Host genomics and infectious disease

Humans differ greatly in their individual responses to pathogens that cause infectious disease (e.g. tuberculosis or HIV). Genomic factors can explain why different people (hosts) may have more or less severe symptoms or no symptoms when infected by the same pathogen.

What is it?

Our genetic background plays a significant role in defining our individual risk when infected by a pathogen. By studying host genomics, scientists can identify genetic signatures specific to disease response. These insights could lead to improvements in the prevention and treatment of infectious diseases.

The interactions between people and pathogens are complex and vary by disease, meaning that the role of host genomics in infectious disease is usually explored in relation to a specific pathogen.

Disease progression can be affected by many other host factors, for example changes in gene regulation and protein production. Beyond genomics, researchers are exploring other biological markers to capture this dynamic picture using different 'omics technologies, such as transcriptomics.

How could it help?

Risk prediction

Understanding host genomics may predict risk in two ways. Genetic variants may be associated with specific risks of disease, symptoms or response to treatment. Such variants can also be combined into a polygenic risk score to identify those people with a high risk of severe disease.

Diagnosis and prognosis

By analysing gene expression patterns (which genes are switched on or off) in a patient, researchers could distinguish between infection types or predict disease severity, informing prognosis and treatment decisions.

Post-infection syndrome

Host genomics and 'omics can be used to research differences in an individual's immune system responses to an infection, such as autoimmune responses or long-term symptoms.

Finding new treatments

Scientists are using host genomics to help them understand the link between infections and genetic variation in individuals. For example, a deletion in a CCR5 gene was associated with reduced susceptibility to HIV infection in people with that genetic variant. This discovery resulted in the development of CCR5 inhibitors as a treatment against HIV.

To support the response to the COVID-19 pandemic, large research initiatives investigating and applying host genomics have been established. This research is still in the early stages, with multiple promising gene candidates identified for drug targeting. This could lead to new treatments for some or all patients.

Ready for patients?

Understanding host genomics could ultimately help protect people from the worst risks or effects of infectious diseases. However, further evidence is needed, and there remain significant research challenges, such as how best to investigate the relationship between a pathogen, symptoms of infection, and the host genome. A patient may be infected by more than one pathogen with similar symptoms, making diagnosis difficult.

Host genomics could undoubtedly improve patient care, but more work is needed to translate knowledge into healthcare applications.

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