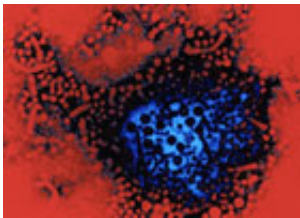


# Study reveals prehistoric journey of hepatitis B

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The hepatitis B virus. Credit: Wellcome Images

(Medical Xpress)—A new study has revealed how the spread of hepatitis B coincides with dates of human migration throughout history, starting around 40 000 years ago. The study could provide a framework for studying the ongoing burden and evolution of the hepatitis B virus.

Hepatitis B is a global public health problem: there are approximately 2 billion infected people worldwide and more than 350 million carriers. There are currently several theories about where the infection in humans might have originated from, but until now there was little evidence to support them.

The new study provides evidence to show that HBV has been following the [migration patterns](#) of human populations for the past 40 000 years. The team of researchers, from the Universities of Athens, Oxford, Sydney and Cambridge, suggest that the [hepatitis B](#) virus (HBV) was infecting us on our journey out of Africa.

The team reviewed and analysed the spread of HBV infection with respect to ancient human populations and examined the relationship between the history of evolution of HBV and the [genetic diversity](#) of humans. They found that the distributions of HBV genotypes are consistent with prehistoric modern human migrations. The most pronounced increase also correlates with the increase in human population over the past 5000 years.

Dr Dimitrios Paraskevis, who led the study at the University of Athens, said: "This is the first consistent evidence to show when the [hepatitis B virus](#) first 'jumped' into humans." Dr Gkikas Magiorkinis, lead author for the University of Oxford, said: "Our approach could be used to shed light on the history of other infectious diseases and how they have evolved in line with their hosts over time."

The study also looked at non-human strains of the virus found in gibbons, orang-utans and chimpanzees and found evidence that the virus jumped from humans no less than 6000 years ago. The orang-utan [HBV](#) strain, in particular, is closely related to the human strain, whereas in chimpanzees it seems the transmission was from an ancient human group that is now extinct.

"Understanding where the virus came from is crucial because it gives us a framework to study how the virus has evolved to become more harmful in [human populations](#) over time," Dr Paraskevis added.

Understanding the emergence and transmission of infectious diseases is one of the Wellcome Trust's core strategic research challenges.

The study is published in the journal *Hepatology*.

**More information:** Paraskevis D, et al. Dating the origin and dispersal of hepatitis B virus infection in humans and primates. *Hepatology*, 2012.

Provided by Wellcome Trust

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