

Cytokine gene expression patterns to predict nosocomial infection in severely injured patients

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Trauma is the leading cause of death in the under 40s. Delayed infection, associated with immune paresis, remains a common avoidable cause of mortality. The dynamic nature of the host immune response, particularly in terms of T helper cell 1 (T_{h1}), T_{h2} , T_{h17} and T regulatory/suppressor cell (T_{reg}) development is incompletely understood in this patient group. Such information could prove helpful in risk stratification and subsequent pre-emptive treatment of those patients at highest risk of developing infectious complications.

Previously, I have demonstrated that a robust T_{h1}/T_{h17} dominated response may be protective in patients with sepsis. Additionally, I observed that falling levels of T_{h1}/T_{h17} cytokines were associated with a five-fold increase in the incidence of pneumonia following thoracic surgery. These pathways are likely to be equally important in trauma populations.

Patients with severe blunt traumatic injuries, presenting to the Royal London Intensive Care Unit (ICU) will be recruited. Blood will be collected daily for the first week and weekly thereafter for as long as the patient remains in the ICU. An extensive panel of $T_{h1}/T_{h2}/T_{h17}$ and T_{reg} cell specific cytokine mRNA and proteins will be assayed from blood. FACS will be used to identify the predominant T cell subtype in individual patients.

The objective is to define a cytokine gene expression pattern, associated with a T cell maturation profile, which is associated with nosocomial infection and is identifiable prior to the clinical appearance of infection. These data may then help target pre-emptive antibiotic therapy and also identify potential novel immunomodulating compounds.