CIBIO EXTERNAL seminar

23 MAY AT 12:30 P.M.
ROOM 102 | POVO 1

LONG-DISTANCE COMMUNICATION BETWEEN LONG AND SHORT NEURONAL GENES MEDIATED BY RNA

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Intronic sequences are spliced out of newly transcribed RNAs and are usually rapidly degraded. Because of their rapid degradation, intronic RNAs have been classically viewed as splicing by-products. Here, we integrate genome-wide maps of RNA-DNA contacts measured by RADICL-seq with genome radiality maps obtained by GPSeq, to illuminate the spatial distribution and fate of intronic RNAs in the nucleus of neuroepithelial stem cells undergoing differentiation. As cells differentiated towards mature neurons, transcription of a set of highly-expressed long neuron-specific protein-coding genes resulted in the production of intronic RNAs that formed long-range contacts either with loci far away (> 5 Mb) from their source gene or on different chromosomes. These long-range interacting intronic RNAs (LIRs) appeared to move radially from the nuclear periphery—where their source genes are located—towards the nuclear interior—where their targets are concentrated. Remarkably, gene ontology analysis revealed that the LIR targets in the nuclear interior are highly enriched with short neuronal lineage-specific genes that get activated in the later stages of differentiation. We propose that, during neuronal differentiation, LIRs transcribed from long neuronal-specific genes act as bridging molecules facilitating chromatin re-organization in the nucleus interior where they mediate cooperative activation of shorter neuron-specific genes.

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