J Gastrointest Dig Syst 2018, Volume 8
DOI: 10.4172/2161-069X-C3-071

Study of the proteomic profile in patients with Crohn's disease, its correlation with diagnosis and disease activity

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Background: Inflammatory bowel diseases (IBD) include two major forms of chronic intestinal disorders: Crohn's disease (CD) and ulcerative colitis (UC). CD can be associated with intestinal granulomas, strictures, fistulas, and transmural inflammation. A single gold standard for the diagnosis of CD is not available. The diagnosis is confirmed by clinical evaluation and a combination of endoscopic, histological, radiological, and/or biochemical investigations. Serum protein profiling of CD was investigated in order to improve the comprehension of the pathologic mechanisms and to support the difficult diagnostic procedures currently available. The aim of the work is to identify plasma proteomic profiles of CD cases and correlating this profile with the other diagnostic markers and activity of the disease.

Methods: We performed a study with 64 plasma samples collected from patients classified in 2 groups (31 crohn's disease, 33 healthy controls) according to accredited criteria. They were subjected to: complete history taking, thorough clinical examination, Laboratory investigations (Erythrocyte sedimentation rate ESR, C- reactive protein CPP, fecal calprotectin, Anti-Saccharomyces cerevisiae antibodies ASCA), ileocolonscopy, histopathology, imaging were done. Plasma proteomic pattern of CD patients and control subjects was determined using Matrix-Assisted Laser Desorption/Ionization (MALDI) Time of Flight (TOF) Mass Spectrometer (MS) analysis, all plasma samples were subjected to solid-phase extraction (SPE). The spectra obtained from all the samples were analysed using ClinProTool software.

Results: There was a statistical significant difference of the plasma proteome profiles of CD group in comparison to health volunteers. 76 peptide peaks were identified by the ClinProt software with a statistically different area, 5 peptide peaks were highly significant. Sensitivity was found to be 91.7%, specificity was 78.6%, PPV was 90, NPV was 77.5 and Youden Index was 0.88. There was a statistical significant difference between active versus inactive CD group, 5 Integration Regions used for classification between active and inactive CD patients using Genetic Algorithm model (GA) which gave 81.43% cross validation and 100% recognition capability. Markers as ESR, CRP, fecal calprotectin, ASCA are statistically correlated to the plasma proteomics found in CD patients. Conclusion: Proteomic profile has the potential to improve diagnosis and evaluate CD activity, reducing the need for more invasive techniques. Plasma proteome profile of CD was statistically correlated to other markers.

Keywords: Proteomics; CD; Biomarkers; (MALDI) TOF MS; Inflammation; Serum profiling

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