Preventive Medicine Reports 58 (2025) 103223

Contents lists available at ScienceDirect

Preventive Medicine Reports

journal homepage: www.elsevier.com/locate/pmedr

Short communication

Prevalence of human T-cell lymphotropic virus type 1 or 2 among blood donors screened at the New Zealand Blood Service: An observational study, 2001–2024

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ARTICLE INFO

Keywords:
Human T-cell Lymphotropic virus
HTLV
Prevalence
Blood donor
New Zealand

ABSTRACT

Objective: To investigate prevalence of Human T-cell Lymphotropic Virus type 1 or 2 (HTLV-1/2) using the New Zealand Blood Service (NZBS) data, to inform whether further HTLV-1/2 prevalence study may be required, in the context of drivers of the inequities in lung cancer for Māori (the Indigenous population).
Methods: This observational cross-sectional study used the NZBS data of all blood donors nationwide (01/01/2001–30/06/2024). Prevalence overall and by ethnicity was calculated as the number of confirmed HTLV-1/2 positive cases per 10,000 donors.
Results: Of 679,946 new donors over the 23.5 years, 25 HTLV-1/2 positive cases were identified. The overall prevalence of HTLV-1/2 in New Zealand was 0.4 cases per 10,000 donors, highest among Middle Eastern, Latin American and African ethnicity (six cases per 10,000 donors), with no positive cases in Māori and Pacific donors. Among the positive cases, the highest proportions were seen separately for those aged 25–34, females, of New Zealand European ethnicity, resident in Auckland, and born in India, compared to their counterparts.
Conclusions: Prevalence of HTLV-1/2 infection among blood donors in New Zealand was very low, with no evidence of infection among Māori and Pacific donors, suggesting that a wider HTLV-1/2 seroprevalence study was unlikely to be necessary.

1. Background

Human T-cell lymphotropic virus (HTLV) is a human retrovirus, most common types being type 1 and 2 among four known types (Ciminale et al., 2014). HTLV-1 and HTLV-2 share similar structures and regulatory mechanisms. Both can transmit via contact with blood or bodily fluids, mother to child (via breast feeding), and sexually (Legrand et al., 2022). In the absence of available vaccines and specific antiretroviral therapies, preventive measures are the mainstay for the control of HTLV infection. However, their pathogenicity significantly differs. While HTLV-2 is usually asymptomatic, it can cause conditions similar or identical to HTLV-I-associated myelopathy/tropical spastic paraparesis (HAM/TSP). HTLV-1 can cause T-cell malignancy and manifest other significant diseases, including HAM/TSP, associated with poor or fatal outcomes (Ciminale et al., 2014; Legrand et al., 2022). The global prevalence of HTLV-1 infection is estimated at 5–10 million people, with 90 % remaining asymptomatic throughout their lifetime (Legrand et al., 2022). The main significant diseases that manifest post-infection in the 10 % of symptomatic people include adult T-cell leukaemia/lymphoma, HTLV-1 associated myelopathy, HTLV-1 associated uveitis, and HTLV-1

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https://doi.org/10.1016/j.pmedr.2025.103223
Received 28 May 2025; Received in revised form 19 August 2025; Accepted 21 August 2025
Available online 22 August 2025

associated pulmonary diseases such as bronchiectasis, bronchitis, and bronchiolitis (Uchiyama et al., 1977; Einsiedel et al., 2021a). HTLV-1 infection is associated with a 60 % increase in mortality from any cause (Schierhout et al., 2020). Given its clinical significance, HTLV-1 is the main focus of this research although testing of it among blood donors in Aotearoa New Zealand does not differentiate between HTLV-1 and HTLV-2.

HTLV-1 can be found worldwide, but is highly prevalent in Southwest Japan, sub-Saharan Africa, South America, the Caribbean area, Middle East and Australo-Melanesia (Gessain and Cassar, 2012). While the disease is endemic in Indigenous Australians and in Melanesia in nearby regions (e.g., 36.5 % [307/840] HTLV-1 positive cases among Indigenous Australian patient cohort in Central Australia), showing evidence of association with chronic lung diseases (Einsiedel et al., 2018), New Zealand has a paucity of research on HTLV-1. This research on HTLV-1 was developed as part of the Te Oranga Pūkahukahu lung health check programme (Te Whatu Ora Waitematā, 2024), which is Māori-focused, and led by Māori (the Indigenous population of New Zealand). The question was asked whether further research is needed on its prevalence, in the context of drivers of the large inequities in lung cancer incidence and mortality between the Māori and non-Māori populations in New Zealand. In New Zealand, the New Zealand Blood Service (NZBS) routinely screens blood donors for HTLV-1 (New Zealand Blood Service, 2023). Using the NZBS screening data, our research aims to provide an updated report on the prevalence of HTLV-1/2 among donors in New Zealand, with a focus on ethnicity to provide understanding of the HTLV-1/2 infection in the Māori population, and to inform whether any further prevalence work may be required in New Zealand.

2. Methods

2.1. Research design and study data

This observational cross-sectional study involved the data of all blood donors recorded at the NZBS over the 23.5 years between 1 January 2001 and 30 June 2024. The NZBS, established in 1998, is responsible for providing blood and blood products, organ donation coordination and tissue typing services (New Zealand Blood Service, 2023). It has nine main collection sites, three manufacturing sites, supported by two testing sites (Auckland & Christchurch) across the country. The NZBS performs testing of donor blood for infectious diseases, including HIV, Hepatitis B & C, Syphilis, and HTLV-1/2.

Ethnicity data is collected on NZBS donors routinely, following the New Zealand Ethnicity Data Standards for the Health and Disability Sector (Ministry of Health NZ, 2017). The ethnicity data output was prioritised for the participants with multiple ethnicities in the following order: Māori, Pacific, Asian, and Middle Eastern Latin American and African (MELAA) and Other, where the Other comprises New Zealand European, and Other European. The Residual category is reserved for these responses: don't know, refused to answer, response unidentifiable, response outside scope, and not stated (Ministry of Health NZ, 2017). It is however noted that NZBS adherence to the Standards for collecting ethnicity information only came into effect approximately 10 years ago, reflected by the residual category figures being diminished over time.

The NZBS perform a routine once-only test for anti-HTLV 1 & 2 antibodies on all new donors using the Abbott antibody enzyme immunoassay (Therapeutic Goods Administration, 2024), processed daily by the NZBS' two Donation Accreditation labs in Auckland and Christchurch. This testing does not differentiate between HTLV-1 and HTLV-2. If the test is negative, no further testing is carried out. If the test is reactive, it is repeated in duplicate. If either or both repeats are reactive, the sample is sent to the Public Health and Forensic Science (PHF Science), the NZBS' reference laboratory. The serology is then repeated using Murex EIA, Fujirebio PPA and MP Bio Western blot assay (MPBio, 2024). If both the NZBS and PHF Science get reactive results, the donor is treated as a true positive, notified and managed by the NZBS as part of standardised result management.

2.2. Ethical considerations

This study used secondary data routinely collected for blood donors at the NZBS. It involved no interventions to the participants. The data obtained from the NZBS were de-identified and transferred for analysis through the secure encrypted ShareFile (ShareFile, 2023) service. An ethics approval was sought from the Health and Disability Ethics Committee for the use of these data, with a formal waiver of consent, which was granted, and to source ethnicity data from the National Health Index where data were missing for positive cases (reference: 2024 EXP 19402). A Waitematā Health New Zealand localities approval was also obtained (registration WAI20145). There are known issues with ethnicity data collection, misclassification and undercount of Māori (Cormack Donna, McLeod M, 2010); these issues are acknowledged, discussed in the limitations and considered in the interpretation of the data by ethnicity.

2.3. Data analysis

The NZBS investigator de-identified and summarised the individual data, grouped by ethnicity for the NZBS donors, and by age, sex, ethnicity, region of residence, and country of birth for all HTLV-1/2 positive cases. With missing values, the NZBS augmented the ethnicity data of HTLV-1/2 positive cases by linking and matching the NZBS records and the National Health Index (NHI) database at the individual level probabilistically. The NZBS transferred the de-identified data to the research team analyst, who analysed the data and presented the disease prevalence by ethnicity and the characteristics of positive cases. The data analysis was conducted using Microsoft Excel.

3. Results

A total of 679,946 new donors were identified over the 23.5 years, giving an average of 28,942 new donors per year (Table 1). The donor pool was predominantly contributed by European (54 %) and residual category (23 %), followed by Asian (9 %) and Māori (7 %), and contributed least by MELAA (1 %). The recording of ethnicity has improved over time; the residual category reduced from 38 % in 2001 to 13 % in 2024. Approximately 6 % of the donors had multiple ethnicities.

Overall prevalence of HTLV-1/2 in New Zealand was 0.4 cases per 10,000 donors. HTLV-1/2 infection was most prevalent in donors of MELAA ethnicity (six cases per 10,000 donors). It was also found in Asian and European ethnicity donors: the prevalence was two cases per 10,000 donors for Asian and 0.3 for European. No HTLV-1/2 cases were detected among Māori and Pacific donors (Table 1). Among the positive cases, the highest proportions were seen separately for donors in the categories of age 25–34 years, female gender, New Zealand European ethnicity, resident in Auckland, and those born in India, compared to their counterparts (Table 2).

4. Discussion

Our study showed that, over the 23.5 years between 1 January 2001 and 30 June 2024, the overall prevalence of HTLV-1/2 infection among New Zealand blood donors was 0.4 in 10,000 donors, with no positive cases reported for Māori and Pacific donors. Although our data is restricted to blood donors, this finding of an overall low prevalence with an absence of Māori and Pacific cases is encouraging, given that a study of seven remote Indigenous communities in Australia between 2014 and 2018 found a very high HTLV-1 prevalence of 30 % (218/720) (Einsiedel et al., 2021b). Their study also suggested that HTLV-1 appeared to increase with age, showing a paediatric prevalence (aged <15) of 3.5 %, which increased to 24.8 % in the 15–24 year group and peaked at 50 % in the 55–64 year group (Einsiedel et al., 2021b). In our

Table 1
Prevalence of Human T-cell Lymphotropic Virus type 1 or 2 among blood donors, New Zealand, 01/01/2001–30/06/2024.

Ethnicity	Donors			HTLV-1/2 positive			Prevalence per **10,000** donors (95 % Confidence Interval)
	Total N	%	Annual N	Total N	%	Annual N	
European	365,408	53.7	15,554	10	40.0	<1	0.27 (0.13–0.5)
Asian	63,687	9.4	2711	11	44.0	<1	1.73 (0.86–3.09)
Māori	47,937	7.1	2040	0	0.0	0	0
Pacific	24,943	3.7	1062	0	0.0	0	0
MELAA	6478	1.0	276	4	16.0	<1	6.17 (1.68–15.8)
Other	14,426	2.1	614	0	0.0	0	0
Residual	157,067	23.1	6686	0	0.0	0	0
Total	679,946	100.0	28,942	25	100.0	1	0.37 (0.24–0.54)

Table 2
Characteristics of Human T-cell Lymphotropic Virus type 1 or 2 positive cases among blood donors, New Zealand, 01/01/2001–30/06/2024.

		N	%
Total		25	100.0
Age [a]			
	15–24 years	3	12.0
	25–34 years	8	32.0
	35–44 years	6	24.0
	45–54 years	6	24.0
Sex			
	Male	11	44.0
	Female	14	56.0
Ethnicity [b]			
	New Zealand European	6	24.0
	Asian	5	20.0
	Middle Eastern	4	16.0
	Indian	4	16.0
Region of residence [c]			
	Auckland	15	60.0
	Christchurch	5	20.0
Country of Birth [d]			
	India	5	20.0
	New Zealand	3	12.0
	Iran	3	12.0
	Unknown	5	20.0

Each of the following categories contributed <3 in number and were omitted from the table: [a] 55–64 years; [b] Other European, European, Korean, South African European, Southeast Asian; [c] Manukau, Hamilton, Lower Hutt, Wellington, Wanaka; [d] Iraq, Malaysia, Pakistan, United States, Republic of Korea, United Kingdom, South Africa, Philippines.

analysis, about one-third of the cases were 25–34 years old, followed by the 35–54 year group (24 %). The 55–64 year group only contributed 8 % to total cases.

The HTLV-1 infection is found to have a strong geographical linkage. Within Australia, the HTLV-1 infection clustered in certain regions, showing high endemicity in the Central Australia region (Einsiedel et al., 2018; Grivas et al., 2014), with low or no prevalence of HTLV-1 in Northern Territory or in Far North Queensland (Smith et al., 2019). Our New Zealand study found that the donors in Auckland contributed the highest proportion (60 %) to total HTLV-1/2 cases among those in other regions. This finding likely reflects the higher proportion of people who originate from the high prevalence areas. Interestingly, in our study, HTLV-1/2 was more common among donors of Asian and Middle Eastern ethnicity and those born in India and Iran compared to their counterparts. Cases appeared to be more strongly linked to ethnicity and were found in people migrating from endemic countries or their descendants, rather than local transmission. This information may help guide the future relevant HTLV-1 studies in selecting the potential high risk areas and populations.

In New Zealand, little evidence has been available on HTLV-1 prevalence since the New Zealand population study in 1987, in which the researchers reviewed blood donor samples including Māori patient samples (Reddy et al., 1987). They concluded that HTLV-1 virus infection was unlikely to occur in the Auckland region. Our study reports the prevalence of HTLV-1/2 in New Zealand using the nationwide blood donor screening data over 23.5 years. Our findings contribute to the limited epidemiological data on HTLV-1 in New Zealand as well as in other Pacific regions, including Polynesia and Micronesia, for broader regional surveillance. A strength is the large dataset recorded over a long time period. Blood donors provide some of the best type of systematic sampling given the range of people who donate blood. However, our study has limitations. The representation of Māori (7 %) in the donor pool was lower than that in the general population (17 %) (Stats NZ, 2024), therefore the findings may have limited generalisability to the total population of New Zealand. The high proportion of residual category ethnicity data, mainly contributed by the poor quality ethnicity data in the earlier period, in the NZBS sample suggests issues with compliance with the Ethnicity Data Standards in the collection of ethnicity data (<2 % residual category indicates high quality ethnicity data (UMR Research, 2009)). Therefore, the ethnicity data may have some level of misclassification or undercount for Māori and other groups.

This analysis overall suggests that HTLV-1 is unlikely a key driver of high Māori lung cancer incidence and mortality in New Zealand. A risk factor based testing approach could be considered for testing HTLV-1/2 in blood donors, or perhaps more likely, in pre-transplant work up for tissue donors, organ donors and hematopoietic stem cell transplantation recipients. Prevention measures for HTLV-1/2 could be integrated into sexually transmitted infections interventions and antenatal care.

5. Conclusions

Prevalence of HTLV-1/2 infection among blood donors in New Zealand was very low. It was observed only in donors from endemic countries with no evidence of infection among Māori and Pacific donors. Although findings from the blood donor sample may not be generalisable to the wider population, this analysis suggests that HTLV-1 was unlikely to be a high impact target for further seroprevalence studies at this time.

Data accessibility

The source data used in the current project contains identifiable individual information. The data are not publicly available due to the data confidentiality and privacy restrictions, but aggregate data are available from the corresponding author on reasonable request and corresponding approvals. Please contact Health and Disability Ethics Committees at hdecs@health.govt.nz for ethics queries.

CRediT authorship contribution statement

Phyu Sin Aye: Writing – review & editing, Writing – original draft, Visualization, Validation, Project administration, Formal analysis. **Lucy**

Gray: Writing – review & editing, Writing – original draft, Conceptualization, Data curation. **Richard Charlewood:** Writing – review & editing, Validation, Data curation. **Wendy Bennett:** Writing – review & editing, Validation, Supervision, Methodology, Data curation, Conceptualization. **Collette Bromhead:** Writing – review & editing, Project administration, Methodology, Conceptualization. **Michelle Balm:** Writing – review & editing, Conceptualization, Validation. **Sue Crengle:** Writing – review & editing, Conceptualization, Supervision. **Karen Bartholomew:** Writing – review & editing, Writing – original draft, Supervision, Resources, Conceptualization.

Ethics approval and consent to participate

This study used secondary data routinely collected for blood donors at the NZBS. It involved no interventions to the participants. The data obtained from the NZBS were de-identified and transferred for analysis through the secure encrypted ShareFile (ShareFile, 2023) service. An ethics approval was sought from the Health and Disability Ethics Committee for the use of these data, with a formal waiver of consent, which was granted, and to source ethnicity data from the National Health Index where data were missing for positive cases (reference: 2024 EXP 19402). The Waitemata localities approval was also obtained (registration WAI20145). There are known issues with ethnicity data collection, misclassification and undercount of Māori (Cormack Donna, McLeod M, 2010); these issues are acknowledged, discussed in the limitations and considered in the interpretation of the data by ethnicity.

Funding

No specific funding was obtained for this study.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have influenced the work reported in this paper.

Acknowledgments

The authors would like to acknowledge the original literature review and considerations paper undertaken by Dr. Lucy Gray that informed the development of this study. We thank Dr. Lavinia Perumal (National Public Health Service) for supervision of the initial project and support and advice on the study. We also thank the NZBS for supporting the analysis and interpretation.

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