

Preface

MicroRNAs: Mechanisms, Functions and Progress

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In 1993 when Ambros and co-workers [1] discovered that a mysterious *Caenorhabditis elegans* gene, *lin-4*, does not encode a protein, but acts in the form of a small RNA and represses the expression of its target gene, *lin-14*, through base-pairing with its 3' untranslated region (3'UTR), nobody would imagine that 20 years later, this category of small RNAs – now widely known as microRNAs (or miRNAs), has ~2000 known members in the human genome (and counting), and that miRNA-mediated gene regulation is deeply involved in virtually all important biological processes in animals and plants.

There is little doubt that recent advances in genomics and bioinformatics technologies and methodologies have made considerable contributions to our understanding of miRNAs [2]. We present this special issue as an attempt to bring readers an update on the current understanding of the biogenesis and targeting of miRNAs, and some of the most recent developments in the exciting field of miRNA research. Grave and Zeng's review entitled "Biogenesis of mammalian microRNAs: a global view" [3] offers an up-to-date overview of the mechanisms by which a miRNA executes its function. Reyes-Herrera and Ficarra's "One decade of development and evolution of microRNA target prediction algorithms" [4] and Ding et al.'s "Finding miRNA targets in plants: current status and perspectives" [5] provide a comprehensive survey of the current methods for the identification of miRNA targets in animals and plants, respectively. In addition, Li and Kowdley [6] bring us an up-to-date review about the involvement of miRNAs in human diseases.

This special issue also includes two mechanistic studies of miRNAs. Kornfeld et al. in an effort to gain insight into the mechanism by which muscle atrophy occurs in extended immobility of mammals, investigated the difference in expression of a few skeletal muscle miRNAs between a non-hibernating state and torpor (a short hibernation) in hibernating bats *Myotis lucifugus*, during which the bats manage to avoid muscle atrophy [7]. In another interesting study, Biggar et al. investigated the roles miRNAs played in regulating stress responses with an intertidal snail species *Littorina littorea*, in response to constantly changing temperature and oxygen levels [8].

Two bioinformatics studies are also presented in the special issue. Bhattacharyya et al. described miRT, a database of validated transcription start sites of human miRNAs [9], and Stähler et al. reported the analysis of differential co-expression characteristics of miRNAs expressed in human whole-blood [10]. These two studies offer novel insights into the genomic organization and co-regulation properties of human miRNAs, respectively.

Finally, a review of the less-known field of bacterial small RNAs and their targeting is also included [11]. Development of this field may provide evolutionary insights into how different domains of life are interconnected in terms of small RNA-based regulation.

We envision that this special issue will inspire more creative research in the exciting field of miRNAs.

References

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