EuroSciCon

11th Annual European Conference on
Gastroenterology

March 11-12, 2019
Amsterdam, Netherlands

Doaa Abdou Mohamed Header, J Clin Gastroenterol Hepatol 2019, Volume:3
DOI: 10.21767/2575-7733-C1-011

STUDY OF THE PROTEOMIC PROFILE IN PATIENTS WITH ULCERATIVE COLITIS, ITS CORRELATION WITH DIAGNOSIS AND DISEASE ACTIVITY

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Background: Inflammatory bowel disease (IBD) comprises primarily 2 disorders: ulcerative colitis (UC) and Crohn's disease (CD). The hallmark of IBD is chronic, uncontrolled inflammation of the intestinal mucosa. The diagnosis is based on a combination of disease history, colonscopy, inflammatory biomarkers, radiological and histological evaluation. Most biomarkers used are not reliable and not disease specific, but reflect generalized inflammation.

Aim: The aim of the work is to identify plasma proteomic profiles of UC cases and correlating this profile with the other diagnostic markers and activity of the disease.

Methods: We performed a study with 70 plasma samples collected from patients classified in two groups (37 UC, 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 (CRP), fecal calprotectin, perinuclear antineutrophil cytoplasmic antibodies (P-ANCA), ileocolonscopy, histopathology, imaging. Plasma proteomic pattern of UC 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). We analyzed the spectra obtained from all the samples using ClinProTool software.

Results: There was a statistically significant difference of the plasma proteome profiles of UC group in comparison to health volunteers. 64 signals were identified by the ClinProTool software and of these 16 peptide peaks were highly significant (sensitivity was 100%, specificity was 84.4%, positive predictive value was 100, and negative predictive value was 82). There was a statistically significant difference between active versus inactive UC group, 5 integration regions used for classification between active and inactive UC patients using Genetic Algorithm model (GA) which gave 88.5% cross validation and 100% recognition capability. Markers as ESR, CRP, fecal calprotectin, P-ANCA are statistically correlated to the plasma proteomics found in UC patients.

Conclusion: Proteomic profile has the potential to improve diagnosis and evaluate UC activity, reducing the need for more invasive techniques. The pattern of these peptides holds the promise of distinguishing disease states and providing clinically important information such as prognosis, response to therapy or perhaps targets of therapy.

Biography

Doaa Abdou Mohamed Abdou Header has currently working as a lecturer in Alexandria Main University Hospital in Internal Medicine and Gastroenterology Department in Alexandria Main University Hospital. She has completed her MD in Internal Medicine in Alexandria University, Egypt.and completed her Master Degree in Internal Medicine in Alexandria University, Egypt.

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