



Recombination in plant chromosome evolution

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Abstract/Resumo

Homologous recombination (HR) or illegitimate recombination (also known as non-homologous end-joining, NHEJ) are essential for the repair of DNA double strand breaks and cell survival. HR is also an essential part of meiosis, ensuring that new genetic combinations are generated, contributing to genetic diversity, and that chromosomes segregate correctly through the physical link between homologous chromosomes established by chiasmata. Although double-strand breaks are the starting point of these processes, different pathways in meiosis may lead to interfering (class I) or non-interfering (class II) crossovers, to non-crossovers (gene conversion) or even to inter-sister repair. In somatic cells, HR happens less frequently than NHEJ and is often ectopic or intrachromosomal (non-allelic), what is related to the sequence similarity among DNA repeats. Recombination is thus associated to the evolution of repetitive DNA, both satellite DNAs and transposable elements, and genome size. It can also lead to chromosome rearrangements. Suppression of recombination in particular chromosome domains, such as centromeres, and chromosome types, such as sex chromosomes, also influences chromosome evolution and repetitive DNA distribution. In this talk, I will review different aspects of homologous and non-homologous recombination and its consequences to repetitive sequence, genome size and chromosome evolution in plants.

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