GENETIC CONTROL OF FLOWERING TIME IN BIENNIAL BEETS

Andreas E. Müller [1], Gretel Schulze-Buxloh[2], Sebastian H. Vogt[2], Markus Wolf[3], Axel Schechert[1]*, Benjamin Stich[4], Christian Jung[2], Elena Orsini[1]
[1]Fr Strube Research GmbH & Co KG, 38387 Soellingen; Germany, [2] Plant Breeding Institute, Christian-Albrechts-University of Kiel, 24098 Kiel, Germany,
[3]Saaten-Union GmbH, 30916 Isernhagen, Germany, [4]Max Planck Institute for Plant Breeding Research, 50829 Cologne, Germany

ABSTRACT

Seed production in hybrid crops such as sugar beet (*Beta vulgaris* ssp. *vulgaris*) is greatly facilitated by synchronous flowering times of the hybrid parents. In the model species *Arabidopsis thaliana*, many of the genes that control flowering time have been identified, but knowledge of the genetic and molecular basis of flowering time control in sugar beet is just beginning to emerge. To start deciphering the genetic landscape of flowering time control in cultivated biennial beets after vernalization over winter, we developed multi-parent QTL populations derived from five breeding lines. Three partially inbred lines were used to generate two segregating populations. One parent was in common. The other segregating populations comprised three full-sib families based on heterozygous parents. The parents spanned a wide range of flowering characteristics and depicted the range of flowering times that can be expected in a common sugar beet breeding population. The offspring (F1) were selfed in the year 2006. In autumn of 2006 we planted the segregating populations (F1:2) in the vicinity of Manosque, Provence (France). In 2007 we evaluated the material on individual plant basis for “Begin of Flowering” (BF) and “Full Flowering” (FF). A total of 185 plants were scored on a daily basis. We noted the days from May 1 to the the occurrence of first open flowers (BF) and the occurrence of open flowers on secondary branches (FF). Individual plants were sampled for genotyping and selfed to create the F2:3 families. In autumn 2007 we planted the F2:3 seed to vernalize the stecklings in open field as done in the previous year. Evaluation of the families has taken place on plot basis in 2008.

The phenotyping revealed for the earliest population an average of 24.5 days and 29.1 days to BF in 2007 and 2008, resp.. The latest populations displayed an average of 31.5 days and 37.5 days to BF in 2007 and 2008, resp.. Standard deviations (SD) ranged from 4.3 to 7.3 and 4.8 to 8.1 days for BF in 2007 and 2008, resp.. The difference between the earliest and the latest population in days to FF was 7 days in 2007 and 5.7 days in 2008. Standard deviations of FF evaluations were comparable to the SD of the BF measurements. The year effect was very pronounced. The difference between the two years we suppose was due to the very hot April in 2007 in Provence, France. The April 2007 displayed a mean temperature that was 6 °C higher than average. This led to a strong year but supposedly also to a strong genotype*year interaction. The year effect was 6.2 days for BF and 2.2 days for FF, resp..

For genetic map construction and QTL mapping, the individual F2 plants were genotyped with 173 EST-derived SNP markers. In addition, we developed markers for a total of 14 recently described flowering time genes in *B. vulgaris* or candidate genes which were identified on the basis of homology to floral regulators in *A. thaliana*. Candidate genes included floral integrators and homologs of key genes in the major floral regulatory pathways. Ten of these genes were

integrated into the genetic map. The map had a total size of 458.0 cM and an average marker interval of 2.5 cM.

By use of a mixed-model approach we identified five QTL with additive effect for flowering time on chromosomes II, V, VI and IX. However, none of the QTL occurred in both 2007 and 2008, possibly as a result of strong genotype*year interaction. Five candidate genes mapped within the confidence intervals of the QTL on chromosomes II, V and IX. Two adjacent QTL on chromosome II were located in a chromosomal region harboring the recently isolated *B* locus for annuality, including the floral activator gene *BOLTING TIME CONTROL 1* (*BvBTC1*), and the *CONSTANS*-like gene *BvCOL1*. One QTL co-localized with the photoperiod response candidate gene *CYCLING DOF FACTOR 2* (*BvCDF2*) on chromosome V. Genes and markers identified in this study can be used for marker-assisted selection of sugar beet genotypes with adequate flowering times for breeding programs and hybrid seed production.