

## **LTR-TE ABUNDANCE, TIMING AND MOBILITY IN *SOLANUM COMMERSONII* AND *S. TUBEROSUM* GENOMES FOLLOWING COLD STRESS CONDITIONS**

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From an evolutionary perspective, retrotransposons (LTR-RTs) activity during stress may be viewed as a mean by which organisms can keep up rates of genetic adaptations to changing conditions. Potato is one of the most important crop consumed worldwide, but studies on LTR-RT characterization are still lacking. Here, we assessed the abundance, insertion time and activity of LTR-RTs in both cultivated *Solanum tuberosum* and its cold tolerant wild relative *S. commersonii* genomes. *Gypsy* elements abounded more than *Copia* ones, suggesting that the former were somehow more successful in colonizing potato genomes. However, *Copia* elements, and in particular the *Ale* lineage, are younger than *Gypsy* ones, since their insertion time was in average ~ 2 Mya. Due to the ability of LTR-RTs to be circularized by the host DNA repair mechanisms, we identified a *Copia/Ale* element active (called *nightshade*, informal name used for potato family) in *S. tuberosum* genome via mobilome-seq, in line with their young insertion time. Our analyses represent a valuable resource for comparative genomics within the *Solanaceae*, transposon-tagging and for the design of cultivar-specific molecular markers in potato.