

Blood test can predict life or death outcome for patients with Ebola virus disease

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The Ebola virus, isolated in November 2014 from patient blood samples obtained in Mali. The virus was isolated on Vero cells in a BSL-4 suite at Rocky Mountain Laboratories. Credit: NIAID

Scientists have identified a 'molecular barcode' in the blood of patients with Ebola virus disease that can predict whether they are likely to

survive or die from the viral infection.

A team at the University of Liverpool, in collaboration with Public Health England, Boston University and other international partners, used blood samples taken from infected and recovering patients during the 2013-2016 West Africa outbreak to identify gene products that act as strong predictors of patient outcome.

Funded by the National Institute for Health Research Health Protection Research Unit in Emerging and Zoonotic Infections and the United States Food and Drug Administration, the new research provides data on the underlying causes of Ebola virus infection and suggests that this type of blood analysis could be integrated into future outbreak responses as a diagnostic tool to help guide treatment strategies.

Since the Ebola outbreak in West Africa much research has been done to further understand the biology of the Ebola virus. In particular, the processes that lead to survival or a fatal infection are unknown, although the amount of virus present in the body (viral load) can be a key determinant.

However, while this premise worked well for predicting outcomes for people with extreme viral loads, it was less clear for people with mid-range counts, the majority of cases, where the outcome prediction was approximately equal between survival and a fatal infection.

The results of this new study, which are published in *Genome Biology*, identified a small number of genes whose expression accurately predicts patient survival, independent of [viral load](#).

Blood samples collected by the European Mobile Laboratory in Guinea of Ebola patients who either went on to survive or die from the [acute infection](#), were analysed using genomic techniques to identify and

quantify messenger RNA (mRNA) expression. These results were compared to [blood samples](#) from a separate group of survivors who had recovered from infection and were now free of the Ebola virus.

The analysis also provided some fundamental information on the host response to Ebola virus infection in humans, and found that an immediate robust immune response didn't affect whether people went on to live or die from the infection. The data also points to the virus causing significant liver damage.

Professor Julian Hiscox, a virologist at the University of Liverpool's Institute of Infection and Global Health, said: "Our study provides a benchmark of Ebola virus infection in humans, and suggests that rapid analysis of a patient's response to infection in an outbreak could provide valuable predictive information on disease outcome."

Professor Miles Carroll, Director of Research at Public Health England, added: "This study helps us to further our understanding of the human response to Ebola [virus infection](#). This understanding should enable more effective patient care resulting in improved clinical outcomes in future outbreaks."

Dr John Connor, Associate Professor of Microbiology, Boston University School of Medicine, added: "It is not just defining how much Ebola virus that is present in a patient that defines whether a patient will survive. How the patient fights the infection is also key. Defining common aspects of how the immune system responds in individuals that survive opens a new window for studying how to keep Ebola virus [infection](#) from being a [fatal infection](#)."

More information: Xuan Liu et al, Transcriptomic signatures differentiate survival from fatal outcomes in humans infected with Ebola virus, *Genome Biology* (2017). [DOI: 10.1186/s13059-016-1137-3](https://doi.org/10.1186/s13059-016-1137-3)

Provided by University of Liverpool

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