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# Novel RNAs along the Pathway of Gene Expression

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The essential roles of messenger RNA, transfer RNA and ribosomal RNA in gene expression in all cells have long been known. Appreciation that additional novel classes of RNAs are critical for gene expression came soon after the discovery of splicing, which removes non-coding segments called introns from the RNA transcripts of most genes in higher organisms. The discovery of small nuclear RNAs (snRNAs), which function in splicing as small nuclear ribonucleoproteins (snRNPs, pronounced snurps), will first be reviewed.

Next, current challenges in the splicing field will be briefly discussed. These include the following questions: Is the spliceosome an example of protein-assisted RNA catalysis? How is alternative splicing (which we now realize is fundamental to the great diversity of proteins encoded by the human genome with only 28,000 genes) regulated? How is splicing coordinated on a molecular level with other events in gene expression? Here, the link between splicing and nonsense-mediated mRNA decay (NMD), which surveys newly-made messages for mistakes and directs them to a degradation pathway before they produce non-functional proteins, will be summarized.

Finally, the latest novel class of small RNAs – microRNAs – will be presented. The initial discovery of RNA interference (RNAi) rapidly led to the development of technologies that allow biologists to easily perform functional gene knockouts even in mammalian cells. However, the cellular machinery that underlies the RNAi phenomenon is normally involved in the production of hundreds, if not thousands, of tiny RNAs (~22 nucleotides) that are encoded by the genomes of higher cells. Defining their roles in regulating multiple aspects of gene expression, and even DNA remodeling, represents an exciting frontier for future research.