

Comprehending the Relationship between the Red Blood Cells of a Protein 4.1 -/- Patient and Those of Healthy Controls: A Comprehensive Analysis of Tandem Mass Spectrometry Data

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Abstract : Protein 4.1 is a crucial component of complex interactions between the cytoskeleton and other junctional complex proteins. When the gene encoding this protein is altered, resulting in reduced expression, or when the protein is absent, the red cell undergoes a significant structural change. This research aims to achieve a deeper comprehension of the biochemical effects of red cell protein deficiency. A Tandem Mass Spectrometry Analysis (TMT-MS/MS) of patient cells lacking protein 4.1 compared to three healthy controls was achieved by the Proteomics Institute of the University of Bristol. The SDS-PAGE and Western blotting were utilized on the original patient sample and controls to partially confirm TMT MS/MS data analysis of the protein-4.1-deficient cells. Compared to healthy controls, protein levels in samples lacking protein 4.1 had a significantly higher concentration of proteins that probably originated from reticulocytes. This could occur if the patient has an elevated reticulocyte count. The increase in chaperone and reticulocyte-associated proteins was most notable in this study. This may result from elevated quantities of reticulocytes in patients with hereditary elliptocytosis.

Keywords : hereditary elliptocytosis, protein 4.1, red cells, tandem mass spectrometry data.

Conference Title : ICHBD 2023 : International Conference on Hematology and Blood Disease

Conference Location : New York, United States

Conference Dates : October 09-10, 2023