24 January 2024

Dipartimento di Biologia Cellulare, Computazionale e Integrata - CIBIO

PhD Colloguia 2023

Alteration of rRNA 2'Ome: a novel translational regulator in cancer







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While the ribosome was considered for over 40 years as a neutral actor of gene expression, it now appears as a key regulator of translation through modulation of its composition, including via chemical modifications of ribosomal RNAs (rRNAs). Using cellular models, we revealed that ribose 2'-Omethylation (2'Ome) of rRNA can be a source of ribosome diversity. We reported that 2'Ome is altered during tumorigenesis and directly affects translational behavior of ribosomes toward mRNA subsets.

Thanks to an innovative omic technology, the RiboMETH-seq, we demonstrated that rRNA 2'Ome is altered in different cancer types, including breast cancer and glioma. Moreover, our data demonstrated that the variability in rRNA 2'Ome level is (i) restricted to particular rRNA sites, (ii) different depending on the pathological context and (iii) associated with particular translational reprogramming. Our data support the recent entry of the ribosome into the emerging field of epitranscriptomics.