

GEL- AND LECTIN-BASED SERUM PROTEOMICS PROFILING IN SEARCH FOR NEW COMPLEMENTARY BIOMARKERS FOR CANCER

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OBJECTIVE

To profile serum samples of patients with different cancers using the gel- and lectin-based proteomics approaches in the search for novel complementary biomarkers for diagnostic and prognostic applications.

METHODOLOGY

Serum samples from patients with nine different cancers and those from age-matched cancer-negative volunteers were subjected to 2-dimensional gel electrophoresis. Separated proteins were either detected using silver staining of the 2-DE gels or probed using enzyme-conjugated champedak galactose-binding (CGB) and mannose-binding (CMB) lectins. Proteins were identified using mass spectrometry and their relative expression was determined by densitometry.

RESULTS

The altered expression of selective serum acute-phase proteins was shown in patients with nine different cancers compared to those of the controls. Different serum acute-phase proteins were apparently altered for the distinct cohorts of patients. Due to this, we have proposed that the acute-phase response patterns may be used as fingerprints for diagnosis and/or prognosis of various types and subtypes of cancers. In addition, we have also detected the aberrant expression of several glycoproteins in selective cohorts of the patients with the use of CGB and CMB lectins as probes. A few of these glycoproteins were not possibly detected by silver-staining. We have isolated one of the lectin-detected glycoproteins using immobilized lectin affinity chromatography and identified it as a fragment of the inter-alpha trypsin inhibitor heavy chain H4 (ITIH4). The potential use of the ITIH4 fragment as novel complementary serum biomarker for cancer diagnosis is currently under investigation.