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Short communication

Performance of a transcription-mediated-amplification HIV-1 RNA assay in pooled specimens

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Abstract

Background: Very limited data exist on the comparative performance of nucleic acid amplification tests (NATs) for the screening of pooled specimens for acute human immunodeficiency virus (HIV) infection.

Study design: In this study, we compared a transcription-mediated-amplification assay (Procleix® HIV-1 Discriminatory Assay, [TMA]) with a branched DNA assay (Bayer Versant HIV-1 RNA 3.0 assay, [bDNA]).

Results: After re-testing 1552 samples that were negative for HIV RNA by bDNA, we found one additional positive sample with the TMA assay.

Conclusion: Our results suggest that TMA could potentially detect acute HIV infections missed by other technologies. © 2007 Elsevier B.V. All rights reserved.

Keywords: HIV; Pooled testing; TMA; bDNA

1. Background

Public health agencies have recently recognized the value of detecting patients with acute HIV infection (Pilcher et al., 2002). Accordingly, several public health departments are routinely screening pooled human immunodeficiency virus (HIV) antibody-negative specimens with HIV nucleic acid amplification test (NAT) assays (Liska, 2005; Patel et al., 2006; Pilcher et al., 2002; Shahkolahi, 2006; Stekler et al., 2005). In this approach, all blood samples are initially screened for HIV antibodies. Seronegative specimens

are then pooled into groups and tested by NAT. A negative pool ends the testing protocol. In the event of a reactive specimen pool, that pool is deconstructed and individual blood samples are re-tested in order to identify the unique patient sample with the positive result. The identification of antibody-negative, RNA-positive patients confirms the diagnosis of acute HIV infection (Centers for Disease Control and Prevention, 1997; Coste et al., 2005; Stramer et al., 2004).

Currently, sample-pooling protocols vary significantly in terms of the size of the master pool and subsequent intermediate pools. Unfortunately, very few data exist on the comparative performance of different NAT assays when used for HIV-RNA detection by sample-pooling protocols (Busch et al., 2005). As a consequence, multiple different NAT assays are currently being used by public health agencies. In this study we evaluated the sensitivity of Procleix® HIV-1 Discriminatory Assay (a transcription-mediated-amplification

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[TMA] assay manufactured by Gen-Probe Incorporated and distributed by Chiron Corp.) (Procleix[®] HIV-1/HCV Assay; Giachetti et al., 2002). The HIV-1 Discriminatory assay is part of the Procleix[®] HIV-1/HCV assay which is routinely used for blood donor screening. This assay consists of the same formulations as the recently cleared APTIMA[®] HIV-1 RNA Qualitative Assay (Gen-Probe Incorporated, San Diego CA), an in vitro nucleic acid assay system for the detection of HIV-1 in human plasma which is intended for use as an aid in the diagnosis of HIV-1 infection, including acute infection. Presence of HIV-1 RNA in the plasma of patients without antibodies to HIV-1 is indicative of acute HIV-1 infection and may also be used as an additional test, when it is reactive, to confirm HIV-1 infection in an individual whose specimen is repeatedly reactive for HIV-1 antibodies (APTIMA®HIV-1 RNA Assay).

Since the APTIMA[®] HIV-1 RNA Qualitative Assay is the only FDA cleared assay for diagnosis of acute infection in HIV antibody-negative samples, we were interested in evaluating samples previously tested negative with the Bayer Versant HIV-1 RNA 3.0 assay (bDNA).

2. Study design

To determine the performance of the TMA HIV-1 Assay on the yield of acute HIV detection in public health practice, we re-tested with this assay all HIV antibody-negative and HIV RNA-negative samples obtained from patients seen at San Francisco City Clinic at the San Francisco Department of Public Health, between November 2003 and December 2004.

Plasma was separated from the whole blood drawn in EDTA tubes, at the San Francisco Department of Public Health Public Health Laboratory within 12 h of collection. The standard Vironostika HIV type 1 enzyme immunoassay (bioMerieux) was used for antibody screening. Remnant plasma was stored frozen at -70 °C until tested for HIV RNA.

HIV antibody-negative samples were routinely tested in pools of 10 with the Bayer Versant HIV-1 RNA 3.0 assay (bDNA) following the procedures recommended by the manufacturer (Versant HIV-1 RNA 3.0 Assay, 2002-2004). HIV antibody-negative samples by Vironostika HIV type 1 enzyme immunoassay and HIV RNA-positive by bDNA assay were re-tested by Genetic SystemsTM HIV-1/HIV-2 PLUS O enzyme immunoassay (Bio-Rad Laboratories) to confirm their antibody-negative status. Specimens from patients with initially HIV RNA-positive samples were retested and confirmed either by repeatedly measurable HIV RNA (bDNA) or HIV-1 antibody seroconversion. As part of the study, HIV RNA-negative samples by this protocol were re-tested in pools of 8 at the Blood System Laboratories in Tempe, Arizona, using the TMA HIV-1Assay (Procleix® HIV-1/HCV Assay; Giachetti et al., 2002). The University of California San Francisco Committee on Human Research approved this study and waived patient consent requirements.

3. Results

A total of 1571 antibody-negative or indeterminate plasma samples were tested in pools of 10 with the Bayer Versant HIV-1 RNA 3.0 assay (bDNA). Nineteen samples were found to be HIV RNA-positive by bDNA testing and confirmed upon re-testing. Samples of those 19 specimens were re-tested by Genetic SystemsTM HIV-1/HIV-2 PLUS O enzyme immunoassay and 9 of them were confirmed to be antibody-negative. Among those 9 patients, viral loads ranged between 1177 and >500,000 copies/mL. A total of 1552 HIV RNA-negative samples by the bDNA assay were re-tested in pools of 8 with the TMA HIV-1 Assay. One additional HIV RNA-positive sample was identified and verified as positive upon re-testing.

4. Discussion

Very few data exist on the performance of different NAT assays for acute HIV infection screening using samplepooling protocols. Procleix[®] HIV-1 Discriminatory Assay, a test developed as part of the Procleix[®] HIV-1/HCV Assay, which is widely implemented in blood donor screening using pools of up to 16 donations (Stramer et al., 2004), is similar to the APTIMA® HIV-1 RNA Qualitative Assay cleared by the FDA for the diagnosis of HIV infection, including detection of acute antibody-negative infections and confirmation of infection when samples have test reactive by a licensed HIV antibody screening assay. With a 50% detection limit of 5.0 copies/mL (confidence interval [CI], 4.5–5.5) and a 95% detection limit of 13.1 copies/mL (CI, 12.1-14.4) (Giachetti et al., 2002; Lelie et al., 2002), this qualitative TMA HIV-1 assay uses a target capture specimen processing system that may offer the potential advantage of decreased false negative results by removing inhibitors and reduced contamination by targeting a specific sequence not included in the amplicon produced by TMA (APTIMA[®]HIV-1 RNA Assay; Kolk et al., 2002; Linnen et al., 2002). On the other hand, Bayer Versant HIV-1 RNA 3.0 bDNA assay has a 95% detection limit of 68 HIV-1 RNA copies/mL (CI, 50-73) (Versant HIV-1 RNA 3.0 Assay, 2002–2004; Collins et al., 1997). Similarly to the TMA HIV-1 Assay, the bDNA assay has shown good correlation with other NAT assays (Elbeik et al., 2000; Galli et al., 2005) and shows a high degree of precision (Kern et al., 1996). However, samples containing less than 50 HIV RNA copies/mL are read as "negative" by the bDNA assay. Whereas, the importance of detecting less than 50 copies/mL when monitoring the response to therapy of patients on antiretroviral therapy is controversial, the detection of low levels of viremia might be of critical importance when testing highly diluted pools of samples. Although the TMA HIV-1 Assay has shown better analytical sensitivity for HIV-1 RNA detection in individual and pooled samples, when compared with other NAT assays (Busch et al., 2005; Lelie et al., 2002), no studies have compared its performance

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with the bDNA assay, when used for the screening of acute HIV infections by sample-pooling protocols.

Our results indicate that the TMA HIV-1 Assay could potentially detect newly HIV infected patients missed by other technologies. This likely reflects the better analytical sensitivity of the TMA assay, compared to bDNA. Although the different number of samples pooled together for testing by the two different assays could have affected the results, it seems unlikely given the rather small difference between the two protocols (pooling of 8 versus 10 samples). The relatively low incremental yield of the TMA HIV-1 Assay relative to bDNA is likely a reflection of the relatively small sample size and the high viral load of acutely infected persons detected in high risk screening settings such as STD clinics (Busch and Hecht, 2005; Stekler et al., 2005).

Differences likely exist in the performance of different NAT assays when used for the testing of pooled samples. Given the paucity of data, the technology with the highest performance in this setting remains to be determined. As HIV RNA screening of pooled patient samples becomes more common, studies comparing the performance of different assays and protocols will be required.

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