The large 8-Gb diploid genome of diploid rye and the 17-Gb genome of allohexaploid bread wheat are major challenges for genome analysis due to their size and complexity. While the wheat genome is composed of three closely related and independently maintained homoeologous genomes, the rye genome is diploid and has undergone a series of rearrangements in comparison to the wheat and the barley genome. We followed different but complementary strategies to work towards highly enriched molecular knowledgebases for both species.

For wheat we used a novel comparative genomics strategy combined with a whole-genome shotgun approach to identify 90 k of wheat genes and assigned a significant proportion to the component A, B, and D genomes. Our analysis reveals a highly dynamic genome, with rapid and extensive loss of gene family members upon polyploidization and an abundance of gene fragments.

For rye, a strategy that involves genome fractionation, development of a dense marker map and syntenic integration (aka GenomeZipper) was employed. The dense marker scaffold allowed to delineate syntenic segments and chromosomal breaks with high resolution and allowed to position 22 k rye genes on the genome. The integration allows to analyse and compare the rye genome with unprecedented depth and allows to generate fundamental insights into the evolution of the rye genome and the genomic consequences of an outbreeding lifestyle.

Grass microRNA gene paleohistory unveils new insights into gene dosage balance in subgenome partitioning after whole genome duplication.

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The recent availability of plant genome sequences, as well as high resolution gene-based genetic maps, have recently offered the opportunity to compare modern genomes and model their evolutionary history from reconstructed founder ancestors on a very precise scale. *In silico* paleogenomic analyses have revealed the evolutionary forces that have shaped present-day plant genomes. They showed that polyploidisation followed by genomic rearrangements such as nested chromosomes fusions (NCFs) that lead to chromosome number reduction, and the return at a diploid state have been driving forces of plant genome evolution.

Comparative genomic analyses combined with a robust scenario of the evolution of modern monocot and eudicot karyotypes from their diploid ancestors, offer an opportunity to gain insights into the evolution of specific sequences. In this work, we studied more particularly the paleohistory of microRNA (miRNA) in plants. The characterization and comparison of miRNAs sequences and associated protein-coding targets in plants allowed us to unravel (i) contrasted genome conservation patterns of miRNAs in monocots and eudicots after whole genome duplication (WGD), (ii) an ancestral miRNA founder pool in the monocot genomes dating back to 100 million years ago, (iii) miRNA subgenome dominance during post-WGD diploidization process with selective miRNA deletion complemented with possible transposable element (TE)-mediated return flows, and (iv) the miRNA/target interaction-directed differential loss/retention of miRNAs following the gene dosage balance rule. Finally, our data suggest that in grass genomes under-retained miRNAs are mainly involved in the basic regulation of plant development while over-retained miRNAs are likely involved in the regulation of genes associated with stress responses and plant adaptation.