

# A new flowering time gene on wheat chromosome 3B; characterization and genetic mapping

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## ABSTRACT

A substitution of the 3B chromosome from the Czech alternative wheat variety Česká přesivka into two spring wheat varieties (Sandra and Zlatka), and two winter varieties (Vala and Zdar), showed a significant effect on flowering time. This suggests an earliness *per se* gene (*eps*) is located on this chromosome. This gene could be homoeologous to the previously known *eps* gene on chromosome 3A. The substitution lines Zlatka (CP3B), Sandra (CP3B), Vala (CP3B) and Zdar (CP3B) were grown under different photoperiod and vernalization regimes. An evaluation of apical shoot development revealed an earlier start to the individual stages of spike development, by, for example, 5 to 7 days in Zlatka as compared to Zlatka (CP 3B) grown under short days. Genetic maps of chromosome 3B were developed using recombinant substitution line populations produced from Zlatka x Zlatka (CP 3B) and Sandra x Sandra (CP 3B) crosses. Combining these with phenotypic data from glasshouse and growth room studies unveiled a QTL in both populations, which mapped to a position near the centromere of 3B.

## INTRODUCTION

Recent studies have made significant advances in our understanding of flowering time control in cereals, particularly on the genetics, physiology and molecular biology of the major genes that control vernalization and photoperiod responses, respectively (Laurie et al.2004; Cockram et al. 2007). There is also growing evidence of the influence of *eps* (earliness *per se*) genes that mainly occur as QTL, controlling flowering time independent of environmental conditions. *Eps* genes are located throughout the wheat genome, having been found on chromosome groups 2, 3, 4, 6 and 7. They supposedly influence the number of floral primordia or rate of floral primordia initiation (Slafer, Rawson 1994, Worland 1996, Islam-Faridi et al.1996).

The presence of a flowering time gene(s) on chromosome 3B had been indicated by the delayed flowering of wheat plants with substitutions of chromosome 3B from the alternative wheat variety Česká Přesivka (CP3B) into the background of a spring variety Zlatka, and the analysis of this effect revealed a probable effect of an *eps* gene(s) (Košner 1987, Košner, Pánková 2002). A detailed analysis of the influence of chromosome 3B substitutions has led to the hypothesis of the presence of an *eps* gene that could be homoeologous to the previously known *eps* gene on chromosome 3A.

## MATERIALS AND METHODS

### *Dynamics of apical development*

Apical development and differentiation were assessed in plants of Zlatka (CP3B) and its parental cultivar Zlatka. The plants were sown into an artificially covered field plot on 20 April and grown under a short day (10 hours) regime. Morphological changes of the apices were analysed under the microscope at weekly intervals. Parallel checks of the time to heading of the plants were carried out. Both the dynamics of apical development and measurements of time to heading were assessed in two seasons, 2006 and 2007.

### *Mapping populations and molecular fingerprinting of chromosome CP 3B substitutions*

Mapping populations of recombinant substitution lines resulting from crosses between Zlatka (CP3B), Sandra (CP3B) and their parental varieties Zlatka, and Sandra, respectively, were obtained for mapping chromosome CP3B using SSR molecular markers.

Monosomic recombinant substitution lines of Sandra/Sandra 3B/Sandra (CP 3B) were grown for phenotypic screening and molecular marker analysis to map the CP 3B flowering time gene. SSR molecular fingerprinting of the Zlatka//Zlatka/Zlatka (CP 3B F<sub>3</sub>) recombinant substitution lines was also carried out to develop a parallel map of chromosome 3B. The data obtained were processed using JoinMap computer software.

## RESULTS AND DISCUSSION

The earlier start of the individual stages of spike development, on average by 5 to 7 days, was detected in the variety Zlatka as compared to Zlatka (CP 3B) when grown under short days, and it took place throughout the period of reproductive development (Fig. 1). This suggests the effect of the flowering time gene(s) act from the very beginning of growth and development of the plant.

A more marked effect on flowering time - up to 19 days - was observed between Vala (CP3B) and Vala (Pánková et al. 2006). The impact of chromosome CP3B substitutions on heading time had been analysed in more detail to reveal that, separate from photoperiod, there was an important influence of interactions between genotype and vernalization (Košner and Pánková 2002).

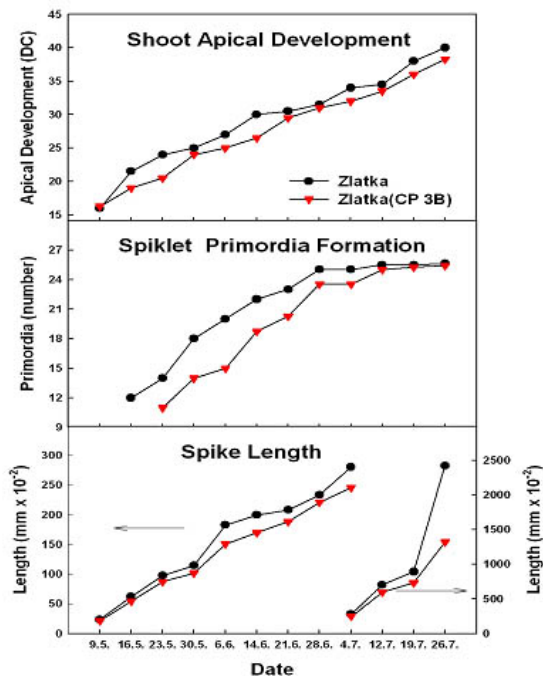


Fig. 1 Shoot apical development of wheat plants under short day conditions (12 hours) was delayed by 5 - 7 days in the substitution line Zlatka (CP3B), compared to the parental variety Zlatka.

A better winter survival had been referred to by Košner (1987) in Zlatka (CP3B) compared to Zlatka. However, a detailed test of frost tolerance under natural winter conditions combined with a laboratory frost test in the winters of 2006, 2007, respectively, has not revealed enhanced survival of the substitution lines compared to the original varieties.

From all experiments it is possible to conclude that the CP 3B chromosome carries an allele for earliness *per se* at a locus located near the centromere on 3BL. This locus is designated *QFT.cri-3B.1*. Using common polymorphic makers it was possible to align the maps for the RSL populations with each other, and also with other chromosome 3B maps available at JIC. Two populations, Spark/Rialto and Charger/Badger, had been extensively genotyped for FT in the field (Snape et al. unpublished). In these crosses a flowering time QTL was distal to the marker locus *Xgwm285*, which was 16 cM proximal to *Xbarc164*. The alignments of the Sandra/Sandra 3B/Sandra (CP 3B) and Zlatka/Zlatka/Zlatka (CP 3B) maps with the Spark/Rialto and Charger/Badger 3B maps are shown in Fig. 2 (Pánková et al. 2008, in press). To localise the QTL more precisely, more SSR primers were used. These primers (*Xgpw*) were kindly provided by Pierre Sourdille from INRA, France. Using them, the previous

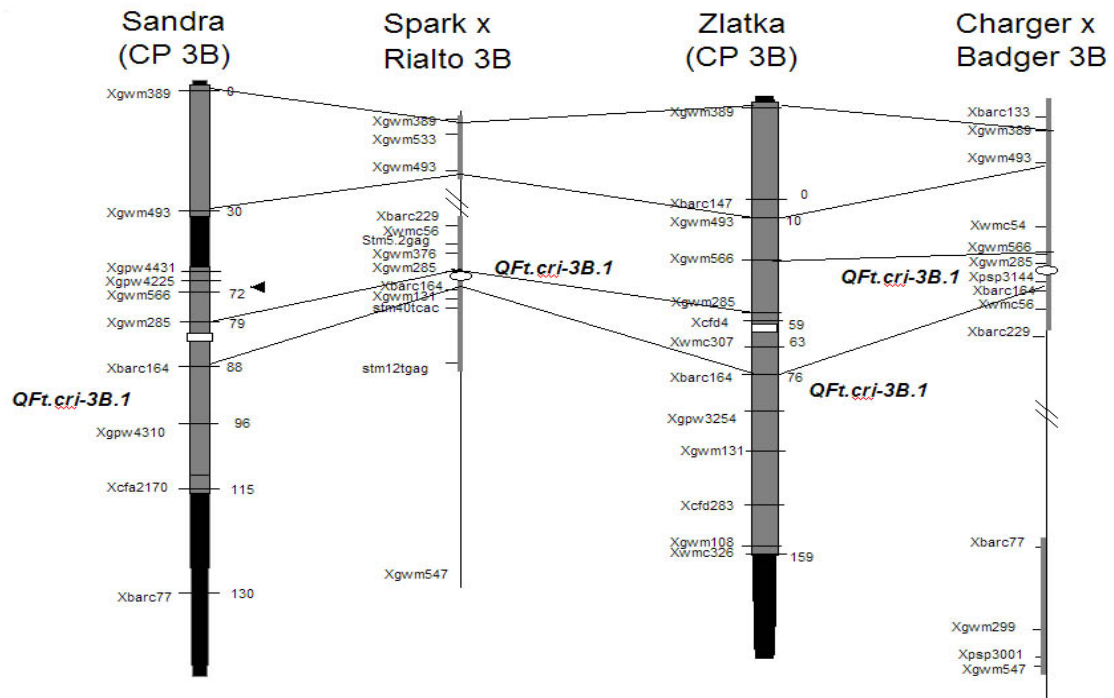
QTL location was confirmed, but unfortunately, closer markers to the QTL were not obtained.

## ACKNOWLEDGEMENT

The work was supported by the grant 521/05/0257 of the Grant Agency of the Czech Republic, by the grant CZ/06/A/PL/13438 of the Ministry of Education, programme Leonardo, and by the research plan MZe CR 0002700602.

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**Fig. 2 Comparative genetic maps and QTL locations for the Sandra//Sandra 3B/Sandra (CP 3B) and Zlatka//Zlatka/Zlatka (CP 3B) recombinant substitution line populations, and comparisons with the 3B maps for the Spark/Rialto and Charger/Badger doubled haploid populations**