Circulation of Multiple Patterns of Unique Recombinant Forms B/CRF02_AG in France

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BACKGROUND

HIV-1 group M is characterised by substantial genetic diversity, and includes nine subtypes, more than 45 CRFs, and numerous Unique Recombinant Forms (URFs).

In France, the epidemic is characterised by:
- predominance of subtype B strains,
- increasing prevalence of non-B subtypes (fig.1), CRF02_AG being the most prevalent,
- increasing at-risk behaviour in the MSM population.

The high prevalence and co-circulation of B and CRF02_AG strains in this population raise the possibility that recombinant forms might emerge and spread.

METHODS

Screening for subtyping discords in different regions of the genome
Near full length sequencing and pattern characterization
Searching for parental strains or minor recombinants using Single Genome Analysis
Analysis of the phylogenetic relationships between the B/CRF02 recombinants

RESULTS

Seven samples were selected from seven patients, of whom five are MSM (tab.1)

<table>
<thead>
<tr>
<th>Patient</th>
<th>Age</th>
<th>Sex</th>
<th>Risk group</th>
<th>Year of diagnosis</th>
<th>Month of sampling</th>
<th>CD4 T cells (cells/mm3)</th>
<th>RNA viral copies/mL</th>
<th>URF identified in patient</th>
<th>Reference sequences</th>
</tr>
</thead>
<tbody>
<tr>
<td>P1</td>
<td>67</td>
<td>M</td>
<td>homosexual</td>
<td>2008</td>
<td>2008</td>
<td>490</td>
<td>5.6</td>
<td>URF1, B503</td>
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<td>P2</td>
<td>46</td>
<td>F</td>
<td>homosexual</td>
<td>2004</td>
<td>2004</td>
<td>584</td>
<td>3.7</td>
<td>URF2, B651</td>
<td></td>
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<td>P3</td>
<td>38</td>
<td>M</td>
<td>homosexual</td>
<td>2006</td>
<td>2006</td>
<td>549</td>
<td>5.5</td>
<td>URF3, B633</td>
<td></td>
</tr>
<tr>
<td>P4</td>
<td>58</td>
<td>F</td>
<td>homosexual</td>
<td>2002</td>
<td>2002</td>
<td>-</td>
<td>-</td>
<td>URF4</td>
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<td>P5</td>
<td>25</td>
<td>M</td>
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<td>2010</td>
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<td>159</td>
<td>5.1</td>
<td>URF5, B636</td>
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<tr>
<td>P6</td>
<td>39</td>
<td>M</td>
<td>homosexual</td>
<td>2006</td>
<td>2006</td>
<td>381</td>
<td>5.2</td>
<td>URF6, B650</td>
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<td>32</td>
<td>M</td>
<td>homosexual</td>
<td>2006</td>
<td>2006</td>
<td>387</td>
<td>4.2</td>
<td>URF7, B638</td>
<td></td>
</tr>
</tbody>
</table>

Tab. 1: Characteristics of the seven patients from whom the samples were selected, and of the corresponding URFs characterized

Two of the seven new URFs involve a 3rd subtype (fig. 2.a). The seven recombination patterns are distinct from each other (fig. 2.a), and from the only two previously described B/CRF02 URFs from Cyprus (Koussiappa et al., 2009) and Spain (Holguin et al., 2008).

In the env gp120 region, URF3 and URF7 appeared to be linked despite their different recombination patterns.

There was no evidence of parental or minor recombinant strains circulation, although polymorphism was observed for all the strains tested (fig. 3).

CONCLUSIONS

The complexity of the molecular epidemiology is growing in France due to the rise of non-B strains prevalence and to subsequent recombinations. The predominant forms, subtype B and CRF02, are co-circulating in the MSM population and frequent co-infections led to local emergence of several URFs. One of those (URF7) being linked with a cluster of CRF02_AG sequences identified in the MSM population of Paris. The absence of parental strains suggests direct transmission of these strains, indicating that they could spread in particular within this population. A surveillance is needed to determine if this dynamic could lead to the genesis of a new CRF_B/CRF02_AG in France.