

**Research Project Proposal**  
Academic year 2017-2018

<b>Project Nº 10</b>
<b>Title: Detection of non-coding rearrangements in Multiple Myeloma</b>
<b>Department/ Laboratory Epigenetic mechanisms of cancer laboratory, Hemato-Oncology program, Center for Applied Medical Research (CIMA)</b>
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<p><b>Summary</b></p> <p>Multiple Myeloma (MM) is an aggressive neoplasm caused by the clonal expansion of malignant plasma cells in the bone marrow. In spite of the advances achieved in MM therapy, this disease remains incurable. Thus, a better understanding of the molecular lesions that lead to MM pathogenesis is a major challenge to develop new therapeutic approaches. The molecular pathogenesis of this disease has started to be elucidated with the identification of several genetic abnormalities. Increasing amount of evidence has shown that beside genetic aberrations, epigenetic abnormalities play an important role in MM (1-2). Besides these epigenetic abnormalities, alteration of the expression of long non-coding RNAs has also emerged as a key mechanism in MM (3). Nevertheless, a vast study that characterizes the known and novel lncRNAs of MM and their alteration mechanisms has not been performed to date. Accordingly, our preliminary analysis has revealed the expression of more than 40.000 novel lncRNAs that are expressed in MM patient samples.</p> <p>The hypothesis of this project is that the deregulation of lncRNAs is a relevant and unexplored mechanism of MM development. This alteration could occur by epigenetic or as in the case of coding genes by chromosomal rearrangements. The goal of this project is the identification of key rearranged lncRNAs (r-lncRNAs) that contribute to MM. r-lncRNAs will be detected from strand-specific-RNA-seq of more than 500 MM patient samples. The validation will be performed by Q-PCR and DNA-FISH; localization of r-lncRNAs by Q-PCR and RNA-FISH and functionality by CHART.</p> <p><b>References</b> References could be added (no more than three)</p> <p>1.- <b>Agirre X</b>, Castellano G, Pascual M, Heath S, Kulis M, Segura V, Bergmann A, Esteve A, Merkel A, Raineri E, Agueda L, Blanc J, Richardson D, Clarke L, Datta A, Russiñol N, Queirós AC, Beekman R, Rodríguez-Madoz JR, San José-Enériz E, Fang F, Gutiérrez NC, García-Verdugo JM, Robson MI, Schirmer EC, Guruceaga E, Martens JH, Gut M, Calasanz MJ, Flicek P, Siebert R,</p>



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3.- Garitano-Trojaola A, **Agirre X**, **Prósper F**, Fortes P. Long non-coding RNAs in haematological malignancies. *Int J Mol Sci.* 2013 Jul 24;14(8):15386-422. PMID: 23887658