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Spatial and temporal distribution of small no coding RNAs (miRNAs and piRNAs) into the cell

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The diffusion of new technologies of high throughput sequencing has resulted in a large amount of sequencing data set that gave us the opportunity to shine the spotlight on different aspects of the intricate cellular networks. The 90% of the genome is transcribed following distinct regulatory pathways, tissue-specific rhythms in specific time-points. The complex regulatory networks control is realized through different types of trans-regulators TFs (transcription factors), different classes of small noncoding RNAs and steps in their maturation. All these evidences have changed the view of cellular networks regulation. However, the advances in methods that analyze RNA populations allowed a quantitative, and rapid characterization of small RNAs in cells and/or tissues producing a picture under a precise condition. All these data are quickly stored in specialized databases that become a source of information, and by a simply changing of the initial question, it can provide surprising results. We performed an analysis of complete subset sequences of small non-coding RNA (miRNA and piRNA) stored in the main data base to identify occurrence of conserved motifs and possible interplay between transcription factors and small non-coding RNAs in genome-scale regulatory networks. In particular, we analyzed the entire subgroup of Homo sapiens mature miRNA (1881 mature miRNAs sequences from <http://www.mirbase.org/ftp.shtml>) and piRNA (32826 piRNAs sequences from <http://regulatoryrna.org/database/piRNA/download.html>).

Biography

Massimiliano Chetta is a biologist with a specialization in medical genetics and PhD. in molecular medicine of the adult and child. He has an extensive international experience in genetics and public health. Currently he is a biologist manager at the Cardarelli Hospital in Naples, hospital of national importance where he carries out activities of molecular biology for the oncology department and post-natal cytogenetic diagnosis. In recent years he has been dedicated to the analysis of big data (whole exome, target sequencing, small RNA-Seq)

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