

ABSTRACT

Repetitive DNA constitutes a major component of plant genomes, playing crucial roles in genome structure, function, and evolution. Despite its significance, the repetitive fraction of the genome has remained relatively understudied in the model grass genus *Brachypodium*. This genus, with its diverse range of diploid and polyploid species and well-characterised evolutionary relationships, offers an excellent system for investigating the dynamics of repetitive DNA evolution.

To address this gap, a comprehensive comparative analysis of the *Brachypodium* repeatome was conducted, integrating both bioinformatic and cytogenetic approaches. Next generation sequencing (Illumina) data were analysed using RepeatExplorer2&TAREAN – repeat identification and quantification tools. Fluorescence *in situ* hybridisation (FISH) and Southern Blot hybridisation were applied to study chromosomal and genomic organisation of selected repetitive elements.

The study focused on characterising the structure, diversity, and evolutionary dynamics of various classes of repetitive DNA, including transposable elements and tandem repeats. The composition and distribution of major repetitive DNA elements were analysed in two accessions of the natural allotetraploid *Brachypodium hybridum*, which originated at different times (0.14 and 1.4 Mya), and in their putative diploid progenitors (*B. distachyon* and *B. stacei*). *B. hybridum* exhibited an overall additive pattern of dispersed repeats. The most prominent changes were observed in the context of tandem repeats. Both analysed *B. hybridum* accessions exhibited divergent landscapes of repetitive DNA sequences, reflecting the gradual evolutionary changes that have shaped their genomes.

Comparative analyses of repetitive sequences in annual and perennial *Brachypodium* species revealed both lineage-specific elements and repeats shared across most of the analysed species. Contrasting evolutionary dynamics were observed among different repeat types. Several conserved satellite DNA families showed variable amplification among related species. Phylogenetic assessment of satellite DNAs across *Brachypodium* species provided insights into the evolutionary dynamics of tandem repeats. LTR-retrotransposon profiles varied among taxa, indicating lineage-specific patterns of proliferation and accumulation. These findings underscore the utility of *Brachypodium* as a model system and provide new insights into the contribution of repetitive elements to genome diversification, polyploid evolution, and structural genome organization in grasses.