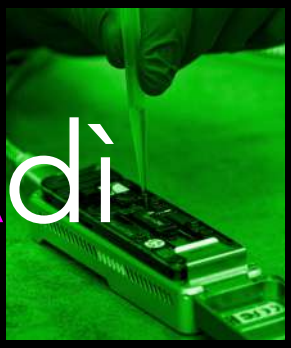
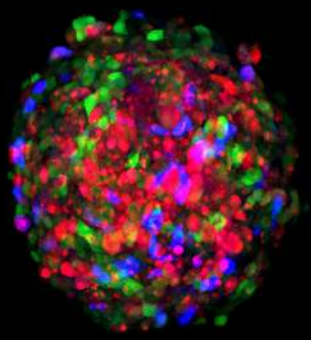
Finanziato dall'Unione europea NextGenerationEU | Ministero dell'Università e della Ricerca | Italiadomani PIANO NAZIONALE DI RIPRESA E RESILIENZA | spoke.6

MUR PNRR National Center for Gene Therapy and Drugs based on RNA Technology

Spoke 6: RNA drug development

veRNAdì





A webinar series about RNA

to share projects and competences,
increase networking, discuss issues
and new ideas, and disseminate results

Every last Friday of the month

https://rb.gy/y40y6

8th veRNAdì: Friday 5 July 2024, 15:00

CELLULAR AND MOLECULAR HETEROGENEITY IN HUMAN CANCER

Dr. Francesco Nicassio

Istituto Italiano di Tecnologia (IIT), Milan

The non-coding genome and regulatory RNAs hold substantial promise for precision medicine, particularly in cancer, where dysregulation of these elements contributes to tumour progression, metastasis, and therapy resistance. Despite technological advancements, the comprehensive understanding of non-coding RNAs and their role in cancer remains fragmented and incomplete. Here we present recent discoveries from our laboratory aimed at overcoming these limitations. On one hand, we investigated the transcriptional and epigenetic programs underlying cancer evolution using single-cell omics and genomic barcoding. In Triple-Negative Breast Cancer models, we found that cancer evolution can be driven by pre-encoded factors. We identified transcriptional states and DNA accessibility profiles linked to tumour initiation and drug tolerance, highlighting the complexity of cancer. In parallel, we are exploiting new third-generation technologies, such as Oxford Nanopore Technology (ONT), which can sequence long, possibly full-length RNA transcripts, enabling the accurate detection of isoforms, alleles, and transcripts that are traditionally difficult to resolve with short reads. Notably, RNA modification pathways are often dysregulated in human cancer and may represent new targets for cancer therapy. Direct RNA sequencing (dRNA-seq) can also capture nucleotide modifications as they alter the signal recorded by the ONT sequencing platform, opening new avenues for epitranscriptomics research.