Entrega de l'Abstract

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Títol de la recerca: Estudi de la metilació del DNA en dos models tumorals
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Abstract (màxim 500 paraules):

I am Elisabet Figuerola a student of University of Barcelona and I've been working in PEBC, a member of IDIBELL, related to the same university. The main purpose of my project was to study how DNA methylation is related to cancer using two well-established models, and it's called "Study of DNA methylation in two tumoral models".

DNA methylation plays an essential role in the regulation of gene expression in cells. It may occur in the CpG dinucleotides of the whole genome by a protein family called DNA methyltransferases (DNMT), to form a new base named 5-methylcytosine. This epigenetic modification, induce a local conformational change in the chromatin fibre compacting it more; thus is directly associated with a transcriptional repression. Aberrations of DNA methylation pattern have been described in many types of cancer, which include a global hypomethylation of the DNA and a concrete promoter hypermethylation in some tumour suppressor genes. The main purpose of our work was to study *in vitro* the changes in the methylation pattern in two well-established tumorigenic models, such the human colon cancer cell line HCT116 and its double *knock-out* of DNMT1 and DNMT3B, DKO line; and a multi-stage progressive tumorigenic model which is the transition from a non-cancerous cell line to a more invasive one with a metastatic behaviour. We have observed these

phenomena analysing the 5-methylcytosine global content by antibody detection, and by quantifying the methylation of the promoter region of candidate tumour suppressor genes after a bisulphite treatment. These studies also revealed a maintenance function of the nuclear architecture related to DNMT, which was clearly observed in the DKO cell line.

In addition, recent advances in the epigenetic field have discovered new nucleotides derived from 5-methylcytosine suggesting a demethylating pathway of DNA. Using the latest antibodies we checked the presence of these marks in our models, highlighting that there is still too much to discover. In this context, the future aim of epigenetic studies should be to increase our knowledge in DNA methylation also considering DNA demethylating pathways, to understand the biology of this disease and develop therapeutic strategies to it.