Evidence of Intra-Familial Transmission of an HIV-1 M/O Intergroup Recombinant Virus

To cite this version:
Paul-Alain Ngoupo, Serge Alain Sadeuh Mba, Fabienne de Oliveira, V Ngono, L Ngono, et al.. Evidence of Intra-Familial Transmission of an HIV-1 M/O Intergroup Recombinant Virus. IRIB, Jun 2015, Rouen, France. hal-02130009

HAL Id: hal-02130009
https://normandie-univ.hal.science/hal-02130009
Submitted on 15 May 2019
HIV-1 is divided into four groups: M (major), O (outlier), N (non-M, non-O) and P. HIV-1 groups M and O co-circulate in Cameroon and dual infections as well as HIV-1 M/O intergroup recombinant viruses have been reported in some patients [1-3]. Recent data has described infection with HIV-1 M/O intergroup recombinant virus in the absence of dual infections thereby suggesting a direct transmission of the recombinant virus [4]. In this study, we described and characterized an HIV-1 M/O intergroup recombinant virus in the absence of dual infection in a couple living in Cameroon. Therefore, we provide for the first time evidence of a direct transmission of an HIV-1 M/O intergroup recombinant virus from one person to another.

## METHODS

### 1- Patients and samples:
- **RECO03 (Husband):** October 2012, March 2013 and September 2013.
- **RECO24 (Wife):** April and September 2013

### 2- Serological and molecular characterization
- **HIV serotyping and Viral load:** Prior to viral load analysis, each sample was subjected to HIV serotyping using envelope (V3 and gp41) peptides. Viral loads were further determined using HIV-1 non-specific, HIV-1 M and HIV-1 O specific techniques.
- **HIV-1 group M and O specific PCRs:** Presence of potential recombinant virus was investigated using HIV-1 M and HIV-1 O specific PCRs targeting the Protease (PROT), Reverse transcriptase (RT), Integrase (INT) and envelope (gp41) genes of HIV-1 M groups and O.
- **PCR for recombination break point:** The previously reported recombination hotspot in the vpr gene was investigated using RT-nested PCRs.
- **Complete genome analysis:** Near full-length genome sequences of the viruses detected in both spouses were determined by amplification and sequencing of seven partially overlapping sub-genomic regions.
- **Phylogenetic and recombination profile analyses:** were performed to investigate the genetic relatedness between viruses from both spouses.

### RESULTS

HIV serotyping (envelope peptides) indicated that both REC003 and REC024 were reactive with only peptides of HIV-1 group O. Using group-specific RT-nested PCRs, we generated HIV-1 M amplicons in the POL (PROT, RT and INT) region from both REC003 and REC024 while HIV-1 O amplicons were obtained ENV (gp41) region. In vpr only the PCR using homologous primers M/O yields a positive result. These results thus indicated the presence of a recombinant virus in both patients.

### Phylogenies of the POL and ENV derived sequences

### REFERENCES


### ACKNOWLEDGMENTS

We would like to thank:
- The Agence Nationale de Recherche sur les Hépatites virales (ANRS N°112256) for the financial support
- The patients for their participation to this study