DNA methylation as a key to new diagnostic and therapeutic technology in oncology

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Di Masi et al. 2016, Ilic et al. 2022, deSouza et al. 2015

Cancer clinical research – main areas of development

Early diagnosis Cancer development monitoring – metastasis/recurrence – Cancer therapy Analysis of DNA methylation in cancer and matched blood samples may contribute significantly to all of these 3 areas!

DNA methylation at cytosine 5th position



Methylated cytosines usually are present cpG site in the CG context





fully-methylated

DNA methylation looking from the perspective of its clinical utility gives us 2 levels of specificity:

- 1. Sequence, as it occurs in a specific regions of the genome
- 2. Binary information of being chemically modified (methylated) or not (un-methylated)

DNA methylation atlas of normal tissues gives a great opportunity of having a reference

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A DNA methylation atlas of normal human cell types

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Proof of concept glioblastoma (GBM) tumors

CANCER GENETICS AND EPIGENETICS

IJC INTERNATIONAL JOURNAL of CANCER

Targeted sequencing of cancer-related genes reveals a recurrent TOP2A variant which affects DNA binding and coincides with global transcriptional changes in glioblastoma

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Proof of concept glioblastoma (GBM) tumors



Looking for technology, rather then for single target-therapy strategies !



Idea of prospective large-scale study

Collect a heterogeneous cohort of patients with different cancer types, including metastatic, recurrent and in-situ cancers, collect tumor samples together with blood samples to analyze DNA methylation markers.

Develop new flexible ways for diagnosis, disease monitoring and therapy based on DNA methylation.



Thank you for listening

