Check for updates





Blood 142 (2023) 5257-5258

The 65th ASH Annual Meeting Abstracts

ONLINE PUBLICATION ONLY

112.THALASSEMIA AND GLOBIN GENE REGULATION

Alterations of Gut Microbiota Related with Status of Iron-Overload in Thalassemia Patients: A Cross-Sectional Pilot Study

Kornkanok Trirattanapa, MD¹, Adisak Tantiworawit, MD², Kanokphong Suparan, MD^{3,4,5}, Sirawit Sriwichaiin, MD^{5,4,6}, Sasiwan Kerdpoo, MSc^{4,5,6}, Teerachat Punnachet, MD⁷, Nonthakorn Hantrakun, MD⁷, Sasinee Hantrakool, MD⁷, Pokpong Piriyakhuntorn, MD⁷, Thanawat Rattanathammethee, MD⁷, Chatree Chaiadisaksopha, MD⁷, Ekarat Ekarat Rattarittamrong, MD⁸, Lalita Norasetthada, MD⁹, Nipon Chattipakorn, MD PhD^{4,5,6}, Siriporn Chattipakorn, DDS, PhD^{10,11,5}

¹Chiang Mai University, Maung, Chiang Mai, Thailand

² Division of Hematology, Department of Internal Medicine, Faculty of Medicine, Chiang Mai University, Chiang Mai, Thailand

³ Immunology Unit, Department of Microbiology, Faculty of Medicine, Chiang Mai University, Chiang Mai, Thailand

⁴ Neurophysiology Unit, Cardiac Electrophysiology Research and Training Center, Faculty of Medicine, Chiang Mai University, Chiang Mai, Thailand

⁵Center of Excellence in Cardiac Electrophysiology Research, Chiang Mai University, Chiang Mai, Thailand

⁶Cardiac Electrophysiology Unit, Department of Physiology, Faculty of Medicine, Chiang Mai University, Chiang Mai, Thailand

⁷ Division of Hematology, Department of Internal Medicine, Faculty of Medicine, Chiang Mai University, Chiang Mai, Thailand

⁸Department of Internal Medicine, Chiang Mai University, Muang, Chiang Mai, Thailand

⁹Chiang Mai University, Chiang Mai, Thailand

¹⁰ Department of Oral Biology and Diagnostic Sciences, Faculty of Dentistry, Chiang Mai University, Chiang Mai, Thailand ¹¹ Cardiac Electrophysiology Research and Training Center, Faculty of Medicine, Chiang Mai University, Chiang Mai, Thailand

Background: Gut dysbiosis can cause an impaired gut-barrier function and may contribute to the pathogenesis of various diseases. Iron overload is a common complication in thalassemia patients and can result in numerous complications, including those affecting the cardiovascular, endocrine, and immune systems. However, it is unclear how iron overload affects the gut microbiota of patients with thalassemia.

Objective: To characterize the profiles of the gut microbiome in thalassemia patients compared with healthy participants, as well as to determine the association of these profiles with iron status.

Method: Transfusion-dependent thalassemia (TDT) patients and healthy controls aged \geq 18 years old were enrolled in the study. Stool samples were collected prior to receiving regular blood transfusions in the thalassemia group. Paired-end sequencing of 16s rRNA bacterial DNA extracted from each stool sample was performed. Serum ferritin levels were assessed in each participant to reflect iron status.

Results: A total of 14 adult TDT patients and 14 healthy controls were enrolled, with a similar proportion of age and sex. The TDT patients had a significantly higher iron overload status than the controls (median serum ferritin level = 1424 in the TDT group and 197 in the control group; p < 0.001). The Shannon diversity index demonstrated a significant increase in gut microbial diversity in TDT patients as compared to healthy controls (7.06 vs. 6.48; p = 0.001). The TDT group showed a higher abundance of several gram-negative bacterial phyla, such as Bacteroidota, but a reduction in the abundance of Actinobacteriota as compared to the control group. Serum ferritin levels showed a positive correlation with higher gut diversity index.

Conclusions: Our study suggests that TDT patients develop gut dysbiotic characteristics compared to the healthy population, with gut diversity associated with serum ferritin levels. This association suggests that iron overload induces gut dysbiosis.

ONLINE PUBLICATION ONLY

Disclosures No relevant conflicts of interest to declare.

https://doi.org/10.1182/blood-2023-172938