RESEARCH TOPIC MECM_5

Multimodal genomic and microenvironmental profiling to predict relapse risk in early-stage epithelial ovarian cancer

Curriculum
MECM Standard

Research Area
Onco

Laboratory name
Unit of Translational Genomics / Laboratory of Cancer Pharmacology

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Abstract
Our previous results showed that the histological subtype of epithelial ovarian cancer (EOC), regardless of stage or grade, can be stratified according to the extent and pattern of somatic copy number alterations into stable (S), unstable (U), or highly unstable (HU) groups. S/U/HU profiles are comparable in bilateral and synchronous lesions and, in multivariate analyses, are associated with survival.
This project proposes that intrinsic tumor features, including S/U/HU status and DNA methylation changes, together with their interaction with the tumor microenvironment (TME), determine whether EOC remains confined to the ovary (stage I), develops micrometastases (stage I, relapsing), or progresses to abdominal macrometastases (stage III/IV).
The aims of this project are to: 1) validate the prognostic value of S/U/HU profiles; 2) link these profiles to methylation patterns; and 3) define how they influence TME composition and spatial organization.
Research activities
1) Validation of the prognostic significance of S/U/HU profiles
- Sample collection
- DNA extraction and purification
- Classification of EOC biopsies according to S/U/HU profiles
- Statistical analyses to assess the prognostic value of S/U/HU profiles in relation to clinical variables and across histological subtypes
- Integration of U/HU profiles with pan-cancer signature analysis, including copy number signatures
2) Methylation landscape analysis
- Generation of a genome-wide DNA methylation dataset for stage I EOC

- Bioinformatic analyses to infer the origin, biological characteristics, and TME composition of S/U/HU profiles
- Statistical analyses to develop a prognostic methylation signature that characterizes clinically relevant subtypes with different risks of relapse
3) Investigation of the mechanisms by which S/U/HU profiles shape TME composition and spatial organization
- Characterization of the immune infiltrate populations in EOC biopsies stratified by S/U/HU profiles
- Investigation of the heterogeneous interactions between tumor cells and the TME
- Spatially resolved quantification of cellular populations within tumor tissues to elucidate the spatial organization of the TME in patients with different clinical outcomes

Main technical approaches

Technical approaches
- Perform Next-Generation Sequencing (NGS) experiments on both liquid and solid tumor biopsies, managing the full workflow from nucleic acid extraction and library preparation to data analysis.
- Conduct genomic, transcriptomic, and epigenomic analyses, including single-cell sequencing and spatial omics approaches.
- Perform immunohistochemical and immunofluorescence analyses on tumor tissue samples.
Required qualifications and skills
- Master's degree (or equivalent) in Biotechnology, Biological Sciences, or a related field.
- Demonstrated hands-on experience in molecular biology techniques; prior experience with NGS workflows and data analysis is highly desirable.
- Ability to work independently in managing laboratory activities while effectively collaborating within a multidisciplinary team of biologists, bioinformaticians, statisticians, and clinicians.

Scientific references

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