

## COHORT PROFILE

# Cohort Profile: The PharmAccess African (PASER-M) and the TREAT Asia (TASER-M) Monitoring Studies to Evaluate Resistance—HIV drug resistance in sub-Saharan Africa and the Asia-Pacific

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## How did the study come about?

According to World Health Organization (WHO) estimates, 33.4 million people were infected with the human immunodeficiency virus (HIV) type 1 globally at the end of 2008.<sup>1</sup> Sub-Saharan Africa and Asia are the two regions that have the highest HIV prevalence, with 22.4 and 4.7 million people infected, respectively.<sup>1</sup> During the 5 years prior, access to combination

antiretroviral therapy (ART) in low- and middle-income countries increased 10-fold to reach 4 million people, providing coverage to 28% of those in need.<sup>2</sup> Several studies have reported significant reductions in HIV-related morbidity and mortality for individuals with access to treatment in these regions.<sup>3–5</sup> In resource-limited settings, to facilitate the rapid expansion of access to ART, WHO recommends a standardized, public-health approach.<sup>6</sup> This is in contrast to

the individualized patient-management strategies in developed countries, based on routinely available diagnostic monitoring.<sup>7</sup> Standardized first-line ART regimens consist of a non-nucleoside reverse transcriptase inhibitor (NNRTI) and a dual nucleoside/nucleotide reverse transcriptase inhibitor (NRTI) backbone, available in some countries as generic fixed-dose combinations.<sup>6</sup> Recommended second-line regimens combine a ritonavir-boosted protease inhibitor (PI) with two previously unused and/or recycled NRTIs.<sup>6</sup>

Routine HIV viral-load monitoring is not generally available in resource-limited countries and treatment failure is frequently identified based on immunological definitions and/or the occurrence of clinical events.<sup>6</sup> Virological breakthrough may be detected late while the failing regimen is continued, thus facilitating the acquisition and accumulation of drug resistance-associated mutations.<sup>8</sup> Drug-resistant HIV variants may compromise the effectiveness of subsequent lines of treatment and their transmission to newly infected individuals has severe public health consequences.<sup>9,10</sup> To date, ART programmes have been implemented without accompanying HIV drug resistance (HIVDR) monitoring. Monitoring studies are hampered by the lack of a molecular laboratory infrastructure required for genotypic resistance testing, logistical challenges related to maintaining specimen integrity in remote settings and the high costs of testing.<sup>11</sup> Challenges to scaling up ART in resource-limited countries, such as absence of routine virological monitoring and limited choices of drug regimen, advocate for the development of a global public-health framework to monitor and prevent the emergence of HIVDR and thus maximize long-term ART effectiveness.<sup>12</sup>

HIV-1 subtype B is the predominant viral subtype in North America, Western Europe and Australia, and antiretroviral (ARV) drugs have been developed on this subtype. However, in sub-Saharan Africa and Asia, the genetic diversity in HIV subtypes and circulating recombinant forms (CRFs), resulting from recombination between subtypes within a dually infected person, is extensive.<sup>13</sup> Although current evidence is limited, some reports have suggested that the propensity to develop HIVDR and the spectrum of mutations that emerge during drug selective pressure, may differ across subtypes and CRFs.<sup>14–17</sup> Viral heterogeneity may, therefore, have implications for rates of disease progression and patient response to ART, warranting further study of inter-subtype differences in mutational pathways to resistance.

To help assess the extent of HIVDR in sub-Saharan Africa and Asia, a collaborative bi-regional programme was established, called LAASER [Linking African and Asian Societies for an Enhanced Response (LAASER) to HIV/AIDS; <http://www.laaser-hiv aids.org>] with the primary aim of increasing regional capacities for the monitoring of HIVDR. PharmAccess Foundation, a non-profit organization dedicated to the strengthening

of health systems and improving access to quality basic health care in sub-Saharan Africa, has developed the PharmAccess African Studies to Evaluate Resistance (PASER). TREAT Asia (Therapeutics, Research, Education and AIDS Training in Asia) is a network of clinics, hospitals and research institutions working to ensure safe and effective delivery of HIV/AIDS treatment throughout the Asia-Pacific and has developed the TREAT Asia Studies to Evaluate Resistance (TASER). Both PASER and TASER programmes incorporate a monitoring and evaluation (M) and a surveillance (S) protocol. Laboratories providing genotyping results for PASER and TASER are required to participate in the TREAT Asia Quality Assurance Scheme (TAQAS), which is an ongoing assessment programme to build genotyping laboratory capacity, described elsewhere.<sup>18</sup> The focus of this cohort profile is the monitoring and evaluation protocols, PASER-M and TASER-M.

## How are PASER and TASER set up and how are they funded?

Through the LAASER programme, PASER and TASER receive financial support from the Dutch Ministry of Foreign Affairs through a partnership with Stichting Aids Fonds, PharmAccess Foundation, TREAT Asia (a programme of amfAR, The Foundation for AIDS research) and International Civil Society Support. PASER-M is coordinated by PharmAccess Foundation, in collaboration with the Amsterdam Institute for Global Health and Development (AIGHD) and the Virology Department at the University Medical Center Utrecht, The Netherlands. TASER-M is coordinated by TREAT Asia and its statistical and data management centre is the National Centre in HIV Epidemiology and Clinical Research (NCHECR), The University of New South Wales in Sydney, Australia.

PASER constitutes a newly established collaboration between HIV treatment clinics, laboratories with the capacity to perform genotypic sequencing and research centres. Thirteen clinical sites and two reference laboratories in six African countries (Kenya, Nigeria, South Africa, Uganda, Zambia and Zimbabwe) are collaborating on PASER-M (Figure 1a). Details of the PASER-M collaborating clinical sites are summarized in [Supplementary Table 1](#) available as [Supplementary data](#) at *IJE* online. Ethics approvals were obtained from the Academic Medical Center Institutional Review Board (IRB) and local IRBs. Sites are government, non-government, faith-based or private clinics and hospitals, situated in major cities or urban areas. ART was introduced at the sites at various time points between 1992 and 2006 (median: 2004). Of the 13 sites, 11 provided drugs, consultations and routine laboratory testing free of charge. HIV viral load testing is available at 8 of the 13 sites.

TASER collaborating sites are selected from within the existing TREAT Asia network, based on their laboratory capacity to perform genotypic sequencing, as described elsewhere.<sup>18,19</sup> Sites that do not have internal laboratory genotyping capacity can participate through collaboration with a TAQAS-certified laboratory. Eleven clinical and laboratory sites in six Asian countries (China, Indonesia, Malaysia, Philippines, South Korea and Thailand) are collaborating on TASER-M (Figure 1b). Ethics approvals were obtained from local IRBs having Federal wide Assurances (FWAs) in place from the United States Office for Human Research Protections. FWAs are required for TASER sites as they participate in the International Epidemiologic Databases to Evaluate AIDS (IeDEA) initiative, described elsewhere.<sup>20</sup> Sites are generally government- or university-based clinics and hospitals or private clinics, situated in major cities and other urban areas. Those with ethics approvals prior to June 2010 are shown in Figure 1b. ART has been available in Asia for more than 10 years, even in less-resourced countries in the region, and all TASER-M clinical sites have on-site viral load testing.

Clinical sites follow their national guidelines to assess eligibility for ART initiation in accordance with the WHO recommendations.<sup>6</sup> Genotypic resistance testing on PASER and TASER clinical specimens are performed in TAQAS-certified genotyping laboratories.<sup>18</sup> Laboratories are encouraged to become accredited members of the WHO/HIVResNet HIV Drug Resistance Laboratory network.<sup>21</sup> Population-based nucleotide sequencing of the HIV protease (PR) and partial reverse transcriptase (RT) gene regions is performed on plasma specimens, which have HIV RNA of more than 1000 copies/ml. Plasma is obtained from blood collected in EDTA tubes which is locally stored at  $-80^{\circ}\text{C}$  and, if required, batch-shipped on dry ice to a genotyping laboratory.

PASER-M genotypic testing is concentrated in two central reference laboratories and thus depends on a robust cold-chain and web-based specimen tracking system for managing specimen shipments. Approximately half of TASER-M clinical sites have an on-site or local genotyping laboratory. Most genotyping laboratories amplify viral sequences using in-house methods, based on assembled commercially available assay components and laboratory-specific sequencing and amplification primers. One TASER laboratory uses the commercial kit TruGene (Bayer HealthCare, Tarrytown, NY, USA). The online Stanford interpretation system is used by most laboratories to identify drug resistance-associated mutations.<sup>22</sup> Resistance genotyping is generally performed retrospectively (i.e. not real-time) for all participants. Details of the genotyping laboratories are summarized in [Supplementary Table 2](#) available as [Supplementary data](#) at *IJE* online. PASER and TASER sequences are submitted to the ViroScore database (Advanced Biological Laboratories SA, France) for data storage.

## What do PASER-M and TASER-M cover and who is included in the sample?

The monitoring studies are multi-centre prospective cohort designs with sequential patient enrolment. Patient eligibility criteria are listed in Table 1. The main study objectives are to assess prevalence and incidence of HIVDR, mutational patterns and factors associated with HIVDR in persons initiating first-line ART or switching to a second-line regimen due to treatment failure under routine circumstances. Participants are required to sign informed consent prior to study enrolment and must initiate or switch ART within 30 days (PASER-M) or 181 days (TASER-M) following baseline specimen collection. Regimen switch due to treatment failure may be determined clinically, as assessed by disease progression, immunologically, by CD4 cell count or virologically, by HIV viral load. A single drug substitution, due to toxicity or intolerance, is not considered a regimen switch. Each site aims to recruit a total of 240 participants. Second-line participants are recruited among first-line participants failing therapy and the clinical site patient population. The recommended maximum site-specific enrolment period is 18 months.

## How often are participants followed-up? What data are being collected?

Participants are followed-up as per local standard of care guidelines. The frequency of follow-up visits for patients varies by site (range: every 1–6 months). The studies make use of clinical data collected during routine visits and recorded in medical records. HIV viral load measurement and, if the HIV RNA value is more than 1000 copies/ml, genotypic resistance testing is performed on plasma specimens taken at baseline, prior to regimen switch due to treatment failure and at annual follow-up. For patients failing a first-line regimen, the treatment failure data collection becomes the new baseline for the second-line regimen. Annual follow-up is then calculated from this point. For patients failing a second-line ART, the treatment failure data collection is the final assessment prior to the patient going off study.

PASER-M clinical data are recorded on standardized hard-copy data forms, which are completed at 3-monthly intervals and entered in a web-based clinical data system, called the HAART Monitoring System. PharmAccess performs quality assurance measures, which include (i) source data verification during 3- to 6-monthly site audits, (ii) checks to identify data entry inconsistencies or suspect data values and (iii) specimen tracking. TASER-M site personnel extract clinical data from site databases and medical

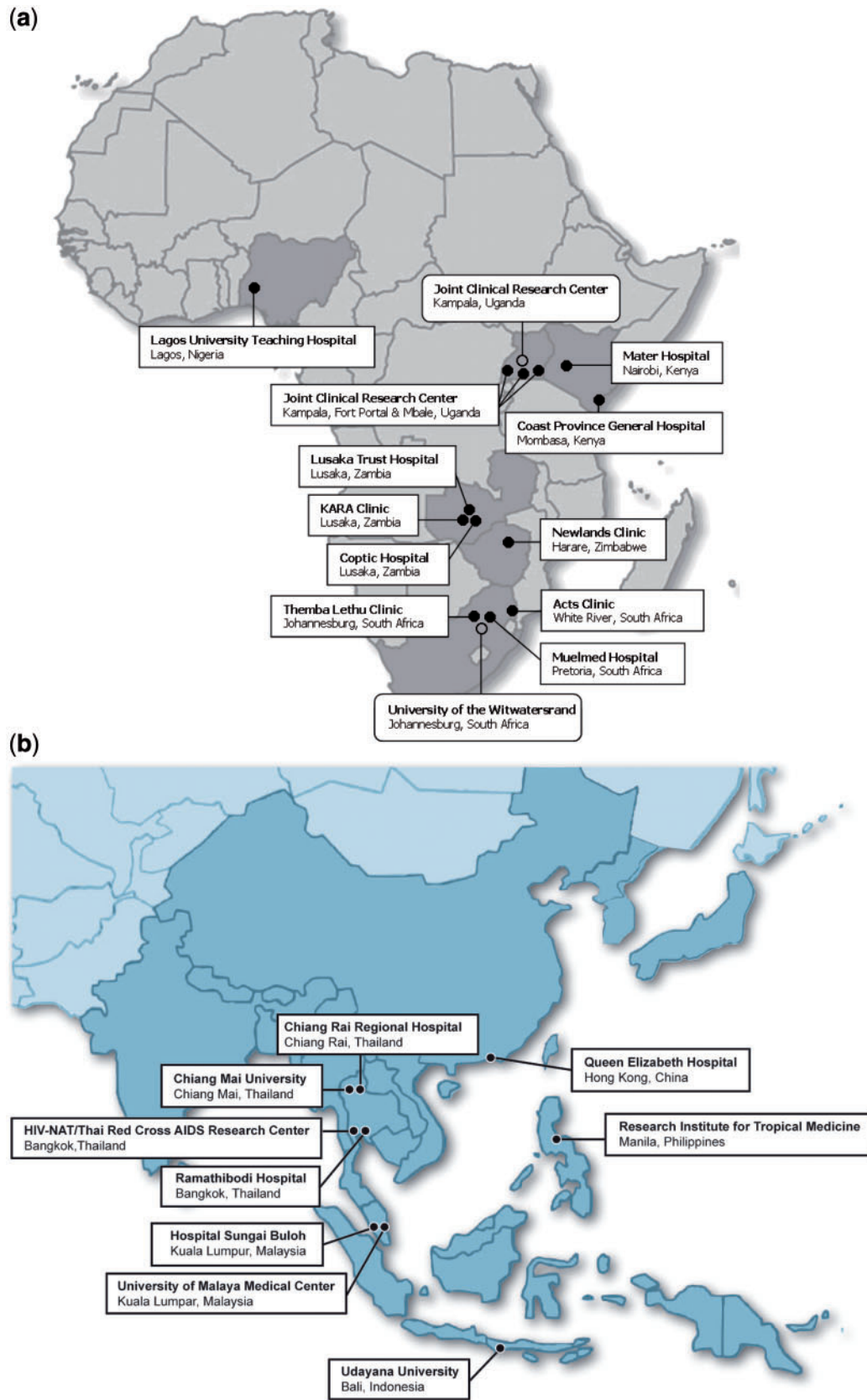


Figure 1 Geographical location of (a) PASER-M collaborating sites and (b) TASER-M collaborating sites

**Table 1** Patient eligibility criteria for PASER-M and TASER-M**Inclusion criteria**

- Confirmed HIV-1 infection
- ≥18 years of age
- Eligible<sup>a</sup> for initiation of a first-line ART regimen or switch from a first-line ART regimen (containing at least three antiretroviral drugs and taken for ≥6 months) to a second-line ART regimen due to virological, immunological and/or clinical failure
- Signed informed consent for study participation prior to enrolment

**Exclusion criteria**

- Currently taking ART (minimum of three-drug regimen), if initiating a first-line ART regimen<sup>b</sup>
- Pregnancy at enrolment<sup>c</sup>
- HIV-1/2 dual infection (in endemic countries only)<sup>c</sup>

<sup>a</sup>Eligibility for ART initiation defined in accordance with national ART guidelines (i.e. advanced immunodeficiency as defined by CD4 cell count less than 200 or less than 350 cells/ $\mu$ l, or advanced clinical disease according to WHO clinical stage/CDC classification).

<sup>b</sup>Specified PASER-M definition: re-initiation of a first-line ART regimen <30 days after stopping previous first-line ART (previous use of antiretroviral prophylaxis or mono/dual therapy is not an exclusion criterion).

<sup>c</sup>Exclusion criteria applicable to PASER-M only.

records collected as part of usual care. From March 2008 to March 2009, TASER-M data were submitted electronically to NCHCECR on a quarterly basis, as part of study start up, then at 6-monthly intervals. At each transfer, NCHCECR performs quality assurance measures, which include (i) checks to identify data entry inconsistencies or suspect data values, (ii) specimen tracking and (iii) ARV history completeness. Annually, a random 10% of TASER-M patients are selected for internal site audit where submitted data are compared with patient medical records.

The studies capture standardized virological and genotypic data at protocol determined intervals. Genotyping data consist of HIV subtype and HIVDR mutations, including insertions and deletions. TASER-M also records discordant subtypes, i.e. when the PR and RT region subtypes differ. Laboratory specimen tracking information is recorded during specimen processing, allowing assessment of pre-analytical and assay validity. Genotyping laboratories complete an annual laboratory survey that includes the dynamic range of the virological assay used, the regions of PR and RT genome routinely sequenced and the interpretation algorithm used. Observational patient data includes demographic parameters, physical measures, Centres for Disease Control and Prevention (CDC) class (TASER-M) or WHO clinical stage (PASER-M), serology of hepatitis and syphilis (TASER-M), opportunistic infections,

current ART regimen, ARV history, concomitant medications, routine laboratory parameters (including CD4 counts) and assessment of drug adherence. Main analyses will include age, sex, ethnicity, HIV exposure category, WHO clinical stage (PASER-M) or CDC class (TASER-M), viral hepatitis co-infection status, CD4 count, HIV viral load, HIV subtype, drug adherence, ARV history and ART regimen as covariates. Predictors of drug resistance will be assessed using logistic regression models. Incidence of drug resistance will be summarized using person-years methods and Kaplan–Meier plots. Cox proportional hazards models will be used to assess risk factors associated with developing drug resistance.

**What is the anticipated attrition?**

The actual attrition in PASER-M and TASER-M cannot currently be accurately estimated because the duration of follow-up in the databases is still limited. In sub-Saharan Africa patient retention in routine ART programmes has been estimated at 61.6<sup>23</sup> to 66.8%<sup>2</sup> at 24 months on ART, attrition being mainly due to loss of follow-up and early death.<sup>23</sup> Therefore, in PASER-M, the original site-specific sample size was calculated accounting for 20% loss to follow-up and 25% mortality after 24 months. Attrition is expected to vary between sites as a result of differences in patient populations, care provided and provisions for tracing lost to follow-up. TASER-M sites are generally sourced from the ongoing TREAT Asia HIV Observational Database (TAHOD).<sup>19</sup> Loss to follow-up for TAHOD was 6.9/100 person-years for the 12-month period from September 2007 to September 2008. Since TASER-M monitors specified outcomes, we speculate that TASER-M follow-up will be similar to TAHOD or better.

**What has been found?****PASER-M**

Patient recruitment commenced in March 2007 and was completed in September 2009. Of the 13 sites, 12 reached the site-specific target of 240 participants, enrolling a total of 3005 participants. Excluding patients with protocol violations ( $n = 16$ ) and key data missing ( $n = 4$ ), 2985 patients were included in the analysis. Of these, 2736 (91.6%) were eligible for a first-line ART regimen and 249 (8.3%) were eligible for second-line ART due to treatment failure. Patient characteristics are summarized in Table 2. For first-line patients, the median age was 36.8 years [inter-quartile range (IQR) 31.3–42.6] and 58% were women. HIV exposure was predominantly reported as heterosexual contact. More than 60% had advanced disease (classified as WHO stages III or IV) and 37% had pre-therapy CD4 counts of less than 100 cells/ $\mu$ l. Across all 13 sites, median baseline CD4 counts of

**Table 2** Baseline patient characteristics, by region and line of ART

	Total	PASER-M (Africa)				TASER-M (Asia)			
		Initiation of first-line ART <sup>a</sup>		Switch to second-line ART <sup>b</sup>	Initiation of first-line ART <sup>a</sup>		Switch to second-line ART <sup>b</sup>		
		ARV-naive	ARV-experienced <sup>c</sup>		ARV-naive	ARV-experienced <sup>c</sup>			
Patients, <i>n</i> (%)	3713	2598 (87.0)	138 (4.6)	249 (8.3)	693 (95.2)	10 (1.4)	25 (3.4)		
<b>Sex</b>									
Female, <i>n</i> (%)	1988 (53.5)	1494 (57.5)	105 (76.1)	124 (49.8)	239 (34.5)	10 (100.0)	16 (64.0)		
Male, <i>n</i> (%)	1725 (46.5)	1104 (42.5)	33 (23.9)	125 (50.2)	454 (65.5)	0 (0.0)	9 (36.0)		
<b>Age (years), median (IQR)</b>	36.9 (31.7–43.3)	37.0 (31.2–42.8)	34.7 (29–40.2)	38.6 (32.9–44.2)	36.5 (31.1–43.2)	33.1 (27.4–38.4)	36.5 (32.4–41.9)		
18–29	707 (19.0)	490 (18.9)	39 (28.3)	28 (11.2)	143 (20.6)	3 (30.0)	4 (16.0)		
30–39	1668 (44.9)	1176 (45.3)	65 (47.1)	112 (45.0)	298 (43.0)	5 (50.0)	12 (48.0)		
≥40	1338 (36.0)	932 (35.9)	34 (24.6)	109 (43.8)	252 (36.4)	2 (20.0)	9 (36.0)		
<b>HIV exposure, <i>n</i> (%)</b>									
Heterosexual contact	2583 (69.6)	1731 (66.6)	108 (78.3)	191 (76.7)	520 (75.0)	10 (100.0)	23 (92.0)		
Homosexual contact	134 (3.6)	4 (0.2)	0 (0.0)	0 (0.0)	128 (18.5)	0 (0.0)	2 (8.0)		
Other <sup>d</sup>	996 (26.8)	863 (33.2)	30 (21.7)	58 (23.3)	45 (6.5)	0 (0.0)	0 (0.0)		
<b>WHO clinical stages, <i>n</i> (%)</b>									
I	493 (16.5)	393 (15.1)	25 (18.1)	75 (30.1)	na	na	na		
II	711 (23.8)	623 (24.0)	33 (23.9)	55 (22.1)	na	na	na		
III	1281 (42.9)	1145 (44.1)	59 (42.8)	77 (30.9)	na	na	na		
IV	500 (16.7)	437 (16.8)	21 (15.2)	42 (16.9)	na	na	na		
<b>CDC classification, <i>n</i> (%)</b>									
A	302 (41.5)	na	na	na	296 (42.7)	0 (0.0)	6 (24.0)		
B	166 (22.8)	na	na	na	152 (21.9)	10 (100.0)	4 (16.0)		
C	260 (35.7)	na	na	na	245 (35.4)	0 (0.0)	15 (60.0)		
Ever pulmonary tuberculosis, <i>n</i> (%)	741 (20.0)	569 (21.9)	25 (18.1)	74 (29.7)	69 (10.0)	na	4 (16.0)		
Hepatitis B <sup>e</sup> , <i>n</i> (%)	36 (4.9)	na	na	na	35 (5.1)	0 (0.0)	1 (4.0)		
Hepatitis C <sup>f</sup> , <i>n</i> (%)	56 (7.7)	na	na	na	55 (7.9)	0 (0.0)	1 (4.0)		

(continued)

Table 2 Continued

	PASER-M (Africa)				TASER-M (Asia)			
	Total	Initiation of first-line ART <sup>a</sup>		Switch to second-line ART <sup>b</sup>	ARV-naive	Initiation of first-line ART <sup>a</sup>		Switch to second-line ART <sup>b</sup>
		ARV-naive	ARV-experienced <sup>c</sup>			ARV-naive	ARV-experienced <sup>c</sup>	
<b>History of ARV drug use, n (%)</b>	422 (11.4)	na	138 (100.0)	249 (100.0)	na	10 (100.0)	25 (100.0)	
ART	334 (9.0)	na	60 (43.5)	249 (100.0)	na	0 (0.0)	25 (100.0)	
Mono or dual therapy	10 (0.3)	na	6 (4.3)	4 (1.6)	na	0 (0.0)	0 (0.0)	
Single-dose NVP for PMTCT	36 (1.0)	na	35 (25.4)	1 (0.4)	na	0 (0.0)	0 (0.0)	
Combination therapy for PMTCT	31 (0.8)	na	19 (13.8)	2 (0.8)	na	10 (100.0)	0 (0.0)	
Unspecified	22 (0.6)	na	22 (15.9)	0 (0.0)	na	0 (0.0)	0 (0.0)	
<b>CD4 cell count (cells/<math>\mu</math>l), median (IQR)</b>	129 (56–205)	133 (62–204)	177 (92–262)	125 (46–196)	99 (33.5–201)	169 (151–222)	197 (109–299)	
<100	1456 (39.2)	975 (37.5)	38 (27.5)	102 (41.0)	337 (48.6)	1 (10.0)	3 (12.0)	
100–199	1215 (32.7)	914 (35.2)	42 (30.4)	81 (32.5)	164 (23.7)	6 (60.0)	8 (32.0)	
$\geq$ 200	1007 (27.1)	702 (27.0)	57 (41.3)	64 (25.7)	171 (24.7)	3 (30.0)	10 (40.0)	
Unknown	25 (0.7)	7 (0.3)	1 (0.7)	2 (0.8)	21 (3.0)	0 (0.0)	4 (16.0)	
<b>HIV-1 RNA (log<sub>10</sub> copies/ml), median (IQR)</b>	4.9 (4.3–5.5)	4.9 (4.3–5.6)	4.8 (4.2–5.5)	4.1 (3.2–5.0)	5.0 (5.4–6.8)	4.8 (4.5–5.0)	4.0 (3.6–4.5)	
<b>ART regimen</b>								
NNRTI-based triple regimen	3330 (89.7)	2590 (99.7)	135 (97.8)	2 (0.8)	593 (85.6)	10 (100.0)	0 (0.0)	
AZT-containing	1302 (35.1)	964 (37.2)	51 (37.8)	1 (0.4)	170 (28.7)	10 (100.0)	0 (0.0)	
TDF-containing	1088 (29.3)	868 (33.5)	49 (36.3)	1 (0.4)	110 (18.5)	0 (0.0)	0 (0.0)	
d4T-containing	833 (22.4)	690 (26.6)	33 (24.4)	0 (0.0)	276 (46.5)	0 (0.0)	0 (0.0)	
ABC-containing	106 (2.9)	68 (2.6)	2 (1.5)	0 (0.0)	37 (6.2)	0 (0.0)	0 (0.0)	
3TC-containing	2387 (71.7)	1746 (67.4)	89 (65.9)	0 (0.0)	542 (91.4)	10 (100.0)	0 (0.0)	
FTC-containing	942 (28.3)	843 (32.5)	48 (35.6)	0 (0.0)	49 (8.3)	0 (0.0)	0 (0.0)	
PI-based triple regimen	351 (9.5)	6 (0.2)	0 (0.0)	247 (99.2)	73 (10.5)	0 (0.0)	25 (100.0)	
Triple NRTI regimen	29 (0.8)	2 (0.1)	3 (2.2)	0 (0.0)	24 (3.5)	0 (0.0)	0 (0.0)	
NNRTI+PI-based triple regimen	3 (0.1)	0 (0.0)	0 (0.0)	0 (0.0)	3 (0.4)	0 (0.0)	0 (0.0)	

Data are n (%) of patients, unless otherwise indicated. na, not available; ART, combination antiretroviral therapy; ARV, antiretroviral; CDC, US Center for Disease Control and Prevention; WHO, World Health Organization; PMTCT, prevention of mother-to-child transmission of HIV-1; TB, tuberculosis; IQR, interquartile range; NVP, nevirapine; d4T, stavudine; AZT, zidovudine; TDF, tenofovir; ABC, abacavir; 3TC, lamivudine; FTC, emtricitabine; NRTI, nucleoside reverse transcriptase inhibitor; NNRTI, non-nucleoside reverse transcriptase inhibitor; PI, protease inhibitor.

<sup>a</sup>Eligibility for ART initiation in accordance with national ART guidelines (i.e. advanced immunodeficiency as defined by CD4 cell count less than 200 or less than 350 cells/ $\mu$ l, or advanced clinical disease according to WHO clinical stages or CDC classification).

<sup>b</sup>Regimen switch due to treatment failure, defined by local standard of care guidelines as determined clinically, immunologically or virologically.

<sup>c</sup>ARV-experienced is defined as any previous use of ARVs, i.e. (first-line) ART, mono/dual therapy and/or PMTCT.

<sup>d</sup>Includes recipients of blood products, injecting drug users, perinatal transmission and unknown exposures.

<sup>e</sup>Hepatitis B positive status was defined as being HBsAg positive.

<sup>f</sup>Hepatitis C positive status was defined as being HCV antibody positive.

**Table 3** HIV subtypes and circulating recombinant forms<sup>a</sup> by region and country

	Total	PASER-M (Africa)						TASER-M (Asia) <sup>b</sup>		
		South Africa	Zambia	Uganda	Kenya	Nigeria	Zimbabwe	Thailand	Hong Kong	Malaysia
<i>n</i> (%)	2523 (100.0)	624 (24.7)	583 (23.1)	410 (16.3)	140 (5.5)	21 (0.8)	17 (0.7)	542 (21.5)	111 (4.4)	75 (3.0)
A	340 (13.6)	2 (0.3)	4 (0.7)	235 (57.3)	97 (69.1)	1 (4.8)		1 (0.2)		
B	114 (4.5)	3 (0.5)						37 (7.0)	55 (49.5)	19 (25.3)
C	1236 (49.2)	617 (98.9)	571 (97.9)	9 (2.2)	19 (13.6)		17 (100.0)		2 (1.8)	1 (1.3)
D	179 (7.1)	1 (0.2)	1 (0.2)	160 (39.0)	17 (12.1)					
G	11 (0.4)		2 (0.3)	1 (0.2)	2 (1.4)	6 (28.6)				
CRF01_AE	585 (23.2)							485 (89.5)	52 (46.8)	48 (64.0)
CRF02_AG	20 (0.8)	1 (0.2)	3 (0.5)	1 (0.2)		14 (66.7)		1 (0.2)		
Other recombinants or discordant subtypes	32 (1.3)		2 (0.3)	1 (0.2)	2 (1.4)			18 (3.3)	2 (1.8)	7 (9.3)
Unclassified	6 (0.2)			3 (0.7)	3 (2.1)					

Data are *n* (%) of subtypes/CRFs, unless otherwise indicated. CRF, circulating recombinant form.

<sup>a</sup>HIV subtypes were determined from the *pol* sequences, using the REGA HIV-1 subtyping algorithm version 2.0 (<http://dbpartners.stanford.edu/RegaSubtyping>) and/or Stanford HIV drug resistance database (<http://hivdb.stanford.edu>).

<sup>b</sup>The collaborating sites in Philippines, South Korea and Indonesia had not yet provided sequence data at time of the current analysis.

first-line patients were less than 200 cells/ $\mu$ l (site median 135 cells/ $\mu$ l, range 93–191). Median baseline HIV viral load was 4.9 log<sub>10</sub> copies/ml (IQR 4.2–5.5). The most frequently prescribed first-line regimens were based on NNRTIs (99.7%), i.e. efavirenz (EFV) and nevirapine (NVP) at 60 and 40%, respectively. First-line dual NRTI backbones were predominantly lamivudine (3TC)/zidovudine (AZT) (37%), emtricitabine (FTC)/tenofovir (TDF) (34%) and 3TC/stavudine (d4T) (26%). Overall, 67% of patients started a 3TC-containing first-line regimen. Among patients initiating first-line ART, 95% (*n*=2 598) reported to be ARV-naïve and 5% (*n*=138) had previous ARV experience, which included ART (*n*=60), mono/dual therapy (*n*=6), single-dose NVP for prevention of mother-to-child transmission of HIV (PMTCT) (*n*=35), combination therapy for PMTCT (*n*=19), and unspecified (*n*=22). Compared with ARV-naïve first-line patients, ARV-experienced first-line patients had higher median CD4 counts (177 vs 133 cells/ $\mu$ l, *P*<0.0001), were younger (median 34.7 vs 37.0 years, *P*<0.0001) and were more likely to be female (76.1 vs 57.5%; *P*<0.001). Other baseline characteristics did not differ between ARV-naïve and ARV-experienced patients.

For the 249 (8.3%) patients switching to second-line ART, the median age was 38.6 years (IQR 32.9–44.2) and sex was equally distributed. HIV exposure was predominantly heterosexual contact and 48% of patients had advanced disease (classified as WHO stages III or IV). Median CD4 count was 125 cells/ $\mu$ l (IQR 46–196). Median pre-switch HIV viral load was 4.1 log<sub>10</sub> copies/ml (IQR 3.2–5.0). Ritonavir-boosted lopinavir (LPV) was the PI used almost exclusively (98%).

As shown in Table 3, analysis of the first available 1795 viral sequences demonstrated that the most common HIV subtypes in the cohort were C (1216, 68.7%), A (338, 18.7%) and D (179, 10.0%). The first PASER report published in 2008 reviewed the available data on HIVDR in sub-Saharan Africa.<sup>11</sup> Baseline HIVDR data from Lusaka, Zambia, has recently been published.<sup>24</sup> International presentations have summarized preliminary baseline HIVDR mutations and subtype distributions.<sup>25,26</sup>

### TASER-M

Patient recruitment commenced in March 2007 and for the March 2009 transfer, seven sites from Thailand, Hong Kong and Malaysia provided data. Of 773 patients, 755 (97.7%) commenced ART within 181 days of baseline specimen collection and 728 (96.4%) participants had genotypic data available. Of these, 693 (95.2%) ARV-naïve patients and 10 (1.4%) ARV-experienced patients, following prior PMTCT, were eligible for first-line regimens. A further 25 (3.5%) patients were eligible for second-line ART following first-line treatment failure. Patient characteristics are summarized in Table 2. For ARV-naïve first-line patients, the median age was 36.5 years. Almost two-thirds of patients were male and HIV exposure was predominantly heterosexual contact. More than one-third of patients were classified as CDC class C and almost half of the patients had pre-therapy CD4 counts less than 100 cells/ $\mu$ l. Median baseline HIV viral load was 5.0 log<sub>10</sub> copies/ml (IQR 5.4–6.8) and the most common first-line regimens were based on NNRTIs (85.6%). Excluding 14 (2.4%) patients on a randomized clinical trial with a blinded NNRTI



component, NVP was more commonly prescribed than EFV at 56 and 42%, respectively. First-line dual NRTI backbones were predominantly 3TC/d4T (47%), 3TC/AZT (29%) and 3TC/TDF (10%). For first-line PI regimens, the favoured NRTI backbone was FTC/TDF (33%) compared with 3TC/d4T (30%) or 3TC/AZT (18%). For the ritonavir-boosted PI component, atazanavir (ATZ) was only slightly favoured over LPV at 43 vs 41%, respectively. Overall, 542 (91.4%) of ARV-naive patients started a 3TC-containing first-line regimen. The 10 PMTCT patients received perinatal prophylaxis of AZT/3TC/NVP ( $n=7$ ), AZT ( $n=2$ ) or AZT/NVP ( $n=1$ ) for between 14 and 102 days and all were prescribed AZT/3TC/NVP as first-line regimens.

For the 25 (3.4%) second-line patients, 22 (88%) were of Thai ethnicity and the median age was 36.5 years (IQR 32.4–41.9). Females were in the majority (64%), HIV exposure was predominantly heterosexual (92%) and 60% of patients had experienced at least one CDC class C event. Of 21 patients with CD4 counts available within 6 months of starting a second-line therapy, the median CD4 count was 197 (IQR 109–299). Median pre-switch HIV viral load was 4.0  $\log_{10}$  copies per/ml (IQR 3.6–4.5). All patients were on PI-based regimens, following failure on first-line NNRTI-based regimens (median duration 30.3 months). The most commonly prescribed PI component was ritonavir-boosted LPV (88%).

As shown in Table 3, from analysis of the 728 available viral sequences, the most common subtypes were CRF01\_AE (584, 80.2%) and subtype B (111, 15.2%). Non-CRF01\_AE recombinants were identified in eight (1.1%) patient specimens. For 21 (2.9%) specimens, the subtype differed between PR and RT regions, suggesting dual infection or recombination. International presentations have summarized 2009 baseline HIVDR mutations and subtype distributions.<sup>27,28</sup>

Complete baseline and prospective outcome data for PASER-M and TASER-M are anticipated to become available in 2010–13.

## What are the main strengths and weaknesses?

Programmes that monitor national and regional levels of primary and secondary HIVDR contribute to evidence-based recommendations to inform treatment guidelines and provide feedback on the success of HIV treatment and prevention programmes. PASER and TASER, with TAQAS, are developing capacity in sub-Saharan Africa and the Asia-Pacific for coordinated HIVDR monitoring and genotypic laboratory testing. The study protocols are harmonized with the WHO HIV Drug Resistance Prevention Survey protocol.<sup>29</sup> An important strength is the large number of patients and sites participating, representing a diverse spectrum of patient populations, clinic types, ART

regimens and HIV subtypes. Opportunities exist to investigate the impact of drug resistance on HIV natural history, rates of disease progression and response to treatment in non-B subtypes. Data from genotypic resistance testing will also provide insight into the population genetics and dynamics of transmitted HIVDR in the region.

PASER-M and TASER-M have several limitations. First, patient samples at each site are not necessarily representative of the site, country or region. Second, data quality depends on the completeness of clinical information captured through routine patient care. In PASER-M, data may have been collected under varying conditions, since some sites had no or limited research experience at study initiation. Third, at some sites, study initiation was delayed by several months due to the time required for contract negotiation, IRB study approval and, in TASER-M, procurement of FWAs. After study initiation, recruiting the required number of patients within the recommended 18-month period proved difficult for some sites, due to asymptomatic patients not seeking care or treatment, cost of medication or low-prevalence in their setting. Fourth, HIVDR monitoring activities in resource-limited countries in sub-Saharan Africa are limited by high costs of laboratory testing. To address this challenge, PASER has initiated a public–private consortium, called Affordable Resistance Test for Africa (ART-A), which aims to develop affordable test algorithms for the detection and interpretation of HIVDR for use in laboratories and clinics (<http://www.arta-africa.org>).

## How can I collaborate? Where can I find out more?

Ownership of individual site data remains with the contributing site. Sites are represented by their principal investigators on the respective PASER and TASER Steering Committees. Research is to be the subject of peer-reviewed publications and analysis priorities are driven by a concept sheet process. Both studies accept concept proposals from external researchers for review, if submitted in collaboration with one or more of the site principal investigators. The PASER and TASER protocols contribute data under the LAASER partnership (<http://www.laaserhivaid.org>) and TASER also contributes data to IeDEA.<sup>20</sup> Collaborating sites are also encouraged to make an appropriate subset of their data available to Ministry of Health in their respective countries in order to contribute to local efforts in monitoring HIVDR. Questions regarding participation, research concepts or requests for data should be sent to Tobias Rinke de Wit, email: [t.rinkedewit@pharmaccess.org](mailto:t.rinkedewit@pharmaccess.org) (PASER), or Thida Singtoroj, email: [thida.singtoroj@treatasia.org](mailto:thida.singtoroj@treatasia.org) (TASER).

## Supplementary Data

Supplementary Data are available at *IJE* online.

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## Appendix 1

### The PharmAccess African Studies to Evaluate Resistance

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