analysis of two intraspecific populations, and several other studies (e.g., Hossain et al., 2010; Rehman et al., 2011). However, its effect at this level seems to be more dependent on environment and the influence of other loci, suggesting that additional variation in this region may have also had a role in post-domestication diversification of flowering behavior. Further clarification of this scenario will require a wider analysis in both interspecific and intraspecific contexts, whether in biparental populations or through association approaches.

In addition to late phenology, wild chickpea is also distinguished from domesticated forms by the greater profusion of branches and prostrate growth habit (Ali et al., 2015), and we found that the same chromosomal region 3A also had a significant influence on both traits, particularly under SD conditions, as reflected by the presence in the region of a major QTL for each of these traits (QTL GH3 and QTL BI3). To date, two major loci, Hg and Hg2, have been reported to determine growth habit differences between C. arietinum and C. reticulatum (Muehlbauer and Singh, 1987; Kazan et al., 1993; Ali et al., 2015). Interestingly, Hg has been mapped to the central region of chromosome 3 by Winter et al. (2000), using a population derived from the same parents as CRIL2, and studies by Cobos et al. (2009), Aryamanesh et al. (2010), Ali et al. (2015) have all reported a locus influencing growth habit in this region. Since the GH3 QTL we describe here for CRIL2 is located within the intervals reported in these studies, it seems likely that all of these studies are detecting the same locus (Hg). Association of flowering with different features of shoot architecture has been previously described in a number of other legume species, including chickpea (Lichtenzveig et al., 2006; Julier et al., 2007; Lagunes Espinoza et al., 2012; González et al., 2016; Yang et al., 2017). In the case of QTL in the chickpea LG3A region, such an association could either represent the action of independent but tightly linked genes, or the pleiotropic effects of a single gene.

The discrete and approximately 1:1 segregation of flowering time in CRIL2 under controlled SD conditions enabled us to map *DTF3A* as a Mendelian trait to a narrower interval, thereby reducing the number of potential candidates. The only remaining clear candidates were a cluster of three FT genes orthologous to the FTa1/a2/c cluster identified in Medicago and pea by Hecht et al. (2005, 2011). FT genes have a widely conserved role as flowering promoters (Wickland and Hanzawa, 2015), and several recent studies show that this is also the case for legume FTa and FTc genes (Kong et al., 2010; Hecht et al., 2011; Laurie et al., 2011; Sun et al., 2011). We identified elevated expression of genes in the FT cluster in the early parents of all three crosses examined (Figure 3), implicating the general derepression of these genes as the likely molecular basis for the DTF3A effect. A comparable situation has been recently described in another legume, narrow-leafed lupin (Lupinus angustifolius), where a strong ancestral vernalization requirement has restricted

production in warmer regions. This limitation has been overcome by the incorporation of dominant alleles at the major locus Ku, which confer de-repressed expression of a tightly linked FTc gene and permit flowering in the absence of vernalization (Nelson et al., 2017; Taylor et al., 2018). However, compared to lupin, where only a single FT gene is present in this genomic location, the presence of three genes in chickpea is clearly a more complex situation, and raises the question of which of them might be responsible for the QTL effects on photoperiod response, or the QTLs for vernalization response that has been localized to the same genomic region on LG3 (Samineni et al., 2015; Pinhasi van-Oss et al., 2016).

The FTa1 gene plays a key role in regulation of flowering in both pea and Medicago, as loss-of function mutants show significant impairment of flowering in both species, and overexpression in Medicago confers early flowering and reduced sensitivity to photoperiod and vernalization (Hecht et al., 2011; Laurie et al., 2011). FTa1 would therefore seem to be the strongest candidate for the causal gene underlying DTF3A. Although the role of FTc has not been systematically explored in either species, both *MtFTc* and *PsFTc* are strong activators of flowering when overexpressed in Arabidopsis, and their induction in apical tissues correlates closely with flowering (Hecht et al., 2011), suggesting that the higher levels of CaFTc expression could also potentially contribute to the earlier flowering of domesticated lines. Intriguingly, the most dramatic expression difference in the two interspecific comparisons was seen for FTa2, which was expressed at a low level in C. reticulatum parents and over 20 times higher in the domesticated parents. However, despite this striking association with early flowering, FTa2 was not expressed at all in the early parent of the intraspecific cross, indicating that the early flowering of domesticated relative to wild chickpea cannot result primarily from the high level of FTa2 expression. Also, in contrast to FTa1 and FTc, FTa2 from pea or Medicago is much less effective for induction of flowering when expressed in transgenic Arabidopsis, and its endogenous expression patterns are not consistently associated with flowering (Hecht et al., 2011; Laurie et al., 2011). Taken together, these observations suggest that FTa2 is less likely to be the basis for the interspecific effects of DTF3A, but it remains plausible that these effects might reflect general derepression across the cluster and a functional contribution from all three genes.

The strong photoperiod-dependence of the *DTF3A* effect can also be interpreted in terms of the known role of *FT* genes in mediating of environmental effects on flowering. In both pea and Medicago, photoperiod and vernalization responses appear to be integrated through *FT* genes, but whereas *FTa* genes are regulated by both photoperiod and vernalization, *FTb* genes are strictly regulated by photoperiod (Hecht et al., 2011; Laurie et al., 2011). In chickpea, a similar LD-specific expression of the single *FTb* gene is seen in both wild and domesticated parents (**Figure 3**) and may be sufficient for maximal promotion of flowering, which could provide an explanation for the minimal effect of *DTF3A* under these conditions. In contrast, under non-inductive SD conditions, the absence of *FTb* expression or other inputs would presumably expose any effects of elevated expression of the *FTa/c* cluster.

Whether one or more of the FT genes are indeed responsible for the effects of DTF3A, it is also of interest to consider what might be the molecular basis of their observed de-repression. The apparently specific effects of the QTL on expression of the underlying FT genes suggests a scenario in which the domesticated parents might have undergone modification of either a cis-acting or a closely linked trans-acting mechanism normally required for repression of the cluster. The absence of other plausible candidates in the defined region favors a cisacting mechanism, and precedent for this is provided by recent studies in two other legumes. In Medicago, insertions in the third intron and 3' flanking region of FTa1 confer gain-of-function phenotypes, with elevated FTa1 expression and dominant early flowering (Jaudal et al., 2013), whereas in narrow-leafed lupin, the derepression of FTc expression that underlies the effects of Ku alleles is associated with deletions in the FTc promoter (Nelson et al., 2017; Taylor et al., 2018). The recently reported role for the polycomb-group protein VRN2 (VERNALIZATION 2) in FTa1 repression in Medicago (Jaudal et al., 2016) points to the likely existence of both epigenetic and transcriptional components to this regulation.

Direct involvement of FT genes would also provide an explanation for the association of growth habit and flowering effects with the chromosome 3A region. It is becoming increasingly apparent that FT genes, in addition to being major flowering regulators, also affect plant architecture and growth habit across a wide range of plant species including Arabidopsis, tomato, rose and rice (Lifschitz et al., 2006; Tamaki et al., 2007; Hiraoka et al., 2013; Huang et al., 2013; Randoux et al., 2014; Tsuji et al., 2015; Weng et al., 2016). However, the most direct and relevant comparison with chickpea is again provided by Medicago, where MtFTa1 overexpression converts the prostrate habit of plants grown under SD to a more erect habit typical of LD (Laurie et al., 2011). This effect is clearly similar to that of the corresponding region on chromosome 3A in domesticated chickpea. In contrast, Medicago fta1 mutants show a highly branched, prostrate phenotype under LD similar to that of wild-type under SD, further emphasizing the multiple roles of FTa1. This observation strengthens the case that the major flowering time and growth habit loci in this region of chromosome 3 represent pleiotropic effects of misexpression of genes in the FT cluster, and possibly of *FTa1* in particular.

An emerging theme in long day legumes appears to be an important adaptive role for dominant genetic variants in the region of the FTa/c cluster that relax the environmental constraints on flowering and permit early flowering (Weller and Ortega, 2015). Whether a common molecular mechanism unites these adaptations and explains their repeated evolution remains to be determined. Among the ancient legume crops, chickpea in particular may represent a unique example in which modification of such a mechanism has been fundamentally important to crop success. Future, more detailed analyses should shed light on its molecular basis and physiological consequences, and its significance for chickpea domestication and adaptation.

AUTHOR CONTRIBUTIONS

JW, RO, VH, and TM conceived the study. JW and RO designed the study. RO, RM, NC-G, RP, JR, and TM carried out the experiments and/or generated the data. RO and JW wrote the manuscript with inputs from the other authors. All authors analyzed the data.

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SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: https://www.frontiersin.org/articles/10.3389/fpls.2019.00824/ full#supplementary-material

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Conflict of Interest Statement: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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cM	LG1		cM	LG2	cM	LG3		cM	LG4		dM	LG	5	cM	LC	36	dM	LG7	cM	LG8		CM LG9
0.0	0	S101p82874	0.0	O 85210954632	0.0	0	\$31605661120	0.0	0	\$34073468	0.0		S52p738001	0.0	_	S176p117949	0.0		0.0	- 0	\$1567p770552	0.0
4.8	_		29	\$521p504171	2.8		S316p5153062	0.0		S34p584702	1.6	-		6.8	-		4.5		1.4	-4-	\$1567p557414	0.0 \$2551p805085
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35.7	-10H0	S2242p178866	16.4	_\\ /{_ \$531p28509	28.6	-0117	_ \$1871p786545	4.3	_@H%	S34p2320862	4.6	-8 .	L S21580213804	23.5		\$24501117366	14.7	\$7880387538	11.0		SR28n3528738	1.4 J L \$2551p1009848
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39.6	-101	\$257p327110	20.2	S529p113809	31.4	- N 10		10.9	-/11/	L S1758p29955	4.6			24.9	- 10		14.7		16.6	-		4.3 - S2414p456056
39.6	-0118	_ C11169874p305	20.2		31.9	- N 12	_ \$687p1128013	14.7	J H I	L S1758p16798	4.6	- 10		25.4	-		14.7		17.6	-H		4.3 524140405161
39.6	-1116	_ \$832p96272	22.1	_ S3387p45149	31.9	- N U	_ \$687p1284744	20.0	-11	_ S1758p13942	4.6	50	S1838p507	25.4	-		14.7		18.5	-H		4.3 \$2414p314584
39.6	-61 10	_ S32p138643	22.1	-\H	31.9		_ S687p1401035	23.3	~	_ \$360p143189	5.3	- 10	10 - S1223p34292	25.4	-	52450308030	14.7		19.4	~#	_ S6289924769	4.3 J S2414p30b397
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54.0	-XHI		30.8		41.4		_ \$498p176803	36.1	-10 - 10	S77p2108888	25.4	-40	_ \$660p2132893	30.4	-48		36.1		40.7	-#	\$307p339784	
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55.4	-41.11		30.8		41.4	_	S545p187498	38.5	4 1 1	_ S77p1108201	26.4	- 18		30.4	-10	S311p192336	36.6		42.1	-11-	_ SZ25p891014	
55.9	-21H		30.8		41.4	-		42.8		L S108p98241	20.4	-76	S660p2743345	30.4	- 1	_ 52051054306	30.0		44.0	-++-	_ 5225095454 5225095454	
56.4	-11		30.8		41.4	-	_ \$726p499774	44.7	4110	S234p3003	20.9	- 10	S66003255022	30.4	- 12	\$131204879	37.0	A \$13480010045	45.4	-++-	S160n24650	
56.4	-24 10		30.8		41.4	-	_ \$726p52047	45.2		L C10437060p6	27.8	- 10	S660n3579281	30.4		\$999p32087	37.0	A - S13480977494	46.9		\$18630173609	
60.0	-74-18		31.4	C10464582p111	41.4	-		45.2		C10431754pE	28.3		S660p3722062	30.4		\$3724087203	38.0	AH 5134801135726		- 0		
60.0	-12-20		31.4		41.9		_ \$364p46113	45.8		L S1252p63434	32.1		S2058p9834	30.4	- 0	S177p74512	38.0					
61.4	$\neg H_{0}$	5751p144558	33.0		42.9	- 1-0		45.8	-11 0	L \$604p79243	33.1	-01	52058p232638	30.4	-		38.5		1	IG	ongth (cM)	Marker density
63.8	-1111	5751p1075392	35.4		43.4	- 18	_ C10391886013Z	45.8		L S1196p54489	34.1	-	S2058p549483	30.4		51070p275817	38.9		-		Length (CM)	Marker density
64.7	-111	5/51p1308040	36.0		43.4	-111	_ 5681p30352	45.0	- M N	L S1/41066810	35.5		_ S2058p935418	30.4	- T		38.9			_G1	74.3	0.17
65.7	-700 M	\$751p1477626	40.0	S005p/95/63	43.4		S1065n103056	45.8	<u>-</u> Ш\!	S500+067363	35.5		- S2058p1203787	31.5	- 11	S1000012100	42.5	S21970214103	I	G2	69.0	0.25
65.7		S751p1875617	42.0	S1180p169047	43.4		S419n348540	45.8	THE AT	5980p43891	38.3	- 10	S205802217321	34.4	- 10	597501251259	42.5	\$21970288132	1	02	44.0	0.20
66.2		S751p2032315	45.4	S18301217607	43.4		\$680p344566	47.2		S192058743	38.8	W	S2058p2626307	36.7		S1301p805655	42.9		1	-03	44.0	0.09
66.2	200 18	S751p2187685	48.7	S183p358031	43.4	3.0	\$3420259472	48.7		L S1619053385	39.2	- 171	_ S2058p3049890	37.6		52480p10422	43.4	S1794p50209	I	_G4	78.4	0.17
68.1	_\8_62	\$751p2344420	51.5		43.4		_ S1008p8589	52.5	-101 138	L \$431p44057	41.1	-401	S2058p3381483	38.1	_	S1096p3025150	43.9	_01 S1794p133746	I	G5	59.0	0.12
68.6		- S751p2489221	53.1		43.4	-		57.8		L S27p1966205	42.6			40.9		110 _ \$1096p1721381	44.3		1	00	64.0	0.12
69.5	-NH0	_ \$751p2790244	57.9	_/ /L \$449p182936	43.4	-		61.1	-0/ 1/0	L S1534p81112	43.6	-\$14	S2058p4206658	44.8	-100	51096p393027	46.7	-WA NA \$3200682432		00	64.8	0.20
70.0		/	62.8	J/{}\L \$449p515924	43.4	-/		65.4	-// 1\\	L \$1534p19136	47 4	-1/1	S205004061794	45.3	-30	S8260187826	50.1	THHE S9550649642	I	_G7	61.2	0.20
70.9	-VEV		67.6		43.4	-	5554p540449	68.7	-/11	L \$308p129629	49.8	- 1/ I	S121102472284	49.6	- 30	S8260212746	52.7	J// S98801408238	I	G8	47.4	0.54
70.9	-474	8751p3229883			43.4	-1	5362p1068	73.0	-101	L S308p296417	55.1	2 '	L \$1211p917524	51.9	30	S91p30971	55.6	JH L \$98802435296	-	CO	0.1	0.11
71.9	-#	5/51p339/467			43.4	78-	- 36/60/6242	11.8	~ \	_ 3699p134/20				54.3	_#	L S91p1032485	57.5	J/ C111053120227	4 1	-09	9.1	0.11
72.4	-7/11	S75103800455			43.4		S/06/15/250							56.2	-4,	L \$1012p266030	59.8		T	otal	507.2	-
72.8	-191	S75104114797			43.0		\$37505173							58.6	-/	L \$3256p572537			1	anaga	56 4	0.20
12.0	-	C oronpertiers/			43.9	700	S816n14879							62.4	~	U C 51097p216935			AV	erage	50.4	0.20

Supplementary Figure 1. High density linkage map of the chickpea interspecific population CRIL2, ICC4958 (*Cicer arietinum*) x PI489777 (*Cicer reticulatum*), which was used to select a subset of markers to contruct genetic maps with the HRM markers designed in this study (Figure S4). The high density map is based on 2956 RAD-GBS SNP markers genotyped in 107 RIL lines (von Wettberg et al. 2018). It comprised nine linkage groups, with a total map length of 507.2cM. The map length of each linkage group varied from 9.1cM (LG9) to 78.4cM (LG4) with an average of 56.36cM (Inset table). A total of 2,956 markers were mapped on all of the 9 linkage groups. The number of markers mapped on an individual linkage group varied from 86 (LG9) to 495 (LG3) with an average of 328.44 markers/LG.



Supplementary Figure 2. Boxplot illustrating the variation in flowering time obtained in different environments for RIP12 (A), RIP5/RIP8 (B) and CRIL2 (C). Note that for RIP12, the flowering values during the 2004 season are relative: the date of the first visible flower in any RIL of the population was considered as day 1 and used as reference for the rest of the population. Box edges denote the lower and upper quantiles with mean (cross) and median (line) values in the middle of the box. Numbers under the boxes correspond to mean ± standard deviation and range (minimum-maximum value). (D) Frequency distribution of flowering time variation measured in CRIL2 parents and RILs grown under long (LD) and short days (SD). Red arrows indicate the phenotypic values of the parental lines.



Supplementary Figure 3. Representation of the chickpea chromosome 3 and the region between markers TA6 and TA64, summarizing the different flowering QTL (vertical coloured bars) described to date in the region (Aryamanesh et al. 2010; Cobos et al. 2009; Mallikarjuna et al. 2017; Rehman et al. 2011; Samineni et al. 2016). Numbers on the left of the linkage group indicate physical position in bp, according to the genome assembly of cultivar CDC Frontier (ASM33114v1; Varshney et al., 2013). Interesting markers from previous reports are shown in blue and markers designed for this study are shown in green. Other interesting flowering-related genes are shown in black while the cluster of *FT* genes is highlighted in red.

LG 1	LG 2	LG 3	LG4
0 0 — — S101p82874	0 0	0.0 m (LHY	0.0 S699p321588
3 3 S101p642643	2.9 \$521p38613	0.8 S316p5661120	3.4 S308p6721
7.4 ~ S101p1155160	3.8 552 lp366 15	2.0 S316p5364679	6.6 S308p296417
8 0 S101p1168572	7.7 ——— S2283p968876	5.0 S316p4956139	9.3
13.1 ~ S101p1400372	10.8 S2283p667718	8.3 📲 S316p4859689	13.2
14.6 S101p2132390	10.0 - 52282522040	10.7 🕼 📓 S316p3874637	16.0 S1534p1913007
17.4 S101p2555175	18.0 S2203p23049	12.3 🐘 🔐 S316p3771776	20.9 / S1534p1037001
21.0 S101p5217051	20 4 S1209p257778	12.8 🐘 📓 S316p3567239	26.0 1 S27p1966205
21.0 010100211001	20.4 S1203p2577765	14.5 🐘 🎆 S316p3273173	27.5 S7355p21026
0101-5011005	23.7 = 0.007 p 0.000	16.1 S316p2511043	32 7 V S431p818339
27.5 510105614995	31.0 $<$ $< S1958n111423$	16.8 S316p2327507	35.5 $\sqrt{10}$ (\$40p845447
0000 00000000	33.1 S215n338782	18.0 S316p1589742	37.9 1 S1610p104504
33.3 5550p435913	35.0 S270p626123	19.3 S316p1178725	39.3 _// S2032p76148
37.0 S550p1402959	38.0 S58p12932	23.7 \$346p384131	40.2 S77p96279
	40 4 S905p486463	27.7 S1208p282429	44.6 S77p1658521
42.4 S1/33p/30/6	42.6 S183p1679651	20.0 S1200p100034	46.1 🔨 🖌 S77p2647267
46.6 S129p121591	45.4 S183p997009	32.3 S1871p1070719	47.7 S77p3281852
50.2 S187n682971	47.4 S183p358031	35.6 S1871p494158	51.0 🔨 📝 S405p2263690
30.2 3107 p00297 1	51.4 S137p193176	35.0 S107 10494 130	54.4 S405p1034880
55.3 S447p573411	55 5 S1186p129714	36.4 S687p402437	55.2 GIGANTEA
		36.7 S687p1003743	56.8 ELF6
60.0 S447p1498195	60.7	37.1 S687p1508322	58.5 🔨 💦 TEMb
62.9 S447p2884249	04.0 0440-545004	37.1 S687p1864511	59.0 S360p1277380
0751-74000	64.9 S449p515924	38 0 CP450	63.6 S1758p608913
67.9 S751p71909	69 5 S449p906646	38 3 ABI5	64.7 PHYA1
72 4 S751p1386566	72 2 S449p1216553	38.5 WUS11 / CDE2d	67.9 S1758p2397602
76.7 S751p2465070	12.2 • • • • • • • • • • • • • • •		71.5 S1758p3016775
70.1 S751p2405070		39.5 ETa1 / NAC100	75.5 S1978p846797
80.7 S751p3569871	LG 6a	30 0 SUIVH4	77.9 S34p2504710
82.8 S751p4286627	0.0 🔨 🛛 🖉 \$565p861121		80.4 - 🔶 S34p1056032
82.8 S751p4200027	0.8 S565p34052	40.0 S28p689334	83.8 - C S34p73468
	3.6 S1097p332078	41.0 SOC1a	
	5.3 S3256p867093	44.1 Scarecrow	
	7.5 S3256p14447	45.1 S28n2932809	
	10.0	46.5 Reptor1	
	11.7 S91p30971	47.4 S714p1327693	
	15.6 S826p761274	50 3 S1202n50545	
	17.9 S826p2714322	50.5 01202p00040	
	19.1 🔨 📄 S1096p715287		
LG 5	24.0 S1096p1969439	LG 7	LG 8
0 0 S52p738001	27.1 S2480p10422	0.0 \carrow C\$175p907087	0.0 c \$1567p770552
3 3 S19p9163	29.8 S976p1251259	6 7 _/ S51p169953	4.1 S1567p247026
5 1 S188p2049560	32.4 S574p9146	7.3 V S51p325307	4.1 S1507p247020
7 2 S188p53345	32.6 S23p627713	17 2 1 S285p98215	8.1 S2046p290232
10.5 S1301p114351	34.2 S1692p26236	18.2 S155p29304	0.1 S2040p30010
	36.4 // S245p598468	18 4 S1866p32734	14.0
16.1 S149p2278159	37.5 ///	19.9 S1124p1059119	18.2 S828p1635634
18.2 S1596p1045628	38.8 /// \\\\ \$1030p18653	22 7 X S744p89991	21.2
20.5 S660p191499	41.0 // S1280p286165	25.0 S744p1554378	21.3
23.2 \$660p916417	43.9 ^{-/} /\ ^L S248p665638	26.9 W S1642p788581	23.2
25.2 S660p2192496	49.2 ⁻⁷ / S248p246648	28.6 W/r S846p324428	27.5
29.5 S660p3/22062	53.1 S2255p362775	32.0 S846p1551131	31.5 S21p59408
31.5 S660p3873897	56.8 //\ S2255p617671	34.9 _// \$1624p622346	40.1
35.5 S2058p413307	57.9 ^{-/} S1028p430704	37.6 _/r S1624p299304	40.1 S26p43752
39.1 S2058p1727283	61.8 ⁻⁷ S176p117949	40.3 _/r \$1348p320085	40.5 41.4
42.2 S2058p2990262		42.9 \\-// \$1348p1325591	41.4
45.0 S2058p3537460	LG 6b	44.0 S3041p336960	42.9
45.7 S2058p3973981	0.0 \ f S2414p1088784	47.1 S2197p288132	45.3 S225p031014
48.4 S2058p4838469	0.5 \/ // S2414p1017084	49.0 \\/ S1794p242596	48 1 S169n24659
51.1 S1211p2611133	2.1 \ S2414p940360	50.8 S320p551481	49.3 S1863n252782
53.5 / S1211p2033994	2.7 S2414p892775	52.8 S320p1357911	-0.0 01000p202702
57.3 S1211p1204220	4.3 - S2414p677622	54.5 S988p812430	
60.2 S1211p795441	5.3 S2414p595966	57.3 S988p1408238	
63.1 - S1211p217054	6.4 //=/` S2414p374580	58.4 S988p1688332	
	7.5 /// S2414p171019	60.6 🔨 🗌 🗅 S988p2589475	
	9.3 // \` S2551p1009848	63.9 S988p4117900	
	10.3 ^J \S2551p852572	64.9 ///\`S6319p211896	
	S2551p776546	66.6 ⁷ S1117p156134	

Supplementary Figure 4. Genetic linkage map constructed for CRIL2 (ICC4958 x PI489777). Numbers on the left of each linkage group represent the absolute distances in cM. The map comprises a total of 226 markers, grouped in 9 linkage groups covering a total distance of 540 cM, with an average intermaker distance of 2.4 cM.



Supplementary Figure 5. Genetic linkage map constructed for RIP12 (ICCL81001 x Cr5-9). Numbers on the left of each linkage group represent the absolute distances in cM. The map comprises a total of 155 markers, grouped in 9 linkage groups covering a total distance of 154.5 cM, with an average intermaker distance of 1.05 cM.



Supplementary Figure 6. Genetic linkage map constructed for RIP5 (WR315 x ILC3279). Numbers on the left of each linkage group represent the absolute distances in cM. The map comprises a total of 64 markers, grouped in 7 linkage groups covering a total distance of 87.3 cM, with an average inter-maker distance of 1.53 cM.



Supplementary Figure 7. Genetic linkage map constructed for RIP8 (ILC3279 x WR315). Numbers on the left of each linkage group represent the absolute distances in cM. The map comprises a total of 95 markers, grouped in 10 linkage groups covering a total distance of 142.7 cM, with an average intermaker distance of 1.76 cM.



Supplementary Figure 8. (A) Maximum parsimony tree derived from the alignment of phosphatidylethanolamine-binding proteins (PEBP) in *Arabidopsis thaliana* (At, blue), *Cicer arietinum* (Ca, red), *Glycine max* (Gm, green), *Pisum sativum* (Ps, purple) and *Medicago truncatula* (Mt, orange). Accession number of the PEBP genes can be found in Supplementary Table 4. Sequences were aligned with MAFFT (full alignment can be found in Supplementary Figure 9) and the tree was build using PAUP* in Geneious 8 software. Numbers beside branches represent bootstrap support from 1000 replications. (B) In next page; Position of the PEBP genes (in red) in the chickpea reference genome. Bars represent chromosomes, with numbers indicated on top. *BFT* and *TFL1c1* are not included as they were located in an unplaced scaffold (NW_004516558.1 and NW_004516523.1, respectively).



Supplementary Figure 8 B.

Supplementary Figure 9. Multiple sequence alignment of the PEBP sequences from five species described in Supplementary Table 1. Proteins were aligned in Geneious 8 using MAFFT. Residues conserved in more than 80% of the sites are presented with black background/while letters. Those with a conservation between 60-80% show grey background/white letters and those between 40-60% with grey background/black letters.

	*	20	*	40	*	60	*	80	
AtMFT :		MAA-SV-DP	LVVGRVIGDV	I – DMFIPTAN	MSVYF-GPKH	ITNGCEI-	K <mark>PS</mark> TAVNP <mark>PKV</mark> I	JISC	: 57
MtMFT :		MAA-SV-D <mark>P</mark>	LVVGRVIGDV	V-DMFIPSVG	MSVYF-GPKH	VTNGCDI-	K <mark>PS</mark> MAINPPKV	FLTG	: 57
PsMFT :		MMS-SA-D P	LVVGRVIGDV	V-DMFIPSVA	MSVYF-GPKH	VTNGCDI-	KPSIAINQPRI	ΓLTG	: 57
CaMFT :		MMAA-SV-DP	LVVGRVIGDV	V-DMFIPSVG	MSVYF-GPKH	VTNGCDI-	KPSIAINPPRV	ΓLTG	: 58
GmMFTa :	MRYLSLSTFSLLCIT	FVVMAA-SV-DP	LVVGRVIGDV	V-DMFIPSVNI	MSVYF-GSKH	VTNGCDI-	KPSIAISPPKL	ΓLTG	: 75
GMMFTD :		MAA-SG-DP	LLVGRVIGDV	V-DMET PSE'NI	MFWYB				: 31
		_							
AtBFT :		MSR-EI-E <mark>P</mark>	LIVGRVIGDV	I-EMFNPSVT	MRVIENSNTI	VSNGHEL-	APSLLLSKPRVE	IGG	: 58
MtBFT :		MSR-PL-EP	LSVGRVIGEV	V-DIFNPSVRM	MNVIY-STKO	VANCHEL-	MPSIVMNKPRVI	DIGG	: 57
PSBFT :		MSR-QL-EP	LSVGGVIGEV	V-DIFNPSVKI V DIFNPSVKI	MNVTY-STKO	VANGHEL-	MPSIVINKPRVI		: 5/
CaBFT :		MCD IMEOR	LSMGRVIGEV	V-DIFNPSVRI V DIFCPSVRI	MNVTY-STKO MNVTY STKO	VANGHEL-		SIGG	: 5/
GMBFIA :		MSR-LMEQE	LVVGRVIGEV	V-DIFSPSVKI	MNVTI-SINO MNVTV-STKO	VANGHEL-	MPSIIMARPRVI	TCC	· 57
GMDIID .		HOIC DIT D						1100	• • • •
									5.0
AtTSF :		MSLS-RR-DP	LVVGSVVGDV	L-DPFTRLVS.	LKV Y-GHRE	VTNGLDL-	RPSQVLNKPIVE	SIGG	: 58
Mt FT 1		MSIN-IR-DP		L-DPENRSITI T-DSEENSTD	LAVII-GORI IDVIV-CNDD	VINGLDL-	KPSQVQNAPRVI		: 38 • 59
Dermal :		MAGS-SR-NP	LAVGRVIGDV	I-DSFENSIP	LRVII-GNRD	VNNGCEL-	KPSQIGNQPKV3		. 50
CaFTal :		MAGS-SR-NP		I-DPFENSVP I-DNFFNSTP	LRVII-GSKD IRVIV-CNRI	VNNGCEL-	KPSOVANOPRA		· 58
MtFTa2		MASG-SRPNP		T-DPFESTIP	LIVIY-GNRT	VTNGGEL-	KPSOVANOPOW	TGV	· 59
PsFTa2		MACS-SR-NP	LVVGRVIGDT	L-DPFESSTPI	LOT Y-GNRN	VSNGCEL-	KPSOVANOPOVS	STGG	: 58
CaFTa2 :		MASG-SR-NP	LVVGRVIGDV	L-DPFESSIRI	LLI IY-GNRN	VNNGCEL-	KPSOVAKOPOVS	SIGG	: 58
GmFTa1/2a :		MPGG-SR-NP	LVVGRVIGEV	I-DPFEISIP	FRVTY-GNRE	VGNGCEL-	KPSQVANQPRVS	SVGG	: 58
GmFTa1/2b :		MPSG-SR-N <mark>P</mark>	LVVGRVIGEV	I-DPFESSIP	FR <mark>VTY-GNK</mark> E	VGNGCEL-	KPSQVPNQPRVS	BIGG	: 58
GmFT-like :			-EEED <mark>LIE</mark> DV	lid dcnnf v g	LKVTY-GSTQ	VTNRCRL-	TSDQTNDRPIVE	EIRG	: 50
MtFTa3 :		MSGS-SR-D <mark>P</mark>	lvvg <mark>g</mark> vigdv	L-VPFQSSIP	IRVSY-NGKE	LNNGCEF-	KPSQVVNQPRVS	SVGG	: 58
CaFTa3 :]	MPSGST-SR-DP	LVVG <mark>G</mark> VIGDV	L-DLFQTSIP	IRVIY-NGKD	VTNGCEF-	KPSQVVNQPRVS	SVGG	: 60
GmFTa3a :		MPSG-SR-DP	LVVGGVIGDV	L-DPFEYSIPN	MRVIY-NNRD	VSNGCEF-	KPSQVVNQPRVI	VIGG	: 58
GmFTa3D :		MPRG-SR-DP	LVVGRVIGDV	L-DPFECSIPI	MRVIY-NNKD	VSNGCEF-	KPSQVVNQPRI	JIGG	: 58
GMFTa3C : GmFTa3d :		MPRG-SRP	LVVGRVIGDV		MRVIII-NNKD	VSNGCEF-	RPSQVVNQPR1	ULGG	: 38 · _
MtFTc .		MPON-LV-P		T-SPETNSVS	SALT-NNRD	TSNGCTV-	KPSOLVNBPRV	JWGG	• 55
PSFTC :		MPRN-MV-DP	HVVRSVTDDV	I-NPETNSVS	LSVVI-NNKP	TSNGCLI -	KPSOLVNRPRVS	SVGG	: 58
CaFTc :]	MPRNNG-GV-DP	LVVGGVIGDV	L-NPFTNSVS	LSVVT-NNKE	ISNGCVL-	KPSOVVNRPRAS	SVGG	: 60
GmFTc1 :		A-RE-NP	LVIG <mark>G</mark> VIGDV	L-NPFTISVS	FT I SI-NNRA	ISNGLEL-	RPSQVVNRPRV	rvgg	: 55
MtFTb1 :		M-NP	LVVCGVIGDV	L-DPFTNSVS	LRVVYENNKE	VS <mark>N</mark> SGEL-	KPSQIVNPPRV(2 <mark>VG</mark> G	: 54
PsFTb1 :		MRMK-SS-N <mark>P</mark>	LVVGNVIGDV	I-DPFINSVS	lrvvyennke	VINSGEL-	KPSQIVNPPRV	2VGG	: 59
MtFTb2 :		MRIK-ST-NP	lvvggvigev	L-DPFTSSVSI	lrvvydnnke	VINSGEL-	KPSQIINSPRV(2VGG	: 59
PsFTb2 :		MRMK-SS-NP	LVVG <mark>N</mark> VIGDV	l-dpfinsvs	LRVVYENNKD	VINSGEL-	KPSQIVNPPRV	2VGG	: 59
CaFTb :		MRSKITM-NP	LVVGRVIGDV	L-DNFTDSVSI	LRVIYDNNKD	VINSGEL-	KPSQIVNPPRVQ	2VGG	: 60
GMFTD1 :				EPEASSIP		VINSGEL-	RPSQIINPPRVE	svGG	: 38 . 15
GmrTb3				T-EPETSSVS		VINCCET -	KPSKTLNBPRT	TGG	• 58
GmFTb4 ·		M-DP	LVIGRVVGDV	L-EPFTSCVS	LBILYDSCSP	VINCCEL-	KPFOTINOPRVE	EVGG	• 54
GmFTb5 :		MPI-SM-DP	LVLGRIIGDI	L-DPFTSSVSI	LRVVYNNQSS	VINSCEF-	KPSQIVNKPRI	VIRG	: 58
At.CEN .		MART-SS-	MVGRVTGDV	V-DNCLOAVK	MTVTYNSDKO	VYNCHET -	FPSVVTYKPKVF	WHC	59
AtTFL1	M	ENMGTR-VI-EP	LIMGRVVGDV	L-DFFTPTTK	MNVSY-NKKO	VSNGHEL-	FPSSVSSKPRV	EIHG	: 61
MtTFL1a		MARM-SO-EP	LIVGRVIGEV	L-DSFTTSMK	MTVSY-NKKO	VFNGHEF-	FPSTINTKPKV	IDG	: 58
PsTFL1a :		MARM-AQ-E	LIVGRVIGEV	I-DSFTTSMK	MTVSY-NKKO	VFNGHEF-	FPSTINTKPKV	IDG	: 58
CaTFL1a :		MARM-SQ-E <mark>P</mark>	LLVGRVIGEV	l-dsftt <mark>sm</mark> ki	MTVSY-NKKO	VFNGHEF-	FPSTINIKPKV	IDG	: 58
GmTFL1a1 :		MARM-PL-E <mark>P</mark>	LIVGRVIG <mark>E</mark> V	L-DSFTTSTK	MIVSY-NKNQ	VYNGHEL-	FPSTVNTKPKV	EIEG	: 58
GmTFL1a2 :		MAKM-PL-E <mark>P</mark>	LIVGRVIGEV	L-DSFTTSTK	MTVSY-NKKO	VYNGHEL-	FPSTVNTKPKV	BIEG	: 58
MtTFL1b :		MSI-VT-DP	LAIGRVIGDV	V-DYFTSTMK	MSVIY-NTKO	VYNGHEF-	FPSSVTTKPKV	2IHG	: 57
PSTFL1b :		MSI-IT-DP	LVIGRVIGDI	V-DDFTTIMKN	MSVIY-NTKO	VYNCHDF-	FPSSLTTKPKV(21 HG 1 TU G	: 57
Contraint :		$PHPIN \perp V V = LA = DP$	LAIGKAAGDA		DRCSCOTION	CENUCIE	COVEON VIUMO	TURC	. 40
GmTFL1b2		MNMT - 99-	VIGRVICDV			VYNCHEF-	FISSTTKE	EFFL	. 40 . 58
MtTFL1c ·		MGSI-TS-DP	ITLGRVIGDV	Т-рүртртткі	MTVTY-NNKE	TFNCYDP-	FPSSVTTKPPTF	TGG	. 58
PsTFL1c :		M-NS-DP	LILGRVIGDV	I-DYFTASTK	MSVIY-NNKD	IFTGYEVP	FPSTVKTKPRT	DIOG	: 56
CaTFL1c1 :		MGSI-SL-DP	LVLGKVIGDV	I-DNFTPSIK	MIVTY-NNKE	IFNGYEP-	FPSTVSTRPRV	IQG	: 58
CaTFL1c2 :		MGSI-SL-E <mark>P</mark>	LVLGKVIGDV	I-DNFTPSIK	MIVTY-NNKE	IFNGYEP-	FPSTVSTRPRV	IQG	: 58
CaTFL1c3 :							MFFNR	ISW	: 9
GmTFL1c1 :		MARM-ST-D <mark>P</mark>	LIIGRVIGDV	I-GSFTPTIK	MTVTY-NKKQ	VYNGYEF-	FPSTITTRPRV	IGG	: 58
GmTFL1c2 :		MAKM-WT-DP	LFIGRVIGDV	U-DSFTPTIK	MTVTYKKQ	VYNCHDF-	FPSTITTRPKV	BIGG	: 57

		* 100	*	120	* 140	* 160	
AtMFT	: -HSDELYTL	VMTDPDAPSPSEPNM	REWVHWIVVD	IP <mark>GG</mark>	TNPSRGKEILPYM	PRPPVGIHRYILVLFR :	: 124
MtMFT	: -NMDNLYTL	VMTDPDAPSPSEPSM	RELIHWIVVD	IP <mark>GG</mark>	TNPKRGKEILPYI	GPKPPVGIHRYILVLFE :	: 124
PsMFT	: -NRSSLYTL	VMTDPDAPSPSEPSL	REFIHWIVVD	IP <mark>GG</mark>	TNPKRGHEILPYI	GPKPPVGIHRFILVLFE :	: 124
CaMFT	: -NIDNLYTL	VMTDPDAPSPSEPSM	RELIHWIVVD	IP <mark>GG</mark>	TNPKRGKEILPYI	GPKPPVGIHRFILVLFK :	: 125
GmMFTa	: -NMDNLYTL	VMTDPDAPSPSEPSM	REWIHWILVD	IP <mark>GG</mark>	TNPFRGKEIVSYV	GPRPPIGIHRYIFVLFQ :	: 142
GmMFTb	:	GPSEPSM	REWIHWIVVD	LEEQTHFVF	hdvacm <mark>s</mark> tggsrk eiv pylo	GPRPPIGIHRYIFLLFQ :	: 94
AtBFT	: QDLRSFFTL	IMMDPDAPSPSNPYM	re <mark>y</mark> lhwmvtd	IPGT	TDASFGREIVRYE	IPKPVA <mark>GIHR</mark> YVFALFK	: 126
MtBFT	: EDMRSAYT-	IMTDPDAPSPSDPHL	rehlhwmvtd	IPGT	TDVSFGNEIVEYE	NPKPVIGIHRYVFILFK :	: 124
PsBFT	: DDMRSAYTL	VMTDPDAPSPSDPYL	rehlhwmvad	IPGT	TDVSFGKEIVEYE	NPKPVIGIHRYVFILFK :	: 125
CaBFT	: DDLRTAYTL	IMTDPDAPSPSDPYL	REHLHWMVTD	IPGT	TDVSFGKEIVEYE	NPKPVIGIHRYVFILFK :	: 125
GmBFTa	: DDMRTAYTL	IMTDPDAPSPSDPHL	REHLHWTVTD	IPGT	TDVSFGKEIVGYE	SPKPVIGIHRYVFILFK :	: 126
GmBFTb	: DDMRTAYTL	IMTDPDAPSPSDPCL	re <mark>h</mark> lhwmvtd	IPGT	TDVSFGKEIVGYE	SPKPVIGIHRIVFILFK	: 125
AtTSF	• DDFRNFYTT	VMVDPDVPSPSNPHO	REYLHWLVTD		TGNAFCNEVWCYE	SPRPPSGTHRTWLWTER	• 126
A+FT	• EDLENFYTI	VMVDPDVPSPSNPHL	REYLHWLVTD	ТРАТ	TGT FGNETVCYE	VESPTAGTHEVVETLER	· 126
Mt FTal	NDL RNLYTT.	VMVDPDSPSPSNPTF	KEYLHWLVTD			RPR PTSGTHREVEVLER	· 126
PsFTa1	NDLENTYTI.	VIVDPDSPSPSNPTF	REYLHWLVTD	ТРАТ	TEVSFGNETVSYE	RPRPTSGTHREVETLER	: 126
CaFTa1	NDMENEYTI.	VIVDPDSPSPSNPTF	REYLHWLVTD	ТРАТ	TGVSEGNEVVGYE	RPRPTSGIHREVEVLER	· 126
Mt.FTa2	NDPTALYTI	VIVDPDAPSPSYPSF	REYLHWMVTD	ТРАТ	NAASEGNEVVSYE	KPRPNI GTHRFVFVLLH	: 127
PsFTa2	NDPVIYTI	VIVDPDAPSPSYPSF	REYLHWMVTD	ТРАТ	TGASEGNEVVSYE	KPRPNI GTHRFVFVLLR	126
CaFTa2	NDL.RIFYTI.	VIVDPDAPSPSNPSF	REYLHWIVTD	TPST	AGASEGNEVVCYE	KPRPNI GTHRYVFVI FR	: 126
GmFTa1/2a	DDLRNFYTM	VLVDPDAPSPSNPNF	REYLHWLVTD	IPET	TGPNFGNEVVSYE	SPRPTMGIHRLVFVLFR	: 126
GmFTa1/2b	DDLRKFYTM	VMVDPDAPSPSNPNF	REYLHWLVTD	IPET	TGPNFGNEIVSYE	SPRPTMGIHRFVFVLFR	: 126
GmFT-like	: -DANSFYTL	VMVDPDSPSRDKPTE	REHLLCOYSS:	RGSNLRY	VLTOFFFGEEVVPYE	SPEPHRWIHRIVFVLFR :	: 122
MtFTa3	: DDLRNFYTL	IMVDPDAPSPSNPNL	REYLHWLVTD	IPAT	TGPTFGHEVVPYE	SPRPSMGIHRIVFVIFR :	: 126
CaFTa3	: DDLRNFYTL	IMVDPDAPSPSNPNL	re <mark>y</mark> lhwlvtd	IPAT	TGPTFGNEVVTYE	NPRPFMGIHRIIFVVFQ :	: 128
GmFTa3a	: DDLRNFYTL	IAVDPDAPSPSDPNL	re <mark>y</mark> lhwlvtd	IPAT	TGASFGHEVVTYE	SPRPMMGIHRLVFVLFR :	: 126
GmFTa3b	: DDFRNFYTL	IAVDPDAPSPSDPNF	re <mark>y</mark> lhwlvtd	IPAT	TGPTFGHEVVTYE	NPRPMMGIHRIVFVLFR :	: 126
GmFTa3c	: DDFRNFYTL	IAVDPDAPSPSDPNF	re <mark>y</mark> lhwlvtd	IPAT	TGPTFGHEVVTYE	NPRPMMGIHRIVFVLFR :	: 126
GmFTa3d	:			<u> </u>		MMGIHRLVFVLFR :	: 13
MtFTc	: DDLRTFYTM	WMVDADAPSPSNPFL	KEYLHWMVTD	IPAT	TSASFGKEVVFYE	SPKPSAGIHREVIALEK :	: 123
PsFTc	: EDLRTFYTL	AMVDADAPSPSNAFL	REYLHWMVTD	IPAT	TSASFGKEAVFYE	SPKPSAGIHR VIVLFK :	: 126
CaFTc	: EDLRTFYTL	VMVDADAPSPSNPVL	REYLHLMVTD	1 PAT	TSANEGKEVVFYE	SENPSAGIHRLVIVLEK :	: 128
GmFTC1	: EDLRIFYTL	VMVDADAPSPSNPVL	REYLHWMVTD	IPAT	TNASFGREVVFYE	SPNPSAGIHRLVFILFQ :	: 123
MCFTD1	: NDLRTLYTL	VMVDPDGPSPSNPNM	REYLHWMVTN	IPAT		NPRPTSGIHRVIFVLFR :	: 122
PSFIDI M+FTb2	NDERILITL			ТРАП			: 127
MCF1D2 DeFTb2	· NDERTLYTI						• 127
CaFTb	• NDERTLYTI				TGTAFGOEIVSTE	VPRPTSCIHRWIFVIER	• 127
GmFTb1	· DDLRTLYTI	VMVDPDAPSPSDPNM	REYLHWLVTN	ТРАТ	TSASEGOEVVSYE	SPRPTSGIHRETFVLFR	· 126
GmFTb2	:			R	TVILIGOEVVSYE	SLOPTSGTHO	: 39
GmFTb3	DDLRTFYTL	VMVDPDAPSPGNPTO	REYLHWLITN	TPAT	TGANFGEEIVSYE	SPRPIVGIHRIVFVLFR	: 126
GmFTb4	DDFRTFYTL	VMVDPDAPSPGNPNO	REYLHWLVTN	IPGT	TGANFGEEVVSYE	SPRPMMGIHRIIFILFR	: 122
GmFTb5	: NDLGIFYTL	IMVNPDAPSPSDPHM	ke <mark>y</mark> lhwlvtn	IPAS	TGATTGEEIVEYE	SPRPTSGIHRIAFVLFR :	: 126
AtCEN	: GDMRSFETL	VMTDPDVPGPSDPYL	REHLHWIVTD	IPGT	TDVSFGKEIIGYE	PRPNIGIHR VYLLFK	: 127
AtTFL1	: GDLRSFFTL	VMIDPDVPGPSDPFL	KEHLHWIVTN	IPGI	IDALEGKEVVSYE	LPRPSIGIHR VFVLFR	: 129
MtTFLIa	: GDMRSFYTL	VMTDPDVPGPSDPYL	REHLHWIVTD	IPGT	TDATFGREVVSYE	LPKPNIGIHRFVFVLFK	: 126
PSTFLIa Commite	: ADMRSFYTL	VMTDPDVPGPSDPYL	REHLHWIVTD		TDATEGREIVSYE	I PKPN GIHRFVFVLFK	: 126 • 126
Calfila CmTFI 1 a 1	CDMRSFIL	TMTDDDVPGPSDPIL	REALAWIVID			IPRPN GIRR VEVLER	120
GmTFL1a2	· GDMRSFFTL		RETITINATION		TDATECKELVSTE	7 DK DNI GI HREVEVI EK	· 120
MtTFL1b	GDMRSFFTL	VMTDPDVPGPSDPYL	KEHLHWIVTD		TDA TECKEVMKYEI	MPR PNIGIHREVELLYK	· 125
PsTFL1b	GDMRSFETT	IMTDPDVPGPSDPVL	KEHLHWIVTD	IPGT	TDATEGKEVMKYE	PRPOIGTHEVELLYK	125
CaTFL1b	: GDMRSFETT	IMTDPDVPGPSDPYL	KEHLHWIVTD	IPGT	TDATEGKEVIKYE	PRPNIGIHREVETLYK	: 129
GmTFL1b1	: SDMRSFFTL	VMTDPDVPGPSDPYL	REHLHWLVTD	IPGT	TDATFGNEVVEYE	IPRPNIGIHRFVFLVFK	: 108
GmTFL1b2	: GDMRSFETL	VMTDPDVPGPSDPYL	REHLHWMVTD	IPGT	TDATFGNEVVEYE	ILRPNIGIHRFVFLVFK	: 126
MtTFL1c	: VDMRSLETL	IMIDPDVPGPSDPYM	KE <mark>H</mark> LHWMVTD	IPGT	TDSTFGKELTSYE	KPKPNIGIHRYVFVLFK	: 126
PsTFL1c	: GDMRSLFTL	IMIDPDVPGPSDPYM	KE <mark>HLHWMVTD</mark>	IPGT	TDSIFGKELTSYE	KPKPNIGIHRYVFVLFK	: 124
CaTFL1c1	: GDMRSLETL	IMIDPDVPGPSDPYM	RE <mark>HLHWMVT</mark> D	IPGT	TDSIFGKELTSYE	IPKPNIGIHRYVFVLFK :	: 126
CaTFL1c2	: GDMRSLFTL	IMIDPDVPGPSDPYM	REHLHWMVTD	IPGT	TDSTFGKELTSYE	IPKPNIGIHRYVFVLFK :	: 126
CaTFL1c3	: NFLFIFELQ	IMIDPDVPGPSDPYM	REHLHWMVTD	IPGT	TDSIFGKELTSYE	IPKPNIGIHRYVFVLFK	: 77
GmTFL1c1	: GDMRSFYTL	IMTDPDVPGPSDPYL	REHLHWMVTD	IPGT	TNASFGKVLVSYE	PNPNIGIHRYVFVLLK	: 126
GmTFL1c2	: GDMRSFYTL	IMTDPDVPGPSDPYL	REHLHWMVTD	11.2G11	INASFGNVLVSYE	MPKPNIGIHRYVFVLFK	: 125

Supplementary Figure 9. Continued

				*	180	1	*		200		*			
A+MFT		ONS	PVG	MVOO	PPSRANE		FACHE	T.GI.PVA	TVYFN	AOKE	PASER	R		173
M+MFT	:	OKC	PTC	-VFO	DTSDVSF				TUVEN	SOKE	DUTKE	P	:	172
DoMET	2		DIC	VEE							DOCKD	D	2	172
COMET	÷	OKG	PIG	VEC						OVE	PQSKK		÷	172
CaMETO	:	OKG	DIC	VEQ						COVE	DAVED		:	100
GIIMFIA	÷	OKG	PLG	VEQ	DDDDAC					COVE	PAVER		÷	142
GIIMETO	:	Qrv	PLG	-veq	PTRASE	-NTR)	вvrql	JLGLPVA	VIEN	SQRE	PAAKR	R	:	142
A+BFT		ORG	BOAM	-KAA	DETRECT		BSSYE		VYFN	AORE		BPSY-		177
M+BFT	:	PC	-RO V	PS	PSSRDNE		N S F NN		VYFN	AORE	TAAPP	P	:	171
DeBFT	:	PC		PA	PNSRDO	STRI		ILCI DVA	VYFN	AORE	AAPP	R	:	172
CORT	:	ORG-		LA	DTEDDNE				VIEN	AQRE			:	172
CmBFT=	:	PC		P D	PSSRDHE	INTRE		LOLL VA	VIIIN	AORE	AAPP	R	:	173
GmBFTh	:	ORG		RP	PSSRDH	-NTRE	RESERVO	LGLPVA	VYFN	AORE	TAARR	R	:	172
OMDI ID	·	eno	- ¥ - 1	1(1						11 <u>Q</u> 101	- 1111111		•	1/2
AtTSF	:	QLG	RQTV	YA	PGWRQQE	-NTRE	FAEIYN	ILGLPVA	ASYFN	CORE	NGCGG	RRT	:	175
AtFT	:	QLG	ROTV	YA	PGWRQNE	-NTRE	FAEIYN	ILGLPVA	VFYN	CORE	SGCGG	RRL	:	175
MtFTa1	:	ogc	RORV	YA	PGWRQNE	-NTRE	FAELYN	ILGSPVA	AVFFN	CORE	SGSGG	RTFR-	:	176
PsFTa1	:	QQC	RORV	YA	PGWRQNE	-NTRE	FAELYN	ILGSPVA	VFFN	CORE	SGSGG	RTFR-	:	176
CaFTa1	:	QQC	RQRV	YA	PGWRQNE	-NTRE	FAELYN	ILGLPVA	VFFN	CQRE	SGSGG	RTFR-	:	176
MtFTa2	:	QQC	RQRV	YA	PGWRQNE	-NTRE	EFIEFYN	ILGSPVA	AVFFN	CQRE	IGSGG	RTFR-	:	177
PsFTa2	:	QQC	RQIV	YA	PGWRQNE	-NTRE	FVELYN	ILELPVA	VFFN	CQRE	AGSGG	RTFR-	:	176
CaFTa2	:	QQC	-QQV <mark>V</mark>	FA	PGWRQNE	-NTRE	FAELYI	DLELPVA	AVFFN	CQRE	IGSGG	RTFR-	:	176
GmFTa1/2a	:	QQF	RQRV	YA	PGWRQNF	-NTRE	FAELYN	ILGLPVA	AVFFN	CQRE	SGSGG	RTF	:	175
GmFTa1/2b	:	QQF	RQRV	YA	PGWRQNE	-NTRE	FAELYN	ILGLPVA	AVFFN	CQRE	IGSGG	RTF	:	175
GmFT-like	:	MKS	GRIV	KA	PEKRTNF	-NTTE	FAAKYF	L-QDVA	GVFFN	SRRR	G		:	163
MtFTa3	:	QLG	RETV	YA	PGWRQNF	-NTRE	FAELYN	ILGLPVA	AYFN	IQRE	HGSGG	RRL	:	175
CaFTa3	:	QLG	RETV	YA	PGWRQNE	-NTRE	FAELYN	ILGLPVS	SVYYN	IQRE	AGSGG	RRLC-	:	178
GmFTa3a	:	QLG	RETV	YA	PGWRQNE	-NTKE	FAELYN	ILGLPVA	AVYFN	IQRE	SGSGG	RRLY-	:	176
GmFTa3b	:	QQG	RETV	YA	PGWRQNF	-ITRE	FAELYN	ILGLPVA	AVYFN	IQRE	SGCGG	RRLC-	:	176
GmFTa3c	:	QQG	RETV	YA	PGWRQNF	-ITRE	FAELYN	ILGLPVA	AVYFN	IQRE	SGCGG	RRL	:	175
GmFTa3d	:	QLG	RETV	YA	PGWRQNF	-NTRE	FAELYN	ILGLPVA	AVYFN	IQRE	SGSGG	RRLYH	:	64
MtFTc	:	QLG	RDTV	FA	PDWRHNE	-NTTN	JFAEINN	ILV-IVA	SVYFN	CQRE	RGCGG	RRC	:	171
PsFTc	:	QLG	RDTV	FA	PEWRHNE	-NTRN	JFAE I NN	ILV-I <mark>V</mark> G:	SVYFN	CQRE	RGCGG	RRC	:	174
CaFTc	:	QLG	RDTV	FA	PEWRHNF	-KTRN	JFAEINN	ILV-IVA	SVYFN	CQRE	RGCGG	RRS	:	176
GmFTc1	:	QLG	RDTV	IT	PEWRHNF	-NSRN	JFAEINN	ILA-PVA	AYAN	CQRE	RGCGG	RRY	:	171
MtFTb1	:	QPC	RHTV	LA	PGWRQNF	-ITRI	FAEFYN	ILGLPVA	ALYFN	CQRE	NGSGG	RRLII	:	173
PsFTb1	:	QPC	RHTI	LP	PGWRQNE	-IIRI	DEAEIYN	ILGSPVA	ALYFN	CQRQ	NGSGG	RRMII	:	178
MtFTb2	:	QPC	RHTV	LA	PGWRQNF	-ITRI	FAEFYN	ILGLPVA	ALYFN	CQRE	NGSGG	RRMVI	:	178
PsFTb2	:	QPC	RHTI	LP	PGWRQNF	-ITRI	DFAEVYN	ILGSPVA	ALYFN	CQRE	NGSGG	RRMIT	:	178
CaFTb	:	QPC	RHTI	la	PGWRQNF	-VTRI	DFAEVYN	ILGLPVA	ALYFN	VQRE	IGSGG	RRMII	:	179
GmFTb1	:	QPR	RMSI	PA	PGWRQNE	-ITRI	DFAEYYN	ILGLPVA	AVYFN	CQRQ	GGSGG	RRLML	:	177
GmFTb2	:		ENVF	TS	SGWRQNY	IMTRI	DFAYN	ILGLPVA	AVYFN	CQRQ	GGSGE	RRLML	:	86
GmFTb3	:	QLR	-RL II	QP	PGWRQNE	'-NTRI	DEADIYN	ILGLPVA	AMYFN	CKRE	NDQSS	GRRR-	:	176
GmFTb4	:	QSG	RQII	YA	PGWRQNE	-NTRI	DESEVYN	ILGLPVA	ATYFN	CKRQ	NNSAR	DGRRT	:	173
GmFTb5	:	QFD	RQIV	HA	PRWRQNE	-NTRI	DEAEVYN	ILGSPVA	AVYFN	CQRE	GGWGG	RRR	:	175
AtCEN		OTR	RGSM	-vsv	PSYRDO	-NTRE	FAHENT	J.GI.PVA	AVFFN	CORE	AARR	R		175
AtTFL1	:	OKO	BRVT	-FPN	TPSRDH	-NTRF	FAVEY	LGI PVA	AVFFN	AORE	TAARK	R	:	177
MtTFL1a	:	OKN	RESV	-TAS	PSSRDY	-NTRN	JFASON	LGI PVA	AVYFN	AORE	TAARR	R	:	174
PsTFL1a		ORA	-RDSV	-RAT	PSSRDHE	-NTRS	FASON	DI GI PVA	VYFN	AORE	TAARR	R		174
CaTFL1a	:	oks	RESV	-MTT	PSSRDHE	-NTRN	JFASON	DLGLPVA	AVYFN	AORE	TAARR	R		174
GmTFL1a1		ŐKR	BOCM	TP	PTSRDHE	-NTRF	FAAEN		AVYFN	AORE	TAARR	R		173
GmTFL1a2	:	ÕKR	RÔCV	TP	PTSRDH	-NTRF	FAAEN	DLGLPVA	AVYFN	AÔRE	TAARR	R	:	173
MtTFL1b	:	okr	ROTV	-MKI	PTSRDLE	-NTKF	FAODN	DLGPPVA	AVFFN	AORE	TAARR	R	:	173
PsTFL1b	:	okr	ROTV	-MKI	PTSRDLE	-NTOF	FAODN	DLGPPVA	AVFFN	AORE	TAARR	R	:	173
CaTFL1b	:	QKR	RQIV	-MKI	PTSRDHE	-NTKI	FAEDN	DLGPPVA	VFFN	AQRE	AARR	R	:	177
GmTFL1b1	:	QKR	RQGV	-LKT	PTTRDLE	-NSRS	FAEENE	LGPPVA	VFFN	AQRE	TAARR	R	:	156
GmTFL1b2	:	QKR	RGSD	EN	snn k x								:	140
MtTFL1c	:	QEKGF	KHSI	VA	PFSRDHE	-N TR A	FSAQN)LGVPVA	AAYFN	ARRA	IAPRR	RAS	:	177
PsTFL1c	:	QKRGN	JKYSI	TC	PFSRDHE	-NTRN	JFADQN	DLGVPVA	AYFN	ARRA	APRR	R	:	173
CaTFL1c1	:	QKK	KHSI	TT	PSSRDHE	-NTRS	SESMQN	DLGVPVA	AYFN	ARRP	IAGRK	PTYI-	:	176
CaTFL1c2	:	Qкк	KHSI	TT	PSSRDHE	-NTRS	SESMQN	DLGVPVA	AYFN	ARRP	TAARK	PTYI-	:	176
CaTFL1c3	:	Qкк	KHSI	TT	PSSRDHE	-NTRS	SESMQN	DLGVPVA	AYFN	ARRP	AGRK	PTYI-	:	127
GmTFL1c1	:	QKR	RQCV	-TRP	PSSRDHE	-NTRF	FSAEN	DLGLPVA	VYFN	AQRE	IAARR	R	:	174
GmTFL1c2	:	QKR	RQCV	-TRP	PSSRDH	-STRF	SAEN	DLGLPVA	SVYFN	AQRE	TAARR	R	:	173



Supplementary Figure 10. Graphic representation of the genomic sequences of the five chickpea *FT* genes. Black boxes indicate exons (sizes over the line, in bp), red boxes the 5' and 3' untranslated regions and lines correspond to introns (sizes under the line).



Supplementary Figure 11. (A) Schematic diagram of the region of chromosome 3 containing the FTa1-FTa2-FTc cluster. The black line represents genomic DNA sequence with FTa1, FTa2 and FTc gene models shown at top in green (triangles representing exons and line corresponding to introns). The position of the primers used are indicated below; forward and reverse primers are presented in dark and light green, respectively. The failure to amplify any region of FTa2 in some lines, shown by the electrophoresis gel of the products obtained with primers FTa2-F6/FTa2-R1b (B) and FTa2-F1/FTa2-R6 (C), suggested a deletion of the gene. 7 chickpea accessions were tested, as follows: 1-ICC4958; 2-PI489777; 3-Cr5-9; 4-CA2156; 5-WR315; 6-ILC3279; 7- ICCV2; 8-SDW. To determine the extent of the deletion, several primers were tested in the FTa1-FTa2 and FTa2-FTc intergenic regions. The primer pair RMK-F1/FTS-R7 successfully yielded a band (D). Since the expected size of the amplicon in (D) is 33.7 kb according to CDC Frontier genome used as reference, the presence of a 2-3 kb band indicated a probable deletion spanning ~ 30kb. Sequencing of the band confirmed the deletion of 32kb that completely eliminates FTa2 and includes part of the FTa1-FTa2 and FTa2-FTc intergenic regions (E). All PCRs were performed in a final volume of 25 μ L containing 50 ng template DNA, 5 μ L of 5x reaction buffer, 10 mM dNTPs, 0.2 μ M of each primer, 50 mM MgCl2, 0.1 µL of MangoTaqTM DNA polymerase (Bioline, Australia) and autoclaved Milli-Q water to final volume. Reactions were performed in a thermal cycler using the following program: an initial denaturation of 5 min at 94°C, followed by 35-40 cycles (94°C for 40 seconds, 58oC annealing temperature and 10 min extension) and a final extension of 10 minutes at 72°C. Primers sequences: FTa2-F6 AAGCCCACAACCCACCTAAGGG; FTa2-R1b ACTAGCCCCAGCAGTTGAAG; FTa2-F1 TAGGCGGAAACGATCTCA FTa2-R6 GCCATAAACCTCTGTCGAACGGC, RMK-F1 ACTGTTCTGCACACAGTGGCTACC; GG; FTS-R7 AGGCCAAAGACAAGATCCCG.



Supplementary Figure 12. Relative expression of flowering-related chickpea genes in CRIL2 parental lines. ICC4958 and PI48977 are represented by red and black lines, respectively. Continuous lines/squares indicate long day condition while dashed lines/circles represent short day. TFL1b and TFL1c expression was measured only in apex and FTa3 expression was measured in both tissues but found only in leaf. The average ± SE of 2 biological and 2 technical replicates is shown, and transcripts were normalized against ACTIN.



Supplementary Figure 13. Variation in growth habit (GH) observed in the CRIL2 population, illustrated by representative examples of the four categories used in the present study: Prostrate (**A**), semi-prostrate (**B**), semi-erect (**C**) and erect (**D**). (**E**) Relationship between GH and flowering phenotype (DTF) of the CRIL2 population grown under SD. Numbers over bars indicate mean DTF ± standard error and those between parentheses correspond to the number of RILs in each category. (**F**) Relationship between GH and branching index (BI) of the CRIL2 population grown under SD. Boxplot illustrating the variation in branching index displayed by CRIL2 parental lines and RILs under LD and SD (**G**). Box edges denote the lower and upper quantiles with median value in the middle of the box. (**H**) Relationship between BI of CRIL2 population grown under SD and LD photoperiod.

Marker	Population	Fw Sequence	Rv Sequence	GeneID
LUV	CRIL2/RIP12	AAACCAACTAAGCATACCCT	TGAGCATCACTCATTCACCA	101500625
LIII	RIPs8/5	CGTCACACTTGTAATCTTCATTCC	AGTTTTCCCCCTTTAATAATGTGG	101500055
CP450	CRIL2/RIP12	CACAAAATAGAGAACAATGACAGC	ACTTTTCCCTTTGCATGTAGG	101502624
CI 450	RIPs8/5	AGAGTTGTATAGTTGTTAAGGATG	GTGTGTGTGTGTTTATCAATTTAAGC	101302024
CDE24	CRIL2/RIP12	TGGTTCCAATTAAGTTTCAAGTG	AGTCAAGTGTTTGGTAAGAGTTG	101500722
CDF 20	RIPs8/5	AGTCGATGCTTAATCTTCAACAGC	AGATCTGCATAAAGATGGTTCC	101300722
WUS11	CRIL2/RIP12	CAGCCTGGTAATTAACTGCATC	ATGATTTTGAGCAATTATTCTGTG	101502157
WUSII	RIPs8/5	GCATAACCTAGAGTGATCGAGC	CTACTCTGACTTAATGGGTTCG	101505157
	CRIL2/RIP12	AATCATCCCCAAGAGATCAA	TGCACAGTCATTGTGTTTCG	
FTa1	RIPs8/5	ACTGTTCTGCACACAGTGGCTACC	AAAGAGATCTAACACATTTTGC	101497376
INC2	CPII 2/PID12	CATCTCATGGCTCTAAGAAAGG		101503708
SUVH41	CRIL2/RIT12 CRIL2/RIP12	TTCGCCGTCACTACCTCG	GGAGATTAAGCATTCGGAGG	101508/28
COLb	CRIL2/RIT12	TGCTACATCATCACCTAGTAACA	TGCCATGATATAGGAAGTCTTAGTT	101504031
SOC19	CRIL2/RIT12		CGACATATAATTCATTGTGGACCG	101510775
SCARECROW ²	CRIL2/RIP12	GAGACATGTTGTTGAACAGC	CTTGATGGTCCTCTAACAGC	101513767
RAPTOR12	CRIL2/RIP12	CCCAATGCCATCCAAATCGG		101514864
ARF9 ²	RIP12	GCAATATGGTGAGAAGAATTTTC	TGAGATAGGCAATTTAGTCCCTG	101491204
ARIS	CRIL2/RIP12	TTAGCACAAGAACGAGCGAGC	GTGAACGAAAAGGTGTTATGAAGG	101490892
GATA91	CRIL2/RIP12	GAGGAATATGTCTTCTTCCATTCC	TGGAAAGAGTAATTTTCCCCCTA	101503040
NAC100 ¹	CRIL2/RIP12	CAGGTCTTAGCAATGACACG	GCCCTATTTCTTCCCATGTC	101500623
GIGANTEA	CRIL2/RIP12	TGTTGAGTACTTGATTCAGTTTAC	TCAGTATATAGATGCATACCTCAGC	101511540
ELF6	CRIL2/RIP12	ACCACCCATTTCAGTTTGTTTAC	CCAGGGTCAAAATTATCATAGTCG	101509509
TEMb	CRIL2/RIP12	GAGTTGAGAAAATCTGTTTCAGCG	AGGTTCCGCGGAAAAGACG	101492303
PHYA1	CRIL2/RIP12	ACAATTGCCTTGTAATCGCC	GCCCAAGATATAACTGCTCAG	101506511
CDF3b	RIPs8/5	AACAACCGAAGAAAAATAGG	GAATTTGTATAATGTTTATCTTCG	101499964
COLg	RIPs8/5	AGAGACTCTGAAGGTGTCCC	CAGTGGCTCGGAGAAAGTGG	101499146
AP2-like	RIPs8/5	AACAAACATCGTCACATCACC	CCTTGTGCTATTTAGTGTTCTGC	101502947
LOB189	RIPs8/5	ACAAAATCAATACAAGCAAACC	TGCAACCGTTAGTTTGTTTGG	101508422
PRSP	RIPs8/5	GATACATTTTCGCTCAAACTATG	TGCGTTGAAAAGTGTTTTATTAGC	101491522
PRT6	RIPs8/5	AAATTTTCATTCTCCTAAGACAGT	ACGGTCCAACCCAACGTATA	101506928
WRKY	RIPs8/5	TTCTGAGAGCACCGTGATGG	AGCATCTCCAACTGTAATTAAATG	101511519

Supplementary Table 1. Details of the HRM markers developed in this study for each population, and identity (NCBI GeneID) of the genes targeted by them.

(1) Primers designed by Saxena et al (2014)

(2) Primers designed for this study based on SNPs described by Saxena et al (2014)

Supplementary Table 2. Sequence and product size of the primers used to measure the expression of flowering related genes in chickpea

Fw primer	R y nrimer	Product s	ize (bp)	
r « primer	Kt primer	Genomic	cDNA	GeneID
ATTGTCTTGAGTGGTGGTTCT	TTCCTCTCTGGTGGTGCTAC	(Ver	ma et al	. 2013)
GAACTTCAGAGTCTGGAACAGC	CATTGTGCCTGTTGTTGAGC	472	188	101488241
TGCAACGCGTAACAGTGAACG	ACGAACAATGCCGTGAGTTCTTG	660	169	101503680
TTGCCAATCAACCCAGAGCG	AGTGGGGTTACTTGGGCTAGG	236	101	101497376
GTTCTGACGGTGGTTCTCTC	CGGAGGTTCACAAAAGAAGG	297	183	101496618
TGTTGGTGGTGAAGATCTAAGG	ATTCCTGCTGAAGGATTCG	6616	186	101508200
GGTGAGCTCAAACCCTCCCA	TCCCTCATATTTGGGTCACTAGG	618	131	101505276
CCATCCCGGAGCATACACAGTC	TGCACCAAGCCCTAGCAATCC	1460	196	101515383
AACGACAACAACAAGGGATCGG	TGCAGCCAACAAGAGTCTGC	120	120	101497661
TATACCGGGCACAACAGATG	GGAGGTCCAAGGTCATTGTC	584	195	101508699
ACGTTCCTGGCCCAAGTGAT	TGGATCCCTATGTTAGGCTTTGGT	1134	136	101491943
	Fw primer ATTGTCTTGAGTGGTGGTTCT GAACTTCAGAGTCTGGAACAGC TGCAACGCGTAACAGTGAACG TTGCCAATCAACCCAGAGCG GTTCTGACGGTGGTTCTCTC TGTTGGTGGTGAAGATCTAAGG GGTGAGCTCAAACCCTCCCA CCATCCCGGAGCATACACAGTC AACGACAACAACAACAAGGATCGG TATACCGGGCACAACAGAGTG ACGTTCCTGGCCCAAGTGAT	Fw primerRv primerATTGTCTTGAGTGGTGGTTCTTTCCTCTCTGGTGGTGCTACGAACTTCAGAGTCTGGAACAGCCATTGTGCCTGTGTGAGCTGCAACGCGTAACAGTGAACGACGAACAATGCCGTGAGTTCTTGTTGCCAATCAACCCAGAGCGAGTGGGGTTACTTGGGCTAAGGGTTCTGACGGTGGTTCTCTCCGGAGGTTCACAAAAGAAGGTGTTGGTGGTGAAGAACCCCCAAATTCCTGCTGAAGGATTCGGGTGAGCTCAAAACCCTCCCATCCCTCATATTTGGGTCACTAGGAACGACAACAACAAGGGATCGTGCACCAAGACCTCACAAACGACAACAACAAGGGATCGTGCAGCCAACAAGAGTCTGCTATACCGGGCACAACAGAGTGGGAGGTCCAAGGTCATTGTCACGTTCCTGGCCCAAGTGATTGGATCCCTATGTTAGGCTTTGGT	Fw primerRv primerProduct si GenomicATTGTCTTGAGTGGTGGTTCTTTCCTCTCTGGTGGTGCTAC(VerGAACTTCAGAGTCTGGAACAGCCATTGTGCCTGTTGTTGAGC472TGCAACGCGTAACAGTGAACGACGAACAATGCCGTGAGTTCTTG660TTGCCAATCAACCCAGAGCGAGTGGGGTTACTTGGGCTAGG236GTTCTGACGGTGGTTCTCTCCGGAGGTTCACAAAGAAGA297TGTTGGTGGTGAAGAATCTAAGGATTCCTGCTGAAGGATTCG6616GGTGAGCTCAAACCTCCCATCCCTCATATTTGGGTCACTAGG618CCATCCCGGAGCATACACAGTCTGCACCAAGCCTAGCAATCC1460AACGACAACAACAAGGGATCGGGAGGTCCAAGGTCATTGTC584ACGTTCCTGGCCCAAGTGATTGGATCCTATGTTAGGCTTTGGT1134	Fw primerRv primerProduct size (bp) GenomicATTGTCTTGAGTGGTGGTTCTTTCCTCTGGTGGTGCTAC(Vermalental)GAACTTCAGAGTCTGGAACAGCCATTGTGCCTGTTGTGAGC472188TGCAACGCGTAACAGTGAACAGACGAACAATGCCGTGAGTTCTG6600169TTGCCAATCAACCCAGAGCGAGTGGGGTTACTTGGGCTAGG236101GTTCTGACGGTGGTTCTCTCCGGAGGTTCACAAAAGAAGG297183TGTTGGTGGTGAAGAATCTAAGGATTCCTGCTGAAGGATTCG6616186GGTGAGCTCAAACCCTCCCATCCCTCATATTTGGGTCACTAGG618131CCATCCCGGAGCATACACAGTCTGCACCAAGACTAGCAATCC1460196AACGACAACAACAAGGGATCGGGAGGTCCAAGGTCATGC584195ACGTTCCTGGCCCAAGTGATTGGATCCTATGTTAGGCTTGGT1134136

Supplementary Table 3. Description, physical position in the chromosome and GeneID of the 59 genes annotated between markers SUVH4 and GATA9, according to the genome assembly of cultivar CDC Frontier (ASM33114 v1; Varshney et al., 2013), available at the National Center for Biotechnology Information (NCBI; https://www.ncbi.nlm.nih.gov).

Marker	Position	GeneID	Description
SUVH4	25748486	101508428	histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH4
	25765688	101509380	CLAVATA3/ESR (CLE)-related protein 4A-2-like
	25787922	101509702	uncharacterized protein LOC101509702
	25849917	101510346	protein Mpv17-like, partial
	25899924	101510883	N-alpha-acetyltransferase MAK3
	25908342	101511521	cytochrome b-c1 complex subunit Rieske-4, mitochondrial-like
	25911181	101511199	uncharacterized protein LOC101511199
	25920520	101511847	uncharacterized protein LOC101511847
	25929005	101512385	uncharacterized protein LOC101512385
	25945170	101512699	LRR receptor-like serine/threonine-protein kinase RPK2
	25987693	101513246	UPF0496 protein At3g19330-like
	26006715	101513575	putative serine/threonine-protein kinase isoform X2
	26029555	101514543	chalcone synthase
	26038727	101505971	uncharacterized protein LOC101505971
	26049105	101514869	jasmonate O-methyltransferase-like isoform X2
	26056836	101506278	jasmonate O-methyltransferase-like
	26073603	101506600	3,7-dimethylxanthine N-methyltransferase-like
	26105741	101515408	7-methylxanthosine synthase 1-like
	26119620	101506937	ethylene-responsive transcription factor LEP
	26135351	101515744	nudix hydrolase 12, mitochondrial
	26162323	101488713	calcium-binding mitochondrial carrier protein SCaMC-1-like
	26169052	101489051	uncharacterized protein LOC101489051
	26187333	101489383	histidine biosynthesis bifunctional protein hisIE, chloroplastic
	26191225	101489915	uncharacterized protein LOC101489915
	26198363	105851804	glycine-rich cell wall structural protein 1-like
	26211557	101490249	syntaxin-22-like
	26221867	101490568	syntaxin-22-like
	26223872	101490780	uncharacterized protein LOC101490780
	26228217	101491110	DNA cross-link repair protein SNM1 isoform X1
	26233285	101491643	uncharacterized protein LOC101491643
	26237155	101491949	uncharacterized protein LOC101491949
	26259086	101492622	uncharacterized protein LOC101492622
	26268535	101492953	probable xyloglucan endotransglucosylase/hydrolase protein B
	26275124	101493288	probable xyloglucan endotransglucosylase/hydrolase-like precursor
	26293522	101493610	glyceraldehyde-3-phosphate dehydrogenase A, chloroplastic

	26300947	101493929	pentatricopeptide repeat-containing protein At3g26630, chloroplastic
	26304938	101494250	WD repeat-containing protein LWD1
	26309206	105851806	pentatricopeptide repeat-containing protein At3g26630, chloroplastic-like
	26315891	101494555	acetyl-coenzyme A synthetase, chloroplastic/glyoxysomal
	26325185	101494873	eukaryotic peptide chain release factor subunit 1-3
	26331419	101495197	importin-13 isoform X2
	26353855	101495954	INO80 complex subunit D-like
	26365580	101496291	omega-hydroxypalmitate O-feruloyl transferase
FTa1	26393854	101497376	protein FLOWERING LOCUS T-like
	26409508	101496618	protein HEADING DATE 3A-like isoform X1
	26437711	101508200	protein FLOWERING LOCUS T-like
	26446273	101497706	transmembrane and coiled-coil domain-containing protein 1-like
	26454060	101498244	aquaporin SIP1-2-like
	26459034	101498578	apyrase 2-like
	26465157	101499141	pentatricopeptide repeat-containing protein At5g15010, mitochondrial
	26476855	101499461	nucleoside-triphosphatase-like
	26505866	101499961	NAC transcription factor 29
	26513981	101500308	uncharacterized protein LOC101500308
NAC100	26542626	101500623	NAC domain-containing protein 100-like
	26551883	101500931	U11/U12 small nuclear ribonucleoprotein 65 kDa protein
	26560819	101501672	thioredoxin-like 1-1, chloroplastic
	26568175	101501985	CCR4-NOT transcription complex subunit 3 isoform X1
	26586013	101503370	glucan endo-1,3-beta-glucosidase 8-like
GATA9	26593826	101503040	GATA transcription factor 9-like

Supplementary Table 3. Continued

Supplementary Table 4. Accession number of the PEBP genes from five plant species; *Arabidopsis thaliana, Medicago truncatula, Pisum sativum* (Pea), *Glycine max* (soybean) and *Cicer arietinum* (chickpea). Soybean accessions were obtained from Wang et al. (2015) and the protein sequences retrieved from the Soybean Knowledge Database [http://soykb.org; Joshi et al. (2012)]. Proteins sequences retrieved from the accessions listed were used in the alignment displayed in Supplementary Figure 10.

A	rabidopsis]	Medicago	Pea	(Chickpea	So	oybean
MFT	AT1G18100	Ме	dtr8g106840	PsCam040701	LOC	2101504081	GmMFTa	Glyma05g34030
							GmMFTb	Glyma08g05650
BFT	AT5G62040	Me	dtr0020s0120	PsCam044479	LO	C101507903	GmBFTa	Glyma09g26550
							GmBFTb	Glyma16g32080
ATC	AT2G27550		-	-		-		-
TFL1	AT5G03840	TFL1a	Medtr7g104460	AY340579	TFL1a	LOC101506075	GmTFL1b1	Glyma12g30940
		TFL1b	Medtr2g086270	AY340580	TFL1b	LOC101508699	GmTFL1b2	Glyma13g39360
		TFL1c	Medtr1g060190	AY343326	TFL1c1	LOC101495644	GmTFL1a1	Glyma03g35250
					TFL1c2	LOC101491943	GmTFL1a2	Glyma19g37890
					TFL1c3	LOC101492277	GmTFL1c1	Glyma10g08340
							GmTFL1c2	Glyma13g22030
FT	AT1G65480	FTa1	Medtr7g084970	HQ538822	FTa1	LOC101497376	GmFTc1	Glyma19g28400
TSF	AT4G20370	FTa2	Medtr7g085020	HQ538821	FTa2	LOC101496618	GmFTa3a	Glyma16g26660
		FTa3	Medtr6g033040	-	FTa3	LOC101515383	GmFTa3b	Glyma16g04830
		FTb1	Medtr7g006630	HQ538824	FTb	LOC101505276	GmFTa3c	Glyma16g26690
		FTb2	Medtr7g006690	HQ538825			GmFTa3d	Glyma02g07650
		FTc	Medtr7g085040	HQ538826	FTc	LOC101508200	GmFTa1/2a	Glyma19g28390
							GmFTa1/2b	Glyma16g04840
							GmFTb1	Glyma08g47820
							GmFTb2	Glyma18g53670
							GmFTb3	Glyma18g53680
							GmFTb4	Glyma18g53690
							GmFTb5	Glyma08g47810
							GmFT-like	Glyma08g28470

Supplementary Table 5. Information about sunrise and sunset times (h = hours, m = minutes) in Cordoba, Spain (Latitude, Longitude: 37 52 51, - 4 46 44) and Jaen, Spain (Latitude, Longitude: 37 45 59, - 3 47 21) during the growing seasons of RIP12, RIP5 and RIP8. Source: Observatorio Astronómico Nacional, Instituto Geográfico Nacional, Ministerio de Fomento, Spain.

Г		Cordoba, 2001															Cordoba, 2	004										Cordoba, 2	2014				
I	Day	Febru	ary	Ma	rch	A	pril	N	4ay	Jı	ne	Day	Febr	uary	M	arch	A	oril	M	lay	Jı	ine	Day	Feb	ruary	Ma	rch	A	pril	M	lay	Ju	ine
	Su	nrise	Sunset	Sunrise	Sunset	Sunrise	Sunset	Sunrise	Sunset	Sunrise	Sunset		Sunrise	Sunset	Sunrise	Sunset	Sunrise	Sunset	Sunrise	Sunset	Sunrise	Sunset		Sunrise	Sunset	Sunrise	Sunset	Sunrise	Sunset	Sunrise	Sunset	Sunrise	Sunset
	h	m	h m	h m	h m	h m	h m	h m	h m	h m	h m		h m	h m	h m	h m	h m	h m	h m	h m	h m	h m		h m	h m	h m	h m	h m	h m	h m	h m	h m	h m
	1 8	323	1843	751	1913	804	2042	723	2110	659	2136	1	824	1842	750	1913	804	2042	723	2110	658	2136	1	823	1842	751	1912	805	2042	723	2110	659	2136
	2 8	323	1844	749	1914	803	2043	722	2111	658	2136	2	823	1843	749	1914	803	2043	722	2111	658	2136	2	823	1843	750	1913	803	2043	722	2110	658	2136
	3 8	322	1845	748	1915	801	2044	721	2112	658	2137	3	822	1844	748	1915	801	2044	721	2112	658	2137	3	822	1845	748	1914	802	2044	721	2111	658	2137
	4 8	321	1846	747	1916	800	2045	720	2112	658	2138	4	821	1845	746	1916	800	2045	720	2113	657	2138	4	821	1846	747	1915	800	2045	720	2112	658	2137
	5 8	320	1847	745	1917	758	2046	719	2113	657	2138	5	820	1846	745	1917	758	2046	718	2114	657	2138	5	820	1847	745	1916	759	2046	719	2113	657	2138
	6 8	319	1848	744	1918	757	2047	718	2114	657	2139	6	819	1847	743	1918	757	2047	717	2115	657	2139	6	819	1848	744	1917	757	2046	718	2114	657	2139
	7 8	318	1849	742	1919	756	2048	717	2115	657	2139	7	819	1848	742	1919	755	2048	716	2115	657	2139	7	818	1849	742	1918	756	2047	717	2115	657	2139
	8 8	317	1850	741	1920	754	2048	716	2116	657	2140	8	818	1849	740	1920	754	2049	715	2116	657	2140	8	817	1850	741	1919	754	2048	716	2116	657	2140
	9 8	316	1851	739	1921	753	2049	715	2117	657	2140	9	816	1851	739	1921	752	2050	714	2117	656	2140	9	816	1851	740	1920	753	2049	715	2117	657	2140
	10 8	315	1853	738	1921	751	2050	714	2118	656	2141	10	815	1852	737	1922	751	2051	713	2118	656	2141	10	815	1852	738	1921	751	2050	714	2118	656	2141
	11 8	314	1854	736	1922	750	2051	713	2119	656	2141	11	814	1853	736	1923	749	2051	712	2119	656	2141	11	814	1853	737	1922	750	2051	713	2119	656	2141
	12 8	312	1855	735	1923	748	2052	712	2120	656	2142	12	813	1854	734	1924	748	2052	711	2120	656	2142	12	813	1855	735	1923	748	2052	712	2120	656	2142
	13 8	311	1856	733	1924	747	2053	711	2121	656	2142	13	812	1855	733	1925	746	2053	711	2121	656	2142	13	811	1856	734	1924	747	2053	711	2120	656	2142
	14 8	610	1857	732	1925	745	2054	710	2121	656	2143	14	811	1856	731	1926	745	2054	710	2122	656	2143	14	810	1857	732	1925	746	2054	710	2121	656	2143
	15 8	609	1858	730	1926	744	2055	709	2122	656	2143	15	810	1857	730	1927	744	2055	709	2123	656	2143	15	809	1858	731	1926	744	2055	709	2122	656	2143
	16 8	808	1859	729	1927	743	2056	708	2123	656	2143	16	809	1858	728	1927	742	2056	708	2123	656	2143	16	808	1859	729	1927	743	2056	708	2123	656	2143
	17 8	807	1900	727	1928	741	2057	707	2124	656	2144	17	807	1859	727	1928	741	2057	707	2124	656	2144	17	807	1900	728	1928	741	2057	708	2124	656	2144
	18 8	305	1901	726	1929	740	2058	707	2125	657	2144	18	806	1900	725	1929	739	2058	706	2125	657	2144	18	806	1901	726	1929	740	2058	707	2125	657	2144
	19 8	304	1902	724	1930	738	2059	706	2126	657	2144	19	805	1901	724	1930	738	2059	706	2126	657	2144	19	804	1902	724	1930	739	2058	706	2126	657	2144
	20 8	803	1903	723	1931	737	2059	705	2127	657	2144	20	804	1903	722	1931	737	2100	705	2127	657	2145	20	803	1903	723	1931	737	2059	705	2126	657	2144
	21 8	302	1904	721	1932	736	2100	704	2127	657	2145	21	803	1904	721	1932	735	2101	704	2128	657	2145	21	802	1904	721	1932	736	2100	705	2127	657	2145
	22 8	600	1905	720	1933	734	2101	704	2128	657	2145	22	801	1905	719	1933	734	2102	704	2128	657	2145	22	800	1905	720	1933	735	2101	704	2128	657	2145
	23 7	59	1906	718	1934	733	2102	703	2129	658	2145	23	800	1906	718	1934	733	2103	703	2129	658	2145	23	759	1906	718	1934	733	2102	703	2129	658	2145
	24 7	58	1908	717	1935	732	2103	702	2130	658	2145	24	759	1907	716	1935	731	2103	702	2130	658	2145	24	758	1907	717	1935	732	2103	703	2130	658	2145
	25 7	56	1909	815	2036	731	2104	702	2131	658	2145	25	757	1908	715	1936	730	2104	702	2131	658	2145	25	756	1908	715	1935	731	2104	702	2130	658	2145
	26 7	55	1910	814	2037	729	2105	701	2131	658	2145	26	756	1909	713	1937	729	2105	701	2132	659	2145	26	755	1909	714	1936	729	2105	701	2131	658	2145
	27 7	54	1911	812	2037	728	2106	701	2132	659	2145	27	755	1910	712	1938	728	2106	701	2132	659	2145	27	754	1910	712	1937	728	2106	701	2132	659	2145
	28 7	52	1912	811	2038	727	2107	700	2133	659	2145	28	753	1911	810	2039	727	2107	700	2133	659	2145	28	752	1911	711	1938	727	2107	700	2133	659	2145
	29			809	2039	726	2108	700	2134	700	2145	29	752	1912	809	2040	725	2108	700	2134	700	2145	29			709	1939	726	2108	700	2133	700	2145
	30			808	2040	724	2109	659	2134	700	2145	30			807	2040	724	2109	659	2134	700	2145	30			808	2040	725	2109	659	2134	700	2145
	31			806	2041			659	2135			31			806	2041			659	2135			31			806	2041			659	2135		

	Cordoba, 2003															Cordoba, 20	08										Jaen, 200	13				
Day	Febr	uary	Mai	rch	Ар	nil	М	lay	Ju	ne	Day	Febr	uary	Ma	rch	Ap	ril	М	ay	Ju	ine	Day	Feb	ruary	Ma	rch	A	oril	М	ay	Ju	ne
	Sunrise	Sunset	Sunrise	Sunset	Sunrise	Sunset	Sunrise	Sunset	Sunrise	Sunset		Sunrise	Sunset	Sunrise	Sunset	Sunrise	Sunset	Sunrise	Sunset	Sunrise	Sunset		Sunrise	Sunset	Sunrise	Sunset	Sunrise	Sunset	Sunrise	Sunset	Sunrise	Sunset
	h m	h m	h m	h m	h m	h m	h m	h m	h m	h m		h m	h m	h m	h m	h m	h m	h m	h m	h m	h m		h m	h m	h m	h m	h m	h m	h m	hm	h m	h m
1	824	1842	752	1912	805	2042	724	2109	659	2135	1	824	1842	750	1913	804	2042	723	2110	658	2136	1	820	1838	747	1908	801	2038	720	2105	655	2131
2	823	1843	750	1913	804	2043	723	2110	658	2136	2	823	1843	749	1914	803	2043	722	2111	658	2137	2	819	1839	746	1909	800	2039	719	2106	655	2132
3	822	1844	749	1914	802	2043	722	2111	658	2137	3	822	1844	748	1915	801	2044	721	2112	658	2137	3	818	1840	745	1910	758	2039	718	2107	654	2132
4	821	1845	747	1915	801	2044	720	2112	658	2137	4	821	1845	746	1916	800	2045	720	2113	658	2138	4	817	1842	743	1911	757	2040	717	2108	654	2133
5	820	1846	746	1916	759	2045	719	2113	657	2138	5	820	1846	745	1917	758	2046	718	2114	657	2138	5	816	1843	742	1912	755	2041	716	2109	654	2134
6	819	1848	744	1917	758	2046	718	2114	657	2138	6	819	1847	743	1918	757	2047	717	2115	657	2139	6	815	1844	740	1913	754	2042	715	2110	654	2134
7	818	1849	743	1918	756	2047	717	2115	657	2139	7	818	1848	742	1919	755	2048	716	2116	657	2139	7	814	1845	739	1914	752	2043	713	2111	653	2135
8	817	1850	742	1919	755	2048	716	2116	657	2140	8	817	1850	740	1920	754	2049	715	2116	657	2140	8	813	1846	737	1915	751	2044	712	2111	653	2135
9	816	1851	740	1920	753	2049	715	2117	657	2140	9	816	1851	739	1921	752	2050	714	2117	657	2141	9	812	1847	736	1916	749	2045	711	2112	653	2136
10	815	1852	739	1921	752	2050	714	2117	656	2141	10	815	1852	737	1922	751	2051	713	2118	656	2141	10	811	1848	735	1917	748	2046	710	2113	653	2136
11	814	1853	737	1922	750	2051	713	2118	656	2141	11	814	1853	736	1923	749	2052	712	2119	656	2142	11	810	1849	733	1918	747	2047	709	2114	653	2137
12	813	1854	736	1923	749	2052	712	2119	656	2142	12	813	1854	734	1924	748	2052	711	2120	656	2142	12	809	1850	732	1919	745	2048	708	2115	653	2137
13	812	1855	734	1924	748	2053	711	2120	656	2142	13	812	1855	733	1925	746	2053	711	2121	656	2142	13	808	1852	730	1920	744	2049	708	2116	653	2138
14	811	1856	733	1925	746	2054	710	2121	656	2142	14	811	1856	731	1926	745	2054	710	2122	656	2143	14	807	1853	729	1921	742	2049	707	2117	653	2138
15	810	1857	731	1926	745	2054	709	2122	656	2143	15	810	1857	730	1927	744	2055	709	2123	656	2143	15	805	1854	727	1922	741	2050	706	2118	653	2139
16	808	1859	730	1927	743	2055	709	2123	656	2143	16	809	1858	728	1928	742	2056	708	2123	656	2143	16	804	1855	726	1923	739	2051	705	2119	653	2139
17	807	1900	728	1928	742	2056	708	2124	656	2144	17	807	1859	727	1928	741	2057	707	2124	656	2144	17	803	1856	724	1924	738	2052	704	2119	653	2139
18	806	1901	727	1929	740	2057	707	2124	656	2144	18	806	1900	725	1929	739	2058	706	2125	657	2144	18	802	1857	723	1925	737	2053	703	2120	653	2140
19	805	1902	725	1930	739	2058	706	2125	657	2144	19	805	1902	724	1930	738	2059	706	2126	657	2144	19	801	1858	721	1926	735	2054	703	2121	653	2140
20	803	1903	724	1931	738	2059	705	2126	657	2144	20	804	1903	722	1931	737	2100	705	2127	657	2145	20	759	1859	720	1927	734	2055	702	2122	653	2140
21	802	1904	722	1931	736	2100	705	2127	657	2145	21	802	1904	721	1932	735	2101	704	2128	657	2145	21	758	1900	718	1927	733	2056	701	2123	653	2140
22	801	1905	720	1932	735	2101	704	2128	657	2145	22	801	1905	719	1933	734	2102	704	2128	657	2145	22	757	1901	717	1928	731	2057	700	2124	654	2141
23	800	1906	719	1933	734	2102	703	2129	657	2145	23	800	1906	718	1934	733	2103	703	2129	658	2145	23	756	1902	715	1929	730	2058	700	2124	654	2141
24	758	1907	717	1934	732	2103	703	2129	658	2145	24	759	1907	716	1935	731	2104	702	2130	658	2145	24	754	1903	713	1930	729	2059	659	2125	654	2141
25	757	1908	716	1935	731	2104	702	2130	658	2145	25	757	1908	715	1936	730	2104	702	2131	658	2145	25	753	1904	712	1931	727	2100	659	2126	654	2141
26	756	1909	714	1936	730	2105	702	2131	658	2145	26	756	1909	713	1937	729	2105	701	2132	659	2145	26	752	1905	710	1932	726	2100	658	2127	655	2141
27	754	1910	713	1937	729	2106	701	2132	659	2145	27	755	1910	712	1938	728	2106	701	2132	659	2145	27	750	1906	709	1933	725	2101	657	2127	655	2141
28	753	1911	711	1938	727	2106	701	2132	659	2145	28	753	1911	710	1939	726	2107	700	2133	659	2145	28	749	1907	707	1934	724	2102	657	2128	655	2141
29			710	1939	726	2107	700	2133	659	2145	29	752	1912	709	1940	725	2108	700	2134	700	2145	29		2.507	706	1935	722	2103	656	2129	656	2141
30			808	2040	725	2108	700	2134	700	2145	30			807	2041	724	2109	659	2134	700	2145	30			804	2036	721	2104	656	2130	656	2141
31			807	2041			659	2135			31			806	2041			659	2135			31			803	2037			656	2130		