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IN THE SEARCH OF EARLY STAGES BIOMARKERS FOR NON SMALL CELL LUNG CANCER

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Although several proteomic approaches have been used in the search for new lung cancer markers, it continues to be the leading cause of cancer related death, mainly due to the advanced stage when the neoplasia is diagnosed. Another issue that difficults the search for novel markers is the overwhelming presence of high abundant proteins, that mask ones that could have a potential role as biomarkers. This inconvenience is being addressed with different removal methodologies, that permit an increase in the detection capability of potential markers.

In this work we attempt to discover novel markers for non small cell lung cancer (NSCLC) performing a prefractionation of the serum with the ProteoPrep 20 Plasma Immunodepletion kit (Sigma-Aldrich), that removes the 20 most abundant proteins, allowing an enrichment of 20-fold and considerably increasing the possibilities of detecting low abundant proteins. The depleted proteomes were then studied by means of DIGE methodology.

For this purpose we chose as patients subjects with adenocarcinoma, as this is the commonest type of NSCLC in Galicia, in which the malignancy was in early stages (localised and regional). As the control group we selected benign subjects with pneumonia, based on the higher interest to discriminate between pathologic stages that could confuse the diagnosis.

Conventional 2D-PAGE and silver staining were performed to check that effectively there was an increase in the resolution of low abundant proteins. Four patients and four matched benign controls were then submitted to DIGE, and differences in the expression level of the spots were analysed with DeCyder software. The statistical analysis revealed twelve proteins differentially expressed between lung cancer and pneumonia subjects, eight of them increased and four decreased in the cancer group compared to the control individuals. These proteins are being identified by mass spectrometry.