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Design and Evaluation of a Human Immunodeficiency Virus Type 1 RNA Assay Using Nucleic Acid Sequence-Based Amplification Technology Able To Quantify Both Group M and O Viruses by Using the Long Terminal Repeat as Target

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Currently available human immunodeficiency virus type 1 (HIV-1) RNA quantification assays can detect most viruses of the group M subtypes, but a substantial number are missed or not quantified reliably. Viruses of HIV-1 group O cannot be detected by any commercially available assay. We developed and evaluated a quantitative assay based on nucleic acid sequence-based amplification (NASBA) technology, with primers and probes located in the conserved long terminal repeat (LTR) region of the HIV-1 genome. In 68 of 72 serum samples from individuals infected with HIV-1 subtypes A to H of group M, viruses could be detected and quantified. In serum samples from two patients infected with HIV-1 group O viruses, these viruses as well could be detected and quantified. In contrast, the currently used gag-based assay underestimated the presence of subtype A viruses and could not detect subtype G and group O viruses. The discrepancy between the results of the two assays may be explained by the number of mismatches found within and among the probe and primer regions of the subtype isolates. These data indicate that LTR-based assays, including the NASBA format chosen here, are better suited to monitoring HIV-1 therapy than are gag-based assays in an era in which multiple HIV-1 subtypes and groups are spreading worldwide.

The human immunodeficiency virus type 1 (HIV-1) RNA level in plasma or serum has become one of the most important markers for monitoring HIV-1-infected patients. Other than HIV-1 DNA, it is the only evidence for mother-to-child transmission, since maternal antibodies present in infant serum hamper antibody-screening assays. The HIV-1 RNA level is the most valuable marker for predicting disease progression in nontreated patients (10, 13, 21, 22, 34) and is highly useful for evaluating the effectiveness of antiretroviral drug therapy (14, 26, 43). The decision to start antiretroviral drug therapy is currently made on the basis of the viral RNA level (31). A patient with an HIV-1 RNA level of less than 10,000 copies per ml generally will not progress to AIDS for at least 5 years (22, 34). Highly active antiretroviral therapy, consisting of treatment with a combination of three drugs, results in a decline of the viral RNA level of approximately 99% (28). The therapy’s goal, for optimal delay of disease, is to decrease the viral RNA level until it cannot be detected by RNA quantification assays. Although HIV-1 subtype B has been the predominant cause of AIDS in Europe and the United States, other HIV-1 subtypes, particularly subtypes A and C, are now taking over. As these different clades of HIV-1 spread rapidly around the world, there is an increased need for assays that can reliably quantify the level of RNA of all known subtypes, i.e., group M subtypes A to H and group O viruses, in plasma, serum, or culture supernatants.

Commercially available RNA quantification assays are based either on the amplification of a fragment of the gag gene of the HIV-1 genome (e.g., NucliSens HIV-1 QT assay [Organon Teknika, Boxtel, The Netherlands] or Amplicor version 1.5 HIV Monitor test [Roche Diagnostics, Basel, Switzerland]) (15, 23, 24, 41, 42) or on the direct detection of HIV-1 RNA by hybridization with labeled probes (e.g., Quantiplex HIV 3.0 assay; Chiron Diagnostics, Emeryville, Calif.) (27, 35, 36, 46). The NucliSens and Amplicor assays were developed with reagents derived from HIV-1 subtype B, but they can detect most group M viruses. The Quantiplex assay uses 45 target probes designed to hybridize with all known HIV-1 group M viruses and is thus more likely than the other two assays to detect and quantify genetically divergent HIV-1 subtypes (7, 12, 25). It has been reported that there is no difference in general performance, for instance, with regard to sensitivity, accuracy, and reproducibility, among the three assays (7, 11, 30, 32, 37, 38) even though some viruses not detected by one assay have been detected by another assay (1, 8, 25). None of the assays can detect HIV-1 group O viruses (12, 20, 29). The sensitivity of both the Quantiplex and the NucliSens assays, if an ultrasensitive protocol is applied, is currently 50 copies of RNA per ml of plasma or serum (5, 44), with an input of 1,000 or 200 µl, respectively. The Amplicor assay has variable sensitivity, with a detection limit of generally ranging from 30 to 60 RNA copies per ml of plasma when an ultrasensitive protocol is applied with an input of 500 µl.

We developed and evaluated a new, broad-clade HIV-1 RNA quantification assay based on nucleic acid sequence-based amplification (NASBA) technology. The evaluation was performed with plasma or serum samples that together contained all group M subtypes and group O viruses. We show that the number of mismatches in sequences of primers and probes

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was the major determinant of accuracy in the detection and quantification of HIV-1 RNA.

MATERIALS AND METHODS

Three-calibrator gag-based NASBA and one-calibrator long terminal repeat (LTR)-based NASBA. The three-calibrator gag-based NASBA is a commercially available assay (NuclSENS HIV-1 QT assay; Organon Teknika). The assay was performed by following the instructions of the manufacturer.

Four regions having highly conserved sequences, which were found in the 5’ end of the genomic RNA (LTR region) after screening of the known HIV-1 genomes (17), were used to develop an LTR-based NASBA. The assay was based on standard NASBA technology (42) but used one internal calibrator (Q) molecule instead of three, as in the gag-based assay (15, 41, 42). A fragment of approximately 135 bases of antisense RNA was amplified and detected with two primers and two probes. Calibrator molecules were added to a 200-μl plasma or serum sample, and RNA was isolated by a silica-based method (4). Five micro-liter volumes of the 50 μl of isolated viral RNA and calibrator RNA were used in the NASBA reaction with a 5’ sense primer (5’ CTCATAAAGCGTGCT TGA) (HIVXBG2G [GenBank accession no. K03455]) nucleotides [nt] 508 to 523) and a 3’ antisense primer elongated with a T7 sequence (in lowercase italics) (5’ attactaatgactcactatggagGGGGCCCATCTGAGAGA) (nt 643 to 628) were used to amplify the LTR fragment. After 1.5 h of incubation at 41°C, 5 μl of the reaction mixture was diluted 31 times in detection diluent (Organon Teknika). From the diluted sample, 5 μl was mixed either with a ruthenium tag-labeled wild-type detection (5’ AATGGTGCAGCCTGGCTGTGTT) (nt 355 to 372) and biotin-labeled capture (5’ TCTGGTAACTAGATAGATCC TC) (nt 580 to 600) probes or with a mixture of Q detection and identical capture probes. The detection probes were labeled so they could be detected by electrochemiluminescence (3). The number of wild-type RNA copies per milliliter of serum was calculated by the ratio between the wild-type signal and the Q signal. Serum samples in which no viral RNA could be detected were reanalyzed by following an ultrasensitive protocol (44).

Ultrasensitive protocol for NASBA. An ultrasensitive protocol for NASBA (UltraSens protocol) (44), which improved the sensitivity of both the gag-based and the LTR-based NASBAs to 50 copies/ml, had already been developed. Briefly, the eluted nucleic acids remaining from the isolation procedure de-

RESULTS

Comparison of the quantitative performance of the gag- and LTR-based NASBAs on HIV-1 subtype B RNA. The gag-based NASBA, based on subtype B sequences, has already shown its ability to detect and quantify HIV-1 subtype B genomic RNA (13, 38, 40–42, 47). We tested whether the new LTR-based NASBA could equal its performance. The two assays were compared with a panel consisting of dilution series of a well-characterized subtype B standard (HXB3) in 0.2 ml of human plasma (19). Analysis of the dilution series yielded similar results for both assays (Fig. 1). The quantification of both assays was linear and accurate over a range of 10^3 to 10^7 copies of genomic HIV RNA per ml when a sample volume of 0.2 ml was applied. The precision and accuracy of the LTR-based NASBA were within 0.2 and 0.1 log_{10}, respectively, for up to 250 copies of genomic HIV RNA per input volume (0.2 ml). This result was determined with a group of 47 human plasma samples mixed with known amounts of HXB3 (19) (data not shown). The analytical sensitivity of the assay, in which ampli-

FIG. 1. Assessed viral RNA levels versus given viral RNA levels in serial dilutions of HIV-1 HXB3 (19) in plasma as determined with the LTR-based (○) and the gag-based (●) NASBAs. The results shown are the means of at least three independently performed experiments.
fication occurred in 50% of the reactions, was approximately 10 genomic RNA copies per reaction. An input volume of 0.2 ml led to a sensitivity of 500 copies of genomic HIV RNA per ml, as only 1/10 of the sample was used in a reaction. The sensitivity was improved to 50 copies of genomic RNA per ml when the UltraSens protocol was applied.

**Linear quantification capacities of the LTR-based NASBA on various HIV-1 subtypes.** The linear quantification abilities of the LTR-based assay were determined by serial dilutions of a viral culture supernatant for each subtype (A to G) of the HIV-1 M group and for four viruses of the HIV-1 O group. The results of representative dilution series for the HIV-1 M and O groups are plotted in Fig. 2A and 3B, respectively. For subtypes A to G of the HIV-1 M group, a linear decrease of the assessed viral RNA levels as the level of dilution increased was observed, indicating that all subtypes were quantified similarly. The variation in initial RNA levels was determined by differences in RNA input. One representative experiment of three that were performed for each subtype was plotted (Fig. 2). The slope of the linear decrease of the viral RNA levels was not as steep for the group O viruses. This finding suggests that the efficiency of quantification was less for the group O viruses than for the group M viruses and was probably due to a greater number of mismatches in the capture probe.

**RNA quantification in serum samples from 72 individuals infected with HIV-1 group M viruses of subtypes A to H and from two individuals (four samples) infected with HIV-1 group O viruses.** Viral subtypes of the viruses were determined based on phylogenetic analysis of the sequences of the gag genes. The serum samples with a viral RNA level below the detection limit...
of either the LTR- or the gag-based assay were reexamined by using the UltraSens protocol, which has a lower detection limit (50 copies/ml). The gag-based NASBA was unable to detect viral RNA in samples containing subtype G or HIV-1 group O viruses, whereas the LTR-based assay could detect the RNA of all tested subtypes or groups. For subtype A viruses, RNA levels were significantly lower \( (P < 0.0001) \) with assessment by the gag-based NASBA than they were with assessment by the LTR-based assay. For all samples, the RNA levels for subtype E viruses as determined by the gag-based assay were lower than as determined by the LTR-based assay, but not significantly \( (P = 0.26) \).

To facilitate analysis, the serum samples were divided into two groups. The first group contained subtypes B, C, and D (Fig. 3A), whereas the second group contained subtypes A, E, and G (Fig. 3B). Only one serum sample each was available for subtypes F and H, and for group O, only four serum samples from two patients were available. Results for these six serum samples were therefore not plotted in the diagrams. The correlation coefficient \( (r) \) for the gag-based and LTR-based NASBA results for all sera together, including those not plotted, was 0.52 \( (n = 76; P < 0.0001) \). For the group containing the subtype B, C, and D viruses, a strong correlation could be found between the two assays \( (r = 0.87; P < 0.0001) \), but this correlation was not as strong for the group with subtype A, E, and G viruses \( (r = 0.29; P = 0.089) \). In total, 16 viruses of various subtypes of the M group (and the four O-group viruses) could not be detected by the gag-based NASBA. Of these, five were subtype A, one was subtype C, one was subtype D, two were subtype E, six were subtype G, and the remaining one was the only subtype H in our serum sample set; therefore, 13 of these 16 serum samples (81%) were in the group containing A, E, and G subtypes.

The LTR-based NASBA was unable to detect viral RNA in four serum samples. Two of these, one subtype A and one subtype D, were negative for viral RNA by both assays. The other two serum samples contained subtype B viruses, which could be detected by the gag-based NASBA only after the UltraSens protocol was applied. This result could indicate that for a limited number of subtype B isolates the detection limit of the gag-based NASBA is lower than that of the LTR-based NASBA. Finally, one serum sample (Fig. 3B) contained a subtype E virus and was positive by both assays; however, it was positive in the LTR-based NASBA only with the UltraSens protocol.

**Analysis of mismatches in primer and probe regions.** To explain the discrepancies in assessed viral RNA levels between the two assays, we sequenced the relevant LTR and gag regions and analyzed the number of mismatches for the primers and the probes. For analysis, insertions and deletions present only in the noncoding LTR region were counted as one mismatch.

For analysis, insertions and deletions present only in the noncoding LTR region were counted as one mismatch for the probes. For analysis, insertions and deletions present only in the noncoding LTR region were counted as one mismatch for the primers and probes of the LTR-based assay (L) and the gag-based assay (G). LDL, lower detection limit. (B) Mean number of mismatches with standard deviation (error bars) for each subtype for the primers and probes of the LTR-based assay (L) and the gag-based assay (G).

**DISCUSSION**

Because various subtypes of HIV-1 are rapidly spreading around the world, HIV-1 RNA quantification assays that can detect all known subtypes of HIV-1 group M and group O viruses are required. We have developed a new NASBA-based assay that uses the conserved LTR region at the 5’ end of the genomic RNA. We have shown that the LTR-based assay is as good in standard subtype B quantification as the existing gag-based assay (NucliSens HIV-1 QT assay; Organon Teknika). The lower detection limits were similar for both assays. By comparing dilution series of a panel of group M subtype isolates from the WHO collection, we have shown that the LTR-based assay quantifies these viruses as efficiently as it does subtype B viruses. In contrast, the group O viruses were less

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**FIG. 4.** (A) Mean log₁₀ RNA level with standard deviation (error bars) for each HIV-1 subtype as assessed by the LTR-based NASBA (L) and the gag-based NASBA (G). LDL, lower detection limit. (B) Mean number of mismatches with standard deviation (error bars) for each subtype for the primers and probes of the LTR-based assay (L) and the gag-based assay (G).
efficiently quantified than group M viruses (i.e., the viral load was underestimated), probably due to mismatches in the capture probe. Adaptation of the capture probe to a group O matching sequence would most likely resolve this matter. By using serum samples for which the viral subtype was determined by phylogenetic analysis of the gag gene, we have shown that the two assays are similar in their ability to quantify subtypes B to F of HIV-1 group M. However, the LTR-based assay is better suited to quantify subtypes A and G of group M and the group O viruses, as well as the only group M, subtype H, virus in our serum sample set. The set also included some proven recombinant viruses (6), which were also detected and quantified by the LTR-based assay.

The most important improvement in the LTR-based NASBA, compared to the gag-based NASBA, is its decreased number of mismatches for primers and probes. We found a strong inverse correlation \( r = -0.78; P = 0.023 \) between calculated viral RNA levels and the number of mismatches found for the gag-based NASBA. It can therefore be concluded that for subtype A and G viruses, as well as for group O viruses, the RNA levels as assessed by the gag-based NASBA will be underestimated or absent. For these viruses, the RNA levels will be detected with more efficiency and accuracy by the LTR-based NASBA.

It has been reported that the three most widely used commercially available assays, namely, NucliSens HIV-1 RNA, Amplicor HIV-1 Monitor, and Quantiplex HIV-1 RNA, are similar in sensitivity, accuracy, and reproducibility (7, 11, 30, 32, 37, 38) but that the Quantiplex HIV-1 RNA assay is slightly more effective for quantification of isolates of certain subtypes (7). Like the gag-based NucliSens assay, the gag-based Amplicor assay underestimates or cannot detect subtype G viruses (2, 8). Neither the gag-based NASBA, the Amplicor assay, nor the Quantiplex assay was able to detect and quantify group O viruses (12, 20, 29), but the LTR-based NASBA could.

A new group of HIV-1 viruses, the N group, was recently reported (33). This group is genetically different from groups M and O. Using a published genomic sequence (GenBank accession no. AJ006022) of a member (YBF30) of this group and analyzing the number of mismatches, we could speculate whether this virus might be detected with either the gag-based or LTR-based NASBA. Since 22 mismatches were present for the gag-based NASBA primers and probes and this number lies between those for subtype G and group O viruses, which are not detected, it is unlikely that the new group can be detected by the gag-based NASBA. With the LTR-based NASBA, however, only four mismatches were found. This is less than was found for group O viruses, so it seems likely that this assay can detect and quantify the new group N viruses, provided that their LTR sequence resembles that of their representative member, YBF30.

Our LTR-based NASBA would be of use for testing infants born of HIV-1-positive mothers. These infants cannot be diagnosed HIV-1 positive based on the presence of antibodies against HIV-1 antigens, because maternal HIV-1 antibodies are present in the serum of these infants. The presence of HIV-1 DNA or RNA must be detected directly in cellular material or serum from the infant to make the diagnosis. Improving the chance of detection by changing the amplification region from gag to the LTR will probably lead to prompt diagnosis of HIV-1 in infected infants, especially if the infants are infected with a subtype A or G or a group O virus. An additional advantage of the ultrasensitive NASBA format over the Quantiplex and the ultrasensitive Amplicor assay format is the smaller serum volume (200 versus 1,000 versus 500 μl, respectively) necessary to detect HIV-1 RNA with similar sensitivity.

Another application of the LTR-based NASBA could be the monitoring of patients receiving antiviral therapy. Decreased efficiency and accuracy in assessments of viral RNA levels could impact not only the start of therapy but also the judgment of treatment failure or success. Often, the decision to start highly active antiretroviral therapy is made on the basis of the viral RNA levels (19). If assay failure leads to a too-low estimation of viral RNA levels, such therapy could be delayed or continued, putting the infected individual at an increased risk for developing AIDS (21, 22). If the gag-based NASBA is used to monitor the treatment of individuals infected with group M, subtype A or G, viruses or group O viruses, the viral RNA levels could be determined, too early, to be below the lower detection limit, falsely indicating therapy success. The viral RNA level will rise above the lower detection limit more slowly, causing an unnecessarily later switch to a new drug regimen when drug resistance does begin to appear.

In summary, compared with the gag-based NASBA, our LTR-based NASBA has improved capacities for quantification of the HIV-1 group M, subtype A, virus as well as for the detection and quantification of the subtype G and group O viruses. This assay is a major advancement in HIV diagnostics, affecting decision management for the start and monitoring of therapy and the diagnosis of HIV-1-infected infants.

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