



Dipartimento di Biotecnologie e Bioscienze – UNIMIB

Thursday, March 14, 2024, 4:30 p.m., U4-Tellus building, room U4-01 / Webex

Genomics regulation by non-coding RNAs

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Human Technopole



Abstract: We have been mapping genome elements, broadly identifying promoters, enhancers, protein-coding, and IncRNAs in the FANTOM projects in a variety of cells. These regulatory elements mapping efforts are currently continued on the Human Cell Atlas in Japan, where we profile transcriptomes while focusing on the simultaneous identification of promoters and enhancers. On the other hand, IncRNAs constitute a large group of transcripts, for the majority of which the function is still unknown. Genetic evidence and conservation suggest a possible function for some 19K, however a more direct assessment of IncRNA function is needed. We started the FANTOM6 Project to directly test the function of IncRNA by systematically knocking down several hundreds of IncRNAs in human primary fibroblasts and ES cells, suggesting a function for >30% of IncRNA tested in each cell type. In the second stage of the project, using our RADICL-seq technology, we broadly map RNAs bound to chromatin, because of the important known role of several IncRNAs in regulating the epigenome/chromatin activity. Our new data identifies a large number of interactions showing various patterns: these include interactome driven by enhancer RNAs, intronic RNAs, IncRNAs, and RNAs from retrotransposon elements. RNA interactions display dynamic interaction patterns during differentiation/cell activation, and specific interactomes for each class of RNAs, suggesting a yet-described regulatory and structural role of RNAs...

Host: Silvia Nicolis

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