

## **SCIENTIFIC MEETING**

## 20 May 2022

13:00 - 14:30

## Hybrid- B6 building and zoom-

near B2 (Allée G. St Hilaire, Talence)

zoom : <u>ID de réunion : 841 0878 6542</u>

13:00 – 14:00 **Dr Gautier Follain**, Postdoctoral Researcher,
Johanna Ivaska lab, Turku Bioscience Centre, Finland

Studying the mechanisms of the intravascular adhesion and extravasation of Pancreatic cancer cells.

14:00 – 14:30 **DEPArray**<sup>TM</sup> digital sorting



Hichem Gallala – Senior Field Application Specialist Béchir Boughaba – Corporate Sales Manager France and Benelux











#### 13:00 - 14:00

**Dr Gautier Follain**, Postdoctoral Researcher, Johanna Ivaska lab, Turku Bioscience Centre, Finland

# Studying the mechanisms of the intravascular adhesion and extravasation of Pancreatic cancer cells.

Solid tumor progression is a dynamic succession of events, happening in different spaces and times in the body, ultimately leading to the formation of life-threatening metastases. To colonize distant organs, cancer cells are exploiting the circulatory networks as natural paths before stopping in small vessels and crossing the endothelial barrier. During transportation, the cells are subjected to harsh physico-chimical parameters and to different cell types compared to their primary tumor of origins. This is a critical situation for them, attested by the massive difference between circulating tumor cell (CTC) counts in patients, and the actual metastatic dissemination. Nevertheless, some of them survive by developing a series of survival, adhesion and migration strategies. All of this remain poorly understood.

My research focuses on the steps of adhesion and extravasation (crossing of the vessel border) of pancreatic ductal adenocarcinoma (PDAC) cell lines. My main objectives are to decipher the mechanisms allowing the cells to break the endothelial barrier, in an attempt to identify key factors and actors during the process. I work with microfluidic models to better reproduce the physiologic conditions of perfused vessels, zebrafish embryos which are transparent and very rapidly develop a complex vascular system, allowing unprecedent live imaging resolution, and mice models. All three are coupled with quantitative and high-resolution imaging and to single cell characterization approaches (scRNAseq and mass cytometry).

My ongoing results support the idea that heterogeneity of cancer cells, even among laboratory cell lines, is driving different adhesion/extravasation modes. My talk will focus on two unpublished aspects: 1. Our extra effort to better understand the biophysicals context during the steps of adhesion and extravasation, using Super Resolution microscopy and AFM. 2. The live and fixed microscopic dissection of the transmigration mechanisms of several PDAC cell lines. Understanding the drivers of such different behavior is necessary to propose novel clinical avenue.

#### Previous work:

Follain et al. Fluids and their mechanics in tumour transit: shaping metastasis. NRC 2020

Follain et al. Hemodynamic forces tune the arrest, adhesion and extravasation of circulating tumor cells. Dev Cell. 2018

To meet Dr Follain, contact Frederic Saltel

14:00 - 14:30

## **DEPArray™** digital sorting

## www.siliconbiosystems.com



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DEPArray digital sorting offers unique options for sorting rare cells in small samples with absolute precision. Major application areas include:

#### **Live Cells**

DEPArray sorting is very gentle with cells due to the absence of Laser light sources and physical stress during the permanence of cells in the flow cell. Cells isolated from live disaggregated tissues or cell culture remains viable and can be cultivated or used for RNA analysis.

## **Liquid Biopsy**

Multiple body fluids can be a non-invasive source of tumor cells. Circulating Tumor Cells (CTCs) in blood is the most common but also ascitic fluid, pleural effusion and cerebrospinal fluid could be assayed using digital sorting.

## Solid biopsy

Low cellularity FFPE samples of epithelial tumors can be disaggregated, stained and loaded on DEPArray™ to isolate pure tumor cell populations, enabling an accurate analysis of difficult quantitative molecular parameters like Somatic mutations, Copy number variation and Loss of heterozygosity. When DNA integrity of the FFPE block is sufficient, whole genome/exome sequencing are possible from pure cells pools.

### Single cell Genomic analysis

Single Cells can be processed using the Ampli1™ WGA workflow for copy number profile and mutation analysis. Low Pass genome NGS produces accurate Copy Number Aberration profiles which enable the real time analysis of tumor heterogeneity and determine the correlation of each clonal population with drug resistance/response. Mutation detection can be further obtained using our Ampli1™ OncoSeek NGS panel

#### Classic Lymphoma

In these samples the Reed Stenberg tumor cell population is distinguished by the combination of CD30 and PD-L1 antibodies, helped by morphological analysis through the cell images. Single or pooled cells can be isolated and analysed in purity, making it possible to obtain valuable molecular information from tumors normally unaccessible to molecular analysis.

