

# MOLECULAR CYTOGENETIC IDENTIFICATION, PHYSICAL MAPPING AND PHENOTYPING OF WHEAT-BARLEY INTROGRESSION LINES

Molnár-Láng, M.<sup>1</sup>, Szakács, É.<sup>1</sup>, Molnár, I.<sup>1</sup>, Kruppa, K.<sup>1</sup>, Sepsi, A.<sup>1</sup>, Cseh, A.<sup>1</sup>, Dulai, S.<sup>2</sup>, Aranyi, N.<sup>3</sup>, Hoffmann, B.<sup>3</sup>

<sup>1</sup>Agricultural Research Institute of the Hungarian Academy of Sciences, Martonvásár, HU

<sup>2</sup>Department of Plant Sciences and Plant Physiology, Eszterházy Károly College, Eger, HU

<sup>3</sup>Department of Plant Sciences and Biotechnology, University of Pannonia, Georgikon Faculty, Keszthely, HU

## Introduction

Wheat and barley are two important cereals worldwide. Sexual hybridization of these species makes it possible to transfer agronomically useful genes from barley into wheat. Wheat-barley hybrids can be produced only with wheat genotypes carrying the crossability alleles *kr1*. Embryo culture and pollinations should be carried out under favourable environmental conditions, and hormone treatment of the pollinated flowers is needed, but even in the best conditions the seed set is extremely low. The main objective of our experiments was to develop new wheat × barley hybrid combination with agronomically adapted barley cultivars in Martonvásár. It was planned to develop genetically stable wheat-barley introgression lines from the hybrids, to characterize the introgressed barley chromosomes with fluorescence *in situ* hybridization (FISH) and with molecular markers. The wheat-barley translocation lines were used for physical mapping of the SSR markers on wheat and barley chromosomes. The drought tolerance of the different lines were tested under rain shelter in Keszthely and Martonvásár.

## Materials and methods

### Plant material:

wheat genotypes –Mv9kr1, Asakaze komugi  
barley cultivars – Betzes, Igri, Manas  
Wheat-barley addition, substitution and translocation lines

### Methods:

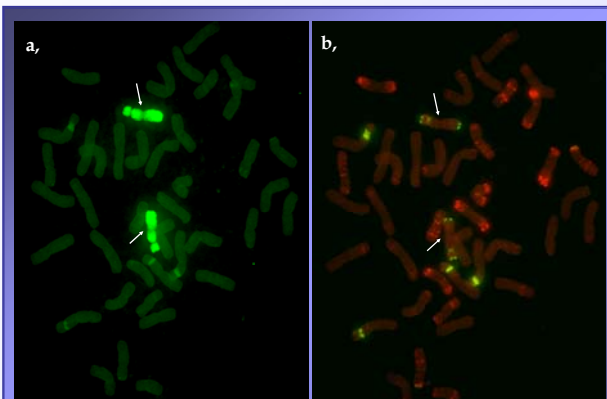
- Pollination, embryo culture  
- *In situ* hybridization:  
FISH-with repetitive DNA probes (HvT01, GAA, Afa-family, pTa71, pSc119.2)  
GISH: probe: total barley genomic DNA  
Labelling: nick translation with biotin-avidin  
FITC and digoxigenin- antidig- rhodamine  
- Wheat and barley SSR markers

### Drought tolerance test in the field:

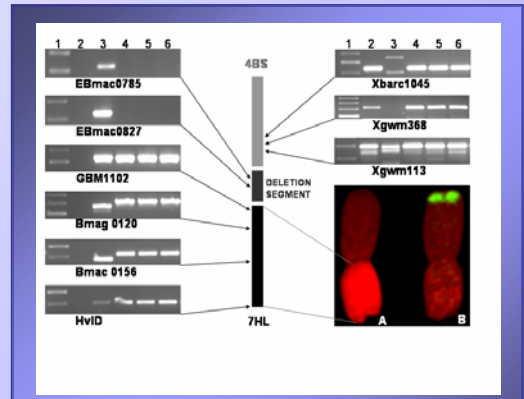
Keszthely: 12 genotypes, the half length of the rows was covered with a plastic folia (Fig.4.)

Martonvásár: 17 genotypes were sown under a rain shelter, and under irrigated conditions in three replications.

Plants were covered with a shelter from April in both places.



**Fig.1.** Detection of a wheat × barley disomic addition line using GISH (a), and identification of the 6H chromosomes using FISH with the probes HvT01, Afa-family and pTa71 (b) (arrows).

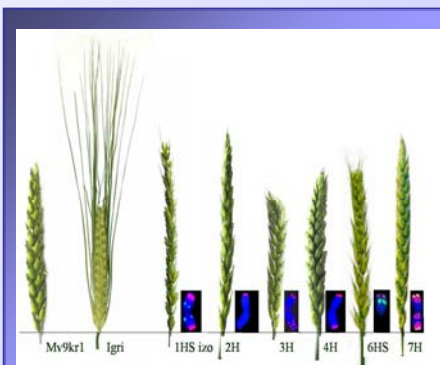


**Fig.2.** Physical map of SSR markers within the 4BS.7HL translocation, including the centromeric deletion of 7HL (A). The electrophoretic patterns of the 7HL specific markers are indicated on the left of the schematic chromosome while the electrophoretic patterns of the 4BS- specific markers are indicated on the right (1: size marker 50 bp; 2: Chinese spring wheat DNA; 3: Manas barley DNA; 4,5,6: DNAs from the translocation lines).

## Results and conclusions

Wheat × barley hybrids were produced in the following hybrid combinations: Chinese Spring × Betzes, Mv9kr1 × Igri, Asakaze komugi × Manas. 2H, 3H, 4H, 6H, 7H wheat/barley disomic addition lines were produced from the Mv9kr1 × Igri and the Asakaze komugi × Manas hybrid combinations (Fig.3).

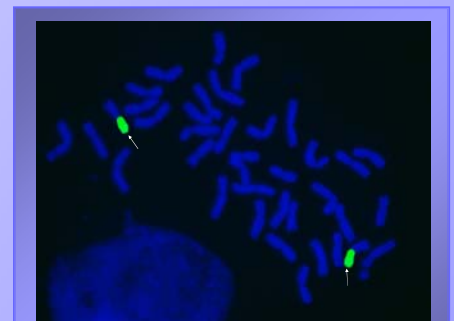
The following wheat × barley translocation lines were produced: 2DS.2DL-1HS, 7DL.7DS-5HS, 3HS.3BL, 6BS.6BL-4HL, 4D-5HS, 4BS.7HL (Fig.5).



**Fig.3.** Spikes of a wheat × barley (Mv9kr1 × Igri) disomic addition line and the FISH pattern of the barley chromosomes using HvT01 (red) and pTa71 (green) FISH probes.



**Fig.4.** Drought tolerance test of the wheat/barley addition, substitution and translocation lines under rain shelter in the field at Keszthely.



**Fig.5.** Detection of a wheat × barley (Asakaze komugi × Manas) translocation line using GISH. Total barley genomic DNA was labelled with Biotin, the barley chromosome arms are green (arrows).

The presence of the barley chromosomes was detected using GISH and FISH (Fig.1.). The cytological identification was confirmed with the help of molecular markers. SSR markers were physically mapped on wheat (7D) and barley (7H) chromosomes with the help of wheat/barley translocation lines (Fig.2.).

The drought tolerance of the wheat/barley introgression lines was analysed under a rain shelter in Martonvásár and in Keszthely in two consecutive years (Fig.4.). Data were obtained for heading date, plant height, root/shoot ratio and components of grain yield.

The most favourable results for root/shoot ratio was measured in case of 7D-5HS and 4H(4D) substitution in Keszthely. The present observations confirmed the earlier data in PEG induced osmotic stress (15%) where the water use efficiency (WUE) of the 4H(4D) substitution line was much higher than the wheat parent.