

## Repetitive DNA sequences and the evolution of the *Brachypodium* genus

Model organisms are simplified tractable systems that are used to study larger scientific questions and to address complex research problems. The data that is obtained from studying such organisms are thought to be applicable to other, more complex organisms. *Brachypodium distachyon* was developed as a model system for grasses (a taxon that includes the key cereals like maize, rice and wheat) approximately 20 years ago. It is now well established in this role and offers substantial experimental and genomic resources, e.g. high-quality whole-genome assemblies and the libraries of large chunks of DNA that has been cloned into high-capacity vectors such as Bacterial Artificial Chromosomes. Some of these resources have also been exploited in evolutionary and phylogenetic analyses of the genus. *Brachypodium* consists of approximately 20 diploid and polyploid species that have small genomes and diverse basic chromosome numbers. Earlier studies showed that chromosome rearrangements, mostly nested chromosome fusions, accompanied the evolution of the genus. These chromosomal changes are very often accompanied by the reorganisation of the repetitive sequences. Repetitive DNA is a major driving force of genome evolution. This fraction of nuclear genomes is often abundant and may contribute to more than 90% of the whole genome, especially in higher plants. Thus, knowledge about this relatively rapidly evolving part of plant genomes is essential for making hypotheses and drawing conclusions on the mechanisms that are involved in genome evolution. NGS (Next Generation Sequencing) technologies have been successfully used to investigate the repetitive sequences in many plant genomes. In this current project, a global analysis of the repetitive fraction of the *Brachypodium* genomes will be performed followed by bioinformatic analyses. The results will then be verified using the cytogenetic (fluorescence *in situ* hybridisation; FISH) and molecular (Southern blotting) approaches in order to estimate the genomic organisation, chromosome localisation and the copy number of the repeats. **We plan to test the following hypotheses: (i) The repetitive DNA composition and organisation in selected *Brachypodium* representatives is correlated with their phylogeny; (ii) After hybridisation and polyploidisation, the repetitive DNA sequences underwent reorganisation in the allotetraploid *B. hybridum* and (iii) Different repeat lineages had different rates and/or patterns of evolution.** The evolutionary trends of the different repetitive sequences that accompany the speciation of a genus can be inferred by comparing the pattern of the distribution of each individual repetitive sequence in different *Brachypodium* species. We expect that such a combined molecular phylogenetic, cytogenetic, molecular and bioinformatic approach will permit a comprehensive picture of repetitive sequence organisation in both diploid and polyploid *Brachypodium* representatives to be drawn. A comparative evolutionary analysis of the repetitive sequences will enable the mechanisms that underlie the diversification and speciation of diploid species and the evolution of parental subgenomes in polyploids to be determined and will possibly also provide additional evidence that would help to elucidate the exact phylogenetic relationships in this model grass genus.