Human Immunodeficiency Virus Type 1 Subtype F Reverse Transcriptase Sequence and Drug Susceptibility

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We sequenced and phylogenetically analyzed the reverse transcriptase (RT) regions of the pol genes of 14 human immunodeficiency virus type 1 (HIV-1) isolates from Romanian patients, which were classified as subtype F on the basis of env gene structure. The RT sequences showed that the strains clustered phylogenetically and were equidistant from other HIV-1 subtypes as shown by the neighbor-joining and maximum-likelihood methods, allowing us to define HIV-1 subtype F according to the pol classification. The subtype F RT sequences differed from reported group M RT sequences by 10.94% (for nucleotides) and 7.6% (for amino acids). Phylogenetic analysis of subtype F susceptibility to three classes of antiretroviral compounds showed an increase in the 50% inhibitory concentration of the tetrahydroimidazol[4,5,1-][1,4]-benzodiazepin-2-(1H)-one and -thione (TIBO) derivate R82913 for one strain which was naturally resistant to this compound. This first report of subtype F pol sequences confirms the perfect correlation between the phylogenetic positions determined by env and pol analyses and suggests that virus variability might influence the efficacy of antiretroviral treatments.

This finding warrants a global evaluation of the phenotypic and genotypic susceptibility of HIV-1 subtypes to antiretroviral drugs.

Most human immunodeficiency virus type 1 (HIV-1) drug susceptibility studies have involved subtype B. Little information on the impact of viral diversity on natural susceptibility to antiretroviral drugs has been reported to date. However, HIV-1 group O viruses are naturally resistant to nonnucleoside reverse transcriptase (RT) inhibitors (8), as is HIV-2 (28). Subtypes are defined on the basis of the env (24, 25) or gag (19) gene. Most RT sequences reported to date belong to subtype B strains, which prevail in North America and western Europe (25), i.e., regions where antiretroviral drugs are developed and clinical trials are conducted. RT sequences of subtypes A to D are also available (25, 32, 34). The full sequences of Thai strains defined as subtype E according to env classification and were equidistant from other HIV-1 subtypes as shown by the neighbor-joining and maximum-likelihood methods, allowing us to define HIV-1 subtype F according to the pol classification. The subtype F RT sequences differed from reported group M RT sequences by 10.94% (for nucleotides) and 7.6% (for amino acids). Phylogenetic analysis of subtype F susceptibility to three classes of antiretroviral compounds showed an increase in the 50% inhibitory concentration of the tetrahydroimidazol[4,5,1-][1,4]-benzodiazepin-2-(1H)-one and -thione (TIBO) derivate R82913 for one strain which was naturally resistant to this compound. This first report of subtype F pol sequences confirms the perfect correlation between the phylogenetic positions determined by env and pol analyses and suggests that virus variability might influence the efficacy of antiretroviral treatments.

This finding warrants a global evaluation of the phenotypic and genotypic susceptibility of HIV-1 subtypes to antiretroviral drugs.

MATERIALS AND METHODS

Study population. We studied 14 HIV-1 subtype F strains isolated from Romanian children (n = 9) and adults (n = 5). All but one of the infected children were nosocomially infected (by injections with nonsterile, reused needles and syringes); the remaining one was vertically infected. Clinical and epidemiological data are described elsewhere, together with virus isolation, env subtype determination, and strain codification (1). None of the patients had received antiretroviral therapy.

HIV-1 RT sequencing. DNA was extracted with phenol-chloroform from cocultured peripheral blood mononuclear cells from (PBMC) infected patients, precipitated with ethanol, and quantified spectrophotometrically. The pol genes were then amplified in a nested PCR with outer primers RT-18 and RT out and inner primers RT-19 and RT-20 as previously described (26). Each nested-PCR product (1,008 bp) was subjected to direct population sequencing with sense primer A 20 (5'-ATTTTCCCATTAGTCCTATT-3') and antisense primer NE150 (5'-ATGTCCATGACGTCGACTT-3'). Sequencing reactions were run with the ABI Prism Dye Terminator Cycle Sequencing Ready Reaction kit with AmpliTaq DNA polymerase (FS, Perkin-Elmer) on an automated sequencer (Applied Biosystems 373A).

Phylogenetic analysis. DNA sequences were analyzed with the multiple-sequence alignment editor Clustal W (35) and improved by visual inspection. The sequences were gapstrapped and a pairwise distance matrix based on 591 sites was generated with the DNADIST program of the PHYLIP package, version 3.56 (12). Tree topology was inferred by the neighbor-joining method with the Kimura two-parameter distance matrix (PHYLIP) and a transition/transversion ratio of 2. Bootstrap analysis was performed with the SEQBOOT (100 resamplings), DNADIST, NEIGHBOR, and CONSENSE programs (PHYLIP package). Phylogenetic analysis was also performed by the maximum-likelihood method, using the DNAML program (12). The tree outliers were the HIV-1 group O sequences (MVP5180 and ANT70). In the tree construction we also included the RT sequences of six subtype B HIV-1 isolates (LAI, SF2, MN, OVI, IRIF, and JRCSF), three subtype D sequences (ELI, NDK, and ZZ26), two subtype A sequences (UG037 and U455), the sequence of a presumed A/G recombinant strain (IBNG) (14), and the sequence of a presumed A/D recombinant strain (MAL) from the Los Alamos National Laboratory database (25). The newly reported sequences for strains CM240 (5), 90CR402, and 93TH253 (14), recombinant A/B strains, were also used in the phylogenetic analyses.

Phenotypic susceptibility assay. The phenotypic susceptibilities of the cellular HIV-1 subtype F isolates were analyzed in a PBMC assay, taking into account the replication kinetics of each strain (3). After conventional isolation of HIV from frozen PBMC, the cell-free HIV-1 subtype F supernatants corresponding to peak RT activity were serially diluted (10−1 to 10−6) and incubated with fresh normal phytohemagglutinin-stimulated PBMC. After being washed, the infected cells were plated in 96-well plates containing six serial dilutions of the antiretroviral...
drugs. Each dilution was tested in triplicate. On days 5, 7, and 10, the supernatants were collected and half the medium was replaced with fresh drug-containing medium. The 50% tissue culture infective dose was assessed by measuring RT activity in control drug-free supernatants collected on the same days. At the peak of RT activity we calculated the drug concentrations inhibiting 50 and 90% (IC50 and IC90, respectively) of the RT activity of 100 50% tissue culture infective doses. For zidovudine (ZDV), an IC50 cutoff of 0.05 M has been defined to classify the virus isolates as ZDV sensitive or ZDV resistant, based on phenotypic analyses of several isolates from treated and untreated patients and on comparisons of these results to genotypic data. For the other antiretroviral drugs, it has not been possible to determine any cutoff value. In this study, phenotypic resistance to these compounds was defined as at least a fivefold increase in IC50s for the HIV-1 subtype F isolates compared to those for HIV-1 subtype B strains.

Antiretroviral agents. We tested the nucleoside RT inhibitors ZDV (Wellcome, Dartford, United Kingdom) and lamivudine (3TC; Glaxo-Wellcome, Dartford, United Kingdom); the nonnucleoside RT inhibitors tetrahydroimidazo[4,5-k][1,4]benzodiazepin-2(1H)-one and -thione (TIBO) derivate R82913 (Janssen, Beerse, Belgium), delavirdine (DLV; Upjohn, Kalamazoo, Mich.), and nevirapine (NVP; Boehringer Ingelheim Pharmaceuticals, Ridgefield, Conn.); and the protease inhibitors saquinavir (SQV; Roche, Welwyn Garden City, United Kingdom) and ritonavir (RTV; Abbott, Abbott Park, Ill.). The purified drugs were kindly provided by the manufacturers.

Nucleotide sequence accession numbers. The nucleotide and amino acid sequences of codons 33 to 235 of the RT genes and proteins from the 14 HIV-1 subtype F isolates have been submitted to GenBank (accession no. Y16138 to Y16151).

RESULTS

Genetic analysis. Figure 1 shows the amino acid alignment of codons 33 to 235 of the RT genes of the 14 HIV-1 subtype F isolates. The sequence of the RO-BCI23 isolate was more similar to that of the subtype B consensus sequence in the first part of the RT gene (subtype B structure in sequences encoding T39, E40, and I135) but was more variable than the other subtype F isolates in the second half of the RT gene (close to the binding pocket). Compared to the subtype B consensus sequence, the RO-BCI23 protein bore four mutations close to the active site of the RT protein (E169D, K173A, Q174K, and D177E).

At position 60, all but one of the strains originating in nosocomially infected Romanian children (RO-BCI7, RO-BCI8, RO-BCI9, RO-BCI11, RO-BCI12, RO-BCI15, and RO-BCI16) bore a valine (as in the subtype B consensus sequence), whereas the strains isolated from adults (RO-BCI17, RO-BCI18, RO-BCI19, RO-BCI20, and RO-BCI23), a vertically infected child (RO-BCI13), and a nosocomially infected child from whom the strain was isolated in 1994 (RO-BCI1) bore an isoleucine. Conversely, at position 39, all but one (RO-BCI17) of the strains isolated from adults bore a threonine, like subtype B strains, whereas all those isolated from nosocomially infected children bore an alanine.

Phylogenetic analysis of HIV-1 RT sequences. Phylogenetic analysis of the RT nucleotide sequences by the neighbor-joining and maximum-likelihood methods gave similar results.
Phylogenetic trees were constructed by using the 14 Romanian HIV-1 RT sequences, representative RT sequences of subtype B strains, and sequences belonging to different subtypes obtained from the database (25). Figure 2 shows the phylogenetic tree constructed by neighbor joining. High bootstrap values were obtained at the relevant nodes, indicating that subtypes B, D, and F each form a consistent clade. Subtype A was composed of five different strains defined as A or E on the basis of the env classification, whereas recombinant strains IBNG and MAL were subtype outliers.

The subtype F phylogenetic tree showed that the strains from nosocomially infected Romanian children formed a cluster, as was previously observed by analyzing the env sequence (1). The RT sequence of a strain from a vertically infected child (RO-BCI13) clustered with the adult sequences. The RT sequence of a strain from a vertically infected child (RO-BCI13) was isolated from a vertically infected child. Strains RO-BCI17, RO-BCI18, RO-BCI19, RO-BCI20, and RO-BCI23 were isolated from HIV-1-infected adults.

F RT amino acid sequences and other group M sequences was 7.6% (range, 6.00 to 11.59%).

Phenotypic susceptibility. The IC_{50}s of nucleoside analogs ZDV and 3TC were similar to those for wild-type subtype B field isolates. Although the IC_{50}s were higher for the subtype F strains than for the subtype B strains, all the subtype F isolates were susceptible to protease inhibitors. All were also sensitive to the nonnucleoside RT inhibitors NVP and DVL. Susceptibility to the third nonnucleoside RT inhibitor, TIBO derivate R82913, was lower for two isolates (Table 2); one isolate (RO-BCI11) showed borderline susceptibility, with a moderate increase in IC_{50} and IC_{90} (0.30 and 1.1 μM, respectively), the second strain (RO-BCI23) showed a significant increase in both IC_{50} and IC_{90} (0.53 and 2.02 μM, respectively). This phenotype was not associated with any of the known mutations linked to TIBO resistance. However, the RO-BCI23 isolate showed the most variable RT sequence of the subtype F isolates and presented different residues close to the active site of the RT. We therefore assessed the phenotypic susceptibilities of all the available subtype F isolates to TIBO. The TIBO IC_{50} (mean ± standard deviation) for 12 subtype F isolates was 0.07 ± 0.06 μM (range, 0.01 to 0.2 μM), and the IC_{90} was 0.4 ± 0.27 μM (range, 0.01 to 0.88 μM), meaning that all 12 strains were susceptible.

![FIG. 2. Phylogenetic analysis comparing the RT regions of HIV-1 pol genes from different strains. Tree topology was inferred by the neighbor-joining method. The tree was based on an alignment of nucleotides from which columns containing gaps have been deleted (597 nucleotides). The tree was rooted with HIV-1 group O sequences. The numbers given at the branch points are the 50% threshold majority consensus values for 100 bootstrap replicates. Vertical distances are given for clarity. The cluster of sequences from nosocomially infected children formed a separate branch within the Romanian sequence cluster with a high bootstrap value.](http://jvi.asm.org/)

### TABLE 1. Nucleotide and amino acid divergences between subtype F and other group M subtype and group O RT sequences

<table>
<thead>
<tr>
<th>isolate group</th>
<th>% Divergence from subtype F (range)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>nucleotides</td>
</tr>
<tr>
<td>Group M</td>
<td>10.94 (8.04–14.84)</td>
</tr>
<tr>
<td>Subtype B</td>
<td>10.04 (8.04–13.15)</td>
</tr>
<tr>
<td>Subtype A</td>
<td>11.90 (9.35–14.84)</td>
</tr>
<tr>
<td>Subtype D</td>
<td>11.01 (9.55–11.96)</td>
</tr>
<tr>
<td>Group O</td>
<td>32.09 (29.9–33.52)</td>
</tr>
</tbody>
</table>

*Average intrasubtype F divergence was 3.56% (range, 1.54 to 6.36%) for nucleotides and 3.7% (range, 1.57 to 6.7%) for amino acids.*
HIV-1 SUBTYPE F RT SEQUENCE AND DRUG SUSCEPTIBILITY

Performing analysis on 11 HIV-1 group O isolates as previously described (9).

**IC50s and IC90s** were measured for isolates from untreated patients (a, b).

**TABLE 2. IC50s and IC90s of nucleoside and nonnucleoside RT inhibitors and protease inhibitors of HIV-1 subtype F isolates, reference HIV-1 isolates, and HIV-2 ROD.**

<table>
<thead>
<tr>
<th>Isolate</th>
<th>ZDV (µM)</th>
<th>3TC (µM)</th>
<th>DLV (µM)</th>
<th>NVP (µM)</th>
<th>TIBO (µM)</th>
<th>SQV (µM)</th>
<th>RTV (µM)</th>
</tr>
</thead>
<tbody>
<tr>
<td>RO-BCI1</td>
<td>&lt;0.002</td>
<td>0.03</td>
<td>0.03</td>
<td>0.10</td>
<td>0.10</td>
<td>0.03</td>
<td>0.03</td>
</tr>
<tr>
<td>RO-BCI16</td>
<td>&lt;0.002</td>
<td>0.04</td>
<td>0.03</td>
<td>0.10</td>
<td>0.10</td>
<td>0.04</td>
<td>0.04</td>
</tr>
<tr>
<td>RO-BCI23</td>
<td>&lt;0.002</td>
<td>0.05</td>
<td>0.03</td>
<td>0.10</td>
<td>0.10</td>
<td>0.05</td>
<td>0.05</td>
</tr>
<tr>
<td>RO-BCI3</td>
<td>&lt;0.002</td>
<td>0.06</td>
<td>0.04</td>
<td>0.10</td>
<td>0.10</td>
<td>0.06</td>
<td>0.06</td>
</tr>
<tr>
<td>RO-BCI7</td>
<td>&lt;0.002</td>
<td>0.07</td>
<td>0.04</td>
<td>0.10</td>
<td>0.10</td>
<td>0.07</td>
<td>0.07</td>
</tr>
<tr>
<td>RO-BCI8</td>
<td>&lt;0.002</td>
<td>0.08</td>
<td>0.04</td>
<td>0.10</td>
<td>0.10</td>
<td>0.08</td>
<td>0.08</td>
</tr>
<tr>
<td>RO-BCI10</td>
<td>&lt;0.002</td>
<td>0.09</td>
<td>0.04</td>
<td>0.10</td>
<td>0.10</td>
<td>0.09</td>
<td>0.09</td>
</tr>
<tr>
<td>RO-BCI12</td>
<td>&lt;0.002</td>
<td>0.10</td>
<td>0.04</td>
<td>0.10</td>
<td>0.10</td>
<td>0.10</td>
<td>0.10</td>
</tr>
</tbody>
</table>

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**REFERENCES**


