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Transmitted Antiretroviral Drug Resistance in the Men Who Have Sex with Men HIV Patient Cohort, Beijing, China, 2008–2011

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Abstract

Transmitted drug resistance (TDR) is an ongoing public health problem in HIV disease treatment. However, little is known about TDR among men who have sex with men (MSM) patients in China. In addition, TDR prevalence among patients with acute HIV infection (AHI) or early HIV infection (EHI) was believed higher than that of patients with chronic HIV infection (CHI), but as AHI is typically either unidentified or crudely defined in large populations, very few direct comparisons have been made. We did a retrospective analysis of TDR in 536 antiretroviral-naive MSM patients from our immunodeficiency clinics at You'an Hospital, Capital Medical University (CMU), in Beijing, China, 2008–2011. The cohort included 266 patients with AHI/EHI and 270 patients with CHI. We analyzed the subtype, estimated the TDR prevalence, and characterized the model of TDR and the predicted drug sensitivity. Additionally, we made a comparison of TDR between the patients with AHI/EHI and patients with CHI.

Our results indicated that among the 536 patients, HIV-1 subtype CRF01_AE accounted for 52.1%, subtype B accounted for 24.8%, CRF07_BC/ CRF08_BC accounted for 21.6% (116/536), and 1.3% were denoted as unique recombinant forms (URFs). A total of 7.8% patients had one or more transmitted HIV-1 drug resistance mutations, representing 6.2% for PI-related mutations, 0.9% for NRTI-related mutations, and 1.7% for NNRTI-related mutations. Although patients with AHI/EHI had a higher TDR prevalence as compared to that of patients with CHI, the difference was not statistically significant. There was no significant difference in TDR model and predicted drug susceptibility between the two groups of patients either.

This study provides important strategic information for public health planning by healthcare officials in China and warrants a comprehensive study with larger patient cohorts from various healthcare centers within China.

Introduction

Mutations associated with drug resistance in HIV-1 can be transmitted to persons who are antiretroviral naive, called transmitted drug resistance (TDR). TDR is an ongoing public health problem all over the world, which has the potential to compromise antiretroviral therapy (ART) at the population level (1). TDR surveillance is an important strategy to monitor the emergence of genetic resistance worldwide.

Since the first HIV case was identified in 1985 in China, the HIV/AIDS epidemic has continued to increase. Epidemic estimates show that at the end of 2011, the estimated number of individuals living with HIV/AIDS in China stood at 780,000 people, with an overall prevalence of about 0.058% (2). Simultaneously, the proportion arising from homosexual transmission increased from 2.5% in 2006 to 13.7% in 2011. Unprotected anal intercourse among men who have sex with men (MSM) has become one of the major factors in the spread of HIV infection in China (2,11). However, little is known about TDR in the MSM HIV patients in China. In addition, it is believed that TDR prevalence is higher among patients with acute HIV infection (AHI) or early HIV infection (EHI) than patients with chronic HIV infection (CHI) (8,16,18), but as

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AHI is typically either unidentified or crudely defined in large populations, very few studies have been undertaken where direct comparisons have been made.

In this study, we did a retrospective analysis of TDR in ART-naive patients from our immunodeficiency clinics at You'an Hospital, Capital Medical University (CMU), in Beijing, China. The aim of our study is to characterize the TDR in our MSM naive patient cohort in Beijing 2008–2011. Furthermore, we compared TDR prevalence between the patients with AHI/EHI and those with CHI, giving us an insight into the effect of ART on TDR among this group of patients, and providing important recommendations for HIV treatment guidelines for clinicians in China.

Materials and Methods

Study population

Our study comprised totally 536 patients, including 266 patients with AHI/EHI and 270 patients with CHI. All the patients belong to the MSM cohorts at the You'an hospital, Beijing, China, between 2008 and 2011, who were enrolled in the AIDS High Risk Cohort Program clinics. This program is supported by the Beijing Science and Technology Committee (6,19). Started in October 2006, more than 2,000 MSM had been enrolled by way of introduction to each other into the longitudinal prospective cohort study. All the participants in this cohort were assessed for HIV-1 antibodies using enzyme-linked immunosorbent assay (ELISA), and HIV-1 RNA using multiplex nested polymerase chain reaction (PCR) every 2 months until HIV-1 antibodies or HIV-1 RNA showed positive results. Acute/early HIV-1 infection was defined as (a) positive HIV-1 RNA with a negative or indeterminate HIV-1 antibody test, followed by HIV sero-conversion within 6 months; or (b) a negative ELISA and Western blot (WB) less than 180 days before a documented positive ELISA or WB (7,18). If a patient was found to be infected at the beginning, he was assigned to the CHI group.

Estimated time of infection (ETI) was estimated as follows: (a) the mid-point between the last sero-negative date and the first sero-positive date; (b) 14 days prior to the date of HIV RNA turned to positive; (c) date of positive HIV antibody testing (ELISA) and indeterminate WB outcomes minus 28 days.

We enrolled patients in the study that met the following three criteria: (a) ≥ 18 years old; (b) baseline genotyping (at the date of diagnosis) was performed; (c) no ART exposure (treatment naive). Patients who were intravenous drug users (IDU) were excluded from the study.

Clinical and laboratory evaluations

Demographic information and behavioral data were collected by trained counselors using a standardized questionnaire at enrolment on HIV diagnosis date. CD4 cell count was measured at baseline and every 6 months. HIV-1 viral load (real-time RT-PCR COBASTM Ampliprep/COBASTM Taqman HIV test; Roche Diagnostics; sensitivity at 20 copies/mL) was measured at the time of diagnose in some patients.

HIV-1 subtype classification and recombination

HIV-1 subtypes were classified according to the phylogenetic analysis of the *pol* sequence (whole protease and entire part of the reverse transcriptase gene). The sequences obtained were edited by Contig Express software (Invitrogen), aligned by the BioEdit program (North Carolina State University, Raleigh, NC: www.mbio.ncsu.edu/bioedit/bioedit.html). Reference sequences representing HIV-1 genetic circulating recombinant forms obtained from the Los Alamos National Laboratory (http://hiv-web.lanl.gov) were included in the alignments. A phylogenetic tree was constructed using the MEGA program (Molecular Evolutionary Genetic Analysis Software, v5.03). The Recombinant Identification Program 3.0 (www.hiv.lanl.gov/content/sequence/RIP/RIP.html) of Los Alamos HIV database was used to verify recombinant sequences.

HIV genotype determinations and drug sensitivity prediction

The HIV genotypic resistance test was done using a published in-house method (18) that targets 1.3kb region of the *pol* gene, covering the complete protease (amino acids 1–99) and part of reverse transcriptase (amino acids 1–305) sequences. TDR was defined as the detection of one or more mutations in the last updated (March 2009) surveillance drug resistance mutations (SDRMs) listed by the World Health Organization (3). This guideline optimizes the specificity of TDR classification for epidemiologic studies by including only mutations that are rarely selected without drugs, by excluding common polymorphic mutations (includes mutations that have a prevalence of at least 1% in treated persons and omits those mutations that are $\geq 0.5\%$ in treatment-naive persons in any subtype). Specific predicted resistance to antiretroviral drugs was calculated using a code developed by Frontier Science as well as scores from the Stanford HIVDB algorithm, v6.2.0 (http://sierra2.stanford.edu/sierra/servlet/JSierra). This tool estimated inferred levels of resistance to 19 FDA-approved antiretroviral drugs. Each HIV-1 drug resistance mutation is assigned a drug penalty score and a comment. Using the total drug score, the program reports one of the following levels of inferred drug resistance: susceptibility, potential low-level resistance, low-level resistance, intermediate resistance, and high-level resistance. Only ''intermediate resistance'' and ''high-level resistance''—that is, as score of ≥ 30—were considered to be resistant to a certain kind of drug in our study.

Ethics statement

Informed consent was obtained from all study participants for the collection of blood samples and subsequent analyses, and the study was approved by the institution's ethical committee of You'an Hospital.

Statistics

Prevalence of TDR was calculated as the number of patients with detectable SDRMs divided by the number of all patients with an available genotype. Confidence intervals (CI) for proportions were calculated using a 95% Wilson confidence interval for binomially distributed data. All statistical analyses were conducted using SPSS v14.0 software (SPSS, Inc., Chicago, IL). We used the chi-square test for comparing categorical data. Differences were considered statistically significant when $p < 0.05$.

Results

Patients' characteristics

A total of 536 patients, including 266 patients with AHI/EHI and 270 patients with CHI, were enrolled into this study between 2008 and 2011. Subjects, all resided in Beijing, had never been exposed to any kinds ART. All subjects were of Han ethnicity, except one patient with AHI/EHI, who was Xinjiang Uygur. One hundred and seventy-one patients (31.9%) had heterosexual contact at the same time as homosexual contact, but 153 (89.5%) of their female partners were negative at the time of diagnosis. The general characteristics of all the patients included in the analysis are shown in Table 1. Briefly, the median age of the patients was 30 years, which was similar between the two groups. The group of patients with AHI/EHI presented a median of 30 days (range, 17 to 50 days) after their EDI at diagnosis. Only 116 of the 270 patients with CHI tracked their approximate time of infection, with a median of 2 years (range 1–5 years). The median CD4 cell count of the AHI/EHI patients was 451.3 ± 191.6 cells/mm^3. The median CD4 cell count of the CHI patients was 365.6 ± 187.8 cells/mm^3 ($p < 0.001$). The viral load of the patients with AHI/EHI was 4.7 ± 1.0 $\log_{10}$ copies/mL. The viral load of the patients with CHI was 4.9 ± 0.9 $\log_{10}$ copies/mL.

Subtype

About half of the patients were identified to be CRF01_AE ($n = 279$, 52.1%). About one quarter of patients were identified as subtype B ($n = 133$, 24.8%), and the remaining were subtype CRF07_BC or CRF08_BC ($n = 116$, 21.6%). Additionally, seven patients (1.3%) were denoted as unique recombinant forms (URFs), consisting of a recombination of A, G, and J. The subtype's distribution was comparable between patients with AHI/EHI and patients with CHI. (CRF01_AE, 54.7% vs. 49.6%, $p = 0.258$; subtype B, 26.0% vs. 23.7%, $p = 0.484$; CRF07_BC or CRF08_BC, 18.4% vs. 24.8%, $p = 0.072$; URFs, 0.8% vs. 1.9%, $p = 0.262$).

Prevalence of TDR

According to the SDRMs listed by the World Health Organization, a totally of 42 patients had one or more transmitted HIV-1 drug resistance mutation (see Table 2), representing a 7.8% [95% CI 5.7–10.5%] overall prevalence of TDR. TDR to nucleoside reverse transcriptase inhibitors (NRTIs) and non-nucleoside reverse transcriptase inhibitors (NNRTIs) were identified among five (0.9% [95% CI 0.3–2.2%]) and nine (1.7% [95% CI 0.8–3.3%]) of the patients respectively. However, the prevalence of TDR to protease inhibitors (PIs) was found in 33 (6.2% [95% CI 4.3–8.6%]) patients. The majority of the patients with TDR displayed a single drug class resistance mutation (39 out of 42 TDR patients, representing 7.3% in the entire cohort). However, there was only one (0.2%) patient in CHI group with TDRs to two classes of antiretroviral drugs (L74V + Y188H), and two (0.4%) patients with TDRs to three classes of antiretroviral drugs (one patient in the AHI/EHI group, T215S + Y188L + L90M; one patient in the CHI group, T215S + Y188L + L90M).

Patients with AHI/EHI had a slightly higher total prevalence of TDR (8.3% [95% CI 5.2–12.3%]) compared to that of patients with CHI (7.4% [95% CI 4.6–11.2%]), although the difference was not statistically significant ($p = 0.710$). NRTIs, NNRTIs, and PIs were identified among 1.1%, 1.9%, and 6.0% of the patients with AHI/EHI respectively, which were all similar to the NRTI, NNRTI, and PI TDR prevalence of 0.7% ($p = 0.641$), 1.5% ($p = 0.720$), and 6.3% ($p = 0.892$) respectively in the patients with CHI.

The pattern of TDR

Among all the patients harboring resistant mutations, the most common TDR mutations were PI-associated mutations (Table 3): RP position M46L/I mutation, which decreases susceptibility to nelfinavir (NFV), was found in 23 patients (4.3%), including 12 (4.5%) AHI/EHI patients and 11 (4.1%) CHI patients. The difference was not significant. Other rare TDR mutations included protease reverse L90M (0.6%), I84V (0.4%), F53L (0.2%), L76V (0.2%), G73S (0.2%), and N88S (0.2%); NRTIs associated reverse transcriptase (RT) position T215 revertants (0.6%), K219Q (0.2%), L74V (0.2%); and NNRTIs associated RT position Y188L/S (0.7%), Y181C (0.4%), V106M (0.4%), K101E (0.2%). There was no significant difference in TDR pattern between the two groups of patients.

Table 1. General Characteristics of 536 Antiretroviral-Naive Men Who Have Sex with Men HIV Patients, Including 266 Acute and 270 Chronic HIV-1 Infected Patients in You'an Hospital, Beijing, China

	Total (n = *536*)	*AHI/EHI* (n = *266*)	*CHI* (n = *270*)	p-*Value*
Age at genotype testing				
Mean ± *SD*	31.7 ± 8.4	31.8 ± 8.7	31.6 ± 8.1	0.767
Subtype				
CRF01_AE	279 (52.1)	145 (54.7)	134 (49.6)	0.258
B	133 (24.8)	69 (26.0)	64 (23.7)	0.484
CRF07_BC or CRF08_BC	116 (21.6)	49 (18.4)	67 (24.8)	0.072
URFs	7 (1.3)	2 (0.8)	5 (1.9)	0.262
Estimated time of infection days, mean (IQR)		30 (17–50)		
CD4 cell count (cells/mm^3)				
Mean ± *SD*		451.3 ± 191.6	365.6 ± 187.8	< 0.001
Viral load ($\log_{10}$ copies/mL)				
Mean ± *SD*		4.7 ± 1.0*	4.9 ± 0.9**	0.394

*$n = 154$; **$n = 50$.

AHI/EHI, patients with acute or early HIV infection; CHI, patients with chronic HIV infection; IQR, interquartile range; URFs, unique recombinant forms.

Table 2. Prevalence of Transmitted Drug Resistance Among 536 Antiretroviral-Naive MSM HIV Patients, Including 266 Acute and 270 Chronic HIV-1 Infected Patients in You'an Hospital, Beijing, China

	Total (536)		*AHI/EHI (266)*		*CHI (270)*		
	n	*% [95% CI]*	n	*% [95% CI]*	n	*% [95% CI]*	p-*Value*
Any class	42	7.8 [5.7–10.5]	22	8.3 [5.2–12.3]	20	7.4 [4.6–11.2]	0.710
NRTI	5	0.9 [0.3–2.2]	3	1.1 [0.2–3.3]	2	0.7 [0.1–2.7]	0.641
NNRTI	9	1.7 [0.8–3.3]	5	1.9 [0.6–4.4]	4	1.5 [0.4–3.8]	0.720
PI	33	6.2 [4.3–8.6]	16	6.0 [3.5–9.6]	17	6.3 [3.7–10]	0.892
Single class	39	7.3 [5.2–9.9]	21	7.9 [5.0–11.9]	18	6.7 [4.0–10.4]	
Two classes	1	0.2 [0–1.1]	0	0	1	0.4 [0–2.2]	
Three classes	2	0.4 [0–1.5]	1	0.4 [0–2.6]	1	0.4 [0–2.2]	

MSM, men who have sex with men; NRTI, nucleoside reverse transcriptase inhibitor; NNRTI, non-nucleoside reverse transcriptase inhibitor; PI, protease inhibitors; single-, two-, or three-class resistance is defined as one or more TDR within one, two, or three antiretroviral drug classes, respectively.

Drug susceptibility

Based on the Stanford HIVdb algorithm, drug susceptibility was possibly significantly reduced in 13 patients (2.4%). There was no significant difference between AHI/EHI and CHI patients (2.3% vs. 2.6%, $p = 0.800$; Table 4). There was no case with mutations conferring resistance to NRTIs, except for one (0.2%) case among CHI patients, who was predicted to be intermediately resistant to abacavir (ABC). When NNRTI mutations were present in eight (1.5%) patients, most of them were predicted to have intermediate to high-level resistance to efavirenz (EFV; $n = 7$, 1.3%) and nevirapine (NVP; $n = 6$, 1.1%). About half of them also were predicted to be resistant to rilpivirine (RPV; $n = 4$, 0.7%). Seven patients (1.3%) were predicted to be intermediate or high-level resistant to PI, and the patients tended to be resistant to SQV/r (5, 0.9%), FPV/r (3, 0.6%), and ATV/r (3, 0.6%). All the subjects remained susceptible or had only a potential low-level resistance to DRV/r and LPV/r. There was no significant difference in predicted drug susceptibility between the two groups of patients.

Discussion

TDR as an inevitable outcome of ART has important clinical and public health implications, and presents in 10–20% (5) of new HIV-1 infections worldwide. Western countries usually have a higher prevalence of TDR than China due to the fact that ART was first introduced in these countries and patients there have been subject to more prolonged periods of ART. The overall TDR prevalence in the United States was reported to be as high as 14.6% (16). ART was scaled up in 2003 in China. The HIV drug resistance (HIVDR) Surveillance Network of China reported that TDR was low (<5%) to all drug classes used since 2007, except for one study that showed moderate (5–15%) rates of transmitted PIs in 2009 (12). The TDR rate in naive MSM patients in the Liaoing province in China was reported to be 4.5%, representing 4.5% for PI-related mutations, 0.5% for NRTI-related mutations, and 0.5% for NNRTI-related mutations (201 patients, 2003–2009) (19). Another study by Lin Li *et al.* reported a TDR rate of 5.3% among naive MSM patients in Beijing (95 patients, 2007–2010) (13). However, in

Table 3. Pattern of TDR Among 536 Antiretroviral-Naive MSM HIV Patients, Including 266 Acute and 270 Chronic HIV-1 Infected Patients in You'an Hospital, Beijing, China

		Total (536)		*AHI/EHI (266)*		*CHI (270)*	
	Mutations	n	*%*	n	*%*	n	*%*
NRTI	T215S	3	0.6	2	0.8	1	0.4
	K219Q	1	0.2	1	0.4	0	0
	L74V	1	0.2	0	0	1	0.4
NNRTI	Y188L/S	4	0.7	2	0.8	2	0.8
	Y181C	2	0.4	1	0.4	1	0.4
	V106M	2	0.4	1	0.4	1	0.4
	K101E	1	0.2	1	0.4	0	0
PI	M46L/I	23	4.3	12	4.5	11	4.1
	L90M	3	0.6	2	0.8	1	0.4
	L76V	1	0.2	1	0.4	0	0
	G73S	1	0.2	1	0.4	0	0
	I84V	2	0.4	0	0	2	0.8
	N88S	1	0.2	0	0	1	0.4
	F53L	1	0.2	0	0	1	0.4

Table 4. Prevalence of Predicted Intermediate or High-Level Resistance to DHHS Recommended Starting Drugs According to Stanford HIVDB 5-Point Resistance Scale Among 536 Antiretroviral-Naive MSM HIV Patients in You'an Hospital, Beijing, China

Resistant to	*Total* n *(%)*	*AHI/EHI* n *(%)*	*CHI* n *(%)*	p-*Value*
Any drug	13 (2.4)	6 (2.3)	7 (2.6)	0.800
NRTIs	1 (0.2)	0	1 (0.4)	0.320
3TC/FTC	0	0	0	
ABC	1 (0.2)	0	1 (0.4)	
AZT	0	0	0	
TDF	0	0	0	
NNRTIs	8 (1.5)	4 (1.5)	4 (1.5)	0.983
EFV	7 (1.3)	3 (1.1)	4 (1.5)	
NVP	6 (1.1)	2 (0.8)	4 (1.5)	
RPV	4 (0.7)	2 (0.8)	2 (0.7)	
PIs	7 (1.3)	3 (1.1)	4 (1.5)	0.718
LPV/r	0	0	0	
DRV/r	0	0	0	
FPV/r	3 (0.6)	1 (0.4)	2 (0.7)	
ATV/r	3 (0.6)	0	3 (1.1)	
SQV/r	5 (0.9)	2 (0.8)	3 (1.1)	

The Stanford HIVDB algorithm estimated inferred levels of resistance to 19 FDA-approved antiretroviral drugs. Each HIV-1 drug resistance mutation is assigned a drug penalty score and a comment. Using the total drug score, the program reports one of the following levels of inferred drug resistance: (i) 0 to 9, Susceptible, no evidence of reduced susceptibility compared with wild type; (ii) 10 to 14, Potential low-level resistance. The virus is likely to be fully susceptible yet it contains mutations that may be indicative of previous exposure to the ARV class of the drug; (iii) 15 to 29, Low-level resistance. Virus isolates of this type have reduced *in vitro* drug-susceptibility and/or patients with viruses of this genotype may have a suboptimal virologic response to treatment compared with the treatment of a wild type virus; (iv) 30 to 59, The genotype suggests a degree of drug resistance greater than low-level resistance but lower than high-level resistance; (v) $>=60$, the genotype is similar to that of isolates with the highest levels of *in vitro* drug resistance and/or patients infected with isolates having similar genotypes generally have little or no virologic response to treatment with the drug.

DHHS, Department of Health and Human Services.

our study, there was a TDR prevalence of 7.8% among naive Beijing MSM patients between 2008 and 2011, representing 6.2% for PI-related mutations, 0.9% for NRTI-related mutations, and 1.7% for NNRTI-related mutations. Although the prevalence was still <5% to all drug classes except for PI, it was still higher than the results of the previous studies. The discrepancies among different studies may be caused by the differences in the study populations, and different drug-resistant mutation lists used to interpret resistance data.

We found that with respect to the pattern of TDR, the most common mutation was RP position M46L/I mutation, which only slightly decreases susceptibility to IDV/r, NFV, FPV/r, LPV/r, and ATV/r. All of the patients with M46L/I mutation belonged to CRF01_AE subtype, except one patient in the AHI/EHI group who belonged to the CRF07_B/C subtype. On the contrary, TDR related to NNRTI and NRTI were much less frequent. Previous studies had similar findings (12,13,19). Lin Li *et al.* found four cases carrying a TDR mutation in 76 strains among Beijing MSM patients. All four cases were M46I mutations, and all of them belonged to CRF01_AE strains (13).

The SDRM list optimizes the specificity of TDR classification by including only nonpolymorphic mutations (3). Nonpolymorphic mutations were defined as mutations present at a frequency of ≤0.5% in ART-naive individuals infected with subtypes for which >1,000 sequences were available in the data set. M46L mutation had been excluded from the previous SDRM list as a common polymorphic mutations, but as more data became available, the newest SDRM list retained M46L/I mutation in the TDR list. Examination of the CRF01_AE sequences with M46I revealed no evidence for sequence artifact or epidemiological clustering. Furthermore, M46I has been reported to disrupt recognition of the HLA-A2-restricted epitope KMIGGIGGFI encompassing protease positions 45 to 54. It reduces susceptibility to several PIs even in the absence of other SDRMSs (3). Our study found a much higher prevalence of M46L/I mutation in CRF01_AE strains compared with other mutations among MSM patients, which indicates the need for further study for the sake of the clinical implications for this group of patients.

It is believed that TDR prevalence is higher among patients with AHI or EHI than patients with CHI based on the assumption that some mutations can be reversed to wild type without ART exposure (15,17).

It was reported that AHI patients had more than twice the prevalence of TDR compared to CHI patients (17), while other studies observed the reversal of some mutations (9,15). Although there was a higher TDR prevalence among patients with AHI/EHI than patients with CHI in our study, the difference was not significant. The TDR model and prevalence in patients who were predicted to be intermediate or high-level resistant to Department of Health and Human Services (DHHS) recommended starting drugs (according to the Stanford HIVDB 5-point resistance scale) were comparable too.

It was confirmed that, without the drug selection pressure, wild type HIV will reappear rapidly in patients with secondary resistance (10). But such a rapid shift of TDR is unlikely after transmission to a new host. Because of the ''genetic bottleneck,'' most HIV infections are initiated by a single variant (14). This means that wild type virus is rarely co-transmitted with drug-resistant variants; there is no ''memory'' of the original wild type in a new host. After transmission,

a novel starting point for viral evolution is created: nucleotide changes in the quasi species are modulated by chance and will be selected only if they have a beneficial effect on viral fitness. In our previous study (4), we observed 10 acute/recently infected patients longitudinally for 24–51 months where, in addition to calculating the replacement rate of TDR measured by bulk population sequencing, we used high-throughput sequencing (Illumina) to quantify the variation of each TDR mutations during the follow-up. As a result, only 1 of 12 baseline TDR mutations was found to be replaced by wild type, although the number of absolute copies of all mutations tended to decline during the follow-up. These data suggest that the reverse of TDR-related mutations do exist, but only occasionally and slowly, and the difference in TDR prevalence between AHI/EHI and CHI patients might be seen in a larger study population.

At present, DHHS suggested HIVDR testing for individual patients after diagnosis as routine care. The study of TDR among new cases of HIV infection in China provides important strategic information for public health planning. Specifically, it provides information to support selection of prevention of mother-to-child transmission regimens, pre- and postexposure prophylaxis, and future first-line ART. In addition, as naive patients are an important media to transmit HIV TDR, this TDR study indirectly provides information about the success of HIV prevention programs in limiting the spread of new infections.

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Author Disclosure Statement

No competing financial interests exist.

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