HTLV-1 and HTLV-2 Prevalence in the United States

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During the 1980s and early 1990s, there was considerable interest in the seroepidemiology of human T-lymphotropic virus (HTLV) types 1 and 2. The limitations of these studies included a focus on areas of described high prevalence, distinct ancient populations, or high-risk groups through social behavior and the use of diagnostic assays that lacked specificity. However, based on these data, de Thé and Bomford could make a crude estimate of 10–20 million HTLV-1 infections in their review of the need for an HTLV-1 vaccine [1]. This was followed by a period of relative epidemiological inactivity, during which the global population increased by approximately 1 billion. The burden of this population growth has been in many of the regions that are endemic for HTLV-1 infection. Gessain et al [2] recently published a revised estimate of 5–10 million infections but took care to note that this was based on only 1.5 billion of the world’s 7 billion inhabitants. Furthermore, Hløla et al [3] found only 17 published studies on the prevalence of HTLV infections in general populations, and none from Europe or North America.

Although it does not completely fill this gap, the article by Chang et al [4] in this issue of The Journal is an extremely welcome addition to the literature. It is the first detailed study of HTLV-1 and HTLV-2 prevalence in new blood donors within the United States for more than a decade. It not only provides contemporary data from 2000–2009, which are sufficient to look in detail at trends over time, but also provides the opportunity for comparison with data from the same risk population during the early to mid-1990s [5].

Chang et al [4] show that HTLVs remain prevalent in the United States, with HTLV-2 more common than HTLV-1, and an overall prevalence of 22/100 000 population. As the authors clearly highlight, these data will underestimate the prevalence of infections in the general population because the aim of screening questionnaires is to identify and exclude high risk populations from blood donation. The authors suggest that this may underestimate the true prevalence of these bloodborne viruses in the general population by 3–5-fold. In data from Europe based on unscreened antenatal clinic attendees, an imperfect surrogate, as the comparator, a 6-fold difference was observed in a multinational study despite widely differing prevalence rates [6].

Comparisons with the general population are further complicated because the prevalence of HTLV infection rises with age, most dramatically among women. However, applying this assumption to the data from Chang et al [4] suggests an overall general population prevalence in the United States of 0.1%–0.2%. Importantly, the authors have identified significant variation in HTLV prevalence by region and have reported that the pockets of high prevalence differ for HTLV-1 and HTLV-2. These are mapped only in the counties in which >5000 first -donors had been tested; thus, the extent of such pockets remains to be fully elucidated. Notable absents are counties in New York and Florida, where patients commonly present with HTLV-related diseases are. Conversely, the data identify some counties that have a high prevalence among blood donors, but are less well recognized for a high incidence of HTLV-1–associated diseases. Further work is needed to complete this important mapping exercise.

As reported in endemic regions, HTLV prevalence among the blood donors is highly age dependent, increasing from 1.3 to 9.3 per 100 000 for HTLV-1 and from 3.6 to 27 per 100 000 for HTLV-2 either side of age 30 years. The peak in HTLV-2 infection among women in the 40–49-year age cohort observed in the 1990–1996 data was attributed to a period during the 1960s and 1970s when injecting drug use was more widespread; this use later tailed off, presumably owing to health concerns related to human immunodeficiency virus. An alternative explanation may have been that HTLV-2 causes premature death. This seemed unlikely in the absence, apart from rare cases of HTLV-2–associated myelopathy, of clear disease associations with...
Transmission of HTLV-1 typically occurs via breastfeeding, sexual intercourse, use of contaminated blood or tissue products and reuse of injection equipment. The observation by Chang et al [4] that HTLV-1 infection is found largely in migrants or the descendants of migrants from HTLV-1–endemic regions of the world, such as the Caribbean and Japan, is consistent with the notion that mother-to-child transmission via breastfeeding continues to contribute significantly to HTLV-1 persistence. Because Adult T-cell Leukemia/Lymphoma is associated with decades of asymptomatic infection, preventing infection during infancy is critical to preventing this aggressive leukemia/lymphoma. The simple measure of screening pregnant women for anti-HTLV antibodies and counseling seropositive mothers to avoid breastfeeding prevents the majority of mother-to-child HTLV-1 transmissions and is proving successful in Japan. In countries with access to clean water and safe infant feeding formulations, formula feeding of at-risk infants is appropriate. Unfortunately, because the burden of disease typically occurs decades after infection, there is no political pressure applied to even wealthy health systems to finance this straightforward measure.

Finally, Chang et al [4] have provided a good reference for future comparative analysis of prevalence rates both within the United States and with other blood services worldwide. Their findings highlight to the many countries that do not routinely screen either blood or organ donations that they should not be complacent, particularly with increasing migration. This has also been illustrated by the recent report of HTLV-1 transmission through organ transplantation, with subsequent disease, in Germany, a country with a very low prevalence of HTLV-1 [8].

As ever, implementation of screening, whether antenatal or of blood or tissue, comes down to a cost-risk analysis. The data from Chang et al suggest that risk, and therefore cost-benefit, varies widely even within a single country and that a one-rule-fits-all approach may not apply. Although HTLV-2 transmission seems to carry little health risk, HTLV-1 is associated with high morbidity in a significant minority, and both viruses have the potential for onward transmission. The true risk of HTLV-1–associated disease after transfusion remains unknown, but data from Japan showed a 16% reduction in new cases of HTLV-1–associated myelopathy in the 2 years after the introduction of donor screening [9]. Even less is known about transplantation-acquired infection, with only anecdotal reporting.

Note

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

All authors have submitted the ICMJE Form for Disclosure of Potential Conflicts of Interest. Conflicts that the editors consider relevant to the content of the manuscript have been disclosed.

References