H2020 MSCA - ITN - 2017 - 766030

CONTRA

Computational Oncology Training Alliance

ESR 3 - Identification of drivers of relapse and metastasis (mostly bioinformatics analyses, with possibility of some experimental validation; 90%/10%)

Research project	In this project, we will aim to specifically uncover the alterations, genes and pathways related with i) the resistance to anti-cancer treatments that result in the relapse of patients, and ii) the metastasis of primary tumours. As in the case of tumourigenesis, we will base the analysis on the assumption that both relapse and metastasis follow a darwinian evolutionary process, and thus we can exploit the signals of positive selection to detect which genomic regions drive it. We will collect publicly mutational data of cohorts of tumours where both the primary and the relapse (or primary and metastases) have been sequenced. Additionally, as part of a project analyzing the mechanisms of relapse of Acute Lymphoblastoid Leukemia –where we have partnered with a hospital– we will have access to newly sequenced samples of primaries and relapse of this disease. We will develop new bioinformatics methods to detect the signals of positive selection on alterations in the processes of resistance to anti-cancer therapies and metastasis, which will employ models of the evolution of tumours upon these two processes. Methods developed in the course of the project will be applied to the publicly available and in-house cohorts of primary-and-relapse/metastasis to produce lists of drivers of these processes. Follow-up experiments of some of the predicted driver alterations (such as comparing the resistance to standard targeted therapies of cancer cell lines with and without them) will be carried out. Although the project implies mostly bioinformatics analyses, we envision that the applicant will have the opportunity to carry out some of the wet-lab experiments as well (90%/10% partitioning of the time between bioinformatics and wet-lab.)
Supervisor	name Nuria Lopez-Bigas e-mail nuria.lopez@irbbarcelona.org website https://bbglab.irbbarcelona.org/
Host institution	Institute for Research in Biomedicine, Spain Programme of Structural and Computational Biology
PhD program	PhD program in Biomedicine, University Pompeu Fabra
Expected results	1) Novel bioinformatics methods to identify drivers of relapse and metastasis, on the basis of evolutionary models of tumours 2) List of experimentally validated drivers of relapse and metastasis across cancer types 3) New biomarkers to improve the stratification of cancer patients for a more accurate prognosis and treatment.
Planned secondments	1) ETHZ/Beerenwinkel (2 months) 2) KTH/J.Lagergren (2 months) 3) KCL/Cicarelli to learn modelling of drug resistance (2 months)
Required profile	The candidate will have a demonstrated mixed background: i.e., comprising both wet-lab experience and bioinformatics expertise. Ideally, the applicant has received basic training in biology via a basic degree in biological or biomedical sciences, or related disciplines, and an MsC in bioinformatics. The candidate must have a I) solid biological background, ii) understanding of the basic concepts of cancer genomics and iii) the methodological basis of NGS technologies and their associated bioinformatics analysis. We expect that the applicant is able to work collaboratively as part of a team, but also to pro-actively take the initiative in the course of the project.