

Preface

More than 60 years ago, in 1954, James Watson and the Russian Physicist George Gamow founded the “RNA Tie club”, a scientific club of selected gentlemen members with the main objective of sharing their ideas and findings not yet mature enough to be published in scientific journals. Brainstorming sessions gave rise to many seminal concepts in cell biology, which were further demonstrated by laboratory experiences. Gamow postulated the concept of a “genetic code” based on the existence of triplets of bases (codons) that will translate the DNA language into protein amino acids. Furthermore, in the last 1950s, another illustrated member of the club, Francis Crick, enunciated the “adaptor theory” based on an intermediate molecule (transfer-RNA) that would be the physical link between nucleic acids and proteins. These ideas were later described in an essential Crick’s article, which is considered by many authors as the embryonic core of the concept of the RNA world. The RNA world stands on the idea that RNA molecules were the first precursors of the living cells, being the origin of the evolution of all biological macromolecules. Several arguments clearly support the theory that the primitive cells could be built over processing units based on RNA molecules, including the existence of catalytic RNA molecules. However, for long time the chemical and structural similarities between DNA and RNA, catalogued RNA as a short-life accessory player in cell physiology. Moreover, the paradigm of the reduced stability of RNA vs DNA prevented for a long time the consideration of RNA as a precursor molecule. In consequence, RNA must be placed at the root of the molecular tree of life.

The central dogma of biology holds that genetic information normally flows from DNA to RNA and to proteins. As a consequence it has been generally assumed that genes code for proteins, and that proteins fulfil not only most structural and catalytic but also most regulatory functions in cells. This is essentially true in prokaryotic organisms whose genomes are almost entirely composed of closely packed protein coding sequences. However, this is not the case in higher organisms in which proteomes and their coding sequences occupy only a tiny fraction of the genome. Around 97–98 % of the transcriptional output of the human genome is non-protein coding RNA (ncRNA). RNA is an ideal molecule to regulate biological networks due

its sequence information and structural plasticity. The intrinsic relevance of ncRNAs in the regulation of genomic output has been rapidly unveiling during the last decade. Nevertheless, functional elements in the primary sequence of the majority of ncRNAs that determine their regulatory role remain unknown. The dominance of ncRNAs in the genomic output of the higher organisms suggests that they are not simply occasional transcripts with idiosyncratic functions, but rather that they may constitute an extensive unrecognized regulatory network within higher organisms. The fact that noncoding RNAs constitute the majority of the transcription of the genomes of humans and other complex organisms suggests that a second tier of genetic output and a network of parallel RNA-mediated interactions has evolved in these organisms, which may enable the integration and coordination of sophisticated suites of gene expression required for differentiation and development.

Recent evidences also pointed out to the pivotal role of ncRNAs in the cell-to-cell communication phenomenon, suggesting a transversal role of ncRNA molecules as modulators in organism interaction. There is a common and central biological language represented by functional RNA molecules. Within a complex multi-cellular organism, cells are able to secrete ncRNAs that can travel using the circulating biofluids to reach distant targets where they will exert their regulatory actions functioning as slow genetic hormones. In pathological conditions such as cancer, experimental evidences suggested the use of ncRNAs by tumour cells to prepare their tissue niche before a metastatic colonization. Different organisms can also take advantage of ncRNAs for their functional associations. This is not only the case of the parasitic associations between infectious agents such as viruses, bacteria and fungi that can hijack the host defenses using ncRNAs, but also this phenomenon can be observed in mutualistic and symbiotic interactions.

The present book is a compilation of selected biological topics where ncRNAs are mediators of inter-kingdom communication. The book is divided in two main sections covering the role of ncRNAs in bacterial and viral interaction with different hosts and the modulatory effect of ncRNAs in the interactions between eukaryotic organisms.

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