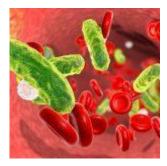# New hope – a potential new treatment for sepsis

Systemic infections may result in sepsis which is more severe in patients with chronic diseases. The bodies exaggerated and uncoordinated immune response to infection can lead to multisystem organ failure with a high mortality rate. There have been no recent advancements in the battle against sepsis, until recently, where a team from the University of California published their work offering some new insights for future treatment of sepsis (interesting read: [SEPSIS is WANTED!](#)).

Qiu, et al., have identified molecular biomarkers, pathways and immune cell dynamics associated with sepsis that can be targeted in order to prevent death from the disorder. These biomarkers were identified using single-cell transcriptomic analysis of the peripheral blood mononuclear cells (PBMCs) of patients with Gram-negative bacterial sepsis with surviving and fatal outcomes. These markers include; the protein CD52 in lymphocytes and the protein S100A9 which is involved in inflammatory processes. These markers were found to be highly expressed in people with sepsis and it was reported that a change in the expression of these markers early in sepsis, specifically within the first six hours from following diagnosis, could determine whether the patient survives or succumbs to the disorder. Through the analysis of two timepoints, diagnosis to six hours, the researchers were able to take a dynamic snapshot of the disease and focus on disease progression.

The authors reported that the biomarkers *were found to uniquely change within six hours in the blood of patients with sepsis and affected specific cellular pathways in specific immune cells*. In addition, changes in CD52 expression were associated with beneficial outcomes through subsequent promotion of activation of protective immune cells. In contrast, S100A9, was a molecular driver of fatal sepsis.

Qiu, et al., also reported similarties between fatal sepsis and COVID-19, highlighting that *platelet (cell types involved in coagulation and blood flow) and erythroid precursor responses are drivers of fatal sepsis, with transcriptional signatures that are shared with severe COVID-19 disease*. In addition, immune and metabolic dysfunction of monocytes and erythroid precursors is driven by hypoxic stress. Further analysis of this may lead to better treatment outcomes for both diseases. More on COVID-19: COVID-19 Cytokine Storm & Paediatric COVID-19.

Following diagnosis of patient with sepsis, patients will be admitted to the intensive care unit, whereby physicians make use of clinical scoring systems, such as the APACHE-2 and SOFA scores, *to help predict severity of illness and probability of mortality*. These systems cannot confirm whether the patient is going to survive or die. They also offer no guidance as to what treatment to provide the patient that may improve the patient's survival chances.

Clinically the treatment of sepsis largely focuses on *early diagnosis, early systemic antibiotics/source control of the infection, and support of failing organ systems*. There is a need to inhibit or reverse the patient's dysregulated immune response to infection.

In their own words taken from the abstract:

"…*data support CD52 as a prognostic biomarker and therapeutic target for sepsis as its expression dynamically increases in*

lymphocytes and correlates with improved sepsis outcomes. In conclusion, this study describes the first single-cell study that analyzed short-term temporal changes in the immune cell populations and their characteristics in surviving or fatal sepsis. Tracking temporal expression changes in specific cell types could lead to more accurate predictions of sepsis outcomes and identify molecular biomarkers and pathways that could be therapeutically controlled to improve the sepsis trajectory toward better outcomes."

Journal Article: Qiu, et al., 2021. [Dynamic changes in human single-cell transcriptional signatures during fatal sepsis](). **Journal of Leukocyte Biology.**

Summary by Stefan Botha