

## **SEQUENCING AND ANNOTATION OF LARGE GENOMIC REGIONS IN NORWAY SPRUCE (*PICEA ABIES* (L.) KARST)**

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*conifers, genome organization, retroelements*

Conifers have huge and complex genomes due to a high content of repetitive DNA. Transposable elements are known to play a major role in the structure and evolutionary dynamics of conifer species. Nevertheless, to date the study of transposable elements in gymnosperms has been largely based on degenerate PCR amplification of conserved domains and the exhaustive characterization of full-length elements is far from complete owing to the scarcity of long range genomic sequences. We report the annotation of four large regions randomly selected from the genome of Norway spruce (*Picea abies*) and accounting for total ~400 Kb. This survey contributes significantly to enlarge the retroelement repertory currently available for genomic analysis of conifer species by the identification of novel families and complete retroelements, including the first non-autonomous LTR-retrotransposons ever reported in conifers. Moreover, we provide the first insight into the local organization of a complex conifer genome showing nests of retrotransposons inserted into each other as commonly found in middle-to-large genome angiosperms. Estimates of retroelement insertion ages reveal an old ancestry dating back to the differentiation of Pinaceae species and insertions of related retrotransposons suggest that different waves of retroelement mobilization may have occurred during the evolution of conifers. The survey of large genomic regions with respect to the content, physical arrangement and age of retroelements may provide a substantial contribution to our understanding of genome organization and evolution in conifers. Finally, the characterization of full-length transposable elements is an essential step required for the satisfactory annotation of genomic libraries from newly investigated conifer species.