Absence of HTLV-I infection in some Indian populations

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A total of 946 adults belonging to ten population groups of Uttar Pradesh and West Bengal were screened for HTLV-I using a gelatin particle agglutination test. The percentage of seroreactive cases varied from 0 to 5.8 per cent. The overall prevalence of seroreactivity was 2 per cent. Of the 19 seroreactive cases, 15 were subjected to Western blot analysis, none could be confirmed. HTLV-I infection is, therefore, absent in these populations.

Key words HTLV-I-India-seroreactive-Western blotting

The human T-cell lymphotropic virus type - I (HTLV-I), is an oncogenic retrovirus which is often involved in the pathogenesis of adult T-cell leukaemia/lymphoma and of tropical spastic paraparesis1. Other clinical manifestations of HTLV-I infection include polyarthritis², infectious dermatitis3, polymyositis4, and uveitis5. HTLV-I is transmitted mainly from an infected mother to her child via breast milk. Other modes of transmission include blood transfusion⁶ and sexual intercourse⁷. Although for understanding the epidemiology of viral infections such as HTLV-I or human immuno deficiency virus (HIV), high-risk groups are generally studied, population studies can also yield extremely valuable information. For HTLV-I, population studies have indicated enormous differences in seroprevalence among defined ethnic populations8. The prevalence varies from 0 per cent in many populations to 14 per cent among the Hagahai, a hunter horticulturist group of Papua New Guinea9. These differences may result from varying life-styles or even from differences in susceptibility, possibly genetic, to HTLV-I infection. On account of prevailing differences in cultural practices and/or differences in genetic susceptibility patterns, it is important to report data on samples from different ethnic populations. Although HTLV-I has, so far, not emerged as a major public health problem in India, it is necessary to screen various populations to estimate the prevalence of carriers because of the potential public health implications.

Material & Methods

In the course of genetic studies conducted by us in Uttar Pradesh and West Bengal during January 1992 and February 1993, we have screened a total of 946 unrelated adults (543 male and 403 female in the age range 16-80 yr), belonging to various socio-religious groups at different levels of the social hierarchy.

HTLV-I serotyping was performed using a gelatin particle agglutination (PA) test (Serodia ATLA/HTLV-I, Fujirebio, Japan). In the assay, 25 µl aliquots of the particle suspension were used with equal volumes of diluted serum. The assays were performed on micro titre plates. The screening dilution for the test sample with sensitized particles was 1:16, while the unsensitized particle control was tested at a dilution of 1:8. A test was scored as reactive when the serum dilution 1:16 showed agglu-

tination and the serum treated with unsensitized particles showed no agglutination. When positive reactivity was detected the test was repeated for confirmation. The dilution was increased serially. For the major fraction of the sample which were scored as seroreactive, we have also performed Western blot (WB) tests using native HTLV-I antigens (Problot HTLV; Fuji Rebio, Tokyo, Japan). Presence of at least one gag product and gp46 was taken to be the criterion for determining positivity in this test.

Results & Discussion

Description of populations, sample sizes and results of PA and WB tests are given in the Table. The percentage of seroreactive cases (observed titre range: 1:16 - 1:32) determined by the PA test varies from 0 to 5.8 per cent. Of the 19 samples that were scored as reactive by the PA test, 15 were subjected to Western blot analysis (WB test on the remaining 4 samples could not be performed because of logistical problems). None of these reactive samples could be confirmed by Western blot analysis. High prevalence of HTLV-I has been reported from southern Japan, the Carribean, South America and equatorial Africa¹⁰. Carriers have also been reported from the Philippines¹¹. While an initial study¹² reported absence of HTLV-I infection in India, subsequent studies have detected HTLV-I carriers from Maharashtra¹³ and in some high-risk groups (sexually promiscuous adults, leukaemia patients) of southern India^{14,15}.

We conclude that HTLV-I infection is absent in the populations studied by us. As in Melanesia¹⁶, although it is possible that HTLV substrains may be detected and isolated¹⁷ in these Indian populations, this possibility is perhaps negligible because sequence alignments and comparisons indicated that several HTLV-I strains from southern India were 99.2 to 100 per cent identical among themselves and 98.7 to 100 per cent identical to the Japanese prototype HTLV-ATK¹⁸. It should also be emphasized that in this study the samples were not selected from a high-risk subgroup. Therefore, although we have not detected any positive case employing stringent Western blot criteria, it is possible that some individuals from these populations who participate in high-risk activities may test positive for HTLV-I. In spite of the limitation of restricted sample sizes, the present study

Table. Populations screened, locations of sampling, sample sizes and results of HTLV-1 PA and WB tests in Uttar Pradesh and West Bengal

Population	Location of sampling	PA test		WB test
		n	n ₊ (%)	n
Brahmin	Lucknow	112	5(4.46)	4
Kayastha	Lucknow	85	2(2.35)	2
Vaishya	Lucknow	52	0(0.00)	0
Chamar	Lucknow	104	6(5.77)	6
Muslim	Lucknow	106	3(2.83)	3
Brahmin	Garhwal	97	1(1.03)	0
Rajput	Garhwal	114	1(0.88)	0
Scheduled castes	Garhwal	84	1(1.19)	0
Muslim	Garhwal	62	0(0.00)	0
Boro Deshi	West Dinajpur	130	0(0.00)	0

None of the 15 seropositive samples tested by WB were positive n, total sample size; n, number of positive samples PA, particle agglutination; WB, Western blot

shows that the prevailing life-styles of these populations have not encouraged rapid spread of HTLV-I even if individuals in these populations were exposed or that intrinsic susceptibility to HTLV-I infection is low among individuals belonging to these populations or, more probably, a combination of both these factors have kept the HTLV-I prevalence to near zero levels in these populations.

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