Advanced approaches to the analysis of genes and alleles influencing growth, development, and yield components of wheat, with the aim of defining better adapted genotypes

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Introduction

Bread wheat encounters a continuous call for improvement of yield and quality under production conditions of reduced climatic conditions. The genome of common wheat with its haploid constitution renders an intricate but extremely flexible system of genes, involved in the growth and development and thus influencing the yield. Diverse approaches to the analyses of these systems are presented here by the use of two types of recombinant inbred line mapping populations of wheat that have been produced with the aim of searching for better adapted combinations of genes and alleles influencing yield. These mainly include genes and alleles controlling growth habit and flowering time, and resistances to biotic and abiotic stresses.

Three mapping populations (SELGEN / CRI) have been produced based on crosses between three different genotypes of wheat, representing different genotype pools grown under the climatic conditions of the Czech Republic. These are being used to evaluate the existing allelic variation, so as to discover the most favourable combinations of genes and alleles, for optimal growth and yield in the field.

Two CP 3B mapping populations based on substitutions of chromosome 3B of the Czech alternative landrace, Cska Presivka, carrying a novel flowering time gene, QFcri-3B, have been subjected to detailed genetic and phenotypic analyses of the 3B chromosome region of interest. This region spans a large genetic distance between the markers Xgwm285 and Xcfa 2170, and fine mapping using segmental recombinants is being carried out to genetically dissect the region.

SELGEN / CRI mapping populations

These mapping populations have been produced based on the SSD (single seed descent) approach, until obtaining F6 generation. Parental wheat genotypes for the original crosses were chosen to represent genes and alleles most successful in the area of the Czech Republic. Stirat and Ilas are among the most important cultivars registered in the Czech Republic, while the breeding line LINDA/SG-3-93/SG-S1267-92 represents a high quality breeding, including the genes of the variety Linda. These genotypes are contrasting in the response to winter conditions.

Stirat is a typical spring, medium early and medium high (75 – 85 cm) genotype with a high yield potential. It was bred from a combination SG-S209/6*BATIT (Selgen, CR, 2005). Its resistance to diseases, especially to moss, powdery mildew and rice blast is mostly high, good baking quality (FT) is combined with high content of protein.

A medium early, medium high (75 – 85 cm) line SG-S5-01 (Selgen-1) represents alternative type having a medium - high yielding quality. It comes from the cross LINDA/SG-3-93/SG-S1267-92. Its resistance to diseases is medium high, achieves the quality group A. Ilas is a typical high yielding late winter cultivar, having a medium yielding potential and high stem (90 – 98 cm), quality A. It was bred in Celchor, Netherlands, in 2005.

In 2012 the mapping populations were screened in a field trial for basic characteristics of the growth habit, earliness, disease resistance and yield. The diagrams show the obtained variability which will be a good starting point for the detailed genotyping and phenotyping of the lines evaluation.

CP 3B mapping populations

Effect on flowering time (FT) was revealed after the substitution of chromosome 3B of Czech alternative wheat landrace Cska Presivka into backgrounds of two spring wheat cultivars, Sandra and Zlatka after growing the plants under the short day conditions (field trial), and this result was repeatedly confirmed (Kolinec,1996; Kolinec & Pánková, 2002).

To map the novel FT gene, two populations of recombinant substitution lines (RSL) were developed from back crosses of substitution lines Sandra (CP 3B) and Zlatka (CP 3B) carrying chromosome 3B of Cska Presivka, by the technique described by Law and Worland (1973). The RSL were developed from the F1 hybrids Sandra (CP 3B) x Sandra and Zlatka (CP 3B) x Zlatka. Each of the individual RSL plants was scored for seed mapping and phenotypic analyses. Dormant recombinants (expected at 25% frequency) were identified by SSR marker analysis as heterozygotes in the selected generation. Phenotypic analyses included FT experiments under a long and short day controlled regimes.

Genetic analyses

Genetic maps of chromosome 3B were developed using the RIL mapping populations of Sandra/Sneček (SBands) (CP 3B) and Zlatka/Zlatka/Zlatka (CP 3B). DNA was extracted from leaf samples using Quest & DNAeasy kits. Mapping was carried out using publicly available simple sequence repeat (SSR) markers sets. Primer giving clearly scorable polymorphisms on the recipient parents and 3B substitution lines were then genotyped on the entire mapping populations. DNA fragments were amplified with PCR and run on 6% polyacrylamide gels for separation. The silver staining technique was used to visualize fragments (Bassam et al. 1991). Data for each population were accumulated into a genotype. Idx; and genetic maps were developed using JoinMap software. The FT gene (QFcri-3B) was genetically mapped to the area between the markers Xgwm285 and Xcfa 2170 (Pánková et al. 2008).

Most recent experiments and analyses

More analyses and more detailed study on growth and development are being carried out to genetically dissect the region and describe the function of QFcri-3B. Production, generation and phenotyping of segmental recombinant lines has been continued while new PCR based markers derived from the Dars have been obtained aiming to the fine mapping and candidate gene analyses.

In parallel, the apical development of parental cultivars, substitution lines and RIL populations has been studied in detail in more FT experiments under different controlled and field conditions (temperature, photoperiod) to define the distinction between present genotypes.