Review Article
Recent updates in heterogenous nuclear (hn) RNA

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Abstract
Ribose nucleic acid (RNA) is known to be a tool for therapeutic purpose and marker in prognosis of diseases. The lineage of heterogenous nuclear RNA (hnRNA) provide a epitranscriptome for the diagnosis and therapeutic potential in various diseases. RNA modifications during the splicing process creates an epigenetic modifications that may serve as marker for diagnosis of diseases. Several new RNA binding proteins take over the splicing mechanism and regulate RNA formation that can be studied by molecular techniques. The coding and decoding of functional messages associated with these hnRNA brought a discovery of new tool for diagnosis of complications associated with diseases.
Keywords: Ribose nucleic acid (RNA),hnRNA,diagnosis, diseases

INTRODUCTION
Ribose nucleic acid (RNA) is a known to be a fascinating molecule ever. The ribosome is the nurturing mother of RNA. RNA possess structural properties as shown for rRNA core.Furthermore, RNA also has protein binding properties like rRNA-protein interactions that can be used for protein translation process (1). Endless properties of RNA also includes enzymatic action. So, RNA is a dynamic molecule with varied functions and properties. During the translation process, the non-coding RNA perform decoding (tRNA) and rRNA (amino acid polymerization) (2). A great statement made by Francis Crick's 'central dogma' of molecular biology it is stated that RNA molecules serve to initiate protein synthesis, decode mRNA and form protein. Apart from RNA molecule the precursor mRNA (pre-mRNA) also known as heterogenous nuclear RNA (hnRNA) also plays a vital role in the biological system (4).
This hnRNA serve as a single premature single strand of mRNA. Transcription enables the DNS template in the cell nucleus to synthesised pre-mRNA. Pre-mRNAs include two types of segments exons and introns. Exons showed hierarchy in final mRNA, while introns are removed under splicing process by the spliceosome.

Characteristics of hnRNA
- First, hnRNA is 4-10 times complex than mRNA (4).
- Spliceosome process the hnRNA.
- The term hnRNA is often used just for the unprocessed primary transcripts.

Precursor mRNA processing in eukaryotes

The pre-mRNA and hnRNA derived eukaryotic sources are extensively edited prior to translation (5). The additional makeover of eukaryotic mRNA impart longer half life compared to prokaryotic mRNA. Moreover, the pre-mRNAs are incorporated firstly in RNA-stabilzing proteins (RSPs) in order to protect precursor-mRNA from degradation during its processing and oozing out of nucleus. Among the most important steps of stabilizing the pre-mRNA, the three predominant steps includes addition of signalling factors at the 5' and 3' ends followed by stabilising proteins and elimination of intervening sequences that are irrelevant to their corresponsding amino acids (6).

5' Capping of pre-mRNA

Post synthesis of pre-mRNA, a 7-methylguanosine capping at the 5' end of the progressive transcript by a enzyme system 5'-to-5' phosphate linkage is performed. This mechanism prevents the further degradation of the nascent mRNA. Additionally some of the initiataion factors involved in protein synthesis recognise this aforesaid cap that assist in translation by ribosomes.

3' Poly-A Tail of pre-mRNA

Endonuclease comprising of protein complex cleave the pre-mRNA between an AAUAAA consensus sequences and a GU-rich sequence (7). This mechanism enable the release of functional pre-mRNA from rest of the transcript. Another enzyme complex called poly (A) polymerase (PAP) cleaves the functional pre-mRNA and immediately add the 200 A nucleaotides which later on form poly A tail at the 3' end of the cleaved pre-mRNA. This addition of A nucleotides protect the mRNA from further degradation and assist in exporting the pre-mRNA into the cytoplasm.

Insights of pre-mRNA splicing

RNAseq-mediated deep mining of the cellulartranscriptome leads to the possibility of definingall alternative RNA splicing (differential removal ofintrons from pre-mRNAs) events that can occur toindividual pre-mRNAs. This has led to the realisationthat more than 90% of human pre-mRNAs arealternatively spliced, while the average pre-mRNAgives rise to around seven different alternativemRNA species. Splicing is controlled by RNAsecondary structure, thestrength of 5´ and 3´ splice sites,splicing enhancer and silencer sequence elements,exon/intron architecture and transcription by RNApolymerase II. However, we do not understand therelative contributions of each of these to determining the final splicing pattern of any one pre-mRNA in development,differentiation or disease.Generationof a ‘splicing code’ that will allowprediction of splicing outcomesfrom RNA sequence is a major goalof current research. Directly related tothis, transcriptome-wide elucidation ofRNA‐protein interactions through HITSCLIP(high-throughput sequencing of RNAby cross-linking immunoprecipitation) (8) and related techniques has allowed theidentification of hundreds of new RNA-bindingproteins that may control splicingand other events in RNA regulation. Despiteidentification, the roles of many of these proteinsare still to be elucidated. Have we abandonedour search for mechanisms of RNA regulationin favour of documenting the complexity ofthe components of the regulatory machinery? Arefocusing on mechanisms of gene regulation willbring new discoveries such as the recent finding thatsplicing factors regulate transcription elongation.

Epi-transcriptome a marker for disease prognosis

Another exciting new field of pre-RNA research isthe RNA ‘epitranscriptome’ and its roles in posttranscriptionalregulation in development anddisease. RNA can be modified by the addition ofover 100 different chemical groups, thus creatingan even more complex diversity of epigeneticmodification with potentially more functionsthan that which occurs on DNA. Althoughsuch modifications are common on non-codingRNAs such as rRNAs, tRNAs and hnRNAs, RNAmodifications are also present on mRNAs, and thesecould change their coding potential. Althoughsome pre-RNA modifications have been known fordecades, such as tRNA pseudouridylation, therecent explosion in their study has been

broughtabout by the discovery of a number of moleculesthat can add and remove modifications and, moreimportantly, decode them into functional messages.
Defects in these pathways lead to loss of embryonicdevelopment and differentiation and congenitaldefects. It is likely that such modifications changethe RNA secondary structure and/or impact onRNA‑protein interactions and recent data showthat they can alter RNA nuclear export, stability andtranslation. However, further studies are required tofully explore this exciting new area of RNA research.

CONCLUSION

The hnRNA research is still need extensive analysis so that hn-RNA molecule can be used in curing and therapeutic approach of several diseases associated with protein translation and defects.

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