Identification of fucosylated proteins in ovarian cancer

Ovarian cancer is the most lethal gynecological cancer. The complexity of the disease make difficult to count with an effective early diagnostic method. At the present, the research is focus on a diagnosis and treatment are but the biochemical complexities surrounding the development and subsequent progression of cancer remain unclear. Fucosylation has been classified as an altered post translational modification in many diseases. When a protein is fucosylated it can acquired new characteristics compared to another one that is not being fucosylated. In relation to the biological implication of this change several cases have been reported, for example in cancer is implicated in processes such as cell adhesion, angiogenesis and ligand-receptor recognition.

The ovarian cancer microenvironment is implicated in epithelial mesenchymal transition. The cells under ascitic fluid stimulation can be changed in morphology and alterations in proteins expression and post translational modifications could be carried out.

The goal of this work was identify fucosylated proteins differentially expressed under ascitic fluid of OvCa stimulation. Through affinity chromatography and mass spectrometry (MALDI-TOF) we identify seven fucosylated proteins, of which 5 was present under the stimulus (KRT10, IFFO1, PHF20L1, IGHV1-2 y ZNF224) and 2 was decreased (BRPF1 y DTNA) as compared with the control condition. This results indicate that the microenviroment generates changes that can up or down regulate protein fucosylation and this changes could be favoring the tumor development.