

Highly conserved synteny despite massive chromosome fusion and fission suggest fragile sites in holocentric plants

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Abstract

Holocentric organisms, unlike typical monocentric organisms, have kinetochore activity distributed along almost the whole length of the chromosome. Because of this, chromosomal rearrangements through fission and fusion are more likely to become fixed in holocentric species, which may account for their extraordinary rates of chromosome evolution. Genome synteny has been reported to be conserved in animals with holocentric chromosomes despite high rates of chromosome rearrangements. Comparing genomes of *Carex* species and a genome of a distantly related Cyperaceae we have characterised conserved vs. rearranged genome regions across pairs of species that range in time since divergence between 2 and 50 million years. We have compared a *C. scoparia* genome with a linkage map of the same species to study rearrangements at a population level and suppression of recombination patterns. We found a surprisingly conserved genome synteny even between very distantly related species and extraordinarily high rates of chromosome evolution in genus *Carex*. Comparing the distribution of repetitive DNA and gene density between conserved and rearranged genomic regions, we found repetitive DNA to be related to holocentromeres and as well as rearranged regions of the genome. This evidence of extremely conserved synteny in sedges and the massive events of chromosome fission and fusion found across the evolution of genus *Carex* suggests the presence of common genomic hotspots of chromosome evolution related to repetitive DNA.

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