MATWIN
MATURATION & ACCELERATING TRANSLATION **WITH INDUSTRY**

TECHNOLOGY OFFER

SUPPORTING INNOVATION AND TECHNOLOGY TRANSFER IN ONCOLOGY

DIAGNOSTIC

PMed-HaeMa

Define assays for precision medicine in haematological malignancies

CONTEXT & BACKGROUND

Multiple myeloma is a rarely curable malignant disease of clonal plasma cells that accumulate in the bone marrow leading to clinical signs and symptoms related to the displacement of normal haematopoiesis, development of bone disease, and production of monoclonal protein. Multiple myeloma is a genetically and clinically heterogeneous disease. Deep genome sequencing studies have recently revealed an even wider heterogeneity and genomic instability with the identification of a complex mutational landscape and a branching pattern of clonal evolution.

All patients invariably relapse after multiple lines of treatment, with shortened intervals in between, and finally become resistant to any treatment, resulting in loss of clinical control over the disease, and death within weeks.
Treatment improvements will come from detailed molecular analyses to develop individualized therapies taking into account the molecular heterogeneity and subclonality evolution. The aim of our project is to define biomarkers and generate assays to develop precision medicine approach in hematological malignancies.

INNOVATIVE COMPONENT & TECHNOLOGY

We developed methods to define biomarkers/gene signatures to predict sensitivity or resistance of hematologic tumor cells to treatments.

SCOPE

Hematological malignancies

KEYWORDS

Biomarker, Theranostics, Hematological malignancies, Cancer

OBJECTIVES

Our aim is to define biomarkers and generate assays to develop precision medicine in hematological malignancies according to the molecular and subclonal heterogeneity.

DEVELOPMENT & MATURATION STAGE

Our team has decades experience in MM research, diagnosis and biological follow-up of the patients. We recently reported gene expression (GEP)-based scores to predict the sensitivity of myeloma cells to different treatments including DNMTi, HDACi or combination. These scores allow the identification of MM patients who could benefit from HDACi, DNMTi or DNMTi/HDACi treatments (3 patents : “Method for predicting multiple myeloma treatment response” (Patent EP12306141.8), “Method for predicting HDACi treatment response in Multiple Myeloma” (Patent EP12306225.9) and “Prediction of multiple myeloma cells sensitivity to DNMTi/HDACi combined epigenetic targeted treatment” (Patent EP14305404). Our method could be extended to other drugs and to other cancers. We are currently expanding our approach to others drugs used in MM treatment with the support of the technology transfer acceleration company SATT AxLR.

INTELLECTUAL PROPERTY & PATENT CO-OWNER(S)

6 patents are already filled and several are in maturation in collaboration between the laboratory, the start-up and the TTO.

We also investigated the interest of our methodology in another B cell malignancy: diffuse large B cell lymphoma (DLBCL), the most common type of non-Hodgkin lymphoma. We recently identified that tumour cells of high-risk patients with DLBCL demonstrated a significant enrichment in genes involved in DNA repair pathway that could represent an adaptive mechanism to drug resistance (Bret et al. Oncotarget 2012). We designed gene-based DNA repair scores that have a strong potential to identify high-risk DLBCL patients and exploit addiction to a specific DNA repair pathway in order to define the best DNA repair inhibitor to use in combination with conventional treatment (Bret et al. BJH 2015) (Patent “Methods for predicting response to DNA repair pathway inhibitors in diffuse large B-cell lymphoma” (EP14306201).

This project associates our research group involved in MM pathophysiology and the laboratory of monitoring Innovative Therapies in charge of diagnosis and residual disease monitoring of multiple myeloma patients. Our diagnostic activity is associated with the biological resource center of the Montpellier University Hospital. Furthermore, we have created a startup company to valorize our academic research in hematology.

Our approach will help to develop the best treatment regimen for each patient according to the disease heterogeneity and reduce the toxicity. It will help clinicians to choose the best treatment strategy (among the large number of molecules available) during the evolution of the disease when previous treatment line-resistant subclones will emerge.

TARGET POPULATION

Patients with Haematological cancers

STRENGHTS & COMPETITIVE ADVANTAGES

Our biomathematic approach to find new biomarkers associated to a specific treatment in hematological cancers is inventive and supported by a solid expertise into haematological malignancies. Moreover, the laboratory has developed more than 40 human multiple myeloma cell lines representative of the molecular heterogeneity of patients and fully characterized (licenced to the start-up). We have also a collection of 18 DLBCL and 10 AML cell lines with ongoing full characterization. The laboratory and the start-up have also developed unique models of drug resistant cell lines and normal plasma cell differentiation.

INDUSTRIAL APPLICATIONS & OPPORTUNITIES

The start-up offers two types of services :

- Assessment of drugs efficiency and characterization of their mechanisms of action/drug resistance. The company provides to pharmaceutical companies a wide range of customized services to optimize new therapeutic agents in Multiple Myeloma and in other haematological cancers.
- Identification of biomarkers to predict sensitivity of malignant cells to new therapeutic agents in Multiple Myeloma and other haematological cancers (DLBCL, AML).

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