TRENDS OF HEPATITIS C VIRUS EPIDEMIC IN AUSTRALIA AND NORTH AMERICA IN 20TH CENTURY: BACK PROJECTIONS FROM MOLECULAR EPIDEMIOLOGY

Rodrigo C1, Eltahla A1, Bull RA1, Grebely J2, Dore GJ2, Applegate T2, Page K3, Bruneau J4, Morris MD5, Cox AL6, Osburn W6, Kim AY7, Shoukry NH4, Lauer GM7, Maher L2, Hellard M9,10,11, Schinkel J8,12, Prins M8,12, Lloyd AR1 and Luciani F1 on behalf of the InC3 Study Group

1School of Medical Sciences, Faculty of Medicine, UNSW Australia, Sydney, NSW, Australia, 2The Kirby Institute, UNSW Australia, Sydney, NSW, Australia, 3Department of Internal Medicine, University of New Mexico, Albuquerque, NM, USA, 4CRCHUM, Université de Montréal, Montreal, QC, Canada, 5Department of Epidemiology and Biostatistics, University of California, San Francisco, San Francisco, CA, USA, 6Department of Medicine, Johns Hopkins Medical Institutions, Baltimore, MD, USA, 7Harvard Medical School, Boston, MA, USA, 8Department of Internal Medicine, Division of Infectious Diseases, Tropical Medicine and AIDS, Center for Infection and Immunity Amsterdam, Academic Medical Center, Meibergdreef, Amsterdam, The Netherlands, 9Burnet Institute, Melbourne, VIC, Australia, 10Alfred Hospital, Department of Infectious Diseases, Melbourne, Australia, 11Department of Epidemiology and Preventive Medicine, Monash University, Australia, 12GGD Public Health Service of Amsterdam, Amsterdam, The Netherlands

Background: Hepatitis C virus (HCV) was identified in 1989. Its epidemiology prior to 1989 is difficult to reconstruct by epidemiological data. Bayesian evolutionary analysis and phylogenetics of full length genomes was used to model the trends of hepatitis C virus epidemics for subtypes 1a and 3a in North America and Australia in the 20th century.

Methods: Full length subtype 1a and 3a sequences from early HCV infections identified across nine cohorts in the International Collaboration of Incident HIV and Hepatitis C in Injecting Cohorts (InC3), as well as public databases from a time window of 1989 – 2012 were used in a Bayesian evolutionary analysis with BEAST software. A combination of General Time Reversible model (as the nucleotide substitution model), Bayesian skyline (as the population prior) and lognormal relaxed clock (as the clock model) was used for each subtype- and continent-specific dataset.

Results: Subtype 3a had more recent origins (1940–1960) than subtype 1a in both continents (1900 – 1930). Both subtypes showed an exponential increase in the number of infections from 1955 – 1975 in both continents coincident with the epidemic rise in injecting drug use during this period. All epidemics have stabilized or showed a decline in numbers over the last 20 years probably attributable to a) reduction in intravenous drug use, b) better needle sharing practices with HIV awareness, c) treatment and d) death of older cohorts with infection.

Conclusions: The findings support the hypothesis that historical events that fuelled the spread of injecting drug use with population mixing (e.g. World Wars, Korean War) could have been a major driver for cross-continental epidemics.

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