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«Plant telomeres: BAL31-NGS in telomere biology»

Per

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This talk will be about plant telomeres in general but also about a specific method to identify as yet undiscovered telomere sequences, which combines next generation sequencing (NGS) with BAL31 digestion of high molecular weight DNA. The method was applied to two groups of plants: i) dicots, genus *Cestrum*, and ii) monocots, *Allium* species (e.g. *A. ursinum* and *A. cepa*).

Both groups consist of species with large genomes (tens of Gb) and a low number of chromosomes (2n=14-16), full of repeat lack typical elements. Both genera telomeric repeats and multiple studies have attempted to characterize alternative telomeric sequences. However, despite interesting hypotheses and suggestions of candidate alternative telomeres (retrotransposons, rDNA, satellite repeats) these studies have not resolved the question.





In a novel approach based on the two general features eukaryotic most of telomeres, their repetitive character and sensitivity to BAL31 nuclease digestion, we have taken advantage of the capacity and current affordability of NGS in combination with the robustness of classical BAL31 nuclease digestion of chromosomal termini. While representative samples of most repeat elements were ensured by low-coverage (less than 5%) genomic shot-gun NGS, candidate identified telomeres were as underrepresented sequences in BAL31-treated samples.









