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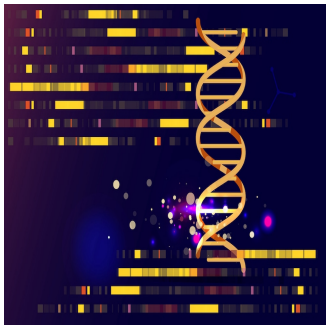
Sepsis Patients Could Get Faster Treatment



Patients with sepsis could be treated based on their immune system's response to infection rather than their symptoms.

New research has revealed that people's genetic makeup significantly influences their response to sepsis. This understanding could help identify those who would benefit from specific treatments and pave the way for developing targeted therapies. The findings are published in Cell Genomics.

The study, conducted by the Wellcome Sanger Institute, the University of Oxford, and their collaborators, builds on previous work that identified different subgroups of sepsis patients. By examining different underlying immune response pathways, the researchers aimed to understand why sepsis responses vary among patients.

The study details the genetic basis for the variability in sepsis responses and identifies the different regulators and cell types involved in each subgroup's immune response.

A more detailed understanding of sepsis at a molecular level could help identify patients who would benefit from different therapies. This knowledge can aid in designing rapid tests, organising clinical trials, and developing targeted treatments based on individual immune responses.

The ultimate goal is for patients to receive the most effective treatment for sepsis quickly, based on their immune response rather than their symptoms. This personalised approach could also be applied to other infections in the future.

Sepsis causes an estimated 11 million deaths worldwide annually, with one death every three seconds. In the U.K., at least 245,000 people are affected by sepsis each year, resulting in 48,000 deaths. Sepsis can progress rapidly, and incorrect treatment can waste valuable time.

Researchers had previously identified a small set of genes that could categorise patients at risk of poorer outcomes from sepsis and COVID-19. Building on this work, the new study investigates the impact of genetic variants that regulate gene expression, known as expression quantitative trait loci (eQTLs). This provides insight into how an individual's genetic makeup influences their response to sepsis, helping classify who would benefit from targeted therapies.

The team analysed data from the U.K. Genomic Advances in Sepsis (GAinS) study, which included 1,400 patients with sepsis due to community-acquired pneumonia and faecal peritonitis from intensive care units across the U.K.

They found that genetic variation among patient groups is associated with differences in immune response during sepsis. By identifying key genetic regulators in each group, they described the biological networks, cells, and mechanisms involved in each response.

Understanding these regulatory networks provides additional information for developing treatments that work with the immune system and move towards a personalised medicine approach for sepsis.

In related research, the University of Oxford is developing rapid tests to identify different subtypes of sepsis. These tests aim to quickly identify those who would benefit from targeted treatments.

The next steps involve further investigating immune responses to find targeted treatments for each immune response or different stages of the immune response.

Source: Wellcome Trust Sanger Institute

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