# New Insights into HIV-1 Group O Diversity

Marie Leoz, Florence Damond, Jude Kfutwah, Jean-Christophe Plantier, French Res-O Network

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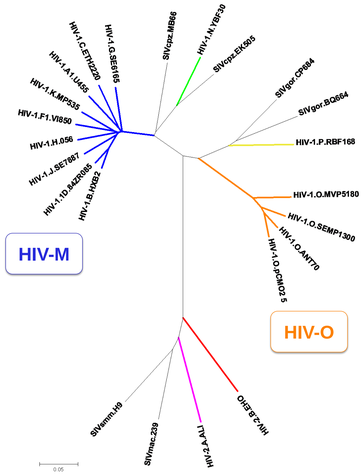
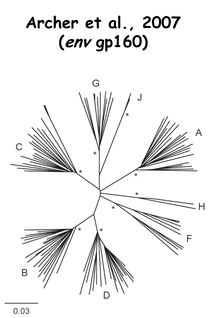
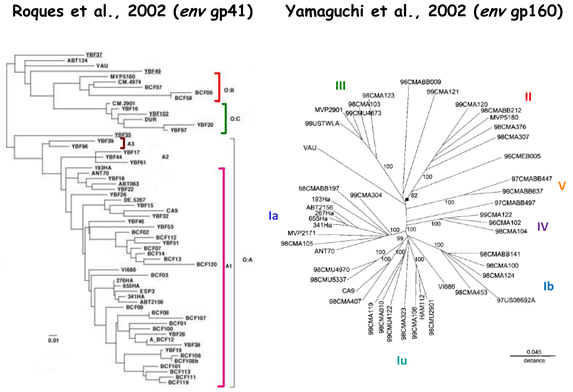
## BACKGROUND




At least twelve cross-species transmissions of SIV (Simian Immunodeficiency Viruses) to humans led to the emergence of 4 HIV type 1 (M, O, N, P) and 8 HIV type 2 (A-H) groups.



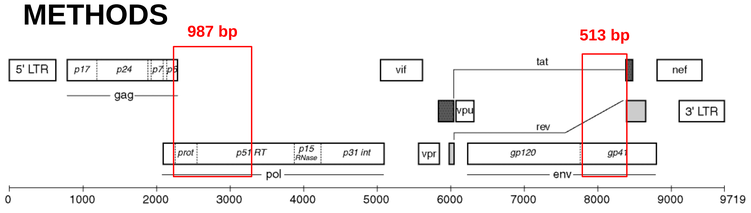

HIV type 1 group M (HIV-M) became pandemic and strain exportations followed by founder effects led to the definition of nine subtypes.




HIV-O remained endemic to Cameroon with limited exportation to some closely related countries. Previous nomenclature proposals, based on few sequences available then, highlighted a broad genetic diversity and opposed strains from a major clade (A or I) to the others.

**OBJECTIVE** : To explore HIV-O diversity through the largest series of HIV-O sequences, from Cameroon (HIV-O diagnosis and follow-up in the Centre Pasteur du Cameroun) and France (RES-O surveillance network)**.**

## METHODS




Sequenced in 241 patient samples

**112 + 125**

Sequenced in 231 patient samples

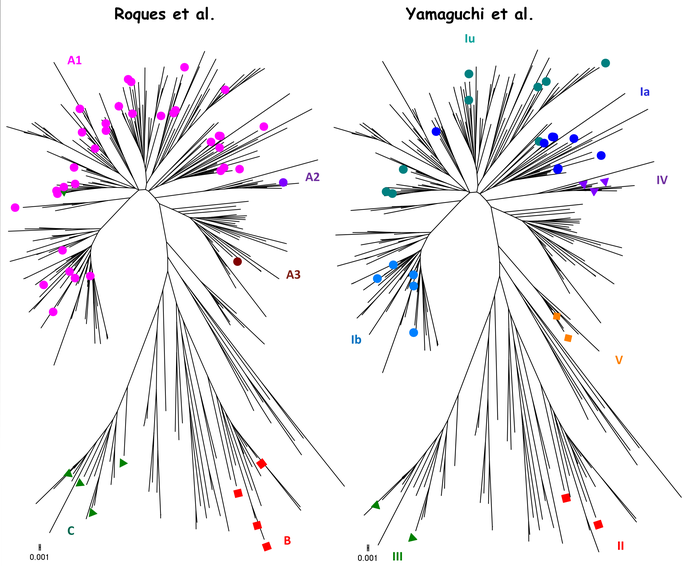
**104 + 123**

Maximum Likelihood Trees inferred from these sequences plus those available in the HIV database and classified in the nomenclature systems proposed before

## RESULTS

### Nomenclature comparison (*env* gp41)

297 sequences (231+58 from HIV database)



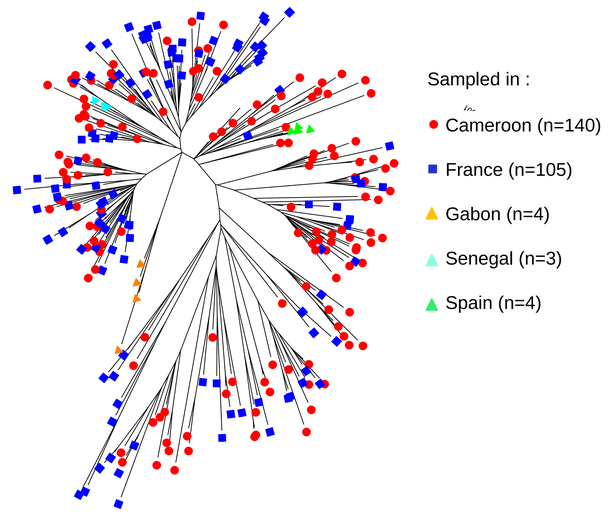

**Classification of 297 HIV-O strains according to the previous nomenclatures**

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| Roques | A 228 (76,8%) | | | | ND 7 (2,35%) | B 14 (4,7%) | C 17 (5,7%) | ND 31 (10,4%) |
| | A1 186 (62,6%) | | | A2 12 (4,0%) | A3 30 (10,1%) | | | |
| Yamaguchi | I 186 (62,6%) | | | IV 12 (4,0%) | ND 30 (10,1%) | V 7 (2,35%) | II 14 (4,7%) | III 17 (5,7%) | ND 31 (10,4%) |
| | Ia 27 (9,1%) | Ib 53 17,8%) | Iu 106 (35,7%) | | | | | |

Current nomenclature systems are partially redundant, partially discordant and fail to describe the whole HIV-O diversity.

### Phylogeographic distribution (*pol* pr-RT)

269 sequences (241+28 from HIV database)




HIV-O are circulating in France due to close history links with Cameroon (136 patients identified).

The distribution of the strains sampled in France and in Cameroon are different, but there is no evidence of a significant French cluster, unlike for the strains sampled in Gabon, Senegal or Spain.

## CONCLUSIONS

- The tree topology is less structured than the one of HIV-M : fewer clusters due to local continuous diversification
- Opposition between a short branch-length major clade and several long branch minor ones : epidemiologic / phylodynamic significance or sampling bias? Distinct phenotypic properties between those clades? (e.g. Y181C mutation in the RT)
- Need for a consensus nomenclature
- No significant clustering of strains sampled in France indicating continuous importations rather than a local spread

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