List of mutations for surveillance of transmitted drug resistant HIV: 2009 update

**RESULTS (CONT.)**

**Exclusion of rare mutations**

We excluded rare drug-resistance mutations, defined as those mutations present at a frequency below 1% among treated individuals in the subtype having the highest prevalence of that mutation. Because the number of isolates from treated persons for some subtypes was low, we also required that the mutation be present in sequences from at least two different persons with the subtype having the highest prevalence of that mutation.

**Sequences analyzed**

We analyzed publicly available RT and PI sequences from drug-naive individuals, with two exclusions:

1. Sequences from primarily infected persons in regions with high rates of transmitted resistance.
2. Sequences with two or more mutations from the 2007 SDRM list based on the premise that the mutations in such sequences could have resulted from previous selective drug pressure.

**Analysis**

- We identified mutations present on ≥4 lists and analyzed the sequences from drug-naive individuals, within subtypes A, B, C, D, F, G, CRF01_AE, and CRF02_AG, for the frequency of those mutations.
- For each of the mutations from the previous analysis that met our criteria for non-polymorphism or for non-occurrence at a highly polymorphic position, we examined publicly available sequences for the frequency of each mutation among individuals reported to be treated with the relevant drug class. Mutations that met the criteria for exclusion were not included in the tables.

**RESULTS**

<table>
<thead>
<tr>
<th>Mutation</th>
<th>Frequency among treated individuals (in subtype)</th>
</tr>
</thead>
<tbody>
<tr>
<td>D80A</td>
<td>5% in subtype B, 2% in subtype C, 0.6% in subtype G, 1.1% in subtype F, and 1.5% in CRF01_AE.</td>
</tr>
<tr>
<td>D80L</td>
<td>0.1% in subtype B, 0.1% in subtype C, and 0.1% in subtype F.</td>
</tr>
<tr>
<td>N34T</td>
<td>0.8% in subtype C, 0.5% in subtype B and CRF01_AG, 0.6% in subtype G, 1.2% in subtype F, and 1.5% in CRF01_AE.</td>
</tr>
</tbody>
</table>

**DISCUSSION AND CONCLUSIONS**

- **The 2007 WHO list of SDRMs was used in several published surveys and has facilitated comparison of results and minimized misclassification of transmitted resistance.** The new list, based on substantially more sequences, includes several new mutations. Namely, the numbers of B and non-B sequences were analyzed for the new list compared to the 2007 list analysis.
- **Among the 93 mutations on the 2009 SDRM list, three occurred at a frequency of more than 3% in subtypes with fewer than 1,000 sequences** and 46 occurred at a frequency between 0.1% and 0.5% in at least one subtype. All lists of mutations used to define transmitted resistance include mutations that are polymorphic to some degree; their contribution to probable overestimates of transmitted resistance should be acknowledged. Our list attempts to minimize this contribution and other elements that could lead to inaccurate estimates of transmitted resistance.