Identification of inflammation related Treg signatures in myelodysplastic syndrome patients

Abstract

Myelodysplastic syndromes (MDS) are a heterogenous group of bone marrow malignancies characterised by irregular haematopoiesis and bone marrow failure. Most MDS patients present with normo- or hypercellular bone marrow, but ~15% present with hypoplastic marrow. Hypoplastic MDS (h-MDS) is more common in Middle Eastern countries and patients tend to be younger, represent a diagnostic challenge due to morphological and clinical similarities with aplastic anaemia (AA), and respond poorly to treatment. MDS patients are currently risk-stratified using clinical features such as blood counts and cytogenetics. T regulatory cells (Tregs) have previously been associated with different MDS stages and may participate in the pathogenesis of MDS by inhibiting the immune surveillance that prevents cancer and facilitating the immune escape of malignant cells. We hypothesise that myeloid-derived inflammation, a well-known phenomenon in MDS, affects Treg phenotype and function to facilitate immune subversion. Our long-term goal is to establish the mechanism of Treg-associated MDS pathogenesis to help further stratify patients and identify potential therapeutic targets. Our specific objectives are: (1) to explore the effect of myeloid-derived inflammation on Tregs in low-risk, high-risk, and hypoplastic MDS using a novel simultaneous whole transcriptome and protein expression profiling approach; and (2) to use a computational approach to identify Treg-specific signatures, biological functions, and potential targets in low-risk, high-risk, and hypoplastic MDS patients. This contribution is significant, since it will detail the Treg phenotypes that could potentially be used as "immunometers" and identify those patients who are most likely to benefit from immunomodulatory treatments. The proposed research is innovative since it exploits an innovative, simultaneous single-cell whole transcriptome and protein expression profiling approach and in silico analyses to investigate Tregs isolated from the bone marrow of low-risk, high-risk, and hypoplastic MDS patients. This proposal also leverages the advantages of a collaboration between King's College London, Qatar University and Hamad Medical Corporation.

Biography

Dr Amal received her MSc in Biomedical Sciences 2010 from University of Hull, and PhD in biomedical sciences in 2019 from University of Salford Manchester, UK. Currently she is an assistant professor at the biomedical department (college of health sciences, QU). Her main teaching courses are human histology, histopathology, cytogenetics and Developmental Biology. In 2022, she was awarded with internal grant for the topic 'Identification of inflammation related Treg signatures in myelodysplastic syndrome patients'. The research still in progress.

Her previous search topics were on the following:

1- Investigation the impact of Fludarabine and Doxorubicin on chronic lymphocytic leukaemia (The medical research laboratory, department of biology, University of Hull, UK) (2010).
2- Investigation the role of Sp1 transcription factor in colorectal cancer progression (School of environmental, biological and medical school, University of Hull, UK) (2011-2013).
3- Effect of omega-3 fatty acid on inflammatory biomarker sin COPD (School of environmental and life Sciences, University of Salford, Manchester, UK) (2015-2019)

Email: amalah@qu.edu.qa

Presenter Name: Dr. Amal Al-Haidose

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Contact Number: +97455542692