

Databases for Research and Development

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To the Editor: I welcome the findings of Mehand et al. in putting together a methodology that can prioritize emerging infectious diseases in need of research and development (1). These approaches are vital in establishing how global research funders and research institutions can best contribute to establishing a knowledge base around what diseases to address and how.

There is also a distinct need to understand ongoing research portfolios at international and national levels. The data emerging from these projects can provide further knowledge and impact in health policy and inform further research priorities.

Our ongoing project involves the Research Investments in Global Health (ResIn) study. ResIn has described research portfolios for cancer and infectious disease research in the United Kingdom (2,3). Internationally, the study has covered investments into global pneumonia research (4) and malaria research across Africa (5). Findings have examined, for example, the burden of disease alongside levels of investment, as well as providing informed comment on research gaps. ResIn also considers how best to implement findings from a research database into health policy and practice, and has presented results and sought opinion from meetings with key stakeholders, including the World Health Organization (WHO), European Commission, and Wellcome Trust.

I encourage WHO and other stakeholders to consider an open-access global research investments portfolio for all areas of health, using open datasets to describe spending on research alongside other areas, such as burden of disease. Alongside the WHO R&D Blueprint (<https://www.who.int/blueprint>), this resource can support decision-making around research knowledge and innovation.

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Self-Flagellation as Possible Route of Human T-Cell Lymphotropic Virus Type 1 Transmission

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To the Editor: Blood donors in Australia who test positive for transfusion-transmissible infections, including human T-lymphotropic virus (HTLV), hepatitis B virus (HBV), hepatitis C virus, and HIV, undergo posttest counseling, as previously described (1). Similar to Tang et al. (2), we identified self-flagellation as a possible unique risk factor for HTLV-1 infection. History of self-flagellation was elicited in 7 (28%) of 25 HTLV-1–positive donors identified during January 2012–December 2018. All 7 donors were men 20–37 years of age, of whom 5 were born in Pakistan and 2 in India; 6 had given blood in Victoria, Australia. The 18 remaining HTLV-1–positive donors were 29–68 years of age; 10 (56%) were men; 1 was born in India and none in Pakistan; and 7 (39%) gave blood in Victoria.

HBV shares transmission routes with HTLV-1 and is highly infectious, including through minor blood exposures

(3). After discussion of recognized infective risk factors, the 610 HBV-positive donors from the same period, of whom 83 were born in India or Pakistan, were asked about any other potential blood exposures. None reported self-flagellation.

At the time of posttest counseling, no previous HTLV results were available for donors reporting self-flagellation or for their family members. Until the known modes of vertical and sexual transmission have been excluded by such results, the likelihood of self-flagellation as an infective risk factor remains unclear. Although India and Pakistan are not known to be geographic risk areas for HTLV-1, few prevalence studies are available (4), and HTLV-1 is commonly present in small geographic foci (5). In addition, a noticeable degree of transmission through communal self-flagellation would first require a raised prevalence of infection among the practicing group. We look forward to further research that may clarify the apparent link between self-flagellation and HTLV-1 infection.

Australian governments fund the Australian Red Cross Blood Service for the provision of blood, blood products, and services to the Australian community.

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Corrections

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Figure 2 contained incorrect values in Cross-Border Movement of Highly Drug-Resistant *Mycobacterium tuberculosis* from Papua New Guinea to Australia through Torres Strait Protected Zone, 2010–2015 (A. Bainomugisa et al.). The corrected figure is provided, and the article has been corrected online (https://wwwnc.cdc.gov/eid/article/25/3/18-1003_article).

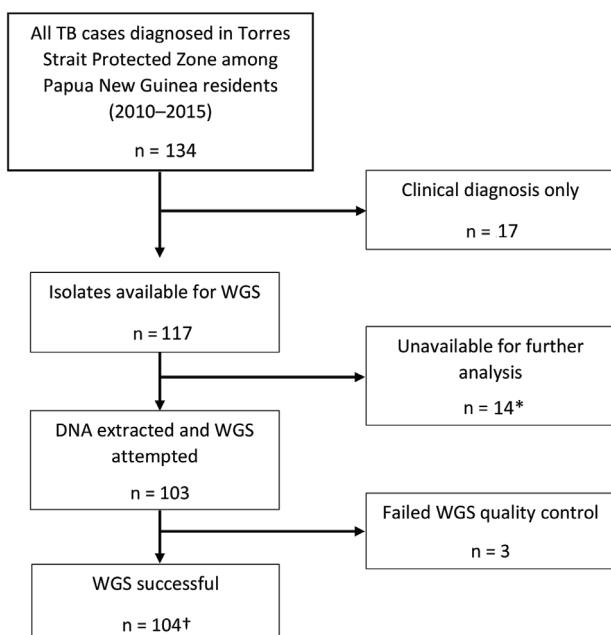


Figure 2. Flow diagram of included *Mycobacterium tuberculosis* isolates from Papua New Guinea citizens residing in Torres Strait Protected Zone, 2010–2015. *Isolates unable to grow or were contaminated. †Included were 4 additional isolates among Queensland residents that were a part of an epidemiologic cluster linked to the Torres Strait Protected Zone. TB, tuberculosis; WGS, whole-genome sequencing.

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Clostridioides was misspelled in Risk for *Clostridioides difficile* Infection among Older Adults with Cancer (M. Kamboj et al.). The article has been corrected online (https://wwwnc.cdc.gov/eid/article/25/9/18-1142_article).