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CHARACTERIZATION OF EXAPTATION EVENTS INVOLVING TRANSPOSABLE ELEMENTS IN CONIFER GENOMES

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Transposable elements (TEs) are sequences able to move in chromosomal sites different from the original one. They heavily contribute to the observed genome size variation across different species and constitute, through their spread within genomes, an endogenous source of variability useful to the evolution of host genomes. When the activity of a TE confers a benefit to the host genome, that element may begin to evolve as a conventional sequence rather than through self-duplication. This process, called TE exaptation, leads to the creation of new genes called exapted transposable element genes (ETEs), that play crucial roles in various biological systems. We are investigating on the exaptation events involving the repetitive component of genomes (especially LTR-retrotransposons) in species belonging to the *Pinophyta* division. In particular we are focusing our analyses on *Picea abies, Picea glauca, Pinus taeda, Pinus lambertiana* and *Pseudotsuga menziesii*. These plants have an ancient origin and large genomes, composed of a large fraction of old and highly diverged repeated sequences. These features make them attractive subjects for studies aimed at identifying ETEs. Furthermore the paucity of genomic studies on conifers increases the interest of this research. In order to analyze these events, we'll adopt a comparative approach, by testing TEs identified in conifer against a panel of species that covers about 400 million years of plant evolution and includes the bryophyite *Physcomitrella patens,* the ancient vascular plant *Selaginella moellendorffii,* the basal angiosperm *Amborella trichopoda,* the dicot angiosperm *Vitis vinifera* and the monocot angiosperm *Oryza sativa*. First we performed a survey aimed at the identification and characterization of LTR-RTs across the available conifer genomes. In this step, we identified 200 representative LTR-RTs for each of the 5 conifer species analyzed. The gag_pol proteins coded for by these elements were then used to build five Hidden Markov Models (HMMs) profiles. The HMMs profiles were mapped on the available aminoacidic sequence of conifer proteins. ETEs differ from TEs for a series of genetic attributes such as expression, repetitiveness, conservation across different species including conservation of the intron/exon structure and microsynteny. Genes showing similarity with TE HMM profiles where further scrutinized for each of these genetic attributes in order to isolate possible ETE candidates. Currently, only in *P.abies,* we identified around 20 candidate ETEs. The material that we are collecting on this species will be used for studying exaptation events in all the others conifers analyzed. Finally identified ETEs will be searched and characterized in all the other plants included in the experimental system. This will provide the opportunity to figure out: when exaptation events occurred, which of these exaptation events were retained over long evolutionary time and what is the frequency of these events. Moreover will be possible infer if some ETEs are able to explain certain aspects of the diversification of the plants considered in this study.