

# Investigating the Origin and Dissemination of Hepatitis B Virus Genotype C in East Asia through Phylodynamic Analysis and Historical Correlates

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## Background/Objective

Hepatitis B virus (HBV) is highly endemic in East Asia. HBV genotype C (HBV/C) has the highest prevalence in almost every East Asia country (China 81%, Korea 98%, Japan 85%, Taiwan 34%), as well as in the United States (41%~23%: West~ East coast) in regions with significant presence of Asian populations.

## Method

We employed high-resolution phylodynamics and phylogeography to study the demographic history and geographic trend of viral spread in East Asia, and investigate, in particular, the introduction source(s) of HBV/C into Taiwan.

## Result

HBV/C most recent common ancestor traced back to China at the beginning of the 1800s (high posterior density intervals, HPD: 1755~1887) and was introduced into Taiwan at least three times after 1842. Dissemination patterns inferred from phylogeography also showed that China was the epicenter of the epidemic from where the virus spread to other adjacent Asian countries, including Korea (1898), and to Japan (1920), followed by a more recent introduction (1952) from Korea to Japan. Reconstruction of viral demographic history through Bayesian skyride showed an overall constant effective population size in Japan and Korea, but exponential growth in China and Taiwan.

## Conclusion

HBV/C dissemination patterns and population dynamics in China may be related to the “Eight-Nation Alliance” war that exploded right after Qing dynasty performed the so-called the Hundred Days Reform in 1898. Ultimately, the comparison of historical records with phylodynamic patterns may provide a powerful interpretation framework for understanding the epidemiological distribution of this important human pathogen.