CASE STUDY

Identification and prognostic impact of a metastases facilitator pattern in resected non-small cell lung cancer IIIA-N2

Who: Hélène Blons, PHD – Head of the Pharmacogenetics and Molecular Oncology Unit, Georges Pompidou European Hospital, INSERM

After an internship and specialist training in medical biology, I started a PhD in "molecular characterization of HNSCC implication on response to neoadjuvant chemtherapy and prognosis" under the direction Professor P. Laurent-Puig. I was then recruited by Trousseau pediatric hospital (2002-2004) to work on hereditary hearing loss and returned to cancer in 2004 as Assistant Professor of Biochemistry (Paris Descartes University), where I started my research on lung cancer. My dual training allows me to work at the interface between a research unit and a medical laboratory. My research is mainly translational and focused on personalized and genomic medicine in solid tumors using liquid biopsies and high throughput sequencing to characterize cancers in terms of response to treatment and prognosis.

Why 3D Biology™ Technology?

Mediastinal lymph node involvement in lung cancer (N2-NSCLC) is associated with poor prognosis. Optimal management of clinical stage IIIA-N2 NSCLC remains controversial but complete tumor resection can be related to long-term survival in some patients. We need to enhance our ability to select IIIA-N2 patients who will benefit from surgical resection. Using 3D Biology technology for research purposes, we want to have the opportunity to test pathways to see if we can find a signature at the expression level that would help us to identify the good responders to the surgery versus the one that will relapse early.

Aim of the project:

Our hypothesis is that tumor heterogeneity is related to higher adaptation capacities (in nodes, in blood stream, and eventually in bone marrow) and to cell plasticity leading to potential resistance to treatment and ultimately to worse prognosis. We believe that IIIA-N2 NSCLC is a good model to study tumor heterogeneity with multiple samples available after surgery. Comprehensive analysis of match pairs (primitive tumors and N2 node) will help analyze differences between long term survivors and early relapse patients to identify those who will benefit from surgery.

Methods:

In this project we plan a comprehensive analysis including oncogene/tumor suppressor genetic profiles and expression data to link genotypes to pathway activation in the primary tumor as well as in N2 nodes to identify the good responders to the surgery versus the one that will relapse early. From a pre-selected set of 18 patients, 9 long term survivors (mean disease free survival 77 months) and 9 with mean disease free survival 9.7 months, we plan to define a specific metastases facilitator pattern associated to prognosis in resected IIIA-N2 NSCLC. Predictive markers will be validated in a planned prospective study and ultimately could be used to help select patients that will benefit from surgery at diagnosis.

nCounter® Vantage 3D™ Assay selection:

nCounter Vantage 3D DNA SNV Solid Tumor Panel + RNA:Protein Solid Tumor Assay for FFPE

"We don't always have frozen tissue for the patients and we don't always have a large amount of tissue available to do whatever we want to do for those patients. The use of techniques that are compatible with small samples is benificial, as low DNA quantity and sometimes low DNA quality is the major challenge that we have to deal with."

Hélène Blons, PHD

Head of the Pharmacogenetics and Molecular Oncology Unit, Georges Pompidou European Hospital, INSERM

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