# ASSIGNMENT: RESEARCH PAPER REPORT

## Screening of Altered Metabolites and Metabolic Pathways in Celiac Disease Using NMR Spectroscopy

Celiac disease (CeD) is an autoimmune intestinal disorder caused by the ingestion of gluten found in various foods like wheat, barley, and rye in genetically predisposed individuals specifically carrying HLA-DQ2 or HLA-DQ8 (human leukocyte antigen) which are genetic markers that are attach to the gluten proteins. Typically, the technique employed for the diagnosis of CeD included combination of specific serological and histological evaluations by biopsy sampling. The need for discovery of an alternative to this traditional method grew as the discrepancies between the clinical, histology, and serology findings make CeD diagnosis difficult.

Microarray-based methods, proteomics, and metabolomics are a few of the methods that could be used to find such novel biomarkers and since metabolomics is helpful in monitoring metabolite changes in body fluids and tissues it was used to evaluate serum metabolite levels. The aim of the study was to identify new biomarkers for population screening. the serum metabolic profile of CeD patients and healthy control was compared using NMR spectroscopy and multivariate statistical analysis.

Since celiac disease is known as a pathology that directly affects metabolism, an NMR profile of serum metabolites may significantly improve the diagnostic process of the disease. This is because the current serologic tests for celiac disease are accompanied by false-negative results due to patients' IgA deficiencies or false-positive results due to other autoimmune diseases and concurrent infections/comorbidities.

To better understand the pathophysiology of various conditions including neurological disorders, cancer, gastrointestinal diseases, and cardiovascular disease, NMR is frequently employed to find relevant diagnostic biomarkers.

The CeD diagnosis was based on positive serology anti-endomysial (EMA) and anti-transglutaminase-2 (TG2) antibodies. Considering pre-existing health factors of the subjects and the controls, blood samples were drawn and was centrifuged to extract the serum supernatant for NMR analysis.

Serum metabolic profiling revealed 25 metabolites. When compared to samples from healthy controls and CeD patients, levels of 3-hydroxyisobutyric acid and isobutyrate exhibited significant differences and this proves that there is a clear relationship between the results and a metabolic signature for CeD in serum samples from celiac patients. Lipid, carbohydrate, and amino acid metabolism are all affected by these changed metabolites.

Nine metabolic alterations were significantly disrupted or altered in CeD patients, as shown by pathway analysis. These enriched pathways are known to be involved in the synthesis of aminoacyl-tRNA, primary bile acid biosynthesis, nitrogen metabolism, glutamine and glutamate metabolism, valine, leucine, and isoleucine biosynthesis and degradation, taurine and hypotaurine metabolism, glyoxylate and dicarboxylate metabolism, and the metabolism of glycine, serine, and threonine, as well as arginine biosynthesis.

Thus, these findings can provide an improved bases for understanding of dysfunctional metabolic pathways in CeD and other such pathology.