

## Proteomic approach for the detection of breast cancer biomarkers using two dimensional gel electrophoresis and mass spectrometry

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### Abstract

**Aims:** The major tool of the proteomic approach in breast cancer is to identify the differentially secreted proteins, which may work as a potential biological marker. We examined the protein expression patterns of infiltrating ductal carcinoma of the breast (IDCA) tissues and serum from Tunisian women using two-dimensional polyacrylamide gel electrophoresis (2D-PAGE) and matrixassisted laser desorption/ionization-time of flight (MALDI-TOF) mass spectrometer.

**Methods:** Serum protein and tumor protein tissues were solubilized and analysed with 2D-PAGE and visualised by a sensitive Colloidal Coomassie G250 stain. Protein expression was identified using MALDI-TOF MS/MS and evaluated using PDQuest 2-D software. The proteins spectrums were identified by searching NCBI and Swiss Prot databases.

**Results:** Comparisons of the protein spots identified on the 2D-PAGE maps from human serum and breast tumor tissues showed that Apolipoprotein AI were up-expressed in both tumor tissue and pre-treatment serum compared with their counterparts.

**Conclusion:** 2-DE and MALDI-TOF/MS offers total protein expression profiles of breast cancer tissues and serum and will give a chance to identify tumor specific diagnostic markers for breast cancer. The differentially up expressed of Apolipoprotein A I may play a key role during tumorigenesis of breast cancer.