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1
2 **THE PREVALENCE OF HUMAN T-LYMPHOTROPIC VIRUS TYPE 1 & 2 (HTLV-1/2) IN**
3 **SOUTH AFRICAN BLOOD DONORS**

4
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18
19 Running Head: HTLV prevalence in SA

20 Research support: Vitalant Research Institute and Abbott Diagnostics for the HTLV reagents

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28

1 **Abstract** (243 words)

2 Background and objectives. Donated blood is not currently screened for human T-cell
3 lymphotropic virus (HTLV) in South Africa. Several small studies have detected HTLV-1 in
4 South Africa, but prevalence by geographic region or population group are unavailable.

5 Materials and Methods. We performed a large seroprevalence study of South African blood
6 donors during three months in 2013. All geographic regions except the Western Cape were
7 included and Black and Coloured (local term for mixed-race) donors were oversampled.
8 Identity-unlinked plasma samples were screened with the Abbott Prism HTLV-1/2 assay and
9 repeatedly reactive samples were tested by the Inno-LIA HTLV-1/2 Score confirmatory
10 assay. **Odds ratios were calculated with multivariable logistic regression.**

11 Results. Of 46,716 donors tested, 133 (0.28%) were initially reactive, 111 (0.24%)
12 repeatedly reactive and 57 (0.12%) confirmed positive for HTLV-1; none were HTLV-2
13 positive. Prevalence was 0.062% weighted to annual **blood donations** but highly
14 concentrated in the Black population group (**OR=20.24 CI 2.77-147.88**); higher in females
15 than males (**OR=1.81 CI 1.06-3.08**); and in donors aged >50 years compared to ages 16-19
16 (**OR=6.4 CI 2.95-13.86**). After controlling for age, sex and population group there was no
17 difference in prevalence between new and repeat blood donors or among geographic
18 regions within South Africa.

19 Conclusions. We conclude that HTLV-1 infection is widespread among the Black population
20 of South Africa and its epidemiology is similar to other endemic areas. Because South Africa
21 is increasing its recruitment of Black blood donors the implications for blood screening
22 require further consideration.

1 Introduction

2 Human T-cell Lymphotropic Virus types 1 and 2 (HTLV-1/2) are closely related retroviruses
3 first reported in the early 1980's[1, 2]. HTLV-1 is the causative agent of Adult T-Cell
4 Leukaemia (ATL)[3] and has been associated with Tropical Spastic Paraparesis (TSP) also
5 called HTLV-1 Associated Myelopathy (HAM)[4]. It is endemic in Southern Japan, the
6 Caribbean Islands and parts of central Africa.[5] Transmission is by sexual contact[6],
7 intravenous drug abuse, from an infected mother to her child, mainly via breast milk[7] and
8 by **non-leukoreduced** blood transfusion[8-10]. HTLV-1 causes ATL in 2-4% of infected
9 individuals and typically after long latency periods[11, 12]. Once diagnosed with ATL life
10 expectancy is typically less than a year. HAM/TSP occurs in approximately 0.25-4% of
11 HTLV-1 infected individuals usually after a latency period of up to 20 years, although
12 HAM/TSP may occur after a few months when HTLV-1 infection is acquired through a blood
13 transfusion[13-16]. Patients with HAM/TSP may live with significant disability for 20-30 years
14 post HAM/TSP diagnosis.[2] HTLV-2 **infrequently** causes HAM/TSP, increased incidence of
15 pneumonia and bronchitis and perhaps higher all-cause and cancer mortality[17].

16
17 In 1993 Bhigjee *et al.* reported a seroprevalence of HTLV-1 in the predominantly Black
18 Ngwelezana area of KwaZulu-Natal of 2.6% (95% confidence interval (CI) 1.62-3.58)[18]. An
19 age-related rise in HTLV-1 seropositivity from 1.3% in the 15-24 year age group to 6.1% in
20 the over 55-year-old group was also noted. In a study performed by van der Ryst *et al.* in
21 1996 in the Free State region of South Africa[19] it was reported that 2% (95% CI: 0.5 to 5
22 %) of asymptomatic urban Blacks and 1.1% (95% CI: 0.14 to 4%) of asymptomatic rural
23 Blacks had HTLV-1 antibodies. An HTLV-1/2 seroprevalence study was conducted in 1996
24 among KwaZulu-Natal blood donors by the Natal Blood Transfusion Service (Sykes, W
25 Personal communication). Donations were tested with an HTLV-1/2 enzyme immunoassay
26 over a 3-month period from March to June 1996. Of 37,422 donations tested (22000 were
27 from white donors) 3 were confirmed positive, for an overall prevalence of 0.008%. Of the
28 three positives detected in this study 2 (0.016%) were female and 1 (0.004%) was male.

1 With increased donor recruitment in the Black community, current HTLV-1 prevalence data
2 are needed for decision making about blood screening within the South Africa National
3 Blood Service (SANBS). In this study we aim to determine the prevalence of HTLV-1 and -2
4 in the South African (SA) donor population and ascertain associations with demographic
5 characteristics and geography

6

7 **Methods**

8 Case Report. In October 2013, a potential HTLV transmission was reported to SANBS[20]. A
9 65 year old Indian-descent male had undergone surgery for carcinoma of the bladder in
10 2011 and had required 6 units of blood. In October 2013 the patient presented with a three
11 month history of progressive lower limb weakness. Examination revealed a spastic
12 paraparesis in the lower limbs. Upper limbs were normal, with normal sensation and intact
13 bowel function. Western blot testing in the blood and polymerase chain reaction assay in the
14 CSF was positive for HTLV-1. Upon trace back SANBS was able to identify one of the six
15 blood donors as being HTLV-1 positive.

16

17 Phylogenetic analysis

18 DNA sequencing of HTLV-1 provirus and phylogenetic analysis was performed on the donor
19 and transfusion recipient samples. High-molecular weight DNA was extracted from
20 peripheral blood mononuclear cells (PBMC) using the QIAamp DNA minikit (Qiagen, Hilden,
21 Germany). The two PBMC samples were first subjected to polymerase chain reaction (PCR)
22 using human beta-globin specific primers to ensure that DNA was amplifiable. Both samples
23 were then amplified by PCR using “env” primers, which were designed to amplify a 885-bp
24 long fragment of the envelop gene: Env11: 5'-TGGCACGTCCTRTACTCTCCCAAC-3' and
25 Env22: 5'-GGCGAGGTGGAGTCCTTGGAGGC-3' corresponding to nucleotides 5,911 to
26 5,934 and 6,774 to 6,796 respectively of the prototype ATK-1 sequence (Genbank: J02029).
27 From each sample, 250 ng of DNA was amplified under the following conditions: 98°C, 1mn;
28 40 X (98°C, 5 s; 72°C, 20 s); 72°C, 1 mn. Reactions tubes were prepared in a dedicated

1 room outside the laboratory with a final volume of 50 µl (DNA matrix, 250 ng; dNTP mix
2 (Roche, Basel, Switzerland), 40 mM; 5X Phire II reaction buffer which contains 1.5 mM
3 MgCl₂ at final reaction concentration (Ozyme, Saint Quentin-en-Yvelines, France), 10 µl;
4 Phire II hot start DNA polymerase (Ozyme, Saint Quentin-en-Yvelines, France), 2 U and 0.5
5 mM of each oligonucleotide primer (Eurofins MWG, Ebersberg, Germany). Ten microliters of
6 amplified DNA was size fractionated by 1.5% agarose gel electrophoresis. The PCR
7 products (40 µl) were sent for purification and sequencing reactions to the MWG Platform at
8 Cochin Hospital, Paris, France. Each PCR product was sequenced using the Env11/Env22
9 pair of primers plus an additional inner pair of primers. A comparison of each generated
10 segment by an alignment of the forward and reverse sequences using the ClustalW
11 algorithm (Mac Vector 14.0.6 software, Oxford Molecular) was implemented to derive a
12 consensus sequence. Then, phylogenetic trees were generated, using both neighbour-
13 joining and maximum likelihood methods, from multiple alignments using the CLC Main
14 Workbench 7.6.4 (Qiagen) software.

15

16 Sampling and Testing. An identity-unlinked cross sectional study to determine the
17 prevalence of HTLV-1/2 in SA blood donors was performed between August 2013 and
18 November 2013. A sample size of 50,000 donations was planned; Black and Coloured (local
19 term for mixed-race) donors were oversampled in a ratio of 4:1 as compared to White/Asian
20 donors to increase statistical power in expected high prevalence population groups (however
21 the over-sampling of Black and Coloured donors was not correctly implemented in the
22 Eastern Cape). Donor samples were collected from all areas of South Africa, excluding the
23 Western Cape Province where another blood service collects and tests donated blood. The
24 donor record was tagged when donations were selected to ensure that if the donor
25 presented to donate again during the study period they were excluded. Donor demographic
26 information (race, gender, age, region and whether the donor was a first time, repeat or
27 lapsed donor) and virology test results were uploaded into the study dataset and linked to a
28 de novo study ID. The donation identifier number was then removed from the specimen prior

1 to testing. The protocol was approved by the SANBS Human Research Ethics Committee
2 (Clearance certificate number 12/01).

3

4 All samples were tested for HTLV-1/ 2 using the Abbott PRISM HTLV 1/2 chemiluminescent
5 assay (ChLIA) (Abbott Diagnostics, Delkenheim, Germany). Initially reactive samples were
6 repeated in duplicate on the same testing platform and repeatedly reactive samples were
7 tested by a confirmatory assay using the Inno-LIA HTLV-1/2 Score Line ImmunoAssay
8 (Fujirebio, Ghent, Belgium) method. Six confirmed positive samples were sent to the
9 National Health Laboratory Service Clinical pathology department at Groote Schuur Hospital
10 in Cape Town for Proviral DNA using a hemi-nested in house PCR targeting a region of the
11 pol gene to validate the Inno-LIA results.

12

13 Statistical analysis. All demographic, donation and laboratory data were captured
14 electronically. HTLV prevalence was calculated overall and by subgroup, and 95%
15 confidence intervals were calculated. Differences in prevalence between groups were
16 assessed with chi-square tests. Multiple logistic regression was performed to determine
17 factors independently associated with HTLV. A p-value of <0.05 was considered significant.
18 Finally, prevalence was extrapolated to annual blood donations at SANBS by weighting
19 according to the original oversampling of Black and Coloured donors. Here we multiplied the
20 HTLV prevalence of each race group in the study by the number of blood donations by that
21 race group annually to determine the number of HTLV positive donations that would be
22 detected annually per race group. These were then added up and the overall prevalence
23 was determined as the total number of HTLV positive donations predicted annually divided
24 by the number of donations collected annually.

1 Results

2 A total of 46,752 blood donors (Black 73%, Coloured 13%, White 12% and Asian 2%) were
3 tested for HTLV-1/2 antibodies (Table 1). Of 133 (0.28% of total) initial reactive samples,
4 111 (0.24%) tested repeat reactive and 57 (0.12%) were confirmed positive. There were 5
5 samples that could not be repeated by the Inno-LIA assay due to insufficient volume; when
6 adjusted for these we estimate that a total of 60 (0.128%) would have confirmed positive. All
7 positives were HTLV-1 according to Inno-LIA and all of the 6 Inno-LIA positive samples
8 tested by PCR were found to contain HTLV-1 provirus. There was one co-infection with HIV
9 and no co-infections with either HBV or HCV.

10

11 HTLV-1 prevalence was 0.16% (95%CI 0.14%-0.23%) in Black donors, 0.02% (95%CI 0%-
12 0.06%) in Coloured donors, 0.02% (95%CI 0%-0.05%) in White donors and 0% (95%CI 0%-
13 0.6%) in Asian donors (Table 1). Female donors showed a significantly higher prevalence
14 than did males (0.16% vs. 0.09% ($p=0.03$)). There was no difference in prevalence between
15 first time (0.11%) and repeat (0.12%) donors. Focusing on the Black population group,
16 HTLV-1 prevalence increased with age and especially ages over 50 years, and females
17 were more likely to be positive than males at all ages (Figure 1). Geographically, there was
18 no significant difference in prevalence among the operational zones of SANBS, which
19 generally correspond to the provinces of South Africa (Figure 2) except that no HTLV-1
20 positives were found in the Eastern Cape where oversampling of Black and Coloured was
21 not properly implemented.

22

23 After extrapolating the study sample back into the population group distribution of current
24 SANBS donations in 2015, the overall number of confirmed infections and estimated
25 prevalence in SANBS donations would be 509 or 0.062% (95%CI 0.0568%-0.068%). The
26 Initial reactive specificity of the antibody screening assay compared to the Inno-LIA
27 (assuming all screen negatives were true negatives) was 99.84% (95%CI 99.75%-99.93%)
28 which would result in 1277 false positives per annum if all 818,000 donations were tested.

1 Logistic regression analysis was used to adjust for confounding between variables (Table 2).
2 The odds of infection rose substantially with age (odds ratio = 6.40 for those aged over 50
3 compared to those aged under 20). Females had nearly twice the odds of HTLV-1 infection
4 compared to males. Black donors had 20 times the odds of HTLV-1 infection compared to
5 White donors, but there was no difference by new versus repeat donor status. Due to the
6 relatively small numbers of positive subjects in any one zone or province, there were no
7 significant differences in the prevalence by geography. Mpumalanga had the highest odds of
8 infection with KwaZulu-Natal having odds similar to Egoli (the Johannesburg/Pretoria
9 region), and lower odds observed in Eastern Cape and Vaal.

10

11 HTLV transmission case

12 The blood donor and recipient HTLV-1 strains were found identical on a 772-bp long env
13 fragment, which comprises the 522-bp fragment used for *env* phylogenetic analyses. These
14 two new sequences (SANBS480 and SANBS900 accession numbers MK496634 and
15 MK496635 respectively) are closely related, but different (1 to 4 bp difference/522bp), from
16 those previously characterized from South Africa and available in GenBank (afs1, 2, 3 and
17 afs 911). Furthermore, several non-South African sequences (i.e. PH757, PH1494 and Ar55
18 from the West-Indies and Argentina respectively) were identical to the two novel sequences
19 generated in this study. The phylogenetic analysis performed on a 522-bp-long *env* region
20 with 1,000 bootstrap replicates showed that both tree topologies were comparable for the
21 neighbour-joining and maximum likelihood methods (data not shown). The main HTLV-1
22 subtypes (a-d) were identifiable and the two new viral strains (SANBS480 and SANBS900)
23 belong to the HTLV-1 Cosmopolitan a-subtype and the transcontinental clade (Figure 3).
24 Furthermore, we also amplified the complete LTR fragment (757 bp) of the donor and the
25 recipient HTLV-1 strains and these were found to be identical. This sequence is slightly
26 different (4 nucleotides difference) from the only other LTR sequence available from an
27 HTLV-1 strain from South Africa (afs911) (see supplemental data). Thus, genetic
28 comparison and phylogenetic analyses, performed on both a fragment of the *env* gene and

- 1 the complete LTR sequence, are compatible with HTLV-1 transmission from the donor to the
- 2 recipient, but evidence falls short of proof as the two identified HTLV-1 strains belong to the
- 3 frequent and widespread a-TC genotype, which exhibits a very low genetic variability.

1 Discussion

2 This study found measurable levels of HTLV-1 infection among South African blood donors,
3 with an adjusted prevalence of 0.062% among blood donations. HTLV-1 infection was
4 localized almost entirely to the Black population group with a prevalence of 0.16%.
5 Associations with female gender (OR = 1.82 versus males) and older age (OR = 6.40 in
6 those over 50 years versus those under 20 years) were similar to reports in other
7 populations [21-24].

8

9 The finding of endemic HTLV-1 among Black South Africans is consistent with data from
10 other countries in Africa. HTLV-1 prevalence in small studies of non-blood donors ranged
11 from 1-2% in Ghana[21], 2-3% in Mozambique, Uganda and Egypt[18, 25-27] and as high as
12 5% and 9.1% in Guinea and Gabon respectively[23, 28]. Caution must be used in comparing
13 these prevalence rates because different population groups were studied and the uncertain
14 use of confirmatory testing.

15

16 Among blood donors, Senegal reported a HTLV-1/2 prevalence of 0.16%[29] of which 88%
17 were HTLV-1, Guinea reported 1.2% [30] and Mozambique reported 0.89% of which all were
18 HTLV-1[31]. In smaller studies with questionable confirmatory methods, Zimbabwe reported
19 a prevalence of 0.1% [32], Ethiopia reported HTLV-1 and HTLV-2 prevalences of 0.19% and
20 0.25%, respectively[27], Mali had an unconfirmed blood donor prevalence of 1.4%[33] and
21 Tunisia found no HTLV positives in 500 blood donors[27]. In Mali, Diarra *et al.* showed the
22 prevalence of HTLV in multi-transfused patients to be 2 and 5.3 fold higher (2.8% and 7.5%)
23 in patients that received 2 and 3 blood transfusions respectively than in blood donors from
24 the same region (1.4%)[33].

25

26 Others have suggested that there is about a 6-fold reduction in HTLV-1 prevalence in blood
27 donors versus the general population due to their younger age[34], selective recruitment and
28 pre-donation risk questioning[35]. HTLV prevalence in the general population is mainly in the

1 elderly whereas at SANBS 80% of the donations are made by donors under the age of 50. In
2 the early 1990s, Bhigjee *et al.* demonstrated a prevalence increasing from 1.3% in 15 to 24
3 years olds to 6.1% in those aged over 55 years in a mostly black community-based sample
4 in the KwaZulu-Natal province of South Africa, a province that has the highest prevalence of
5 HIV[18]. Overall, this is about 10-fold higher than the age-specific prevalence we found in
6 Black blood donors, demonstrating selection for safer donors as noted above. If we were to
7 apply a similar factor of 6-10 to extrapolate the current data, it would suggest that the
8 prevalence of HTLV-1 in the general Black adult population of South Africa is at least 1%,
9 suggesting endemic infection but at perhaps a lower prevalence than in certain countries in
10 sub-Saharan Africa.

11

12 SANBS implemented a strategic objective in 2005 to increase blood donations from the
13 majority Black population to correct historical racial imbalances and improve sustainability.
14 At the time of this study in 2013, the proportion of Black donors was 39% compared to 6% in
15 2005[36]. Because our study found HTLV-1 infection to be evident in the Black population,
16 efforts to increase donations from Black donors may be expected to increase the overall
17 prevalence in blood donations above 0.062% and this will need to be monitored
18 prospectively.

19

20 During this study SANBS was informed of a potential HTLV transmission. Findings based on
21 sequence comparison and phylogenetic analysis, are compatible with transmission from the
22 donor to the recipient. There is one other previously reported potential blood-borne HTLV-1
23 transmission in the late 80's from South Africa however this case was not studied
24 molecularly[37]. Possible reasons for so few reported transmission events are many: 1) lack
25 of HTLV awareness among health care providers and a poor haemovigilance system with
26 under reporting; 2) an assumed 50% mortality after transfusion[38], asymptomatic infection
27 in most patients[2], and a prolonged asymptomatic phase before rare disease outcomes[34];
28 and 3) aspects of blood processing may reduce transmission including storage time prior to

1 transfusion but SANBS transfuses 80% of its red cell products in less than 11 days following
2 collection[34] and white cell reduction by buffy coat removal (84%) or filter leukoreduction
3 (16%)[39].

4

5 HTLV-1 antibody testing of all blood donations has been implemented in a number of high
6 income countries however some have questioned the cost effectiveness of these strategies
7 considering that money spent to prevent rare HTLV-1 infections is diverted from other health
8 priorities[40-43].

9

10 Strengths of the study include its large sample size, oversampling of the endemic Black and
11 Coloured populations, broad geographic scope, and use of state-of-the-art assays for HTLV-
12 1 antibody screening and confirmation. Weaknesses include relatively low power for
13 subgroup analyses due to the limited number of positives and the lack of more detailed risk
14 factor information due to its unlinked design. In addition, the over-sampling of Black and
15 Coloured donors was not correctly implemented in Eastern Cape, which likely explains the
16 observed zero prevalence in this Province. Cellular blood samples were not stored from
17 positives and so molecular epidemiologic studies to compare HTLV-1 subtypes are not
18 possible. Finally, as mentioned above, the data need to be extrapolated to the general
19 population with caution because blood donors are selected to be low risk and healthy.

20

21 In conclusion, this large study has allowed the measurement of contemporary HTLV-1
22 prevalence in South African blood donors and provides strong evidence that the virus is
23 endemic in the South African Black population and is not limited to KwaZulu-Natal province.
24 It raises the question as to whether HTLV-1 antibody screening or other measures should be
25 implemented to prevent transfusion transmitted infections in the country. The findings from
26 this study along with a budget impact tool were used to assess implications of different blood
27 screening options for HTLV in South Africa using the Alliance of Blood Operators Risk Based
28 Decision Making framework (see Vermeulen et al in this issue). At this time SANBS has

- 1 decided not to implement screening for HTLV due to financial constraints in the South
- 2 African health sector.
- 3
- 4

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3 for providing a portion of the HTLV test kits. A special thanks to all the Donation Testing staff
4 at SANBS for performing the testing in addition to their normal work. We would also like to
5 thank Dr. Diana Hardie of the South African National Health Laboratory Service for
6 performing the HTLV proviral DNA testing for confirmation of the Inno-LIA results.

7

8 Author contributions:

9 Marion Vermeulen, Wendy Sykes, Edward Murphy, Brian Custer, Charlotte Ingram and Ravi
10 Reddy provided input into the design of the research

11 Wendy Sykes, Charl Coleman, Genevieve Jacobs, Jabulisile Jaza, Colwyn Poole, Antoine
12 Gessain and Olivier Cassar acquired the data

13 Marion Vermeulen, Wendy Sykes, Edward Murphy, Brian Custer, Zhanna Kaidarova,
14 Antoine Gessain and Olivier Cassar analysed and interpreted the data

15 Marion Vermeulen, Edward Murphy and Brian Custer drafted the paper and the other
16 authors revised the Paper.

17 All authors approved submission.

1 **Figure Legends**

2

3 Figure 1. HTLV-1 seroprevalence by age and sex, South African blood donors, 2013.

4

5 Figure 2. HTLV-1 seroprevalence according to province of blood collection, South African
6 blood donors, 2013.

7

8 Figure 3. Phylogenetic analysis of HTLV-1 *env* sequences. Phylogenetic comparison was
9 performed on 522-nucleotide-long *env* gene fragment of 53 HTLV-1 isolates, including the
10 two sequences generated in this study (SANBS 480 and SANBS 900; in red frame); other
11 South African isolates afs1, afs2, afs3, afs911 and 47 previously published sequences. The
12 phylogeny was derived by the neighbour-joining method using the GTR model. Numbers on
13 each node indicate the percentage of bootstrap samples (of 1,000) in which the cluster is
14 supported (threshold value $\geq 50\%$).

1 Table 1: HTLV-1 prevalence, by demographic and geographic characteristics as well as
 2 donor status. Zones indicate SANBS blood collection regions that correspond roughly to
 3 South African Provinces.

		N Tested	HTLV-1 Positive, n (%)	P- VALUE(Adjusted)
	All donors	46 752	57 (0.12%)	
Age	16-19	9 521	10 (0.11%)	<.0001
	20-29	14 254	12 (0.08%)	
	30-39	9 904	4 (0.04%)	
	40-49	7 426	9 (0.12%)	
	50+	5 647	22 (0.39%)	
Gender	Male	26 701	25 (0.09%)	0.03
	Female	20 051	32 (0.16%)	
Race	White	5 643	1 (0.02%)	0.0023
	Asian	909	0 (0.00%)	
	Coloured	6 033	1 (0.02%)	
	Black	34 166	55 (0.16%)	
	Other	1	0 (0.00%)	
Zone	Egoli	11 318	15 (0.13%)	0.0568
	Eastern Cape	4 604	0 (0.00%)	
	Free State	2 287	3 (0.13%)	
	Kwa-Zulu-Natal	7 826	10 (0.13%)	
	Mpumalanga	4 750	12 (0.25%)	
	Northern	10 109	12 (0.12%)	
	Vaal	5 858	5 (0.09%)	
Donor status	New	7 214	8 (0.11%)	0.6885
	Re-Join	5 548	8 (0.14%)	
	Repeat	33 966	41 (0.12%)	

4

5 * In South Africa, Coloured ethnicity is a multiracial group made up of five source populations
 6 namely: African San, African non-San, European, South Asian, and East Asian[44]

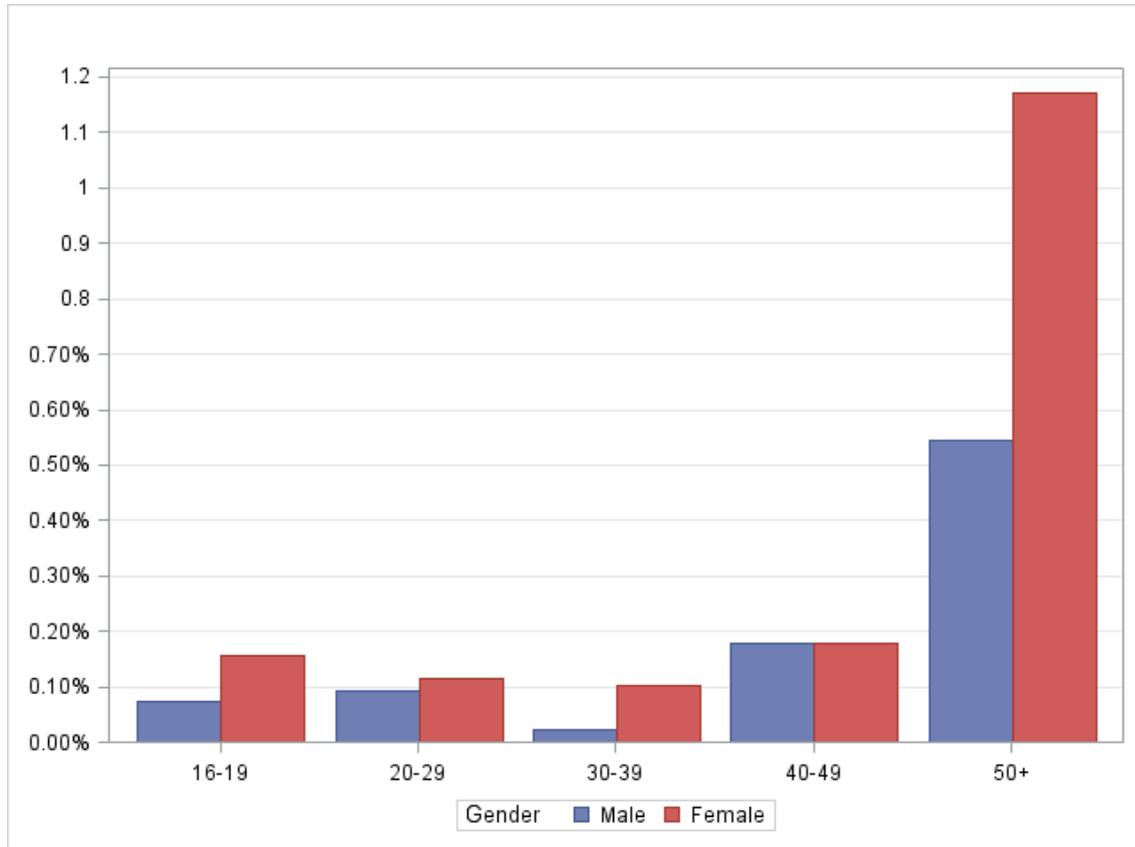
7 ** Lapsed donors have made at least one donation but none within the past year.

- 1 Table 2: Logistic regression model of factors associated with HTLV-1 infection. Adjusted
 2 odds ratios and 95% confidence intervals are shown. Zones indicate SANBS blood collection
 3 regions that correspond roughly to South African Provinces.

Variable	Groups	Odds Ratio	95%CI	
Age	16-19	1.00	---	
	20-29	0.80	0.34	1.88
	30-39	0.44	0.14	1.41
	40-49	1.68	0.65	4.13
	50+	6.40	2.95	13.86
Gender	Male	1.00	---	
	Female	1.81	1.06	3.08
Race	White and Asian	1.00	---	
	Black	20.24	2.77	147.88
	Coloured	1.65	0.10	26.49
Zone / Province	Egoli	1.00	---	
	Eastern Cape/Vaal	0.36	0.13	1.00
	Free State	1.33	0.38	4.61
	Kwazulu-Natal	1.04	0.46	2.33
	Mpumalanga	1.84	0.85	3.97
	Northern	0.75	0.35	1.60
Donor type	First time	1.00	---	
	Repeat	1.25	0.57	2.75
	Lapsed	1.56	0.57	4.24

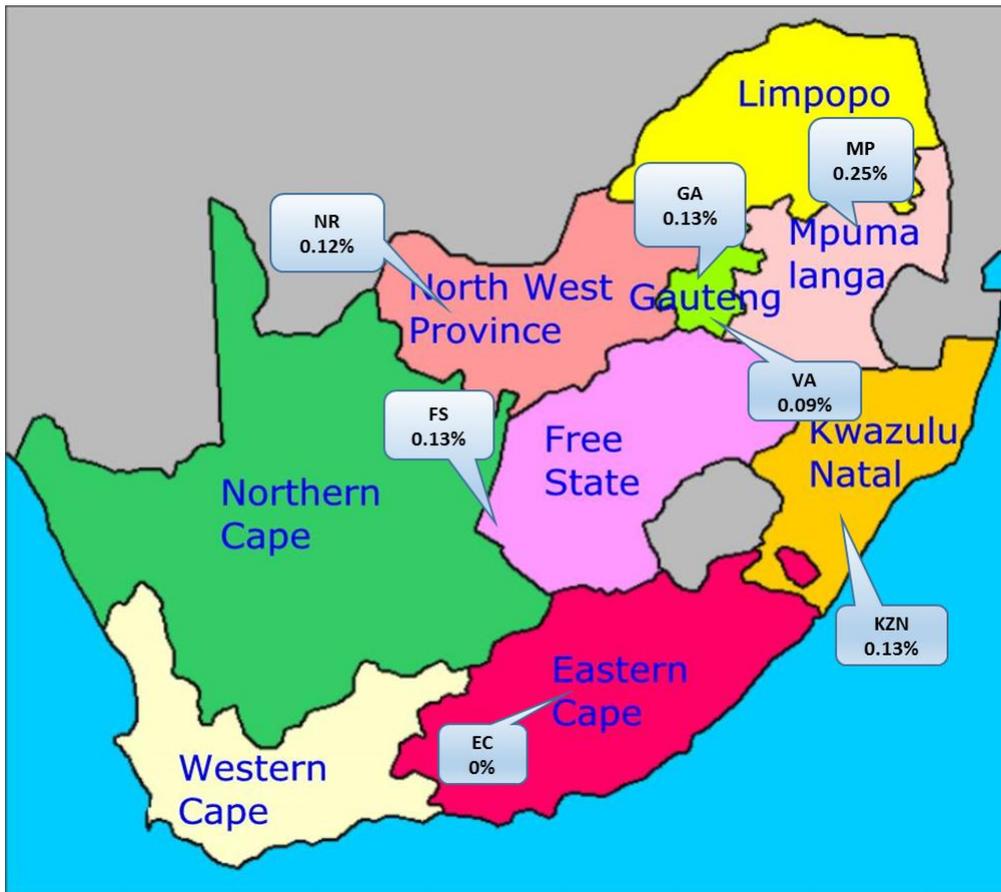
1 Fig 1: HTLV-1 prevalence by age and sex, South African blood donors from the
2 Black population group only.

3



4

- 1 Fig 2: HTLV-1 prevalence by SANBS collection zones, which correspond generally to South African Provinces.
- 2



3

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