

Preface

RNA has been an interesting molecule in biology displaying a multitude of functions in all cellular systems. According to the RNA world hypothesis, it is proposed that RNA was the first macromolecule to arise in the universe even before DNA and proteins came into existence. However, modern biology has seen a great influence of DNA as the information storage house, while the proteins are really the final functional actors in various cellular functions. RNA was thought to have only a supporting role in maintaining the functional homeostasis. Messenger RNA carries the information encoded in DNA. Ribosomal RNA organizes the ribosome structure to facilitate the translation of the messenger RNAs. Transfer RNAs carry the amino acids to be incorporated into the proteins. Other small RNA molecules like 5S RNA and 5.8S RNA contribute to ribosome function. Small nuclear and nucleolar RNAs (snRNAs and snoRNAs) play significant roles in splicing machinery. For a long period of time, it was a common notion that the entire DNA in eukaryotic cells is not transcribed, and the junk DNA hypothesis prevailed for a few decades. However, subsequent to the completion of the Human Genome Project and the advent of NGS technology, we have seen that much of the DNA is pervasively transcribed to generate a large repertoire of RNA molecules which are now being classified as non-coding RNAs. This includes both short (22–33 nucleotides in length) and long RNA species (>200 nucleotides in length). Presently it is estimated that there are more genes coding for long noncoding RNA genes than the estimated ~25,000 protein-coding genes in humans and mice. It is becoming increasingly clear that long non-coding RNAs (lncRNAs) have ubiquitous biological function(s) in almost every aspect of cellular biology, regulating gene expression and contributing to the final functional output of protein-coding genes. lncRNAs are found in all eukaryotes from unicellular organisms to higher mammals. The present book is an attempt to briefly describe the most recent developments in the area of long noncoding RNA biology which is one of the emergent hot topics in the field of molecular and cellular biology today.

The first chapter by Jarroux, Morillon, and Pinskaya introduces the area of lncRNAs beginning with the history and their discovery. This is followed by a description of their characteristic features in comparison with messenger RNAs.

They also discuss the different classes of lncRNAs based on their genomic organization, cellular localization, and functions. This chapter lays an excellent foundation for the ensuing chapters in the book. The second chapter by Kanduri and associates discusses the role played by lncRNAs in genome organization and chromatin organization and regulation along with their varied mechanisms of action. They also discuss the role of lncRNAs in nucleolar and centromere functions. This chapter is followed by an exhaustive description of lncRNAs in an invertebrate model system, *Drosophila melanogaster*, by Subhash Lakhotia (Chap. 3). This model organism, owing to its richness in genetics and genetic approaches, has contributed significantly toward our understanding of the biology of lncRNAs. This chapter also includes a vast amount of information on the lncRNA *hsrw* that was discovered in the author's laboratory. Zapulla et al. have focused, in the fourth chapter, on the functions of lncRNAs in the widely studied unicellular eukaryote *Saccharomyces cerevisiae*. From transcription regulation to acting as a scaffold in the telomere region, the chapter sheds light upon how these single-celled organisms have evolved to add an extra layer of regulation in the form of lncRNAs. In the fifth chapter, Wang and Chekanova have categorized and detailed the lncRNAs involved in gene expression regulation in the plant kingdom. With an emphasis on the well-characterized plant *Arabidopsis thaliana*, the chapter deals with diverse roles that the lncRNAs play in plants. From acting as miRNA sponges and decoys to transcriptional silencing, they are involved in the coordination of crucial physiological phenomena such as flowering.

The sixth chapter by Mishra and associates discusses the role of lncRNAs in genomic imprinting, dosage compensation, body patterning, tissue development, and organogenesis and also the role of lncRNA in the etiology of human diseases and disorders. The following chapter (Chap. 7) by Felley-Bosco and Arun Renganathan summarizes the recent developments on the role of lncRNAs in cancer and their therapeutic potential. It is becoming apparent that every type of human cancer is associated with one or several of the lncRNAs and expression of many of them is perturbed in any given cancer. Current efforts worldwide are being directed toward developing these lncRNAs as biomarkers as well as potential targets for molecular intervention. Chapter 8 by Debosree Pal and M. R. S. Rao discusses the role of long noncoding RNAs in the biology of stem cells both with respect to their pluripotent properties and cell fate specification and differentiation. Stem cells are increasingly perceived as promising candidates for regenerative medicine, and the importance of the long noncoding RNAs in the biological features of stem cells provides additional opportunities for better understanding of the players involved in the maintenance of stemness as well as their differentiation properties. It is likely that lncRNAs may play a significant role in the application of stem cell technologies in regenerative medicine in the near future. In Chap. 9, Clark and Blackshaw describe the present scenario of the role of lncRNAs in brain function and more particularly in nervous system development. At present, neuroscience is one of the most challenging areas of human biology, and in this context, our understanding of the functional role of lncRNAs in nervous system development will be very valuable in the future prospects of neural function and neurodegenerative diseases.

The concluding chapter by Tripathi and associates provides a detailed yet comprehensive view about the technologies and methods that have been developed in the last decade or so to decode the functions of these lncRNAs. Experimental methods related to sequencing of these transcripts, understanding their localization, and solving their complex structures have been dealt with in this chapter, along with a listing of the bioinformatic and computational methods as well.

I am extremely thankful to all the contributors for taking their valuable time off and assembling each of the chapters very eloquently. The field of long noncoding RNA biology is expanding very fast and is one of the areas wherein a large number of papers are being published in the scientific literature today. In this context, all the chapters have been written very lucidly incorporating very up-to-date information. In such a rapidly expanding area covering almost every aspect of cellular biology, it is difficult to avoid any overlap of some of the information between the chapters. I would urge the readers to bear with this.

I should also express my deep sense of gratitude to Steinmetz and Pelechano who have been in the forefront of human genomics sciences for consolidating their thoughts in this emergent area of lncRNA biology in their foreword. I would like to personally thank Ms. Debosree Pal who has been involved with me from the beginning of the conceptualization of this book until the final execution of the project. Many of my former graduate students and postdoctoral fellows have contributed significantly toward the growth of long noncoding RNA biology in my laboratory to take the mrhl RNA biology to where it is today. I am extremely grateful for their efforts and the intellectual inputs in making mrhl RNA as one of the important molecules in epigenetically regulating gene expression during mammalian spermatogenesis. Finally, I would like to acknowledge all the help I received at every step of the execution of this project from Dr. Suvira Srivastava and her colleagues at Springer, New Delhi.

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