QTL for flowering date in three mapping populations of Medicago truncatula

Jean-Baptiste Pierre, Thierry Huguet, Philippe P. Barre, Christian C. Huyghe, Bernadette Julier

▶ **To cite this version:**

HAL Id: hal-02754135
https://hal.inrae.fr/hal-02754135

Submitted on 3 Jun 2020

QTL for flowering date in three mapping populations of *Medicago truncatula*

Jean-Baptiste Pierre[1], Thierry Huguet[2], Philippe Barre[1], Christian Huyghe[1], Bernadette Julier[1]
[1] **INRA, UR 4, Unité de Recherche Pluridisciplinaire Prairies et Plantes Fourragères, 86600 Lusignan, France,** [2] **INP-ENSAT, Laboratoire Symbiose et Pathologie des Plantes, 31326 Castanet-Tolosan, France. Email: bjulier@lusignan.inra.fr**

Date of flowering is a major step in plant life cycle. The objective of this study was to describe genetic architecture of the flowering date of the model species for legume crops, *Medicago truncatula*, in a multiple mapping population. Three recombinant inbred lines (RILs) populations involving four parental lines were used: LR1 (196 RILs in F5 generation), LR4 (199 RILs in F7 generation), LR5 (173 RILs in F7 generation). They were obtained from the crosses DZA315.26 x DZA45.6, Jemalong6 x DZA315.16 and Jemalong6 x F83005.5, respectively. Quantitative variation was evaluated in several years and locations, and QTL detection was carried out. A large variation for flowering date was observed, with a large effect of lines and seasons or locations, but the interactions between lines and seasons or lines and locations were low or non significant. Transgressive lines compared to the parents were observed. Within populations, the heritability was high, ranging from 76 to 82%. QTL detection showed a QTL on chromosome 7 that was common to all populations and seasons, with LOD scores between 4 and 19. Taking advantage of the multiple mapping populations, it was condensed into a single QTL with a support interval of only 0.9 cM (Pierre et al. submitted). In a bioanalysis, six candidate genes, known to be involved in flowering date in *Arabidopsis*, were identified in this interval: Constans, FD, PKS and three copies of FT. Other genomic regions were involved in flowering date variation more specifically in one population or one season. These QTLs confirm that genetic variation for flowering date is controlled by several genes, and explain the transgressive lines. The main conclusion of this analysis on three different mapping populations is that (1) a common QTL was found, and its position was estimated more precisely than with a single population (Julier et al., 2007), (2) more alleles were revealed, (3) other QTLs were detected. Identification of candidate genes was a result of integration of QTL analysis and genomics in *M. truncatula*.

References

Julier B, Huguet T, Chardon F, Ayadi R, Pierre JB, Prosperi JM, Barre P, Huyghe C (2007) Identification of quantitative trait loci influencing aerial morphogenesis in the model legume *Medicago truncatula*. Theor Appl Genet 114:1391-1406

Pierre J.B., Huguet T., Barre P., Huyghe C., Julier B. Detection of QTLs for flowering date in three mapping populations of the model legume species *Medicago truncatula*. Theor. Appl. Genet., under review.