



New Insights into HIV-1 Group O Diversity

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French Res-O Network

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New Insights into HIV-1 Group O Diversity

Marie Leoz¹, Florence Damond², Jude Kfutwah³, Jean-Christophe Plantier¹ and the French RES-O Network

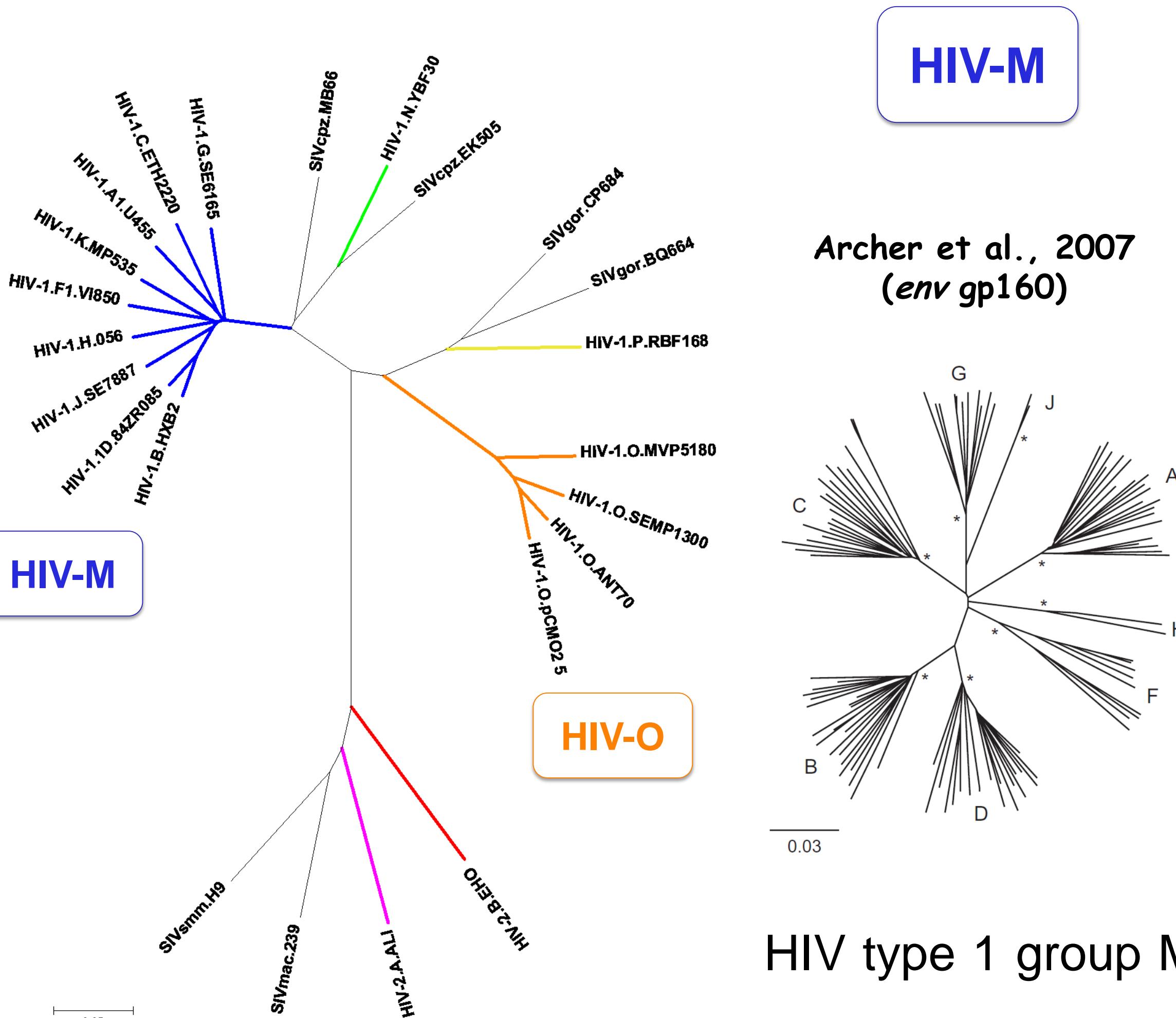
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BACKGROUND



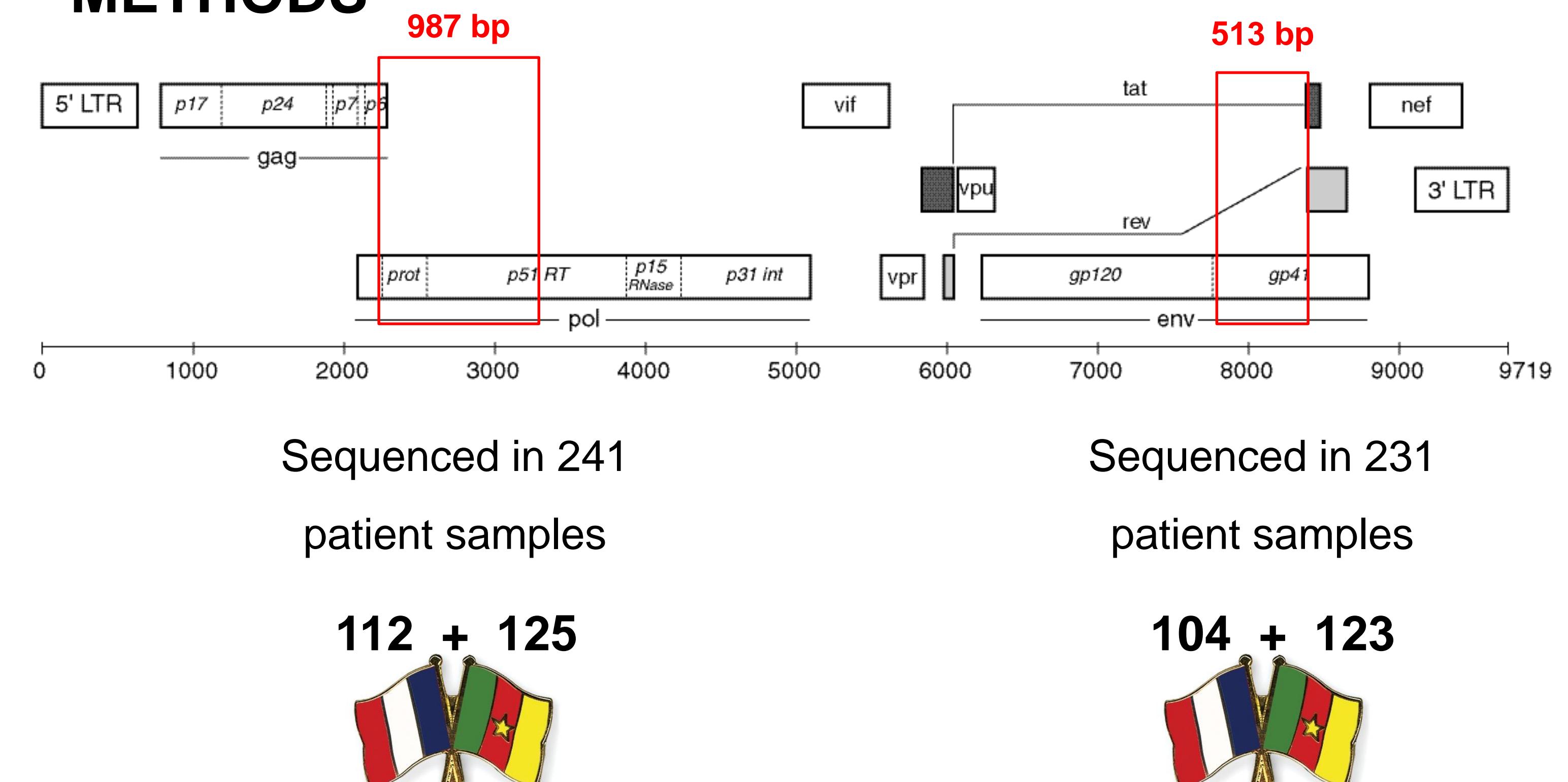
HIV type 1 group M (HIV-M) became

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-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.

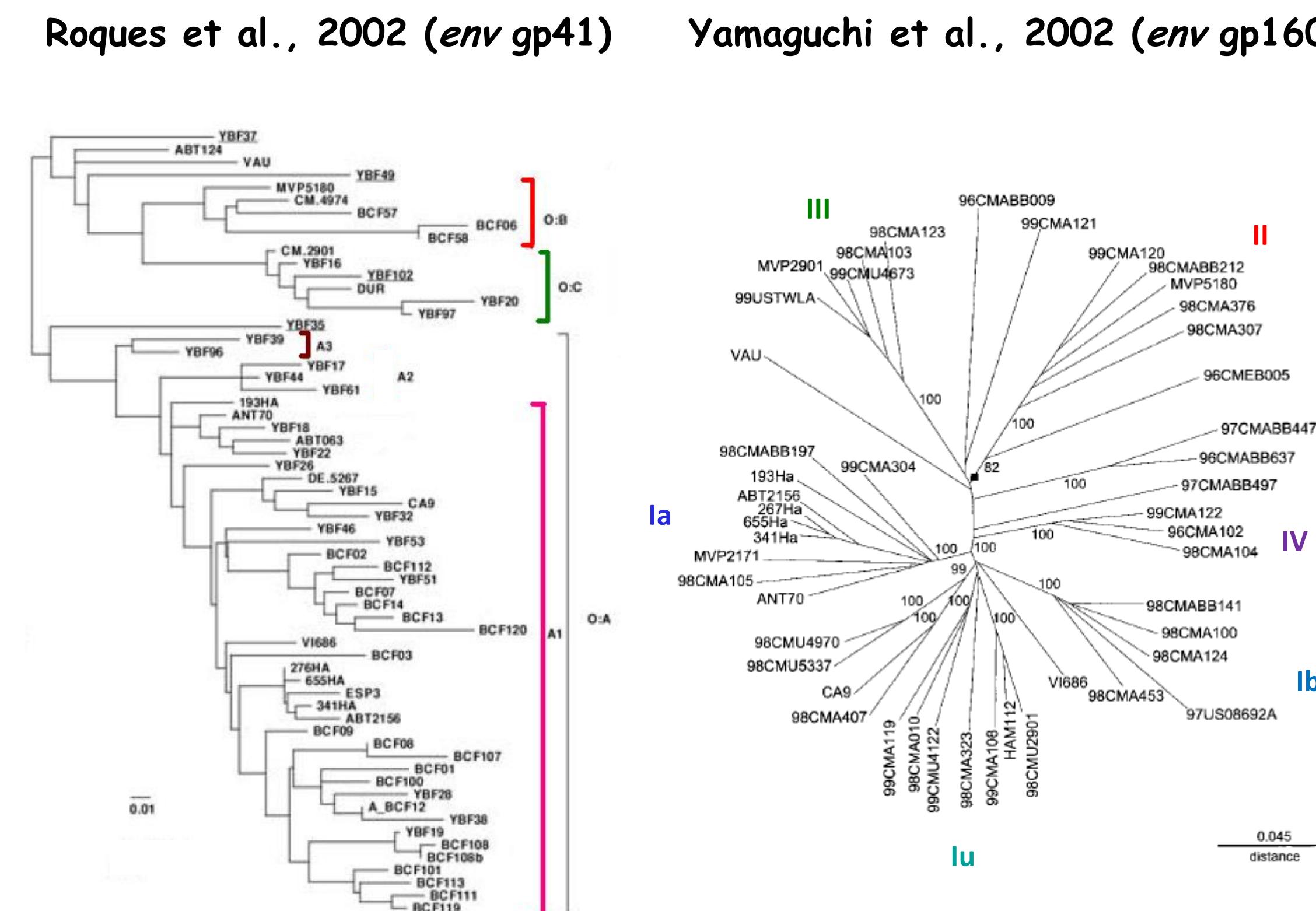
OBJECTIVE : To explore HIV-O diversity through the largest series of HIV-O sequences, from Cameroon (HIV-O diagnosis and follow-up in the Centre Pasteur du Cameroun) and France (RES-O surveillance network).

METHODS



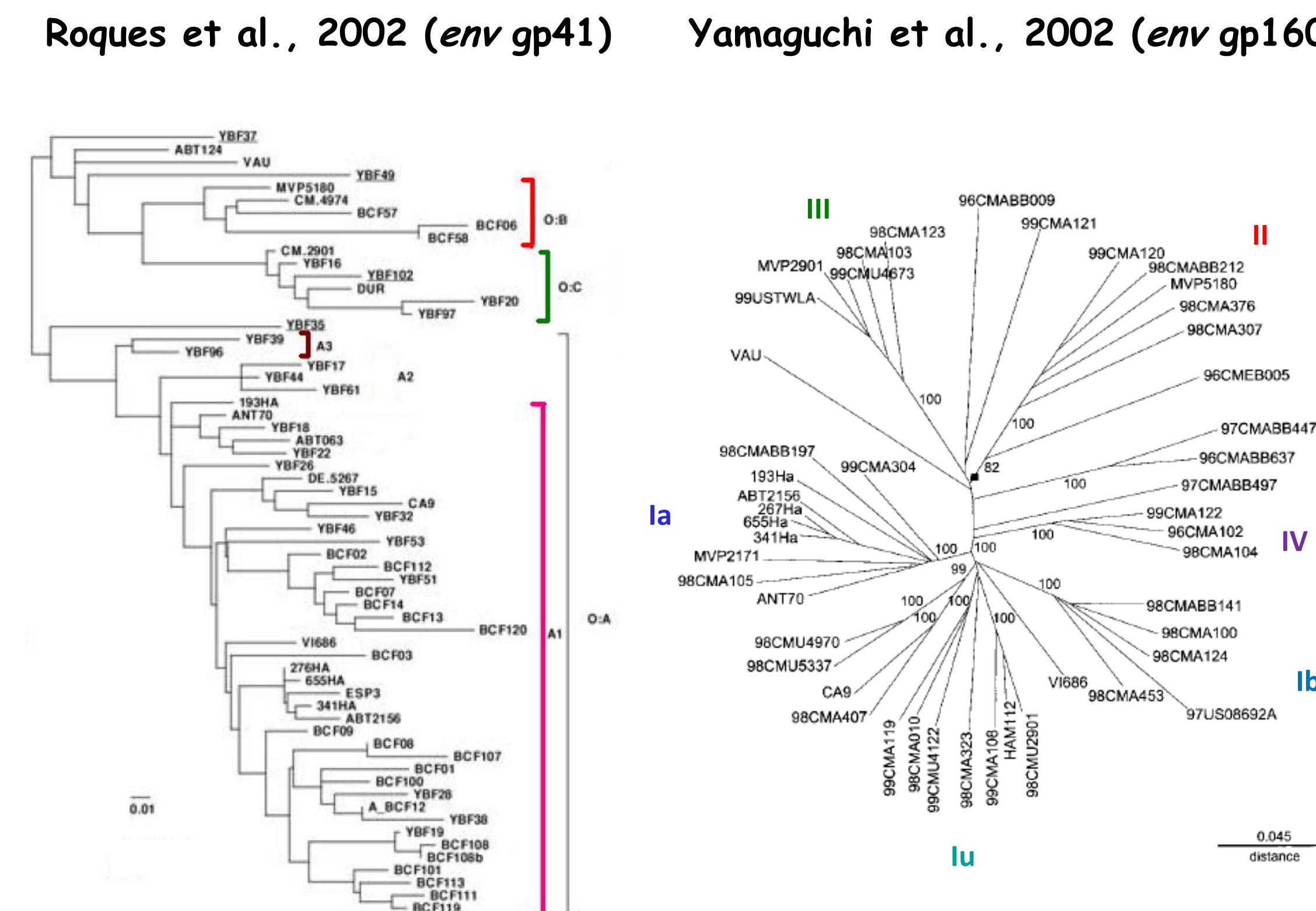
HIV-M

Archer et al., 2007 (env gp160)



HIV-O

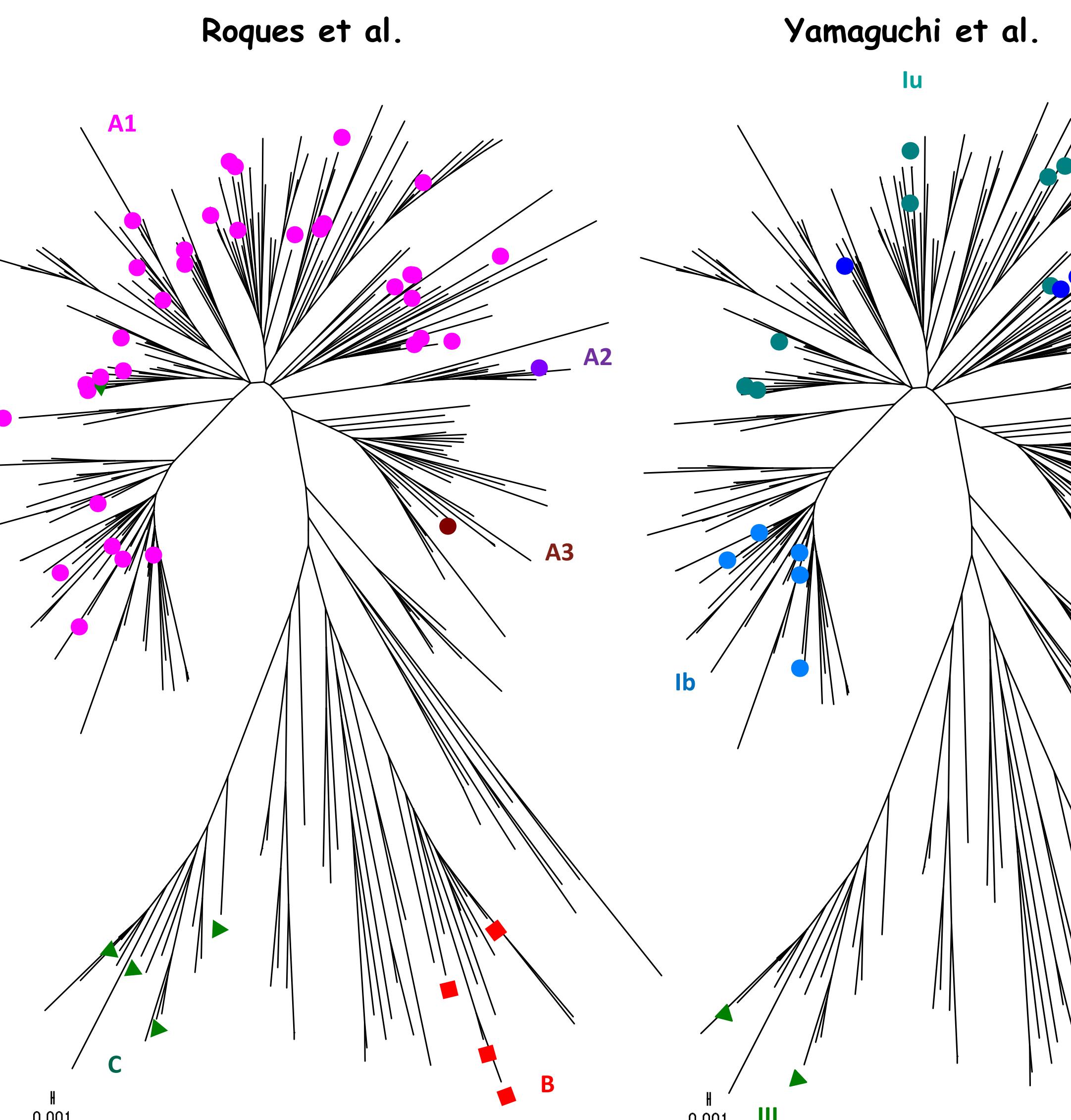
Roques et al., 2002 (env gp41) Yamaguchi et al., 2002 (env gp160)



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	B	C
	A1 186 (62,6%)	A2 12 (4,0%)	A3 30 (10,1%)	7 (2,35%)	14 (4,7%)	17 (5,7%)
Yamaguchi	I 186 (62,6%)	IV 12 (4,0%)	30 (10,1%)	7 (2,35%)	14 (4,7%)	17 (5,7%)
	Ia 27 (9,1%)	Ib 53 (17,8%)	Iu 106 (35,7%)			31 (10,4%)

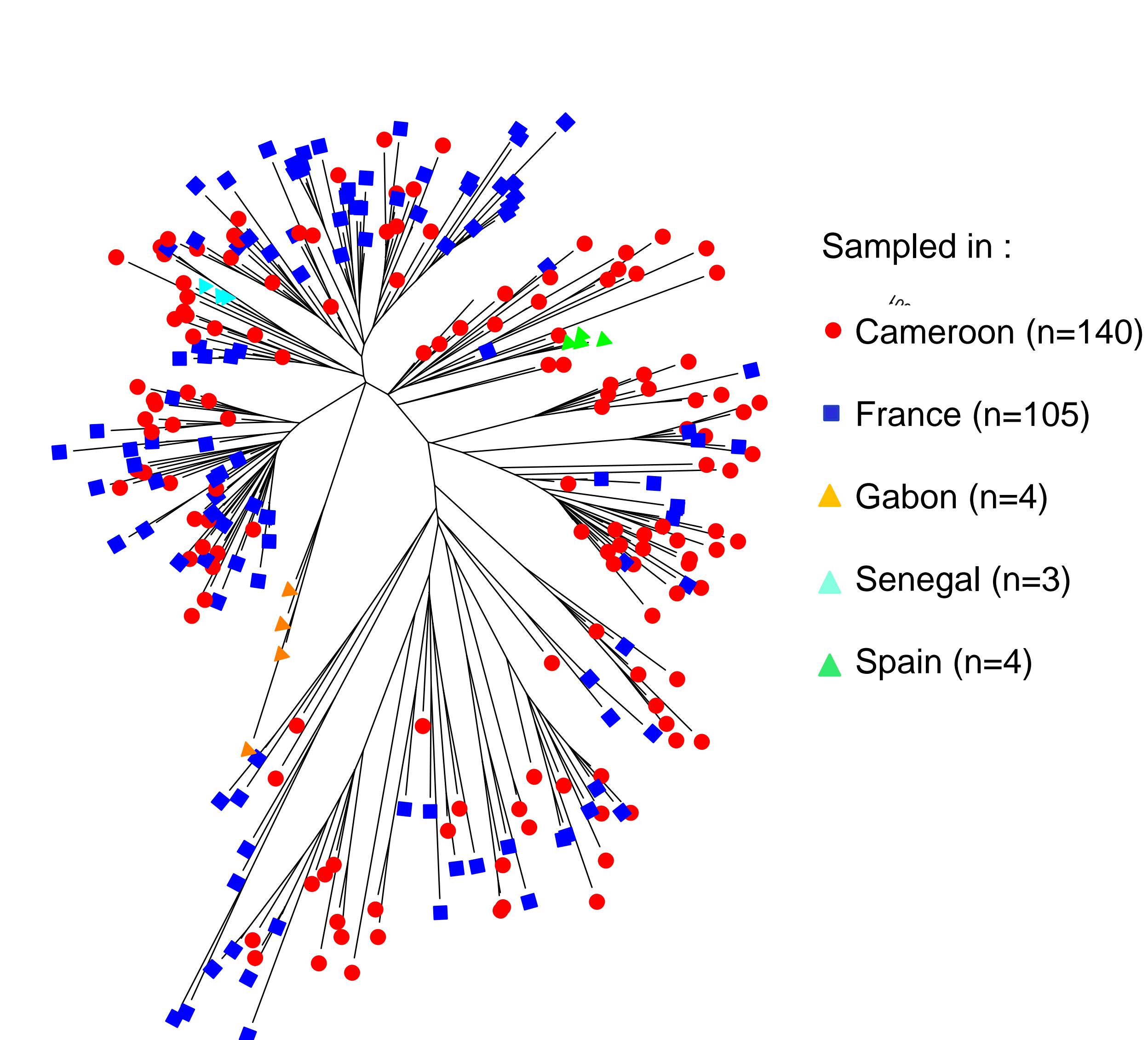
Current nomenclature systems are partially redundant, partially discordant and fail to describe the whole HIV-O diversity.

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

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.