microRNAs in development
Methods and protocols
Tamas Dalmay (ed), 2011
Methods in molecular biology; vol. 732
Humana Press – Springer Verlag
Heidelberg, Germany
ISBN: 978-1-61779-082-9
210 pp – 36 figs – 94,95€

The fascinating process of organ formation and patterns of forms acquistion stick together in plant and animal development intriguing the observers, from the great greek philosopher to the great Johann Wolfgang von Goethe, from D'Arcy Wentworth Thompson and Conrad Hal Waddington to present day biologists, scientists and laypeople! Each of us is fascinated by these natural phenomena and wondering how the genome, the same genome (constantly the very same genome in each cell, from the fertilized egg, with the only exception of those organisms were gene expression is primarily controlled by pre-transcription coarse mechanisms like chromatin elimination, not infrequently occurring in Nematoda, Insects and Crustacea to name a few) reach such a fine tuning capacity to modulate and direct gene expressions patterns towards specific organ formation and form acquisition. Which are ultimately based on the production of specific sets of proteins characterizing the different cell types.

The 2006 Nobel Prize in Physiology or Medicine (http://nobelprize.org/nobel_prizes/medicine/laureates/2006/) awarded jointly to Andrew Z. Fire and Craig C. Mello *for their discovery of RNA* interference - gene silencing by double-stranded RNA partly answered to our questions highlighting the microRNA word: short RNAs (21-24 nucleotides in lenght) capable of post-transcriptional regulation of mRNAs translation efficiency. Now, this well edited book by Prof. Tamas Dalmay provides a complete (as for today!) overview of the role played by microRNAs in modulating such processes in animal and plant development so that the question beginning his preface *how do a lion or an orchid develop from a single cell*? get a (still inevitably only partial) satisfactory answer. In a remarkably concise and well written *Preface*, the Editor is giving us a very clear introductory remark to the field: in this case it provides the reader with both a needed historical view and some conceptual tools to better understand the microRNA world and to orientate yourself in the fifteen chapters following one after the other without any formal partition eventhough we are told by the Editor that the conceptual partition is as follow:

chapters 1-6 *describes various techniques to detec and profile miRNA expression either spatially or at different time point*. In fact, there are chapters with detailed protocols to detect miRNA in animals, plants and prostate cancer cells using different techniques, namely *in situ* hybridization, Northern blotting, real-time PCR, deep sequencing and microarray technologies;

chapters 7-10 *are protocols to manipulate the activity of miRNAs in various organisms.* Here we face *Arabidopsis, Drosophila* mutants and mouse pancreas coltures;

chapters 11-15 *describe different methods to identify and validate miRNA targets in animals and plants*. Among the immunoprecipitation of Argonaute protein complexes (RNA binding proteins), the use of a Luciferase reporter system and others tricky techniques it is particularly noteworthy to tell of the chapter illustrating the identification of miRNA target sites in live *Caenorhabditis elegans* thanks to the *in vivo* crosslinking of miRNAs to the Argonaute protein.

Thanks to this book I think that a multitude of readers can better understand how the genome express itself in time and space. In other words, I think that the books gives to the scientific community a clear vision of a five dimensional world in which to investigate: the three anatomical spaces (x, y and z) plus the heterochronic and heterotopic dimensions of gene expressions thanks to the microRNAs.

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