

Alternative splicing is a mechanism of gene expression regulation that maintains, regulates, and creates genomic diversity and tissue specificity in plants. It involves the differential joining of exons in precursor mRNAs, leading to multiple mRNA isoforms from a single gene. The formation of these isoform variants and their subsequent translation leads to subfunctionalization of proteins, generating diversity in structure and function. Therefore, alternative splicing is often important in various biological processes in plants, such as development, stress response, immunity, and reproduction. Key types of alternative splicing events include intron retention, exon skipping, alternative 5'/3' splice sites, and mutually exclusive exons. Regulation of alternative splicing involves cis-regulatory elements and trans-acting protein factors such as serine/arginine-rich (SR) proteins and heterogeneous nuclear ribonucleoproteins (hnRNPs). This thesis aims to summarise the mechanisms and consequences of alternative splicing in plant development, including maturation of male and female gametophytes, meiosis, stress, and cell differentiation. It also describes methodological approaches that allow for a genome-wide study of alternative splicing, including microarrays, RNA-seq, and PCR. A better understanding of alternative splicing will provide insights into plant biology and may facilitate agricultural and biotechnological applications.