

Comparative analysis of the evolutionary dynamics of alternative splicing in *Arabidopsis thaliana* and *Solanum lycopersicum*

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Motivation and aim: Alternative splicing plays a key role in the formation of transcriptomic and proteomic diversity in plants. Previous studies have demonstrated that it regulates essential biological processes, including growth, development, and adaptation to environmental conditions. Despite this, its evolutionary dynamics remain largely unknown. The aim of this study is to determine the evolutionary dynamics of alternative splicing in *Arabidopsis thaliana* and *Solanum lycopersicum*.

Materials and methods: We conducted a comparative analysis of alternative splicing in *A. thaliana* and *S. lycopersicum*. Isoforms for both species were reconstructed from ONT long-read sequencing data using our previously developed tool FLIC (<https://github.com/albidgy/FLIC>). The consistency of structural isoform features was assessed across genes grouped into orthogroups based on sequence homology.

Results: First, we assessed the relationship between the mean intron length, mean exon length, and the number of splice sites across species. The results indicated that the number of splice sites is conserved, whereas intron and exon lengths vary significantly between species. Next, the neighborhood of splice sites was examined, identifying conserved sites present in both species. We also analyzed the origin of unique splice sites to determine whether their sequence context occurs elsewhere within isoform structures of another species. Finally, the relationship between the presence of unique splice sites and isoform expression profiles was evaluated, based on the assumption that expression patterns are indicative of the biological function of genes.

Conclusions: Our study demonstrates that the number of splice sites and their surrounding regions are conserved between *A. thaliana* and *S. lycopersicum*. These features remain stable despite variations in intron and exon lengths, suggesting the evolutionary stability of the regulation of splicing. Our findings highlight the important role of conserved splicing mechanisms in the evolution of genes.

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