Research Project Proposal
Academic year 2018-2019

Project Nº 47

Title: Analysis of transcriptional profile in patients with Acute Myeloblastic Leukemia as a tool for prognoses and target identification

Department/ Laboratory

Genómica Avanzada/ laboratory 1.04/ CIMA

Director 1 *: Felipe Prósper*

Contact: *fprosper@unav.es*

Codirector: *Teresa Ezponda*

Summary Acute myeloid leukaemia (AML) is a malignant disease characterized by the uncontrolled proliferation and differentiation of immature progenitors. This leukemia in adults over the age of 60 has a poor prognosis and is associated with a low chance for long-term disease-free survival.

Although current therapies offer a 20-30% chance of response, most patients eventually relapse an understanding factors that predict the response as well as mechanisms involved in the resistance to therapy are essential to improve the results in this disease. In the context of the PETHEMA group, we have completed a clinical trial in which over 250 patients have been randomized to receive hypomethylating agents versus fludarabine with ara-C, an samples from these patients have been collected at the time of diagnoses.

IN the current work, we will determine using RNAseq the trascriptoma of AML patients and compare the transcriptome between patients who response or are refractory with the aim of identifying transcrional profiles associated with response. Additionally we will identify profiles associated with certain genomic in order to identify new potential targets and mechanisms of transformation.

To answer these questions we will use RNAseq along with NGS in leukemic cells from patients at the time of diagnoses.

The development of next generation sequencing techniques (NGS) has allowed clinicians and researchers to better comprehend patients not only at clinical levels, but also from a genomic point of view. In order to retrieve useful information from NGS, the generated data must be carefully processed and analysed by bioinformaticians or computational biologists. This joint analysis leads to a better understanding of different subjects such as the relationship between a transcriptomic signature and the response to treatment.

In this project, we expect the candidate to understand how NGS data is generated from a wet-lab approach and the computational analysis of RNA-Seq data to compare the transcriptomic signature of patients with positive and negative response to this two different treatments.

yes		**Does the project include the possibility of supervised animal manipulation to complete the training for animal manipulator?**
no	X	