Epigenomic maps of the bread wheat chromosome 3B

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Eukaryotic genomes are organized in chromatin, which not only packages the DNA, but also functions as a carrier of epigenetic information, including DNA methylation, nucleosome positioning, histone variants and their post-translational modifications. Together these epigenetic marks impact many cellular processes operating on DNA such as transcription, replication, recombination and repair. They are further essential players in the vital control of potentially deleterious DNA sequences such as transposable elements. In large plant genomes, like wheat, where genes are interspersed in considerable amounts of transposable elements that can make up to 80% of the genome, epigenetic marks are likely to play a pivotal role in the regulation of gene expression and maintenance of genome integrity.

In wheat, genome-wide (or chromosome-wide) epigenetic studies have long been hampered by the lack of a reference sequence. However, using a chromosome-based approach, the INRA GDEC recently produced the first reference sequence of a wheat chromosome: 3B.

Taking advantage of this unique genomic resource, we initiated a project aiming at exploring the epigenetic landscape along the bread wheat chromosome 3B in order to better understand the two main chromatin structures: euchromatin and heterochromatin in a polyploid and highly repetitive genome.

The strategy relies on a combination of immunoprecipitation targeting either methylated DNA (MeDIP) or chemically modified histones (ChIP) with sequence capture to focus on the chromosome 3B gene space. DNA fragments are then sequenced on an Illumina HiSeq2000 and reads are aligned to the chromosome 3B genes in order to explore the localization of each mark at each genetic loci and at the chromosome level. The combination of these epigenetic marks will allow us to define chromatin states along the bread wheat chromosome 3B and investigate the distribution patterns of these marks according the gene density or particular motifs of the gene space.