The importance of Splice Site Secondary Structure Stability: A Comparative Analysis of Alternative Splicing Regulation in Humans and Plants.

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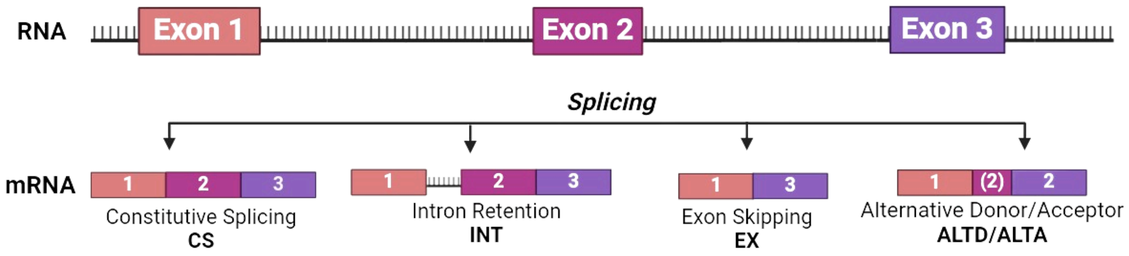
INTRODUCTION

Splicing is a crucial process for pre-mRNA maturation in eukaryotes, significantly contributing to transcriptome and proteome diversity and regulating gene expression. Despite its importance, the regulation of splicing events remains poorly understood, especially in plants.

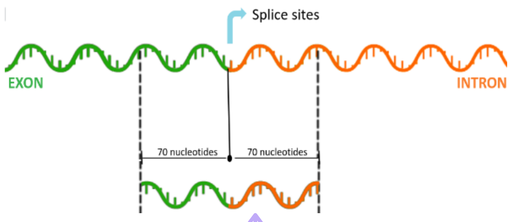
Previous studies in humans have suggested that the stability of secondary structures (SS) around splice sites could be a regulatory mechanism, with more stable structures associated with alternative splicing events.

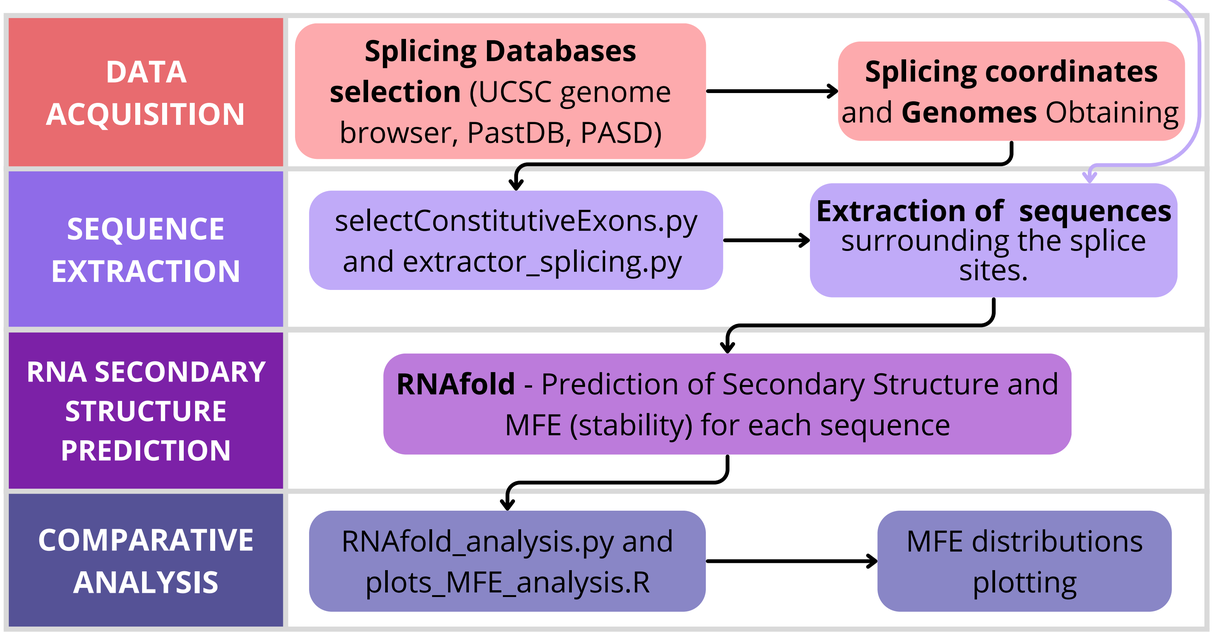


This study aims to investigate the dispersion pattern of RNA SS stability at splice sites for alternative and constitutive splicing in humans, *Arabidopsis thaliana*, and *Zea mays*.

METHODS

To investigate the relation between the dispersion pattern of RNA secondary structure (SS) stability in splicing regulation, we have analyzed RNA secondary structure (SS) stability in constitutive (CS) and alternative splicing (AS) events (INT, EX, ALTD, ALTA) across human (HG18 and HG38), *Arabidopsis thaliana*, and *Zea mays* genomes.





RESULTS

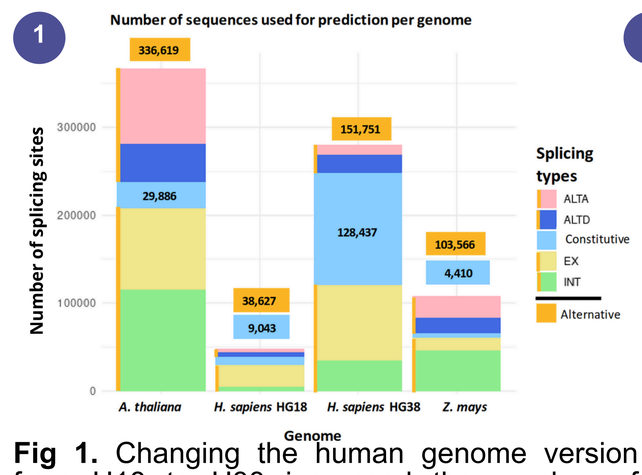


Fig 1. Changing the human genome version from H18 to H38 increased the number of detected splicing sites by six-fold.

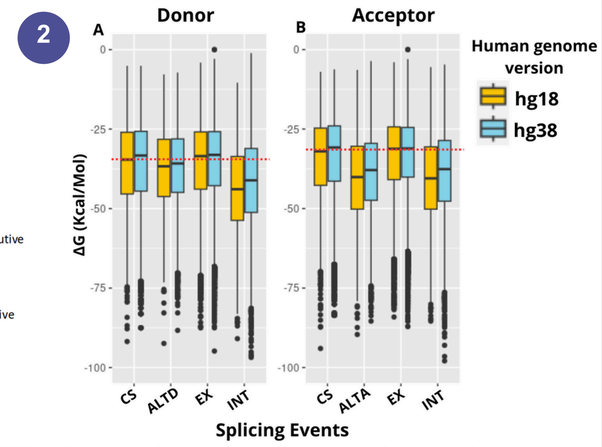


Fig 2. Signals reported for HG38 are highly similar to previous results in HG18 .

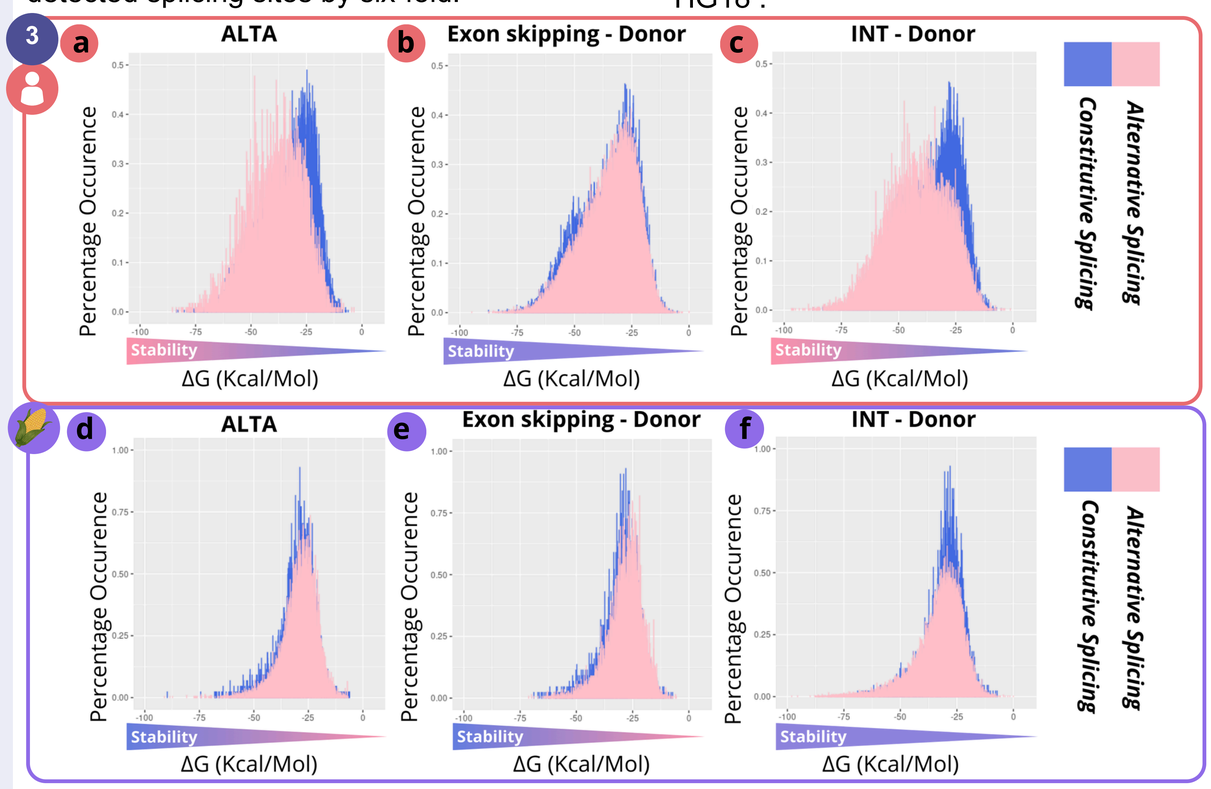
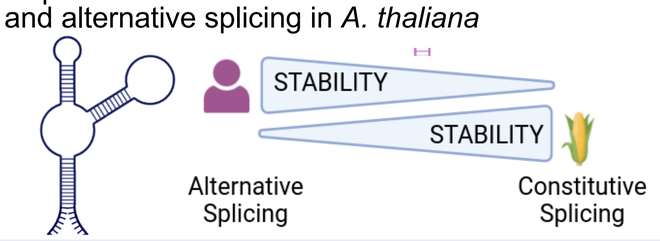
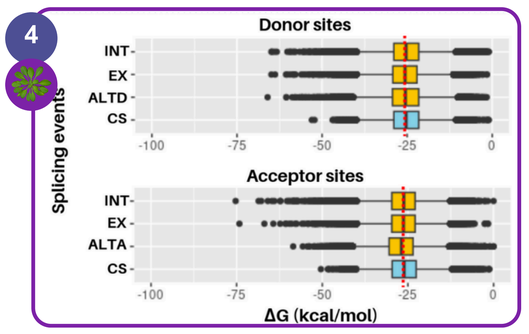


Fig 3. Comparing SS stability of the same events between maize and human shows different patterns, including opposite patterns.

Fig 4. No significant difference in stability dispersion was observed between constitutive and alternative splicing in *A. thaliana*





CONCLUSIONS AND NEXT STEPS

- The relation between SS stability at splice sites and alternative splicing (AS) is different for humans and plants.
- In humans, more stable SS are linked to AS sites, suggesting a regulatory role. In *Arabidopsis thaliana*, no significant SS stability difference between CS and AS events. In *Zea mays*, AS events generally show less SS stability than CS.
- Findings highlight species-specific splicing regulation mechanisms, offering insights into gene expression evolution.

NEXT STEPS

- To improve the knowledge on splicing and splicing regulation in plants, given the lack of splicing data in plants and promising results, our next goal is to systematically identify alternative splicing in grasses such as sorghum, maize, rice, barley, and *Arabidopsis thaliana* to perform analysis comprehanding splicing regulation using principally bioinformatics techniques.