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HIV-1 Subtype B Epidemic and Transmission Patterns in Slovenia

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A B S T R A C T

In the present study the epidemic of human immunodeficiency virus type 1 (HIV-1) subtype B in Slovenia during the 10-year period was investigated using phylogenetic analysis of pol gene sequences. 119 pol sequences generated on samples dated from January 1996 to December 2005 were retrieved from the database of Slovenian HIV/AIDS Reference Laboratory. The phylogenetic analysis revealed 14 potentially significant transmission clusters (bootstrap value ≥ 98%), comprising 34 HIV-1 strains. The vast majority of clustered individuals were men (91%), and of them, 79% were men who have sex with men. Factors significantly associated with clustering were: recent infection (HIV-1 infection during or after year 2003), diagnosis of primary HIV-1 infection, higher CD4 cell count and acquiring HIV-1 infection in Slovenia. Recent subtype B HIV-1 infections are the important driving force of current HIV-1 epidemic in Slovenia.

***Key words**: HIV-1 transmission, pol gene, subtype B, Slovenia*

Introduction

The human immunodeficiency virus type 1 (HIV-1) epidemic in Slovenia started in 1986, and from then on, the HIV infection surveillance has been based on mandatory reporting of newly diagnosed cases of HIV infection and acquired immunodeficiency syndrome (AIDS)[1–3]. Until recently, Slovenia has been considered as a country with a relatively low HIV-1 infection prevalence. Thus, by the end of 2005, a total of 278 HIV-1 infected individuals were cumulatively reported in Slovenia. However, a higher incidence was noted during the last two years, when the annual incidence rate based on newly diagnosed infections peaked to 17.5 (in 2005) cases per million population[1,2]. Surprisingly, men who have sex with men (MSM) still constitute the most affected population group. Fortunately, a rapid spread of HIV infection has not yet been recorded among injecting drug users and their sexual partners in Slovenia[1,2,4].

Recent molecular epidemiological studies on HIV-1 in Slovenia revealed that subtype B is predominant HIV-1 subtype (84%), although a relatively high proportion (16%) of non-B subtypes was found[4–7]. Moreover, in contrast to a recent increase in the proportion of HIV-1 infections acquired through heterosexual contact recognized in the majority of Western European countries, an unexpected and statistically significant increase in the proportion of MSM among the newly diagnosed HIV-1 infected patients was observed during the last four years (2002–2005). An analogous, but statistically insignificant increase in the proportion of subtype B infections among the newly diagnosed HIV-1 infected patients was observed in the same period[7].

The genetic variability of HIV-1 makes it possible to trace the HIV-1 epidemic within a certain geographic region[8–11]. To date, phylogenetic analysis has been successfully used for providing evidence of HIV-1 transmission, not only for epidemiological purposes, but also for the resolution of legal cases[12–17]. However, the choice of the most appropriate genetic region of HIV-1 phylogenetic analysis is still subject to debate[18–21]. To date, most studies on HIV-1 transmission using phylogenetic analysis have relied on the V3 loop region of the *env* gene, and to a lesser degree on the fragments of the *gag* gene[19,22–24]. The *pol* gene has recently been considered to hold sufficient genetic variability to permit the reconstruction of HIV-1 transmission pathways by phylogenetic methods[18,21,22,25,26]. Moreover, since the genotypic drug resistance

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testing is widely used, a huge amount of sequence data is nowadays available for the protease (PR) and reverse transcriptase (RT) region located in the *pol* gene. Therefore, the *pol* gene has become recently an attractive target for phylogenetic studies[18,21,22,25–27].

In order to gain a better understanding of the spread and transmission of subtype B HIV-1 in Slovenia, we performed a phylogenetic analysis based on *pol* sequences and collected clinical and epidemiological data in 119 individuals infected with this HIV-1 subtype that were diagnosed in the Slovenian HIV/AIDS Reference Laboratory over the last ten years (1996–2005). The factors associated with transmission clustering were also investigated.

Material and Methods

Study population

Of 140 *pol* sequences generated on the samples dated from January 1996 to December 2005, all sequences of subtype B were retrieved from the database of the Slovenian HIV/AIDS Reference Laboratory and were used for phylogenetic analysis to investigate transmission events. The epidemiological and clinical data about the individuals included in the study were gathered prospectively, and in some cases, retrospectively by sending a questionnaire to the clinician. The study was approved by the Medical Ethics Committee at the Ministry of Health of Slovenia (Approval Ref. No.: 126/12/03). Confidentiality and anonymity of the individuals enrolled in this study were protected by using a code number for each individual.

HIV-1 RNA extraction, amplification and sequencing

HIV-1 RNA was extracted, reverse transcripted, amplified, and sequenced using either the ViroSeq HIV-1™ Genotyping System version 2 (Celera Diagnostics, Alameda, Calif.) or TRUGENE® HIV-1 Genotyping Kit (Visible Genetics, Toronto, Canada) following the manufacturer's recommendations. Using these two commercial assays, the nucleotide sequences of *pol* region, including the entire PR and a part of RT gene of approximately 1,200 bp, were obtained.

Phylogenetic analysis

The *pol* sequences were aligned using ClustalX, version 1.81[28]. The alignment was edited using the BioEdit program, version 5.0.9[29]. The gaps were removed manually and the sequences were trimmed to obtain fragments of equivalent length (918 nucleotides). Phylogenetic relationships between the *pol* sequences were estimated using the Neighbor-joining (NJ) method of MEGA software, version 3.1[30]. Evolutionary distances were calculated using the Kimura two-parameter distance model with a transition/transversion ratio of 2. The statistical robustness of the NJ tree and reliability of the branching patterns were confirmed by bootstrapping (1,000 replicates). Two other phylogenetic methods were also used: minimum evolution and unweighted pair group method using arithmetic averages with both the Kimura two-parameter and the Jukes-Kantor substitution module. In addition, we used a maximum parsimony method implemented in the Mega 2 software[31]. Because the trees constructed by all the algorithms resulted in the same topology, only the NJ tree is presented.

The phylogenetic clusters with bootstrap value of ≥98% and average genetic distance (i.e., branch length) lower than 0.015 nucleotide substitutions per sites within cluster were considered significant. To evaluate such criteria, five pairs or triplets of multiple sequences from intra-patient follow-up samples were incorporated within the sequence alignment as positive controls.

Statistical analysis

Statistical comparisons of individuals in a cluster with those not in a cluster were performed using Chi-squared tests, Fisher's exact tests or Mann-Whitney U test, as appropriate. All statistical analyses were performed using the SPSS for Windows, version 13.0 (SPSS Inc., Chicago, IL). P values were two-sided and considered significant at a level of <0.05.

Results

Baseline characteristics of the population

One hundred nineteen patients infected with subtype B HIV-1 were enrolled in this study. One hundred eight (90.8%) were males and 11 (9.2%) were females. Their mean age was 36.3±12 years. With respect to the mode of infection, 91 patients (76.5%) reported homo/bisexual contacts, 18 patients (15.1%) reported frequent high-risk heterosexual contacts, and five patients (4.2%) were intravenous drug users. Mother-to-child transmission was the cause of infection in three individuals (2.5%), and for two individuals (1.7%), the data regarding the mode of infection were not available. The primary HIV-1 infection (PHI) was documented in 28 out of 119 (23.5%) individuals. Twenty-four out of 28 (86%) individuals with documented PHI were diagnosed during or after the year 2003. Eighty three out of 119 (70%) patients were most probably infected in Slovenia, 22% (26/119) were infected in Western and Central Europe, and the remaining 8% (10/119) in Eastern Europe, USA, Australia, Brazil or Asia.

Identification of philogenetically significant transmission clusters

The NJ tree derived from the 119 HIV-1 subtype B *pol* sequences is presented in Figure 1. Five pairs or triplets of sequential sequences from a single patient were used as positive controls. Phylogenetic analysis revealed 14 potentially significant transmission clusters (bootstrap value ≥ 98% and branch length <0.015 nucleotide substitutions per site), including one cluster of five individuals, one of four individuals, one of three and 11 clusters of

two individuals. As shown in Figure 1, all positive controls conformed to the above mentioned criteria for the determination of a significant transmission cluster.

Characteristics of individuals within 14 transmission clusters

Viruses from 34 out of 119 (28.6%) individuals appeared within 14 transmission clusters (Figure 1). As shown in Table 1, 31 out of 34 (91%) clustered HIV-1 infected individuals were men and the majority of them (27/34; 79%) were MSM. The diagnosis of PHI was documented for 16 out of 34 (47%) individuals and all of them were MSM. Thus, within 11 out of 14 clusters, there was at least one individual with PHI. For 21 out of 26 (81%) individuals within 11 clusters with PHI, the estimated date of infection was during or after the year 2003.

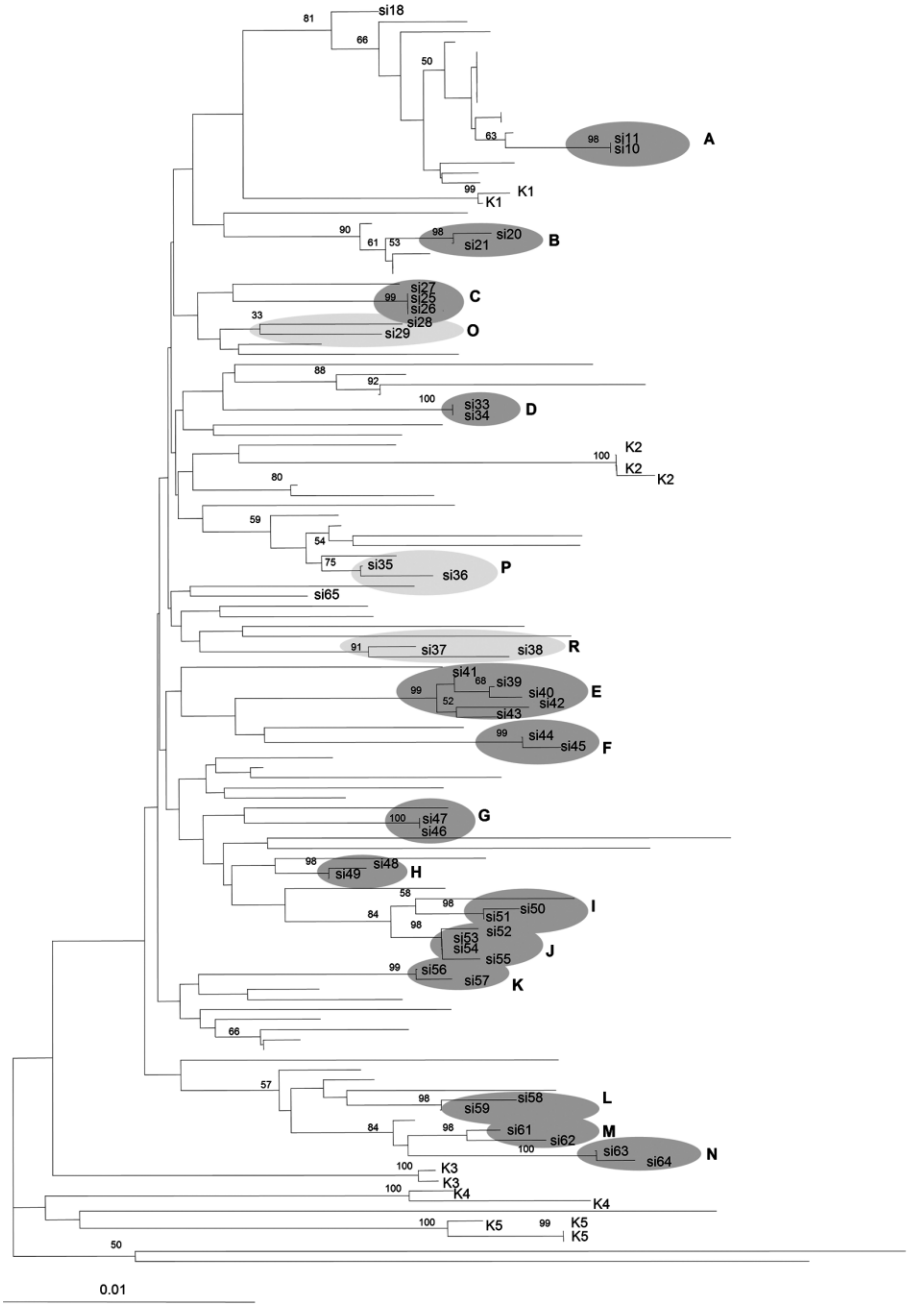

Fig. 1. Neighbor-joining phylogenetic tree based on pol sequences from 119 patients infected with subtype B. Possible transmission clusters are circled and labeled with letters A-M. Linkages confirmed by clinical and epidemiological data are indicated by letter in bold face. Five pairs or triplets of multiple sequences were used as positive controls for relatedness and are indicated by letters K1-K5 (e.g. K1 indicates multiple sequences from patient K1). Bootstrap values higher than 50% are indicated on the branches.

TABLE 1
CHARACTERISTICS OF 34 CLUSTERED HIV-1 INFECTED PATIENTS COMPARED WITH 85 NONCLUSTERED HIV-1 INFECTED PATIENTS

Characteristics	In cluster	Not in cluster	p value
Number of patients	34	85	
Male sex	31 (91%)	76 (89%)	1.000
Age at time of diagnosis (X±SD)	35±13	36±11	0.636
Homosexual risk group	27 (79%)	64 (75%)	0.812
Infection acquired in Slovenia	31 (91%)	54 (63%)	0.003
Primary HIV-1 infection	16 (57%)	12 (14%)	0.001
Recent infection (during or after year 2003)	23 (68%)	28 (16%)	0.001
Evidence of epidemiological linkage	24/34 (70%)	8 (9%)	0.0001
CD4 (cells/mm^3) (X±SD)	450±313	281±227	0.002
HIV-1 RNA (log copies/ml) (X±SD)	5.19	4.95	0.182

Therefore, as shown in Table 1, significant associations with clustering were: recent infection (HIV-1 infection during or after year 2003), diagnosis of PHI, higher CD4 cell count, and acquiring HIV infection in Slovenia (Table 1). Within clusters, similar drug resistance associated mutations (including secondary resistance mutations) were observed in 9 out of 14 clusters (Table 2). No primary drug resistance mutation was observed in the PR or in RT gene.

Epidemiology linkage and clusters

Eleven out of 14 clusters were supported by evidence of clinical and epidemiological linkage. In two clusters comprising five (cluster E) and four individuals (cluster J), the evidence of epidemiological linkage was not documented for all individuals, but only for two and three of them, respectively. Namely, within the cluster E, epidemiological information about the linkage was known only for two individuals (Si41 and Si42) diagnosed in the year 2005. The obtained epidemiological information suggests that the source (Si41) was probably infected in the year 2003, meanwhile the contact (Si42) was diagnosed in 2005 during the PHI. Both were MSM. For three individuals whose viruses appeared also within the cluster E, the epidemiological information about the linkage was previously unknown. All of them were diagnosed during the PHI in the year 2004 or 2005. Two of them were MSM and one reported high-risk heterosexual contacts.

Within another large cluster (J), the epidemiological link was documented for three out of four MSM within the cluster. Two of three individuals for whom epidemiological data existed were diagnosed during PHI in the year 2003 and the estimated date of infection for the third epidemiologically linked individual was in the year 2005. The fourth individual within this cluster was probably infected in 1996. All four patients were most probably infected in Slovenia.

After a careful review of epidemiological data, we found out that the epidemiological linkages were formally documented for four additional couples (two heterosexual and two homosexual), but these linkages were not phylogenetically confirmed. More specifically, the viruses from three epidemiologically linked couples appeared in the clusters with bootstrap values <98% (O, P and R; 33%, 75% and 91%; Figure 1). Additionally, the phylogenetic analysis revealed that the viruses of homosexual couple (Si18, Si65), for which epidemiological data about linkage existed, were clustered separately, indicating that no evolutionary relationship between the two HIV-1 strains existed.

Discussion

It has recently been shown that the HIV-1 *pol* gene sequence data obtained by routine HIV-1 resistance genotypic testing could be also utilized effectively to track the presence of transmission clusters within a geographic region from where the sequences were obtained[18,21,25–27].

Therefore, in the present study, we investigated the epidemic of HIV-1 subtype B during the 10-year period (1996–2005) in Slovenia using the phylogenetic analysis of *pol* gene sequences. In order to obtain a better understanding of HIV-1 transmission networks among the individuals infected with subtype B HIV-1 in Slovenia, 119 *pol* sequences generated on the samples dated from 1996 to 2005 were retrieved from the database of Slovenian HIV/AIDS Reference Laboratory.

The data of the present study revealed some important findings regarding the HIV-1 transmission in Slovenia. First, among 119 *pol* sequences, we identified 14 possible transmission clusters (n=34), representing mostly (79%) MSM infected with closely related viruses. These clusters are suggestive of HIV-1 transmission groups. Second, our data showed that most individuals (22/34; 64%) whose sequences appeared within the phylogenetic clusters were infected recently (during or after the year 2003), pointing out the evidence of multiple transmission clusters during the period of higher incidence. Recently, an increase in the number of newly diagnosed HIV cases was noted in Slovenia[7]. Thus, in the year 2005, there were twice as many newly diagnosed HIV cases than dur-

TABLE 2
EPIDEMIOLOGICAL AND DRUG RESISTANCE MUTATION INFORMATION FROM THE 14 CLUSTERS OF *POL* SEQUENCES

Cluster	Sequences	Year of sampling	Epid. data	Drug history	Resistance associated mutations	
					PR	RT
A	Si10	2005	yes	naive	L63P, A71T, V77I, I93L	None
	Si11	2005	yes	naive	L63P, A71T, V77I, I93L	None
B	Si20	2005	no	naive	L63V	None
	Si21	2005	no	naive	L63V	None
C	Si25	2005	yes	naive	L10I, L63P, I93L	None
	Si26	2005	yes	naive	L10I, L63P, I93L	None
	Si27	2005	yes	naive	L10I, L63P, I93L	None
D	Si33	2000	yes	naive	M36I, L63T	None
	Si34	2000	yes	naive	M36I, L63A	None
E	Si39	2004	no	naive	L63A	None
	Si40	2004	no	naive	L63A	None
	Si41	2005	yes	naive	L63A, I93L	None
	Si42	2005	yes	naive	L63A, I93L	None
	Si43	2005	no	naive	L63A, I93L	None
F	Si44	2004	yes	naive	L63P, V77I, I93L	None
	SI45	2004	yes	naive	L63P, V77I, I93L	None
G	Si46	2001	yes	naive	L63P, I93L	None
	Si47	2001	yes	naive	L63P, I93L	None
H	Si48	1999	yes	naive	L63P, I93L	None
	Si49	2000	yes	naive	M36I, L63P, I93L	None
I	Si50	2005	yes	naive	I93L	None
	Si51	2005	yes	naive	I93L	None
J	Si52	2005	no	naive	None	V179D
	Si53	2003	yes	naive	None	V179D
	Si54	2003	yes	naive	None	V179D
	Si55	2005	yes	naive	L10I, V77I	V179D
K	Si56	2004	no	naive	L63P	None
	Si57	2004	no	naive	L63P	None
L	Si58	2004	no	naive	L63P, V77I	None
	Si59	2005	no	naive	L63P, V77I	V179D
M	Si60	2002	yes	naive	L63P, V77I	None
	Si61	2002	yes	naive	L63P, V77I	None
N	Si62	2005	yes	naive	L63P, V77I, I93L	None
	Si63	2005	yes	naive	L63P, V77I, I93L	None

ing the year 2003, and the vast majority (almost 85%) were MSM. Third, importantly, the diagnosis of PHI was documented for 16 out of 34 (47%) individuals within the transmission clusters and all of them were MSM. Within 11 out of 14 transmission clusters identified, there was at least one individual with PHI, suggesting, like in some previous studies[32,33], that HIV-1 epidemic in Slovenia is driven by the transmissions occurring during early phases of HIV-1 infection, in our case, mostly among MSM.

Since the comparison with epidemiological data is important for the validation of the linkages characterized at the molecular level, the clinical and epidemiological data for 119 HIV-1 infected individuals were collected. Surprisingly, the existence of 11 out of 14 transmission clusters identified in the present study was epidemiologically confirmed. In addition, the information about the epidemiological linkage was known also for 8 individuals whose viruses failed to fulfill the arbitrary criteria of a bootstrap support ≥98% and branch length <0.015 nucleotide substitutions per site. Probably, due to within-individual evolution, the viruses of three epidemiologically linked couples (two heterosexual and one MSM) failed to fulfill the arbitrary criteria, since the sequences were generated from the plasma samples obtained over a longer time span (estimated date of infection between 1995–1997, date of collecting the plasma samples for sequences 2003–2004). The presence of multiple sexual partners often compromises the characterization of linkages between HIV-1 infected individuals. This was most probably the case in the forth couple of MSM whose viruses did

not even form the cluster. Therefore, it should be kept in mind that characterization of transmission patterns within a group of HIV-1 infected individuals might be more problematic when using the sequences collected over a long time period[18].

Furthermore, it should be stressed that, when undertaking these analysis, it is very important to distinguish between epidemiological and individual or legal purposes of studies performed[17,18].

Although our study was performed on individuals infected with the HIV-1 subtype B only, we are persuaded that the results of our study have provided a realistic insight into the complete HIV-1 epidemic and transmission patterns in Slovenia as a population of 70% (119/169) of all HIV-1 infected individuals diagnosed during the 10-year period was studied. A more complete understanding of the dynamic of the incidence of HIV-1 infection, behavioral trends in the MSM population can be very useful in predicting epidemic trends and improving HIV prevention strategies. Since in the first five months of the year 2006, no signs of decreasing nor in the number of newly diagnosed HIV-1 cases neither in the number of PHI within the population of MSM has been noted, additional and more effective HIV preventive efforts are urgently needed in Slovenia to reduce risk behavior within the groups of MSM, and the monitoring coverage of this most affected risk population should be increased.

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EPIDEMIJA I NAČINI PRIJENOSA PODTIPA B HIV-A U SLOVENIJI

SAŽETAK

U radu je prikazano istraživanje epidemije HIV-1 podtipa B u Sloveniji u posljednjih 10 godina koje temelji na filogenetskoj analizi područja pol. U analizu je bilo uključeno 119 sekvenci područja pol dobivenih od siječnja 1996. do prosinca 2005. godine, izabranih iz zbirke podataka Referentnog laboratorija za HIV/AIDS Republike Slovenije. Pomo-

ću filogenetske analize, utvrdili smo postojanje 14 genetskih porodica sa statističkom potporom ≥ 98%. U navedene porodice uvrstili smo 34 HIV/AIDS bolesnika. Među tim bolesnicima prevladavali su muškarci, a među njima bilo je 79% takvih koji imaju spolne odnose s muškim osobama. Čimbenici koji su bili statistički značajno povezani s uključivanjem u genetske porodice su: nedavna zaraza s HIV-om (prije ili za vrijeme 2003. godine), dijagnoza primarne zaraze s HIV-om, visok broj CD4+ stanica te zaraza s HIV-om u Sloveniji. Trenutna HIV epidemija u Sloveniji uglavnom je posljedica velikog broja nedavnih i/ili primarnih zaraza s podtipom B HIV-a.