Closing the hepatitis B treatment gap: A longitudinal analysis of C4 sub-genotype infection from the Hep B PAST program

Authors:
Martin GE[1-3], Hosking K[1,2], Banz K[2], Gargan C[2], Stewart G[2], Greenwood-Smith B[2], Ramsay P[2,4], Tate-Baker J[2], Connors C[2], Binks P[1], McKinnon M[1], Vintour-Cesar E[1], Batey R[2], Marshall C[1,2], Nihill P[2], Fernandes TA[2], Fuller K[5], Tong S[1,3], Boettiger D[1,6], Davis JS[1,7], Bukulatjpi S[4], Davies J[1,2] on behalf of the Hep B PAST Partnership.

[1] Global and Tropical Health Division, Menzies School of Health Research, Darwin, Australia [2] Northern Territory Health, Northern Territory, Australia [3] Department of Infectious Diseases, University of Melbourne, Melbourne, Australia [4]Miwatj Aboriginal Health Corporation, Nhulunbuy, East Arnhem Land, Northern Territory, Australia [5]Katherine West Health Board, Katherine, Northern Territory [6]Kirby Institute, UNSW, Sydney, NSW, Australia [7]School of Medicine and Public Health, University of Newcastle, NSW, Australia

Background: In the Northern Territory (NT), Aboriginal and Torres Strait Islander people with chronic hepatitis B (CHB) are infected with a unique sub-genotype. C4 sub-genotype virus contains mutations linked to progressive fibrosis and HCC development. Whilst early evidence suggests a severe phenotype of C4 infection, progress through disease phases is incompletely understood. This study aimed to describe the phase distribution of C4 sub-genotype infection and estimate how many untreated individuals may benefit from therapy.

Methods: Hep B PAST (2018-2023) is a co-designed program to improve the cascade of care for individuals living with CHB in the NT. It has recorded the hepatitis B status of >40,000 individuals creating an electronic care facilitation tool (the “Hep B Hub”) which has undergone continuous quality improvement cycles. All individuals with CHB were identified; clinical/laboratory information and treatment status was collated. Disease phase, cirrhotic status and treatment need were determined algorithmically where data completeness permitted.

Results: 812 people were living with CHB at study completion (24% on therapy). 16% of individuals had identified cirrhosis, most of whom (70%) were treated. Among those not on therapy, data were available to determine disease phase and treatment need in 422 (69%). The majority (94%) were in phase III (immune control). Only 33 individuals not currently treated (7.8%) are eligible for antiviral therapy under current guidelines. Amongst individuals with prior or current infection, loss of eAg occurred at 9.4/100 person years at median age 36 years (n=107). sAg loss occurred at an older age (median 53 years) at 1.5/100 person years (n=885) equating to 92% still sAg-positive after 5 years.

Conclusion: A small treatment gap (7.8%) for CHB in the NT shows the success of the Hep B PAST program. Insights from this largest ever analysis of C4 sub-genotype infection will be used to further improve care.

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