DUAL HIV-1/M+O INFECTIONS AND HIV-1/MO RECOMBINANTS IN FRANCE FROM 2004 TO 2014
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The aim of this study was to determine the circulation level of dual M+O recombinants (MOrecs). The first dual M+O infections were described in Benin in 1995 and HIV-1 exhibits a high genetic diversity. It is currently divided into 4 groups: M, N, O and P as recombinants now account for more than 20% of HIV-1 infections links with Western Central Africa, sporadic cases of superinfection/dual infections.

The presence of both M and O genomes were detected in 10/141 (7%) HIV-O infected patients. For each of these MO recombinants, whole genome or partial sequences were analyzed. All the MO recombinant genetic patterns were different with breakpoints in LTR (1 in 8), gp120 (1 in 8), RT (3 in 8), IN (2 in 8), gp41 (1 in 8) and/or accessory genes (9 in 8) as shown in the figures 2 and 3. Heterogeneity of accessory genes pattern was observed (at least 2 and 5 respectively).

The 2 viruses found in the same patient RBF221 exhibited multiple breakpoints in the accessory genes (at least 2 and 5 respectively).

The presence of both M and O genomes were detected in 10/141 (7%) HIV-O infected patients. The analysis of these cases allowed us to identify different situations:

- 6 MO recombinants without parental strains
- 3 MO recombinants associated with the HIV-O parental strain
- 2 MO recombinants with both the M and O parental strains in 1 patient
- 2 MO recombinants involving accessory genes

Although all described in Cameroonian native patients, we show 11 HIV-M+O dual infections and/or HIV-MO recombinant infections in the last decade in France, highlighting these phenomenons are not so rare. Moreover, the presence of MO recombinants circulating without the presence of parental O or M strains, and in epidemiologically linked patients demonstrate they are fit enough to be transmitted and spread. Finally, as HIV-O are naturally resistant to NNRTIs, the transmission of dual HIV-M+O infections or MO recombinants carrying HIV-O genomic fragments underline the importance of searching for these forms, evaluating their spread dynamics and following the possible emergence of a CRF_MO.

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