CCR – Impromptu Seminar

Monday, January 15th 2024, 13:00

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Fusion-driven sarcomas: From epigenetic profiling to developmental disease models

Sarcomas constitute a diverse group of mesenchymal cancers that affect bones and soft tissues. They account for 2% of all cancers, with a higher incidence in children and young adults (20% of pediatric solid tumors are sarcomas). Sarcomas are among the most deadly childhood cancers and provide few genetic targets for molecularly targeted therapy. We were among the first to investigate the epigenome of Ewing sarcoma, a pediatric sarcoma characteristically driven by a fusion oncogene, showing that these tumors exhibit a unique epigenome with thousands of fusion-driven gene-regulatory elements. Moreover, we performed the first large-scale analysis of epigenetic heterogeneity in Ewing sarcoma tumors, revealing an epigenetic memory of the disease's cell-of-origin and an association of epigenetic signatures with metastatic status at diagnosis. Based on these findings, we have developed a liquid biopsy assay for tumor detection and classification that is based on whole genome sequencing and a machine learning algorithm that detects tumor-associated chromatin from cell-free DNA fragmentation.

In this talk, I will introduce our work toward precision medicine for pediatric sarcomas, with a specific focus on regulatory processes that go beyond the genome. Using state-of-the-art technologies, patient samples as well as stem cell derived tumor models, and the combination of wet-lab with computational methods, we aim to: (1) Uncover non-genetic mechanisms of sarcoma development and exploit them for new therapeutic approaches. (2) Create minimally invasive biomarkers for disease monitoring. (3) Develop sarcoma models to expedite drug discovery and molecular precision medicine.

Venue: Lecture Hall B1, Borschkegasse 4a
Time: Monday, January 15th, 2024 at 13:00
Host: Maria Sibilia

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