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MicroRNA pathways as new functional axes in cell fate determination

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The identification of a series of non-coding RNA (ncRNA) families, with regulatory roles in several biological processes, represents one of the most relevant advances derived from transcriptome analysis. These ncRNAs are actively transcribed from the genome of many organisms. Among them microRNAs (miRNAs) are small regulatory, single-stranded, RNA molecules (19–25 nucleotides in length) that are generated in the nucleus as hairpin primary transcripts. miRNAs processing is carried out initially in the nucleus and later on in the cytoplasm, where the mature miRNAs molecules, through a limited base-pairing complementarity, destabilize or block the translation of their phylogenetically conserved target transcripts [1].

miRNAs exert their function assembled in the RNA-induced silencing complexes (RISCs), where members of Argonaute (Ago) family of proteins provide a unique platform for target recognition and gene silencing. Interestingly, recent evidences also suggest that miRNAs and epigenetic pathways appear to form a complex regulatory circuit that modulates the expression of an increasing number of genes in the genome. miRNAs are not only modulated by epigenetic regulation but it is now emerging that miRNAs also have specific epigenetic functions for the regulation of the transcriptional landscape of the cell.

Following the identification of a functional miRNAs pathway in C. elegans, their contribution to both embryonic development and maintenance of tissue homeostasis in adults has rapidly emerged also in mammals. miRNAs exhibit a developmental stage- and tissue-specific expression and are present in critical regulatory pathways to regulate stem cells function, cell lineage specification/differentiation, maintenance of cell identity and tissue induction, growth and morphogenesis.

The identification of the molecular pathways involving miRNAs and specific RNA-binding proteins, responsible for the regulation of their production, localization, stability and activity, is gaining crucial importance for the characterization of physiological and pathological processes of human development.

References

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Key words

MicroRNA, cell fate determination, differentiation, tissue homeostasis and morphogenesis.