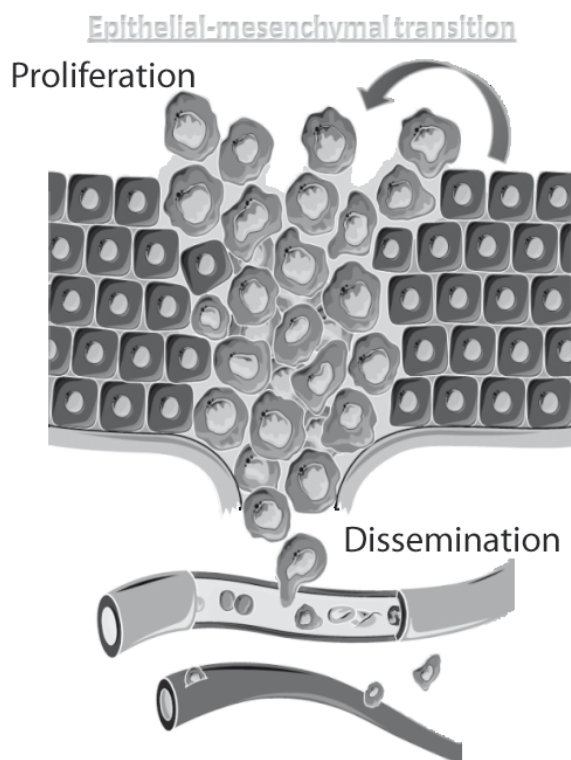


## Regulation of epithelial-mesenchymal transition in colon cancer by $1\alpha,25$ -dihydroxyvitamin D3: a proteomics approach

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Epithelial-mesenchymal transition (EMT) is a typical feature of cells undergoing proliferation and it is a fundamental process in the early stages of carcinoma invasion and metastasis [1-3]. It is a process characterized by loss of cell adhesion, repression of E-cadherin expression, and increased cell mobility (Figure 1).



**Figure 1.** Epithelial-mesenchymal transition. During EMT epithelial cells lose polarity and cell-cell contacts, become migratory, and divide at a faster rate. The cells can intravasate into lymph or blood vessels, allowing their passive transport to distant organs.

There is an increasing interest in the active vitamin D metabolite  $1\alpha,25$ -dihydroxyvitamin D3

[ $1\alpha,25(\text{OH})_2\text{D}_3$ ] and its analogs as preventive and therapeutic anticancer agents [4, 5].  $1\alpha,25(\text{OH})_2\text{D}_3$  drastically alters the gene expression profile of many cell types, inhibiting the proliferation and promoting the differentiation to a normal adhesive epithelial phenotype of human colon cancer cells [6].

In this study we have investigated the regulation and biological activity of  $1\alpha,25(\text{OH})_2\text{D}_3$  in EMT of colon cancer cells. We present evidence of the direct regulation of a number of proteins by  $1\alpha,25(\text{OH})_2\text{D}_3$  in colon cancer cells.

SW480-ADH colon cancer cells were treated with  $1\alpha,25(\text{OH})_2\text{D}_3$  for 8 and 48 hours. Nuclear extracts of treated and non-treated cells were used by triplicate for a proteomic analysis. Proteins were labeled with CyDye Fluor for their subsequent separation by 2D-DIGE. Comparative analysis of protein expression patterns was performed with Progenesis SameSpots and Ludesi Redfin software. Differentially expressed proteins were identified by mass spectrometry (MS) MALDI-TOF/TOF and subsequently validated by western-blotting.

An average of 1600 spots was detected on 2D-DIGE gels. A total of 31 and 19 spots were found to be differentially expressed at 8 hours with Ludesi and Progenesis software ( $p < 0.05$ ; fold-change  $> 1.2$ ), respectively; and a total of 84 and 71 spots at 48 hours ( $p < 0.05$ ; fold-change  $> 1.3$ ). A 36% of overlapping in spot detection was found between the 2 software. By MS and MS/MS were unequivocally identified 17 and 72 proteins from treatment at 8 and 48 hours, respectively. These proteins were mainly involved in DNA and RNA regulation, affecting cell morphology, cell assembly, cell organization as well as cellular repair. A

number of these proteins were further validated by western-blotting confirming previous results.

In summary, we have investigated the regulation and biological activity of  $1\alpha,25(\text{OH})_2\text{D}_3$  in EMT of colon cancer cells. Through the use of proteomics tools we have identified numerous proteins whose expression levels were altered with  $1\alpha,25(\text{OH})_2\text{D}_3$  treatment, and some of them have been further validated. Our results show evidence of the direct role of  $1\alpha,25(\text{OH})_2\text{D}_3$  treatment in EMT in colon cancer through the transcriptional regulation of a number of genes mainly related to cell morphology, cell assembly, cell organization as well as cellular repair.

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## Comprehensive proteomic analysis of human endometrial fluid aspirate

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## Abstract

The endometrial fluid is a non-invasive sample which contains numerous secreted proteins representative of endometrial function. We show here, for the first time, an in depth analysis of the protein content of the EFA using proteomic techniques [1]. To achieve this objective, three different but complementary strategies were used. First, in solution digestion followed by reverse phase high-performance liquid chromatography coupled to tandem mass spectrometry (HPLC-MS/MS); second, protein separation by denaturing one dimensional elec-

trophoresis (SDS-PAGE) followed by HPLC-MS/MS analysis. Finally, two dimensional polyacrylamide gel electrophoresis (2D-PAGE) followed by MALDI-TOF/TOF analysis. The combination of the three strategies led to the successful identification of 803 different proteins. An extensive description of the endometrial fluid proteome will help provide the basis for a better understanding of a number of diseases and processes, including endometriosis, endometrial cancer and embryo implantation. We believe that the thorough catalogue of proteins presented here can serve as a valuable reference for the study of embryo implantation and for future biomar-