Brachypodium: A Model Genus to Study Grass Genome Organisation at the Cytomolecular Level

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Abstract : In contrast to animals, the organisation of plant genomes at the cytomolecular level is still relatively poorly studied and understood. However, the Brachypodium genus in general and B. distachyon in particular represent exceptionally good model systems for such study. This is due not only to their highly desirable 'model' biological features, such as small nuclear genome, low chromosome number and complex phylogenetic relations, but also to the rapidly and continuously growing repertoire of experimental tools, such as large collections of accessions, WGS information, large insert (BAC) libraries of genomic DNA, etc. Advanced cytomolecular techniques, such as fluorescence in situ hybridisation (FISH) with evermore sophisticated probes, empowered by cutting-edge microscope and digital image acquisition and processing systems, offer unprecedented insight into chromatin organisation at various phases of the cell cycle. A good example is chromosome painting which uses pools of chromosome-specific BAC clones, and enables the tracking of individual chromosomes not only during cell division but also during interphase. This presentation outlines the present status of molecular cytogenetic analyses of plant genome structure, dynamics and evolution using B. distachyon and some of its relatives. The current projects focus on important scientific questions, such as: What mechanisms shape the karyotypes? Is the distribution of individual chromosomes within an interphase nucleus determined? Are there hot spots of structural rearrangement in Brachypodium chromosomes? Which epigenetic processes play a crucial role in B. distachyon embryo development and selective silencing of rRNA genes in Brachypodium allopolyploids? The authors acknowledge financial support from the Polish National Science Centre (grants no. 2012/04/A/NZ3/00572 and 2011/01/B/NZ3/00177)

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