



Federal Ministry
of Food
and Agriculture

AppleClimateBreeding

Establishing the tools for breeding of new apple (*M. domestica*) cultivars with altered flowering time that are better adapted to climate change

country/countries	Germany/New Zealand
funding agency	Federal Ministry of Food and Agriculture – BMEL
project management	Federal Office for Agriculture and Food – BLE
project coordinator	
project partner(s)	Dr. Vincent Bus The New Zealand Institute For Plant & Food Research Limited (PFR), Hawke’s Bay Research Center, Havelock North 4157, New Zealand
project budget	99.828,00
project duration	01.03.2020–31.03.2023

key words	Apple breeding, climate change, dormancy, flowering time, genetic mapping
background	<p>Climate change poses a number of challenges for fruit growing. The influence of higher temperatures on winter dormancy is very serious. In mild climates, warmer winters mean that there are not enough cold hours and the passage of winter dormancy is disrupted. This leads to irregular flowering patterns and poor yields. In our climate, increased spring temperatures lead to an ever earlier start of flowering and thus to an increase in damage caused by late frosts. To counter these phenomena, more knowledge is needed to efficiently breed new varieties that are adapted to warmer temperatures. For this purpose, segregating populations between apple varieties and species were produced, genotyped and phenotyped. The results were used to determine genomic regions that influence winter dormancy, bud burst and flower development.</p>
objective	Mapping of QTL that determine flowering time, identification of candidate genes and development of molecular markers for flowering time.

results	<p>Genetic maps were generated for MAL0940 and 'Rote Sternrenette' consisting of 2457 and 3660 SNPs, respectively, and 56 SSR markers segregating in both genotypes. QTL mapping of phenology data detected significant gene loci for the dormancy and BBCH53 to BBCH65 stages at the top of chromosome 9 in 2021 and 2022. At the bottom of chromosome 15 is another locus linked to phenology. Further, SSR markers were developed for the QTL at the top of chromosome 9, which has the greatest phenotypic effect and influences the most traits. In addition, candidate genes located in this chromosomal region and their expression patterns during dormancy were determined in both parents. The gene MdICE1, known from <i>A. thaliana</i> as Inducer of CBO Expression 1, showed a significant genotype effect in expression during dormancy. The gene was isolated from both parents and four alleles were sequenced. An SSR marker was developed for the identified sequence variation that can distinguish all four parental alleles. It was shown that this marker is significantly associated with bud burst and flowering time. The greatest effect has an allele of 'Rote Sternrenette', which leads to later bud burst. Thus, this marker is a potential marker that can be used in breeding programs for late bud burst and late flowering varieties. The results were compared with the New Zealand project partner, which led to an increase in confidence and the identification of further candidate genes for the regulation of bud burst.</p>
recommendations	<p>There are clear differences in the flowering time of apple cultivars, which are genetically determined. The development of methods for the early selection of seedlings with different flowering times is possible and should be continued in order to develop markers that can be used in different populations.</p>

photos

