Human immunodeficiency virus and tuberculosis in Argentina: prevalence, genotypes and risk factors

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The objective of this study was to determine the prevalence and genetic variability of human immunodeficiency virus type 1 (HIV-1) and other sexually transmitted infections (STIs) among 205 patients with clinical diagnosis of tuberculosis (TB) in Buenos Aires in 2001. Infections with hepatitis B virus (HBV), HIV-1, hepatitis C virus (HCV), *Treponema pallidum* and human T-cell lymphotropic virus types I/II were diagnosed in 37/187 (19.8%), 35/205 (17.1%), 22/187 (11.8%), 13/187 (7.0%) and 4/181 (2.2%) patients, respectively. Almost one in three participants (33.1%) presented at least one infection in addition to TB. Multiresistance to TB drugs (isoniazid plus rifampicin) was detected in the isolates recovered from three patients. Injecting drug use was detected as the main risk factor for HIV, HBV and HCV infections. Of ten patients who died, eight were infected with HIV. HIV genetic characterization showed the presence of two different subtypes. Env subtype F was found in 13/24 samples (54.2%) and subtype B in 11/24 samples (45.8%) by heteroduplex mobility assay. Sequencing of the protease/RT region was performed in ten samples: three were characterized as subtype B and seven as B/F recombinants by bootscanning analysis. Phylogenetic analysis of four full-length

Received 3 July 2007
Accepted 10 October 2007

sequences showed that three were the circulating recombinant form CRF12_BF. The results of this study suggest an urgent need to detect HIV infection in high-risk groups to prevent future HIV transmission as well as morbidity and mortality associated with TB by providing highly active antiretroviral therapy (HAART) and/or TB treatment. Collaboration between TB and HIV programmes seems to be the best approach to decrease the incidence of these diseases, especially in high-prevalence HIV settings.

INTRODUCTION

Tuberculosis (TB) is the second most common infectious disease causing death worldwide after human immunodeficiency virus/acquired immunodeficiency syndrome (HIV/AIDS). The incidence of TB varies widely by region, with the highest incidence (356 per 100 000 of the population) and mortality (81 per 100 000) in Africa and the lowest in the Americas (incidence: 41 per 100 000; mortality: 5.9 per 100 000) (Frieden *et al.*, 2003; WHO, 2006).

Since 1980, much of the increase in the incidence of TB has been attributable to the impact of HIV/AIDS. Globally, an estimated 13 % of adults with newly diagnosed TB in 2004 were also co-infected with HIV, but there was great variation among regions, from 34 % in the African region to 1.4 % in the Western Pacific region (Dye, 2006; WHO, 2006).

HIV is the highest single risk factor for progression to active TB disease in adults (Frieden *et al.*, 2003). TB may occur relatively early in the course of HIV infection: the immunosuppression it induces modifies the clinical presentation of TB, and TB influences the prognosis of HIV infection. In addition, anti-TB drugs interfere with antiretroviral drugs (Aaron *et al.*, 2004).

The last epidemiological data for TB from Argentina in 2002 showed an incidence of 30.5 per 100 000 inhabitants, with the highest rates in the north (Jujuy: 87.3; Salta: 72.7). In Buenos Aires city and surroundings, the incidence of TB is similar to that in the whole country. The mortality rate in Argentina is 2.6 per 100 000 inhabitants, with the highest rate in the north (approx. 9 per 100 000 inhabitants) (Liga Argentina Contra la Tuberculosis, 2003).

Previous studies (1988–1994) have reported an HIV prevalence of 3.1–21 % in TB patients from Buenos Aires city (Musella *et al.*, 1990; Putruele *et al.*, 2006). However, no systematic research on HIV/TB co-infection is currently being undertaken. Therefore, the objectives of the present study were to estimate the prevalence and risk factors of HIV and other sexually transmitted infections (STIs), as well as the genetic variability among HIV strains in TB patients from Buenos Aires city.

METHODS

Study population and enrolment procedures. From July to December 2001, patients ≥ 18 years old with a clinical diagnosis of TB

who attended one of three public hospitals in Buenos Aires (Tornú, Durand and Rivadavia Hospitals) were invited to participate.

Participants were recruited through physicians, who explained the study objectives and procedures, and obtained written informed consent and clinical and epidemiological data in a confidential manner. Participants were invited to receive HIV testing and were offered pre-test and post-test counselling. All HIV-positive participants were subsequently referred for medical follow-up and a blood sample was collected for viral load, CD4 counting and HIV molecular genotyping (described below).

Hepatitis B virus (HBV), hepatitis C virus (HCV), *Treponema pallidum* and human T-cell lymphotropic virus type I/II (HTLV-I/II) infections were tested retrospectively in most of the samples after 1 year.

Blood sample collection and STI diagnosis. Anticoagulated blood (10 ml) was collected in a sterile fashion. HIV was diagnosed by ELISA and agglutination (GENSCREEN Plus HIV Ag-Ab, Bio-Rad; Serodia HIV, Fujirebio). HBV infection was screened by ELISA (Wiener Laboratorios); reactivity to HBV surface antigen and/or anti-core antibodies was considered as evidence of previous HBV infection. HCV infection was screened by ELISA (anti-HCV ELISA; Wiener Laboratorios). Screening for HTLV-I/II was performed by particle agglutination (Serodia HTLV-I; Fujirebio) and ELISA (Platelia HTLV-I New; Bio-Rad). Reactive samples were confirmed by Western blotting for HIV (Novapath HIV-1 Immunoblot; Bio-Rad) or HTLV-I/II (HTLV Blot 2.4; Genelabs Diagnostics). Past *T. pallidum* infection was screened by VDRL test (Wiener Laboratorios).

HIV viral load was assessed using a Quantiplex HIV DNA (bDNA) assay (Chiron Diagnostics). The CD4 T-cell count was estimated using a Beckman Coulter EPICS XL flow cytometer.

Bacteriological studies. Sputum analysis was performed by direct examination of bacilli presence using Truant auramine–rhodamine staining. Bacterial culture was performed in parallel in Löwenstein–Jensen medium and Bactec 460 TB (following the manufacturer's recommendations). Bacterial sensitivity to isoniazid, streptomycin, rifampicin and ethambutol was performed for 102 isolates in parallel by the Canetti methodology in Löwenstein–Jensen medium and with Bactec 460 TB (following the manufacturer's recommendations).

Genotyping procedures. DNA extraction was performed with peripheral blood mononuclear cells (Qiagen). All 35 HIV-positive samples were subjected to PCR amplification of *env* and the protease/reverse transcriptase (RT) regions, and four samples were subjected to almost full-length amplification. The *env* region was amplified and a heteroduplex mobility assay (HMA) was performed with second-round PCR products using nine reference standards, as described previously (Delwart *et al.*, 1993). The protease/RT region was amplified using primers Pro5F/RT3474R in the first round and Pro3F/ProRT in the second round. Almost full-length sequences were determined using primers MSF12b/OFMR1 in the first round and F2NST/UNINEF 7 in the second round. The amplified products were sequenced with Big Dye terminators using an ABI 3100 automated

sequencer (Applied Biosystems), assembled using Sequencer software (Genecodes) and examined in a multiple alignment with standard subtype references using CLUSTAL_X. Phylogenetic analyses were conducted by the neighbour-joining method with Kimura's two-parameter model of distance calculation and a bootstrap computed with 100 replicas using MEGA. Bootscanning and distance scanning were performed to determine the presence of recombination using Simplot (Lole *et al.*, 1999).

Resistance profile. An antiretroviral drug resistance profile was performed considering mutations that have been associated with reduced susceptibility to protease and RT inhibitors, as reported by the International AIDS Society-USA (Stanford University HIV Drug Resistance Database).

Statistical analysis. Fisher's exact test or a χ^2 test was utilized to compare proportions. Student's *t*-test or a Mann-Whitney U-test was used to compare continuous variables. Association of risk factors with HIV, HBV, HCV or *T. pallidum* infection were expressed as odds ratios (ORs) with 95% confidence intervals (95% CI). ORs were adjusted for age and education in multiple logistic regression analyses. Risk factors with a value of $P < 0.25$ in univariate analysis were selected for inclusion in stepwise forward multivariate logistic regression analyses with threshold values of $P = 0.10$ for entry into and $P = 0.05$ for removal from the model. All reported *P* values were two-sided. Statistical analyses were conducted using Stata version 8.0.

RESULTS AND DISCUSSION

Study population

A total of 205 patients with clinical diagnosis of TB infection were enrolled, 65.9% of which were men. The mean age of participants was 34.8 ± 14.1 years. Sixty-two per cent of the participants were Argentinean; the rest were mainly from Peru (16.7%) and Bolivia (15.8%). Almost all of the participants lived in Buenos Aires city (43.1%) and surrounding areas (52.9%). A high educational level (approximately equivalent to high school) was reported by 59% of the participants, with women showing a significantly higher educational level (70 vs 53.3%, $P = 0.025$); 80.5% of the participants were employees.

Irregular use of condoms (defined as 'occasional or no use at all') was reported by 58.6%, whilst 6.4% reported

experiencing condom tears. Previous STIs were declared by 20.6%, with gonorrhoea being the most frequent. A history of transfusion was reported by 11.1%. Tattoos were reported by 19.4%, and were more frequent in men than in women (24.8 vs 8.8%, $P = 0.008$). Ten per cent had been in prison, which was also more common in men (15.3 vs 1.5%, $P = 0.001$). Approximately 4% of men defined themselves as homosexual. Illicit drug use was declared by 27.5% of men and 2.1% of women ($P < 0.0001$), and 9.4% were intravenous drug users (IDUs), also reported more frequently among men (12.7 vs 2.9%, $P = 0.023$). Twelve per cent reported having had sex with an IDU partner and 12.4% reported having an HIV-positive partner. In men, 6.7% reported that they had exchanged sex for money, drugs or food occasionally during their lifetime. With regard to sexual attitudes, 16.3% of men and 5.8% of women reported having had more than one partner over the last 6 months ($P = 0.024$).

Previous BCG vaccination was reported by 75% of the study population. Eighty per cent were inpatients at the hospitals. Of the 205 patients, 20.7% were under TB treatment and in all of these TB disease was clinically confirmed by bacteriology or culture assays.

Prevalences

Infection with HBV, HIV, HCV, *T. pallidum* and HTLV-I/II was diagnosed in 37/187 (19.8%), 35/205 (17.1%), 22/187 (11.8%), 13/187 (7.0%) and 4/181 (2.2%) participants, respectively (Table 1). HIV and HCV prevalence was found to be significantly higher among men, showing a risk of 2.5 and 10.7, respectively. Among the HTLV-positive cases, three were HTLV-I and one was HTLV-II. Table 2 shows the risk factors that were found to be statistically associated with higher prevalence of the infections analysed. Most HIV-positive cases (90%) reported having previous HIV testing.

Bacteriological results

Sputum samples were analysed in 156 patients and 119 (76.3%) were found to be positive. In 102 patients,

Table 1. Prevalence of HIV, HBV, HCV, HTLV-I/II and *T. pallidum* among 205 patients with TB in Buenos Aires, Argentina, 2001

Organism	Total		Women		Men		<i>P</i> value
	No. positive/ no. studied	% Prevalence (95% CI)	No. positive/ no. studied	% Prevalence (95% CI)	No. positive/ no. studied	% Prevalence (95% CI)	
HBV	37/187	19.8 (14.3–26.2)	9/64	14.1 (4.8–23.4)	28/123	22.8 (14.9–30.6)	0.109
HIV	35/205	17.1 (12.2–23.9)	6/70	8.6 (1.3–15.8)	29/135	21.5 (14.2–28.8)	0.020*
HCV	22/187	11.8 (7.5–17.3)	1/64	1.6 (0.04–8.4)	21/123	17.1 (10.0–24.1)	0.001*
<i>T. pallidum</i>	13/187	7.0 (3.8–11.6)	3/64	4.7 (1.0–13.1)	10/123	8.1 (2.9–13.4)	0.548
HTLV-I/II	4/181	2.2 (0.6–5.6)	0/62	0	4/119	3.4 (0.9–8.4)	0.301

*HIV and HCV infections were significantly more frequent in men than in women.

Table 2. Prevalence of HIV, HBV, HCV and *T. pallidum* by potential risk factors among 205 patients with TB in Buenos Aires, Argentina, 2001

The total number of cases tested in each group varied because of missing data. Statistically significant variables ($P < 0.05$ by χ^2 or Fisher's exact test) are shown in bold.

Feature	HIV		HBV		HCV		<i>T. pallidum</i>	
	%	No. positive/total	%	No. positive/total	%	No. positive/total	%	No. positive/total
Age group (years)								
18–24	3.6	2/55	6.0	3/50	8.0	4/50	2.0	1/50
25–29	11.9	5/42	13.9	5/36	8.3	3/36	5.6	2/36
30–44	33.3	20/60	33.3	18/54	22.2	12/54	7.4	4/54
≥45	16.7	8/48	23.4	11/47	6.4	3/47	12.8	6/47
Nationality								
Other	3.8	3/78	18.9	14/74	6.8	5/74	5.4	4/74
Argentinean	25.6	32/125	20.4	23/113	15.0	17/113	8.0	9/113
Level of education								
High school or higher	10.7	13/121	17.3	19/110	8.2	9/110	4.6	5/110
Primary or less	26.2	22/84	23.4	18/77	16.9	13/77	10.4	8/77
Employment								
Yes	11.8	20/170	17.4	27/155	8.4	13/155	7.7	12/155
No	48.0	12/25	36.4	8/22	31.8	7/22	4.6	1/22
Imprisonment								
No	12.4	22/178	16.6	27/163	6.1	10/163	7.4	12/163
Yes	57.1	12/21	50.0	9/18	61.1	11/18	5.6	1/18
Tattoos								
No	13.0	21/162	19.6	29/148	7.4	11/148	8.8	13/148
Yes	33.3	13/39	20.0	7/35	28.6	10/35	0.0	0/35
Use of injected drugs								
No	9.2	17/187	15.3	26/170	5.3	9/170	6.5	11/170
Yes	94.7	18/19	73.3	11/15	86.7	13/15	13.3	2/15
Sexual partner use drugs								
No	8.8	14/159	13.8	20/145	6.2	9/145	7.6	11/145
Yes	81.8	18/22	60.0	12/20	65.0	13/20	10.0	2/20
Do not know	13.6	3/22	25.0	5/20	0.0	0/20	0.0	0/20
Sexual partner HIV-positive								
No	3.5	5/141	13.5	18/133	4.5	6/133	7.5	10/133
Yes	80.0	16/20	61.1	11/18	55.6	10/18	11.1	2/18
Do not know	33.3	14/42	23.5	8/34	17.7	6/34	2.9	1/34
Prior history of STI								
No	13.3	21/158	16.4	24/146	11.6	17/146	4.8	7/146
Yes	34.1	14/41	36.1	13/36	13.9	5/36	16.7	6/36
Exchanged sex for goods								
No	15.4	30/195	18.3	33/180	11.1	20/180	6.7	12/180
Yes	55.6	5/9	66.7	4/6	33.3	2/6	16.7	1/6
Use of illegal drugs								
No	10.0	18/180	16.8	28/167	7.8	13/167	7.2	12/167
Yes	70.8	17/24	47.4	9/19	47.4	9/19	5.3	1/19
Condom breaking								
No	15.2	28/191	18.9	33/175	11.4	20/175	7.4	13/175
Yes	46.2	6/13	36.4	4/11	18.2	2/11	0.0	0/11
Anal sex with condom in the last 6 months								
No	58.3	7/12	54.6	6/11	63.6	7/11	9.1	1/11
Yes	13.6	18/132	16.9	20/118	10.2	12/118	5.1	6/118

Mycobacterium tuberculosis was isolated and an antibiogram was performed. Ninety-one isolates (89.2 %) were sensitive to all drugs and 10 presented the following resistance

patterns: four were resistant to isoniazid, three to streptomycin and three were multiresistant (isoniazid plus rifampicin).

Fig. 1. Distribution of co-infections among 181 patients with TB in Buenos Aires, Argentina, 2001. Others indicates other co-infections between HIV, HBV, HCV and *T. pallidum*.

Co-infection

Co-infection was studied in 181 participants (88.3%) for whom full serological data were available. Almost one in three (33.1%, $n=60$) presented at least one infection in addition to TB. Of these patients, 36 (19.9%), ten (5.5%),

ten (5.5%) and four (2.2%) were diagnosed with two, three, four or five infections, respectively. The three most common co-infections were TB/HIV/HSV/HCV (4.4%), TB/HIV/HSV (2.2%) and TB/HIV/HCV (1.7%). The distribution of co-infections is shown in Fig. 1. A significant association between HIV and HBV ($P < 0.001$), HIV and HCV ($P < 0.001$), HBV and HCV ($P < 0.001$), HBV and HTLV-I/II ($P = 0.025$) and HCV and HTLV-I/II ($P = 0.006$) was observed.

Risk factor analyses

Table 3 shows the multiple logistic regression analyses of risk factors associated with HIV, HBV, HCV and *T. pallidum* infection. The significant risk factors for HIV infection were: age 25–44, Argentinean nationality, primary or lower level of education, unemployment, history of imprisonment, presence of tattoos, injected drug use, an IDU partner, an HIV-infected partner, a history of STI, sexual contact with men, exchange of sex for goods, illegal drug use and a history of condom tears. For HBV infection, risk factors were older age (30–44 years), unemployment, a history of imprisonment, injected drug use, an IDU partner, an HIV-infected partner, a history of STI,

Table 3. Multiple logistic regression analysis of risk factors associated with HIV, HBV, HCV and *T. pallidum* infection among 205 patients with TB in Buenos Aires, Argentina, 2001

AOR, odds ratio adjusted for gender, age and level of education. Categories in parentheses indicate the reference category for odds calculation. Statistically significant variables are shown in bold. NA, Not applicable.

Risk factor	HIV		HBV		HCV		<i>T. pallidum</i>	
	AOR	95% CI	AOR	95% CI	AOR	95% CI	AOR	95% CI
Age group								
25–29 (<25 years)	7.6	2.2–26.2	2.7	0.7–11.0	1.3	0.7–2.3	3.2	0.7–14.7
30–44 (<25 years)	23.2	4.2–128.5	8.0	1.7–36.3	2.7	0.7–10.6	3.3	2.8–4.0
≥45 (<25 years)	8.2	0.58–116.1	4.9	1.2–19.3	0.5	0.02–13.7	5.7	1.2–26.7
Argentinean nationality (other)	6.8	1.5–31.1	0.85	0.47–1.5	2.4	1.2–4.7	0.9	0.1–7.3
Primary or lower level of education (high school or higher)	2.0	1.5–2.7	1.0	0.44–2.3	2.4	0.42–14.2	1.5	0.4–5.5
No employment (yes)	5.7	4.6–7.1	3.3	2.6–4.1	3.7	2.7–5.0	0.6	0.2–2.3
History of imprisonment (no)	10.9	4.4–26.6	5.9	2.1–16.7	17.6	4.8–64.3	0.8	0.3–2.4
Presence of tattoos (no)	3.3	1.3–8.0	1.1	0.47–2.6	3.2	1.5–7.0	NA	NA
Use of injected drugs (no)	177.0	11.3–2780.7	16.2	2.0–132.4	189.5	7.1–5072.4	2.3	0.5–10.5
Sexual partner using drugs (no)								
Yes	73.9	31.7–172.5	12.5	4.2–37.1	39.2	21.7–71.0	1.6	0.3–7.6
Do not know	3.0	1.1–8.2	2.8	1.6–5.0	NA	NA	NA	NA
Sexual partner HIV-positive (no)								
Yes	328.5	44.9–2405.4	12.1	3.4–43.8	46.9	11.3–194.6	1.9	0.7–5.7
Do not know	18.3	6.1–55.0	2.1	0.8–5.6	4.6	0.9–22.3	0.4	0.1–1.1
Prior history of STI (no)	3.2	1.7–5.9	2.3	1.1–4.7	1.4	0.9–2.2	2.7	0.5–15.1
Sexual contact with men (no)	4.7	3.2–6.9	NA	NA	NA	NA	NA	NA
Exchanged sex for money/goods (no)	3.7	1.6–8.6	7.6	3.6–16.0	2.1	0.7–7.0	1.9	1.3–2.7
Use of illegal drugs (no)	42.0	19.0–92.5	5.5	3.9–7.7	7.7	5.6–10.5	0.9	0.6–1.6
Condom breaking (no)	9.0	5.4–15.0	4.1	1.3–13.5	4.1	0.8–20.9	NA	NA
Anal sex without condom (with condom)	5.9	0.5–68.3	5.3	1.6–17.9	14.4	2.8–74.4	1.7	0.5–6.3

exchange of sex for goods, illegal drug use, condom tears and unprotected anal intercourse. In contrast, Argentinean nationality, unemployment, history of imprisonment, presence of tattoos, injected drug use, an IDU partner, an HIV-infected partner and use of illegal drugs were the main risk factors associated with HCV infection. For *T. pallidum* infection, only older age and exchange of sex for goods were associated risk factors. Among HTLV-I/II infected patients, two were IDUs who were also HIV-infected; one was from Peru and the other one had a history of transfusion.

When a stepwise forward multivariate logistic regression analysis was applied, only some variables remained associated with HIV, HBV and HCV: age (OR 1.1, 95 % CI 1.0–1.1), unemployment (OR 15.5, 95 % CI 2.8–83.0), having a sexual partner with HIV (OR 41.8, 95 % CI 4.7–370.6) and use of injected drugs (OR 132.2, 95 % CI 8.3–2111.1) for HIV; age (OR 1.04, 95 % CI 1.01–1.07), use of drugs in the sexual partner (OR 5.17, 95 % CI 1.38–19.33) and use of injected drugs (OR 6.65, 95 % CI 1.53–28.89) for HBV; and use of drugs in the sexual partner (OR 11.58, 95 % CI 6.78–19.80), being male (OR 24.15, 95 % CI 4.71–123.95) and use of injected drugs (OR 62.92, 95 % CI 1.65–2398.94) for HCV.

The univariate analysis to identify the association between illicit drug use and other variables showed that the presence of tattoos, a history of imprisonment, an IDU partner, an HIV-infected partner, a higher number of sexual partners and exchange of sex for goods were highly reported in patients who reported being drug users. Stratified analysis of the study population showed that, in non-IDUs, condom tears, having an IDU partner and having an HIV-infected partner were the main risk factors associated with HIV infection.

Retrospectively, the outcome of the patients was disclosed: 143 patients were cured, 25 left the treatment, eight were referred to another hospital, five continued treatment when the study was concluded, ten died and no information was available for the remaining 14 participants. Of the ten patients who died, nine had at least one of the diagnosed infections and eight were HIV-positive.

Genotyping, resistance profile, CD4 count and viral load in HIV-positive patients

An *env* HMA was completed in 24 HIV-positive samples. *Env* subtype F was found in 13 samples (54.2 %) and subtype B in 11 samples (45.8 %). Ten samples were sequenced in the protease/RT region: three samples were found to be subtype B and seven were B/F recombinants by bootscanning analysis (Fig. 2). Three *Env* subtype F samples were sequenced in the protease/RT region and were found to be B/F recombinants. Phylogenetic analysis (neighbour-joining and bootscanning analysis) of the full-length sequences of four protease/RT B/F samples showed that three were the circulating recombinant form CRF12_{BF} and the other was a unique recombinant form.

Of the ten HIV-positive samples analysed, primary antiretroviral resistance was detected in three: ARG3002 (I54V, V82A, L90M, T69N, F116Y, Q151M and M184V), ARG3011 (L100I and K103N) and ARG3015 (G48V, L90M, V118I, K103E and Y181C).

The median viral load for the HIV-positive patients was 5.2 log viral RNA copies ml⁻¹ (158 489 copies ml⁻¹) and the median number of CD4⁺ T cells was 84 cells ml⁻¹.

The results of this epidemiological study provide a better understanding of the status of the HIV/TB epidemic in Argentina. This study clearly indicates that a high proportion (17.1 %) of patients with TB are also infected with HIV. The high viral loads and low CD4 counts registered, together with the absence of previous opportunistic infections, suggest that TB was probably the first AIDS-defining illness. In HIV-infected patients, TB most often results from reactivation of latent TB infection (Aaron *et al.*, 2004; Frothingham *et al.*, 2005).

Different risk factors were detected in this study, but the use of injected drugs was by far the main risk factor associated with HIV and hepatitis infection. The overwhelming majority of patients who used injected drugs were infected with HIV (18/19), HCV (13/15) and HBV (11/15). This is consistent with previously reported data from our group among injecting drug users in Buenos Aires (Weissenbacher *et al.*, 2003).

TB is the main cause of hospitalization among HIV-infected injecting drug users at Muñiz Hospital (the national reference hospital for infectious diseases in Argentina). Two out of three HIV-positive IDU patients experience at least one TB episode following infection. Moreover, it was observed that among HIV-infected individuals, the chance of developing pulmonary or extra-pulmonary TB is twice as high in IDUs as it is in non-IDUs (Moscatello, 2003).

In those patients who do not use injected drugs, sexual risks (condom tears, or having an IDU or HIV-positive sexual partner) were the main risk factors associated with HIV infection. As previously reported for other risk groups in Buenos Aires, these variables related mainly to a low socioeconomic level, and included unemployment, exchange of sex for goods and history of imprisonment, and were also associated with hepatitis infection (Pando *et al.*, 2003, 2004, 2006).

Multiresistant TB was detected at high prevalence in Argentina during the 1990s and was particularly associated with AIDS patients attending some hospitals in large urban centres such as the Muñiz Hospital (Palmero *et al.*, 2006). In 1999, a countrywide survey depicted 1.8 % multi-resistant TB (WHO/IUATLD, 2004). In this study, only three patients who had already received TB treatment presented multiresistance (isoniazid plus rifampicin). These three patients declared very low or no treatment adherence and one was also HIV-positive.

The results of genetic characterization showed the presence of two different subtypes, as was previously detected in heterosexual men and women (Ávila *et al.*, 2002). HMA showed the co-existence of subtypes B and F (54.2 vs 45.8 %) and sequencing analysis showed that all of the Env subtype F samples sequenced in the protease/RT region were B/F recombinants as previously noted (Ávila *et al.*, 2002; Carr *et al.*, 2001). The high prevalence of B/F recombinants and CRF12_BF described in this group is in accordance with previous studies performed in IDUs (Espinosa *et al.*, 2004).

ACKNOWLEDGEMENTS

Jackson Foundation for the Advancement of Military Medicine, Inc. or any other organization listed.

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