

Quantification of the innate immune function in whole-blood infection assays reveals pathogen-dependent immune defence of different sepsis phases

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Quantification of the innate immune function in whole-blood infection assays reveals pathogen-dependent immune defence of different sepsis phases

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Introduction

- Marked heterogeneity of sepsis as a clinical syndrome
- Caused by highly diverse pathological conditions and shows variable kinetics in individual patients
- Classification of sepsis patients by their immune status is necessary for immunomodulatory therapy approaches

Are there pathogen-specific patterns of immune activation during whole blood infection?
Are there immune effector functions that allow stratification of sepsis patients?

Approach

Within this project, we will use data from a human whole blood model of infection combined with advanced mathematical modelling.^{1,2}

Results

Analysing pathogen association and immune activation in blood from healthy volunteers

Activation of immune cells (MNC, C. albicans, S. aureus), Association with immune cells (MNC, C. albicans, S. aureus), Model simulation results, Immune reaction rates.

Comparison of infection with C. albicans and S. aureus:

- Greater association of S. aureus cells with MoC
- Larger number of C. albicans cells
- S. aureus infection causes steeper slope of immune cell association kinetics

Analysing pathogen association and innate immune activation in blood from HLM patients

White blood cell count, Association with immune cells (C. albicans, S. aureus), Immune reaction rates.

Blood samples were obtained before cardiac surgery (pre-operative), immediately after surgery (post-operative), and 1 day after admission to ICU.

- Increase in white blood cell count after surgery with a maximum at one day
- Higher white blood cell count exceeding the reference range after surgery
- Monocyte number increases
- Lymphocyte number decreases

Conclusions

Once optimized, analyses of blood samples from sepsis patients and patients who have survived severe sepsis will follow. This will allow identifying patterns of dysregulated immune homeostasis providing functional classifiers for the differentiation of sepsis patients, and thereby forming a basis for future patient stratification.

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