

## **PROTEOMIC APPROACH TO IMPROVE THE DIAGNOSIS OF MALIGNANT PLEURAL EFFUSIONS**

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Pleural effusion is an accumulation of pleural fluid that can appear in patients with congestive cardiac failure, pneumonia, tuberculosis, pulmonary embolism, cancer (mainly lung and breast cancer), or physical trauma. Therefore, a cytologic study is commonly needed to confirm the etiology of this malignancy, and in a relevant number of patients surgical techniques are also required. Although several studies have been performed on pleural effusion, their purpose were more a description of the protein content than a comparative analysis to discriminate differentially expressed proteins. For this reason, the aim of this work was to find new protein biomarkers that could improve the diagnosis of malignant pleural effusions in order to avoid the use of invasive diagnostic procedures.

We have compared, by means of proteomic techniques, pleural effusion samples from four patients with tuberculous pleural effusion and four patients with non-small cell lung cancer. Since large portions of pleural effusion proteins are common to those found in plasma, we performed a previous fractionation of samples using multiple affinity removal spin cartridges for the depletion of six high-abundant proteins (Agilent technologies) in order to detect low abundance proteins that could serve as novel biomarkers for the malignancy.

After depletion, to test the efficiency of the removal process, a global analysis of pleural effusion proteome was made using conventional two-dimensional electrophoresis (2-DE). Gels were silver-stained and analyzed using PDQuest software, revealing more than 1200 spots per gel.

Comparison of proteomes from neoplastic origin versus benign ones was carried out using two-dimensional differential in-gel electrophoresis (2D-DIGE) technology and analyses of differences were made with Decyder Software. Those proteins presenting statistical significant differences will be submitted to mass spectrometry for identification.