Seroprevalence of Human T-Cell Lymphotropic Viruses Types 1 and 2 Antibodies in Hepatitis C Virus-Positive Patients: Manitoba, Canada, 2012–2014

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Human T-cell lymphotropic viruses types 1 and 2 are probably among the most neglected blood-borne pathogens that have experienced significant changes in their epidemiology since discovery, which could be attributed to globalization and intravenous drug use practices as well as enhanced screening recommendations; however, systematic prevalence studies, especially in high-risk populations in North America, are not updated.

Keywords. hepatitis C; HTLV; seroprevalence.

Human T-cell lymphotropic viruses types 1 and 2 (HTLV-1/2) belonging to the Retroviridae family of viruses infect up to 20 million persons around the world. The seroprevalence of HTLV, especially HTLV-1, varies widely by locality and ethnicity. Human T-cell lymphotropic virus type 1 is typically transmitted from mother to child (after birth through breastfeeding or, less often, through premastication or before or during birth), but it is also transmitted through blood transfusion and intravenous drug use (IVDU) in both endemic and nonendemic regions [1]. Human T-cell lymphotropic virus type 2 infection, on the other hand, has been highly associated with transmission

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through IVDU. Another blood-borne virus, hepatitis C virus (HCV), infects more than 185 million persons around the world [2], many of whom develop chronic HCV infection, which can cause liver failure. Intravenous drug use has been the main route of transmission of HCV in industrialized countries since the implementation of blood and blood products screening for HCV in 1992 [1]. An estimated 3.9 million and 242 500 persons live with HCV infection in the United States [3] and Canada [4], respectively, making this population a reasonable target for a HTVL seroprevalence investigation.

The Study

To assess HTLV seroprevalence among HCV-positive patients, 1049 deidentified stored residual serum specimens were obtained from HCV-positive patients (confirmed positive by antibody, regardless of RNA status). These specimens were collected and submitted for other diagnostic purposes to Cadham Provincial Public Health Laboratory in Winnipeg, Canada, during January 2012-July 2014, and they were screened using a commercial random-access platform for HTLV-1/2 antibodies followed by immunoblot confirmation of positive sera at National Laboratory for HIV/HTLV Reference Services in Winnipeg, MB, Canada. There were 2 age cohorts in the study: 652 born between 1945 and 1965 and 397 born in other years. The positivity rate in the 1945–1965 cohort was (15 of 652) 2.3% (95% confidence interval [CI] = 1.3%-3.8%), all typed as HTLV-2, whereas that of the other cohort was (4 of 397) 1.0% (CI = 0-2.0%). Three were typed as HTLV-2 and 1 was typed as HTLV-1. The overall positivity rate was 1.8% (CI = 1.0% - 2.6%), whereas the HTLV positivity rate in the laboratory since 2000 has been 0.25% (CI = 0.1%-0.4%) among 6671 patients not selected on the basis of HCV seropositivity; however, they included a mix of all patients with a variety of reasons for testing. Of the 19 patients who tested positive in this study (19 of 1049), 18 tested positive for HTLV-2 antibody, suggesting IVDU as the route of transmission, although other routes of transmission cannot be reliably excluded. Two patients with indeterminate immunoblots but with high screening readouts were not included in the above calculations.

CONCLUSIONS

Screening of HCV-positive patients for HTLV infection at least once, especially screening those with unexplained signs and symptoms (eg, a neurological disease resembling HTLV-1-

Received 27 October 2014; accepted 19 December 2014.

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associated myelopathy/tropical spastic paraparesis, upper and lower urinary tract infections, and bronchitis among others), might be considered [5, 6]. More studies on additional (such as those with hepatitis B and human immunodeficiency virus infection) and larger patient populations (multicenter) will be useful to have an updated and synoptical knowledge of HTLV subtypes prevalence. This is especially the case for HTLV-2, considering the possibility of future development of emerging virulence mechanisms and given its faster evolution rate (up to 350 times faster than that of HTLV-1), which is a result of its association with IVDU route of transmission [7]. Because HTLV infection is not notifiable in United States or Canada, its spread can go unnoticed, making notifiability a potentially important public health consideration.

Acknowledgments

Financial support. This work was supported by Cadham Provincial Laboratory internal research funds.

Potential conflicts of interest. All authors: No reported conflicts.

All authors have submitted the ICMJE Form for Disclosure of Potential Conflicts of Interest.

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