



RESEARCH TOPIC DASMEN2
Dissecting spatial transcriptomics in stage I ovarian cancer
Curriculum DASMEN Standard

Laboratory name and address

Cancer Pharmacology Lab, via Manzoni 56, 20089 Rozzano - Milan, Italy

Datascience Supervisor

Sergio Marchini

sergio.marchini@humanitasresearch.it

Laura Mannarino

laura.mannarino@humanitasresearch.it

Research Supervisor

Rosanna Asselta

rosanna.asselta@hunimed.eu

Maurizio D'Incalci

maurizio.dincalci@hunimed.eu

Abstract

Stage I epithelial ovarian cancer (EOC) is a tumor confined to the ovary, causing the relapse after front-line therapy of 20% of patients. To date, there are no molecular biomarkers for predicting the response to therapies.

Our research group has recently demonstrated that stage I EOC can be classified into 3 groups based on tumor chromosomal alterations, which correlates with prognosis. The hypothesis behind this project is that chromosomal aberrations can shape not only the aggressiveness of cancer cells, but also their interaction with the tumor microenvironment (TME). For this purpose, we will analyze the various cell types present in the tumor using spatial transcriptomics. Clinical biopsies of stage I EOC will be analyzed to detect any difference in cancer cells and TME among the different histotypes and according to the clinical evolution (n=10), considering the different regions within the tumor.

Main technical approaches

- Bioinformatic analysis of data from scRNAseq, spatial scRNAseq, RNAseq, and spatial transcriptomics.
- Analysis of DNA shallow whole-genome sequencing (sWGS).
- Handling, manipulation and analysis of large datasets.



Scientific references

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Type of contract

Scholarship of € 21.000 gross per year awarded by Istituto Clinico Humanitas. This sum is subject to IRPEF income tax and exempt from social security contributions.

Borsa di studio pari a € 21.000 annui lordi erogata da Istituto Clinico Humanitas. Importo soggetto a tassazione IRPEF ed esente da contribuzione previdenziale.