7.1 INTRODUCTION (1)

Post-transcriptional gene regulation involves controlling gene expression after R
is transcribed from DNA but before it is translated into protein, affecting mRNA stabi
localisation, and translation efficiency. Although we have already discussed one componen
post transcriptional regulation in previous chapter in the topic, small regulatory RNA-media
regulation, yet there are several other key mechanisms which may not be directly rela
to epigenetic modifications discussed previously. Hence, we will discuss those remain
post-transcriptional regulations here in this chapter. In particular our focus will be on R
splicing, RNA stability, RNA editing and RNA surveillance. Among the common types
post-transcriptional mechanisms are include RNA splicing, RNA editing, RNA stabi
regulation and control of RNA localisation. **RNA splicing** (the term was already introdu
in molecular biology, chapter transcription), where alternative splicing generates multi
mRNA variants from a single gene, increasing protein diversity. For example, the Drosophi
Dscam gene can produce thousands of protein isoforms through alternative splicing. **mR
stability** is regulated by elements like AU-rich regions in the 3′ UTR, influencing mR
degradation rates; for instance, the rapid degradation of cytokine mRNAs allows tig
control of inflammatory responses. Yet another component of RNA stability is the regulat
through regulatory RNAs such as the action of microRNAs (miRNAs), like miR-21, wh
downregulates tumor suppressor genes in cancer. **mRNA localisation** ensures proteins
synthesized where needed, such as β-actin mRNA localisation to the leading edge of fibrobla
for cell motility and hence also controls the spatial regulation of gene expression. **RNA editi
such as the A-to-I editing in the glutamate receptor gene, alters RNA sequences, impacti
mRNA stability and protein function. Additionally, **mRNA surveillance** mechanisms preve
the production of faulty proteins by degrading mRNAs with premature stop codons a
inability to stop translation. Post-transcriptional regulation of gene expression plays a critic
role in maintaining cellular homeostasis, responding to environmental changes, and ensuri
proper development and function in organisms. These processes are essential for the preci
control of gene expression and protein production, and their dysregulation can lead to numero
diseases and metabolic disorders. In cancer, aberrant alternative splicing can produce oncogen
protein variants or result in the loss of tumor suppressor functions, with mutations in splici
factors being common in several cancers. Alterations in RNA stability and turnover can al
lead to the overexpression or under expression of critical genes, and dysregulated microRN
(miRNAs) frequently influence tumor growth. In neurodegenerative diseases, mis regulati
of RNA splicing and editing is implicated in conditions like amyotrophic lateral scleros
(ALS) and frontotemporal dementia, where mutations in RNA-binding proteins can caus
widespread splicing defects. RNA surveillance mechanisms, such as nonsense-mediated deca
(NMD), are vital for eliminating faulty mRNAs; failures in these pathways can result in toxi
protein accumulation, contributing to diseases like Huntington's and Alzheimer's. In metaboli

disorders, post-transcriptional regulation is crucial for metabolic control, with RNA editing of apolipoprotein B (Apo B) mRNA affecting lipid metabolism, and disruptions in RNA binding proteins and miRNAs linked to insulin resistance and diabetes. In this chapter we will discuss these well-established post-transcriptional regulatory mechanisms in greater detail.

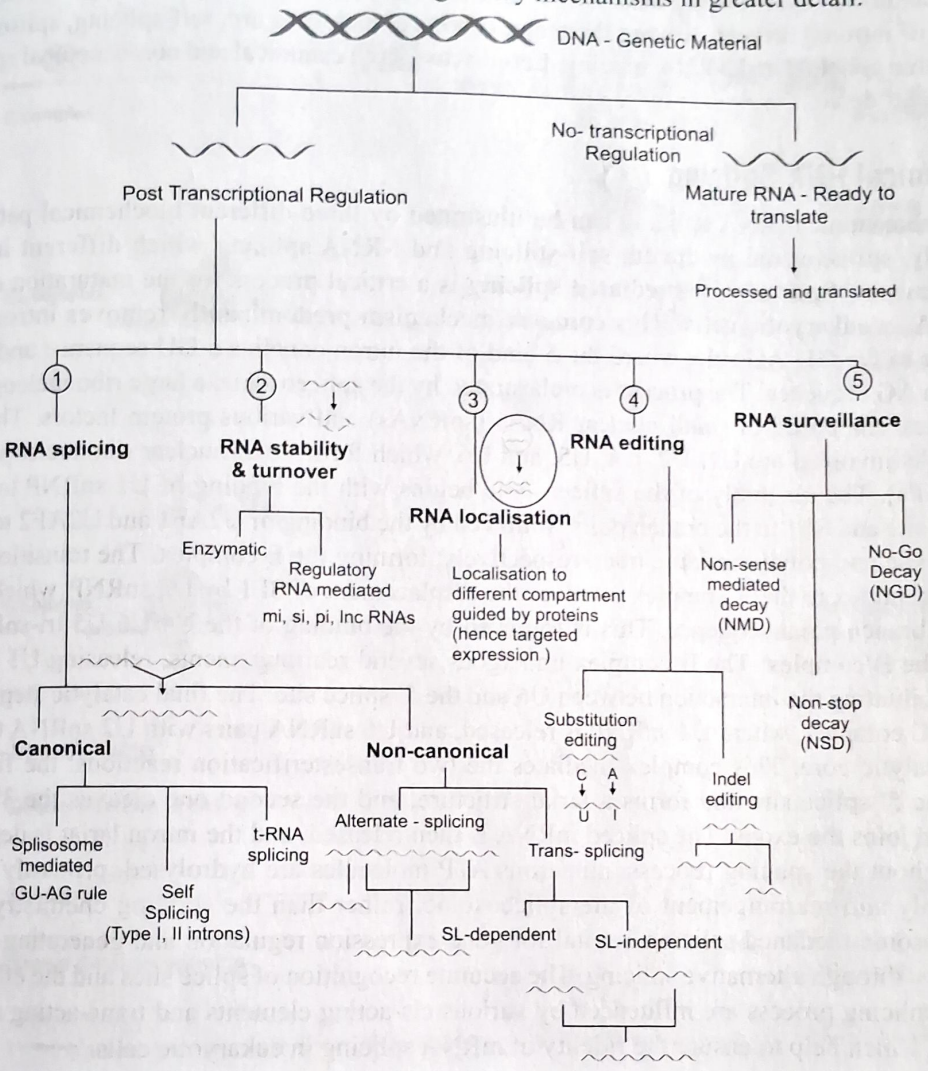

Fig. 7.1. *General outline of various of post-transcriptional regulatory mechanisms.*

7.2 RNA SPLICING

As we learnt in previous unit, during our discussion on transcription, that most of the RNA in eukaryotes is processed after its formation. One of the prominent features of RNA processing, especially for those RNAs which contain intervening sequences (introns) is called **RNA splicing**. The literaric meaning of splicing is to join two pieces of rope, film, etc. together at their ends in order to form one long piece. Likewise, the RNA with intervening sequence is first cut to remove those sequences (or introns) and join together into a final product called mature RNA. There are several mechanisms of RNA splicing known to us till date, some of which lead to a single final product from a single precursor or unprocessed RNA, is called simple or **canonical splicing**, while the another one called, **non-canonical splicing**, is less common and

does not apply to all RNAs. Here, more than one precursor RNAs may be involved from different genes (**trans-splicing**) or there can be single precursor RNA which can splice in than one way and lead to different transcripts from same pre-mRNA called **alternate spli** The canonical RNA splicing also, may follow various paths depending upon types of RN types of introns) present. Among the major canonical pathways are, self-splicing, splisos mediated splicing, and t-RNA splicing. Lets discuss, both canonical and non-canonical spl in greater detail.