



# CHROMOSOME GENOMICS IN WHEAT

## IMPORTANCE OF WHEAT

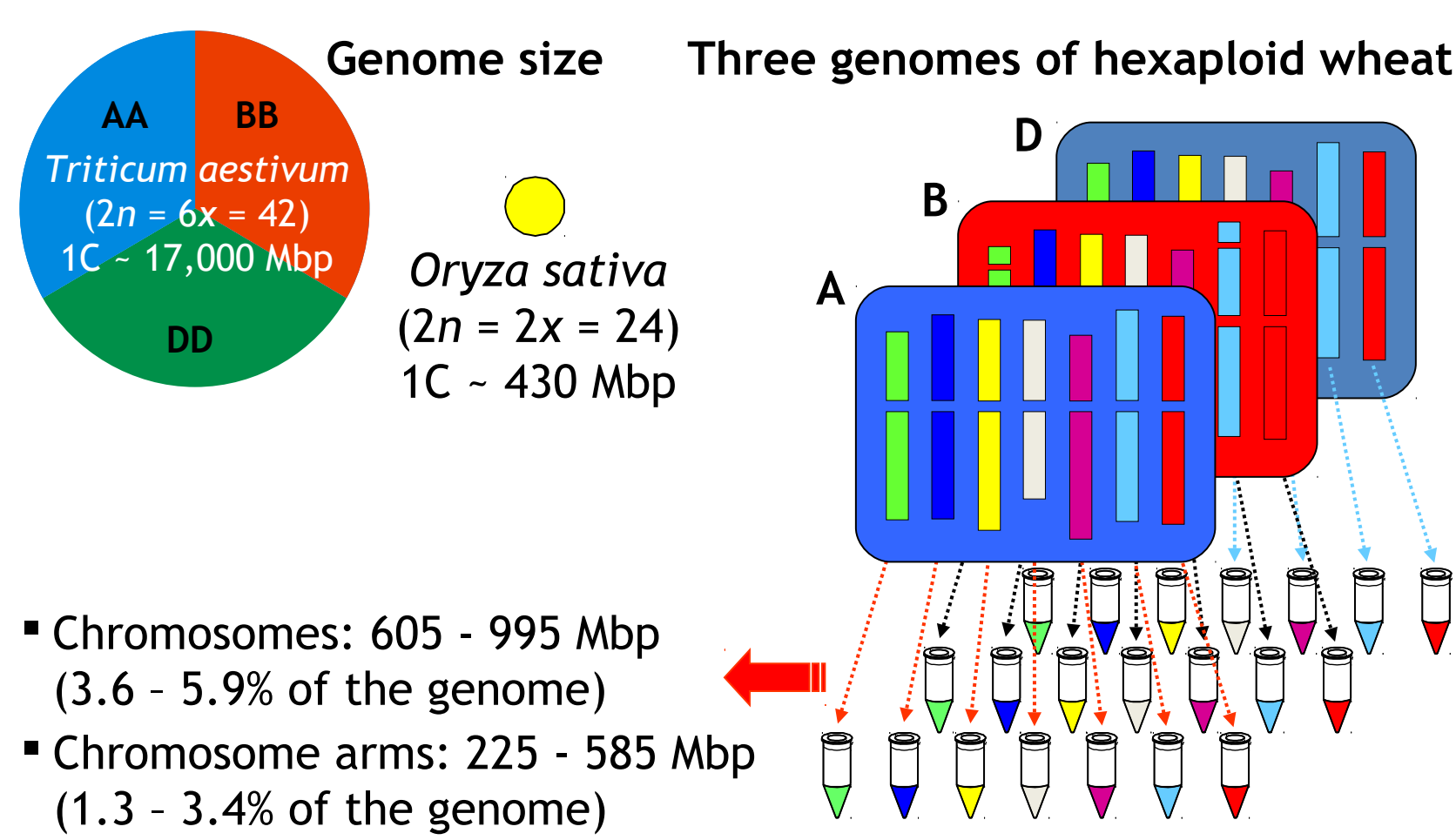
Bread wheat (*Triticum aestivum* L.) is one of the world's most important crops providing staple food for 35% of the world's population and 20% calories consumed (<http://www.CIMMYT.org/>). The bread wheat is grown in all areas of temperate zone and its global significance could be compared only with rice. As the World's population is supposed to reach 9Bn by 2050, the production of wheat must increase by 60%. Wheat (*Triticum aestivum*,  $2n = 6x = 42$ ) is characterized by a large genome (1C - 17,000 Mb) and presence of three homeologous genomes. These features hamper gene isolation, mapping and genome sequencing and assembling

## CHROMOSOME GENOMICS

The concept of chromosome genomics is based on dissecting nuclear genomes to individual chromosomes, whose DNA can be analyzed separately. This approach brings a dramatic reduction in DNA sample complexity and facilitates genome mapping, sequencing and positional cloning. In polyploid wheat, it helps to avoid problems due to sequence redundancy and occurrence of homoeologous sequences.

## WHAT WE ARE DOING

### DISSECTING THE GENOME

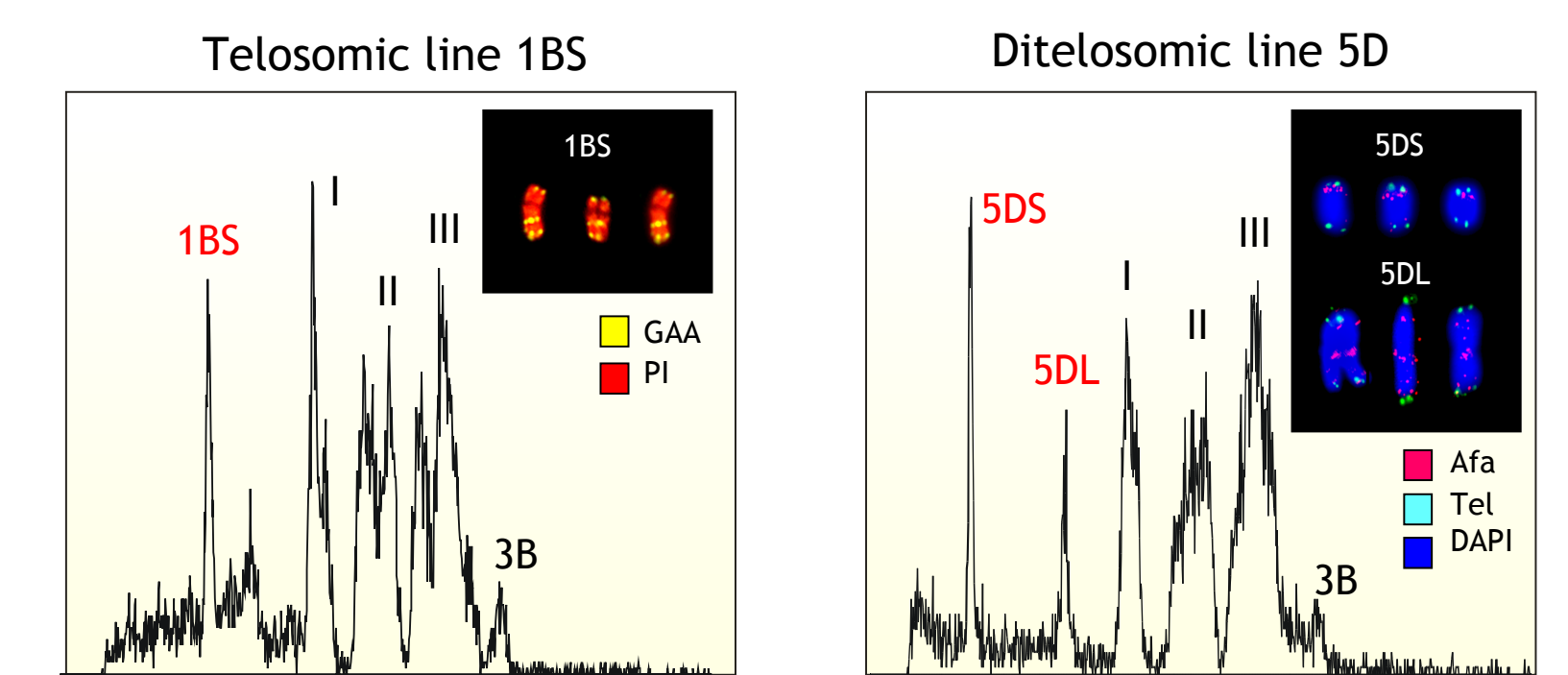


### WHERE WE ARE

- Flow cytometry can be used to sort chromosomes in bread wheat
- Due to similarities in DNA content, only chromosome 3B can be flow-sorted in most of bread wheat cultivars. Other chromosomes can be sorted in groups.
- All chromosome arms can be sorted from telosomic lines. In these lines, the arms are stably maintained as telocentric chromosomes.
- Flow-sorted chromosomes are intact, and high molecular weight DNA can be prepared from them, suitable for molecular biology and genomics applications

### SORTING CHROMOSOME ARMS

Chromosome arms can be sorted from telosomic lines. Two different arms can be sorted simultaneously from most of ditelosomic lines

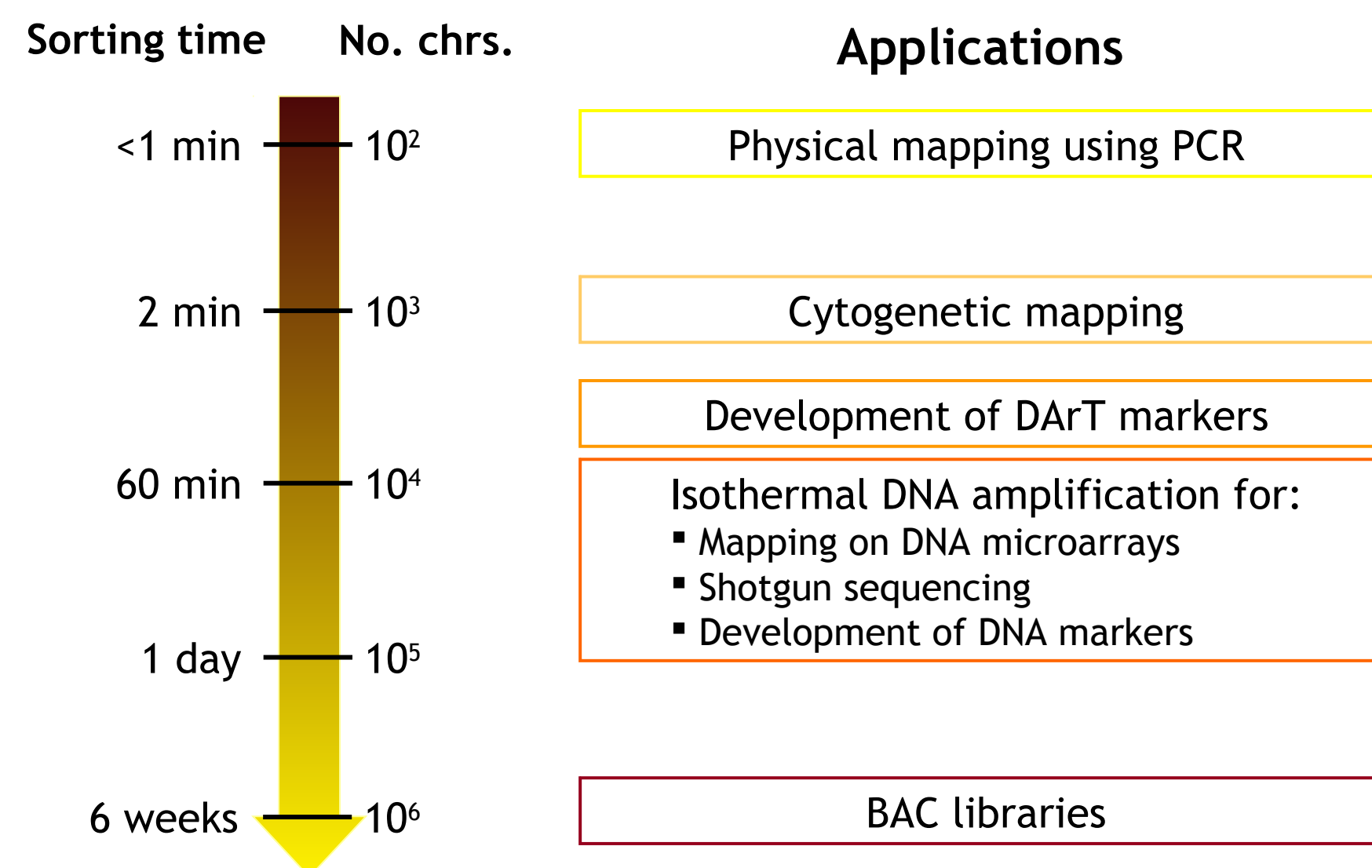


### CHROMOSOME-SPECIFIC BAC LIBRARIES

Chromosome-specific BAC libraries have a much smaller number of clones than genomic libraries and are easy to use. They facilitate targeted development of DNA markers, positional gene cloning and assembly of ready-to-sequence physical maps. Construction of BAC libraries from all chromosomes of hexaploid wheat is in progress. To date, BAC libraries are available for 19 out of the 21 chromosomes of wheat.

<http://olomouc.ueb.cas.cz/dna-libraries/cereals>

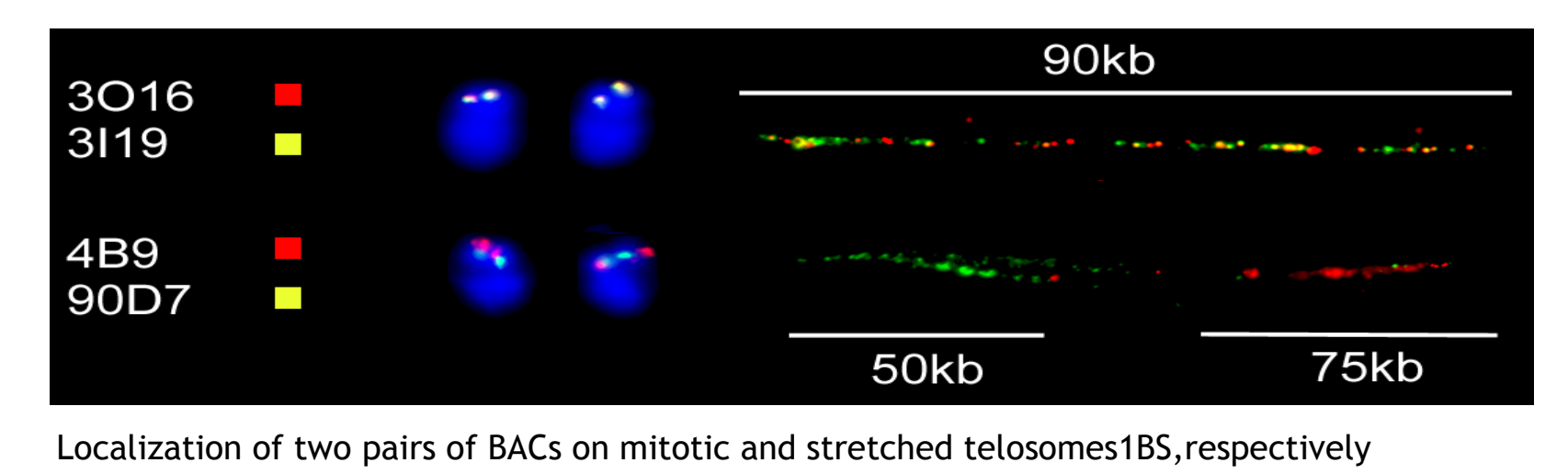
### APPLICATIONS OF SORTED CHROMOSOMES



### CYTOGENETIC MAPPING

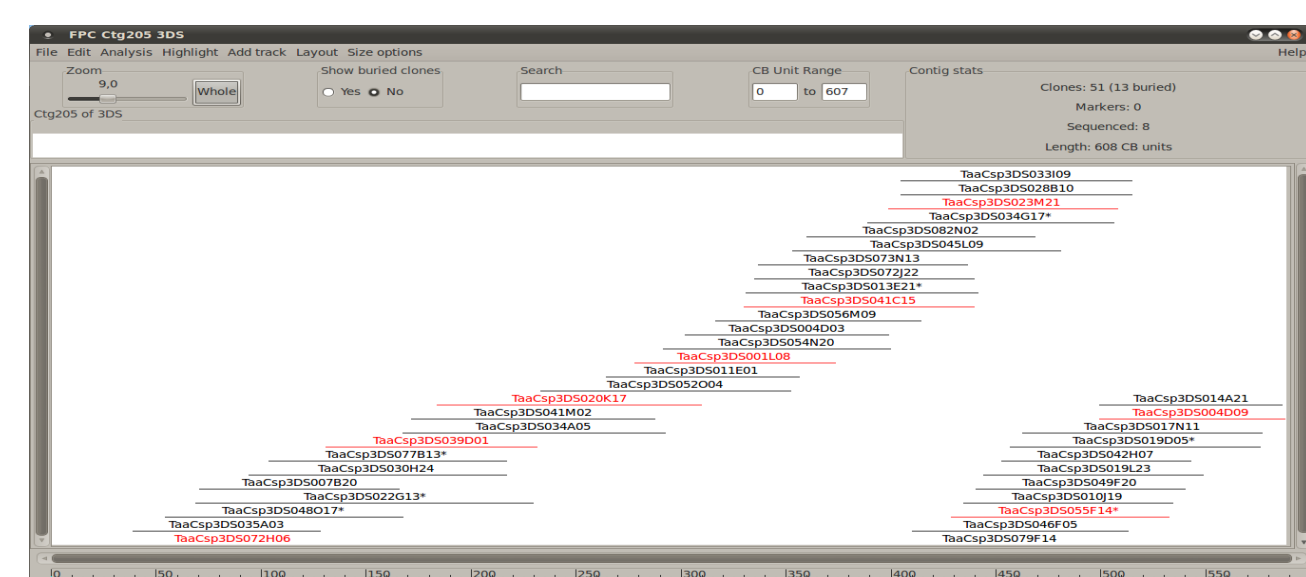
Advantages of using flow-sorted chromosomes for FISH:

- Higher throughput (mapping on large populations of chromosomes)
- Higher sensitivity (localization of short DNA sequences ~2 kb)
- Higher spatial resolution



### PHYSICAL BAC CONTIG MAPS

The chromosome-based strategy simplifies BAC contig assembly and construction of physical map of hexaploid wheat

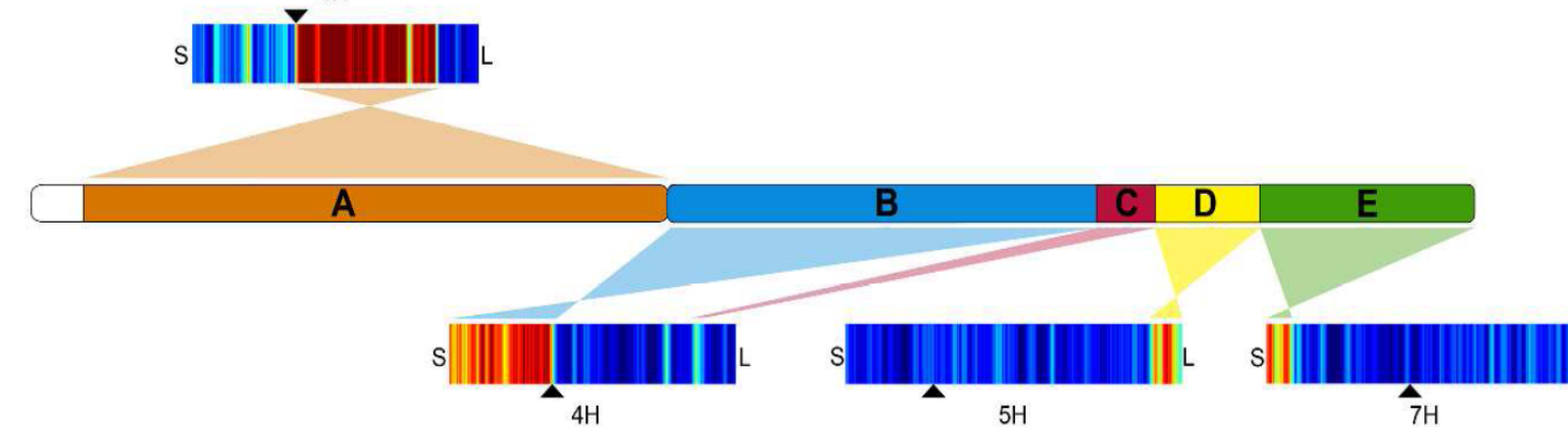


Ctg205 from 3DS physical map. Red BAC clones belong to 3DS Minimum Tiling Path (MTP).

### NEXT-GENERATION SEQUENCING

Next generation sequencing of flow-sorted chromosomes enables the assembly of genes and low copy regions. Syntenic relationship between wheat (barley, rye) and sequenced genomes of related species is used to produce annotated syntenic builds whereby genes are placed in an approximate order and orientation. These assemblies can be used to identify candidate genes, discover SNPs and investigate genome evolution.

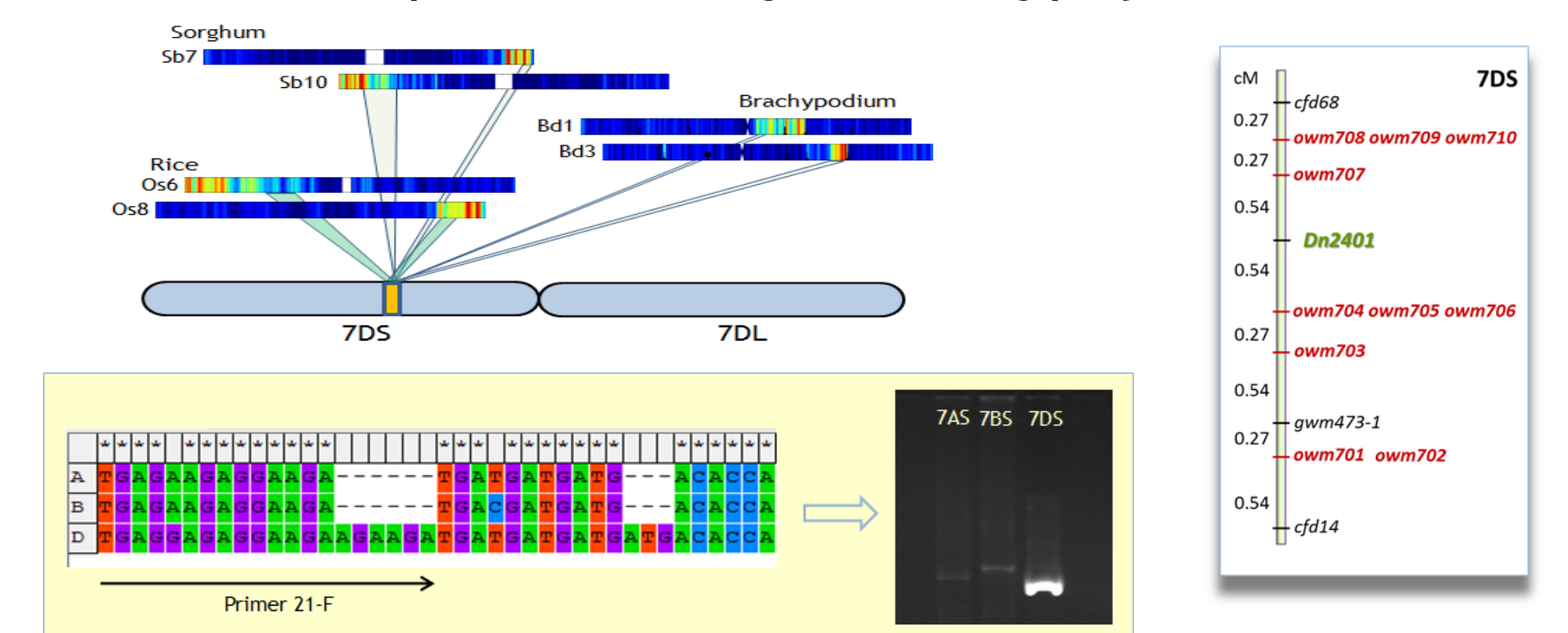
#### Comparison of wheat chromosome 4A sequence with that of barley chromosomes



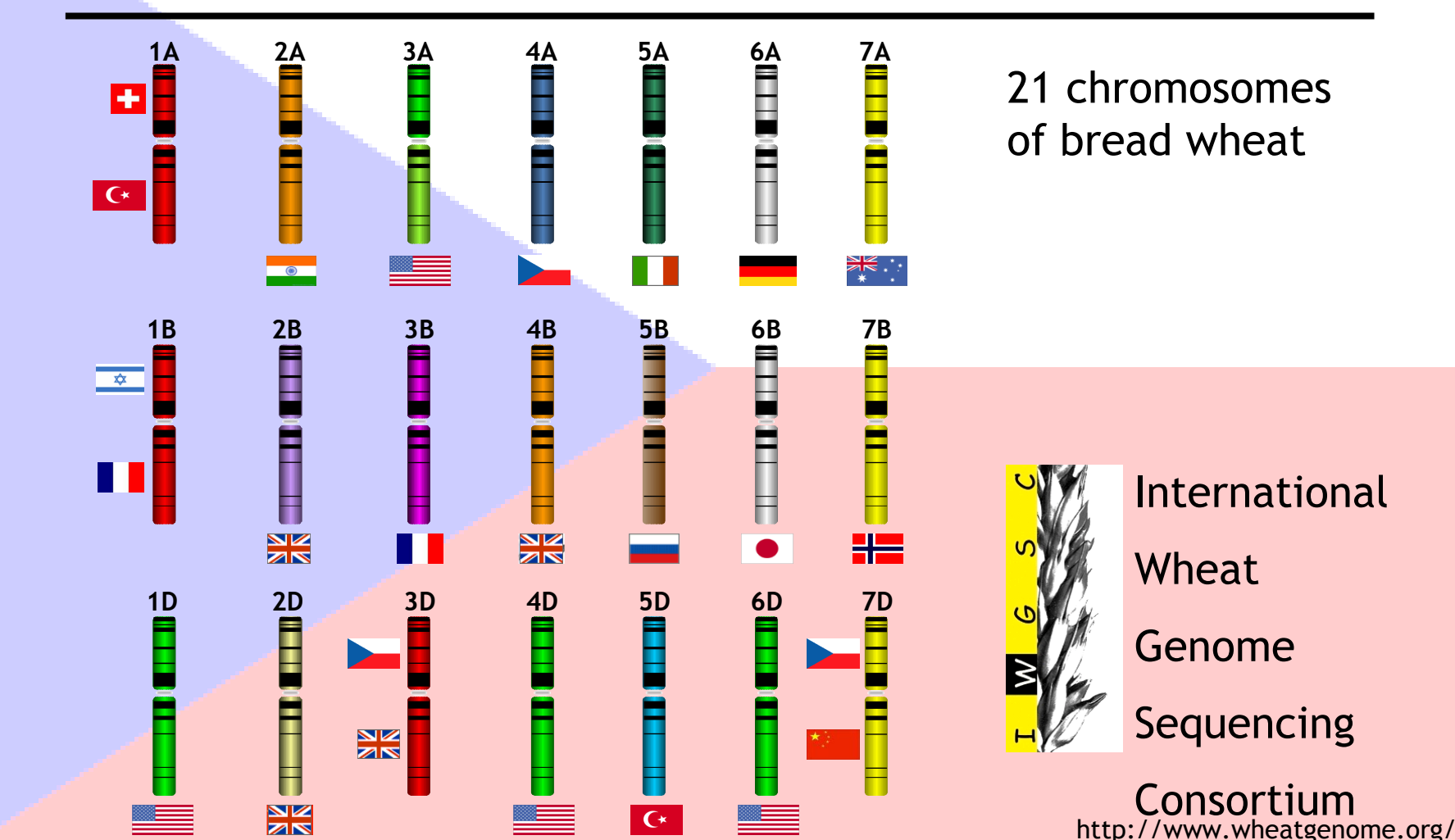
### POSITIONAL GENE CLONING

Cloning of agronomically important genes should accelerate conventional breeding efforts and production of new efficient crop cultivars. Projects for cloning Russian wheat aphid resistance gene, powdery mildew resistance gene as well as a gene controlling flowering time are underway.

#### Russian wheat aphid resistance gene cloning project



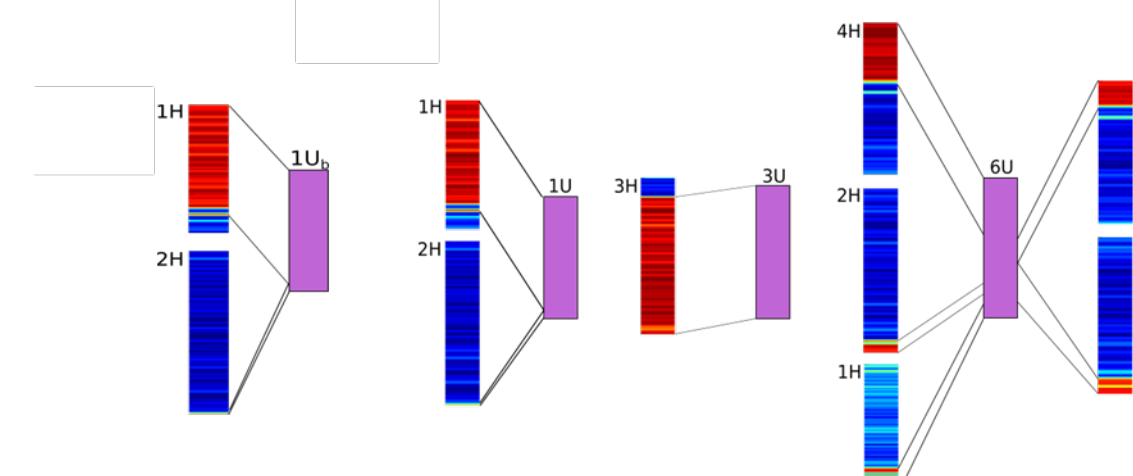
### International collaboration on the wheat genome



### ALIEN INTROGRESSION

The gene pool of elite bread wheat is relatively narrow. Introgression of additional variation found in genetic resources should to increase yield stability under environmental and biotic stress and further improve wheat. To support these efforts, we have developed chromosome genomics in two wild diploid wheats, *Aegilops umbellulata* and *Ae. comosa*, and their allotetraploid hybrids.

Syntenic relationships between the chromosomes of *Ae. biuncialis* (1U<sup>a</sup>), *Ae. umbellulata* (1U, 3U, 6U), and barley



### FUTURE RESEARCH TARGETS

- Chromosome sequencing and assembly
- Functional gene analysis
- 3D organization of wheat nucleus
- Chromosome specific proteomics
- Epigenetic status of chromosomes