

The global dynamics and spread of Hepatitis C virus 1a and 1b: A phylogeographical analysis

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Research published this week in *PLoS Medicine* finds that the global spread of Hepatitis C virus (HCV) coincided with widespread use of transfused blood and with the expansion of intravenous drug use but slowed before wholesale implementation of anti-HCV screening.

Angelos Hatzakis and colleagues used phylodynamic and phylogeographic methods to analyse sequences of HCV subtype 1a and 1b samples (these subtypes cause 60% of global HCV infections) collected over the past 20-30 years in the Los Alamos HCV sequence database. These analyses also suggest that the most plausible route for the spread of [hepatitis C](#) virus was from the developed to the [developing world](#).

More information: Magiorkinis G, Magiorkinis E, Paraskevis D, Ho SYW, Shapiro B, et al. (2009) The Global Spread of Hepatitis C Virus 1a and 1b: A Phylodynamic and Phylogeographic Analysis. *PLoS Med* 6(12): e1000198. [doi:10.1371/journal.pmed.1000198](https://doi.org/10.1371/journal.pmed.1000198)

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