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The wheat genome: swimming in an ocean of Transposable Elements

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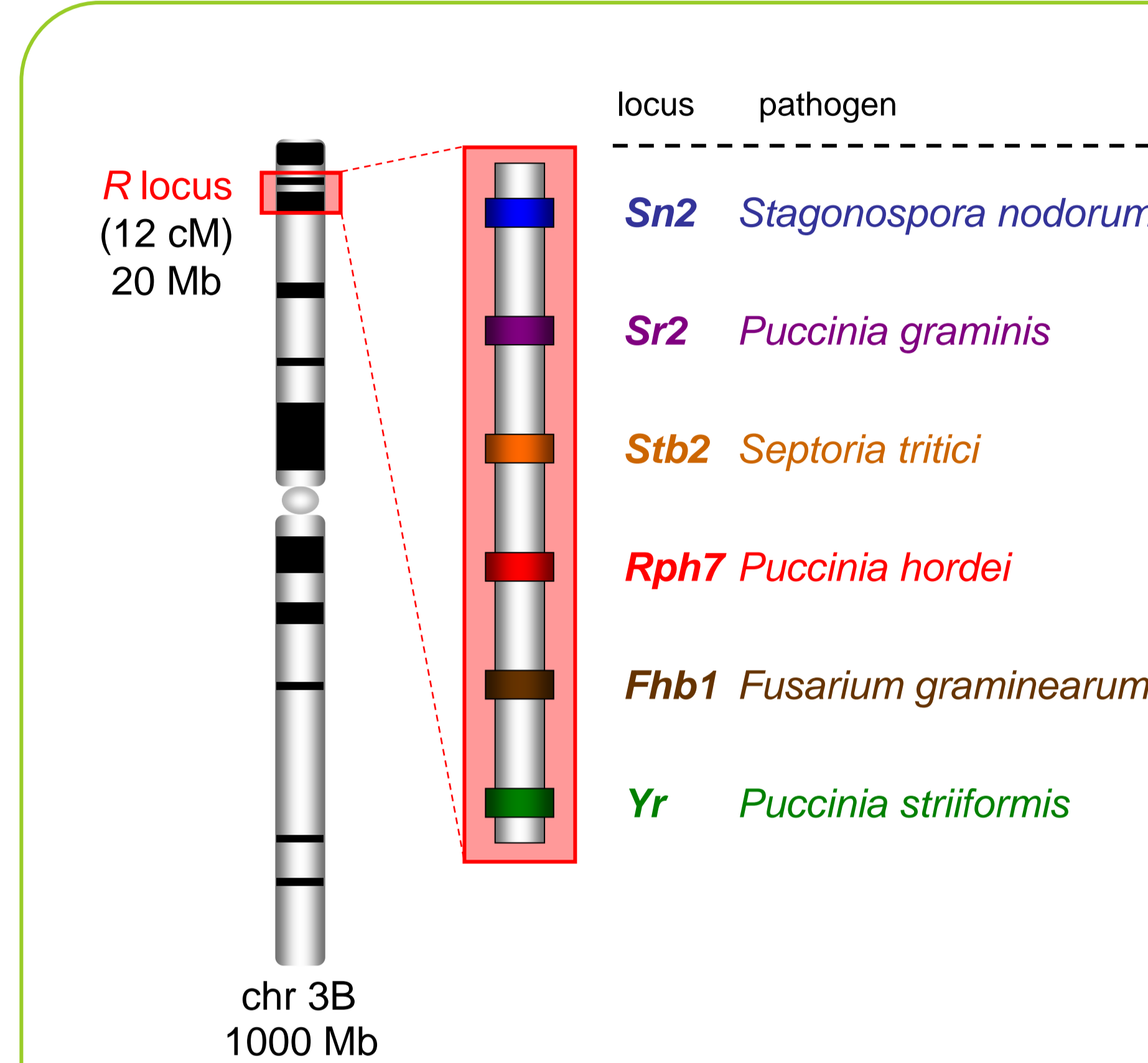
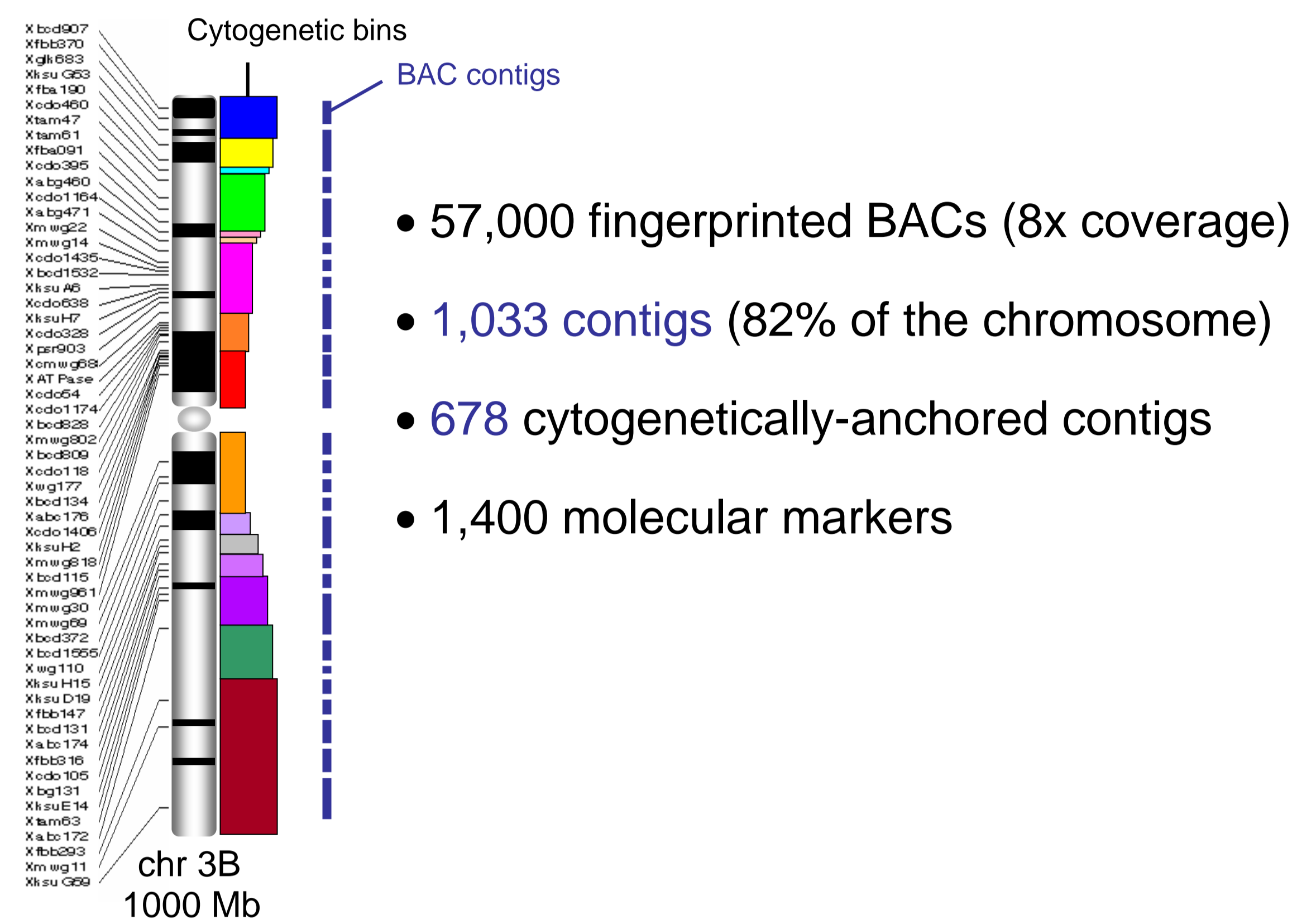
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With **17 Gb** and an **hexaploid** structure, the bread wheat (*Triticum aestivum* L.) genome composition and organization is largely unknown and its molecular characterization remains a challenge. Our current knowledge is limited to the analysis of small fragments (150 kb) and random BAC end sequences.

Using a chromosome-specific approach, we have constructed an integrated physical map of the largest wheat chromosome, 3B (1 Gb), to enhance our knowledge of the structure, function and evolution of the wheat genome.

Establishment of a physical map of the 3B chromosome



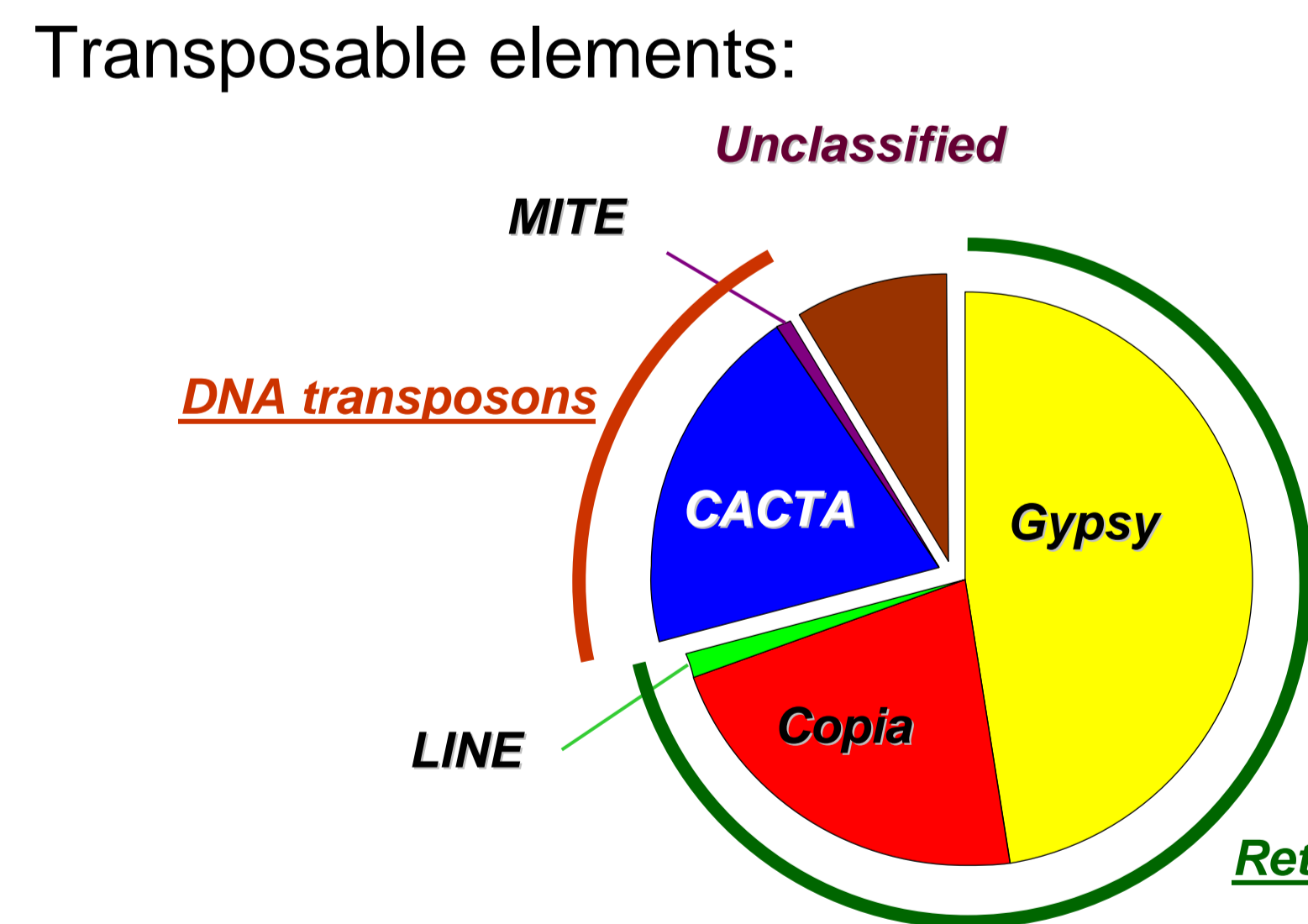
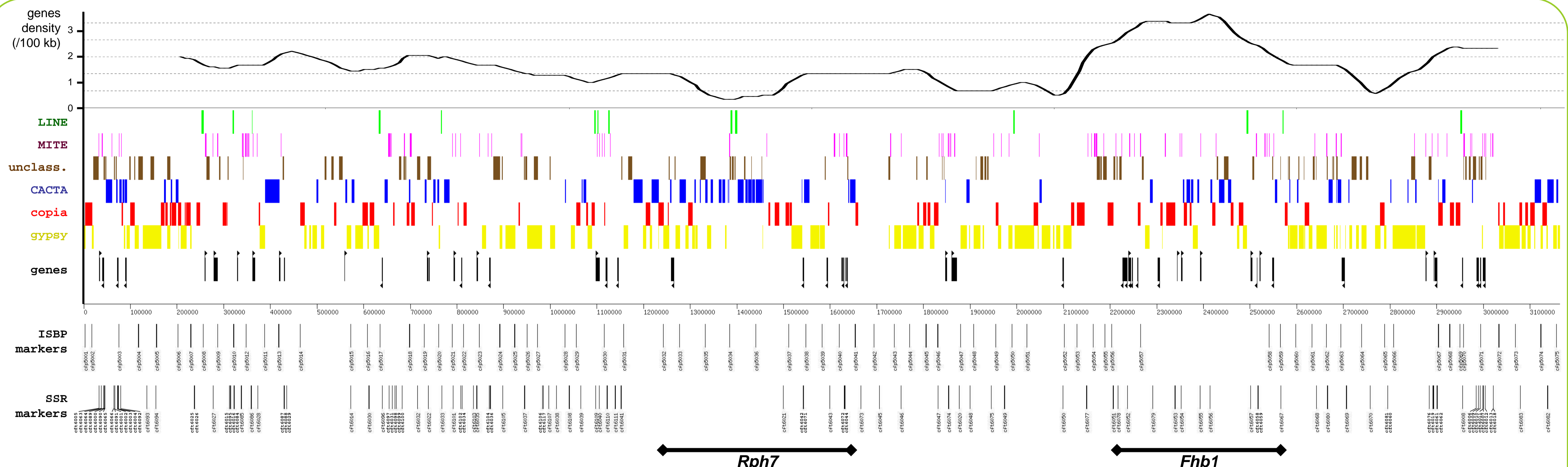
The R locus:

A cluster of at least 6 fungal disease resistance loci has been identified on the short arm of chromosome 3B in hexaploid wheat.

15 contigs (~20 Mb in total) are located in this region and 2 contigs spanning disease resistance loci are currently under sequencing and annotation.

One of them represents **3,2 Mb** and spans the **Rph7 and Fhb1** resistance loci.

Sequencing, annotation and marker development at the Rph7-Fhb1 locus



contig size	3.165 Mb
predicted genes	50
TE (and derivatives)	609

- TEs represents **60%** of the sequence, the majority of them being **LTR-retrotransposons (72%)** and **CACTA family DNA transposons (20%)**. The curated annotation has lead to detect **609 TEs** and truncated derivatives showing variable levels of nested structure.

- The genes and TEs are not randomly distributed along the locus: the length of intergenic regions varies from **500 bps to 283 kb**.

This project aims at sequencing and annotating the first Mb-sized contigs available from the hexaploid wheat genome. Preliminary analyses of this 3.2Mb region revealed the presence of **61** different families of repeated elements, of which **15** are represented by more than 10 copies. Furthermore, the 2 major families (**Fatima** and **Sabrina**, LTR-retrotransposons) alone represent **84** TE copies and cover 15% of the contig.

In addition, these first large wheat genome sequences are an important resource for new TE discovery. Here, about **30** annotated features are potentially unknown TEs. Deeper analyses now remain to be done to confirm, classify and characterize these new elements. Thus, the sequencing of large contigs provides additional insights, compared to random BAC sequencing, into the genome structure and composition and supports the discovery of new TEs.

The high TE content of the wheat genome can be exploited as an endless source of **molecular markers** (ISBP: Insertion Site Based Polymorphism). Here, a potential of more than **1200 ISBPs** (2 markers per TE) can be designed along the 3.2 Mb.

The data generated by this project provides original and new data on the wheat genome structure, function and evolution at a scale of Mb-sized contigs that has never been studied in wheat so far. In addition, it will allow the cloning of economically important disease resistance genes and QTL and enable the development of perfect markers for marker-assisted selection of these genes.

