

Wednesday
February 2, 2022
15.00 (GMT+1)



Davide Bedognetti

Human Immunology Department
and Cancer Program
Sidra Medicine, Doha, Qatar

The seminar will be held on line. Please register at <https://bit.ly/3H8GmLB>

You will receive an invite with the link to the seminar.

Visit <https://cqb.dieti.unina.it/index.php/events> for the event series.

Systems biology as a compass to understand tumor-immune interactions in humans

Cancer progression is influenced by complex interactions between cancer cell, the immune system, and the microbiome. Deciphering this interplay is critical to develop novel therapeutic approaches and more efficient stratification systems. We use systems biology approaches to dissect the relationship between cancer-cell intrinsic (somatic) and host-related modifiable (microbiome) and unmodifiable (germline genetics) factors with tumor immune responsiveness. In the TCGA, we observed that a significant proportion of immune microenvironmental features are influenced by the genetic background of the host and identified potential drivers of this phenomenon. Furthermore, we assembled a genomic dataset (AC-ICAM) that combines paired tumor-normal whole exome, tumor transcriptome, deep T Cell Receptor sequencing of tumor samples, and tumor-normal colon tissue microbiome characterization. Using such a resource, unreported cancer-immune-microbiome interactions associated with favorable outcome were observed.

Davide Bedognetti, MD, PhD is the Director of the Human Immunology Department and Cancer Program at Sidra Medicine. He also serves as an Adjunct Associate Professor at the Hamad Bin Khalifa University in Doha, Qatar, and as an Associate Professor of Internal Medicine at the University of Genova, Italy. Dr. Bedognetti joined Sidra in 2014. The main focus of Dr. Bedognetti's Lab is to define determinants of immune responsiveness in tumors by using integrative genomic approaches. The ultimate goal is to develop novel and personalized therapeutic strategies. The team employs systems biology approaches to dissect the molecular network of host-tumor interactions, and to understand its relationship with treatment effectiveness.

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