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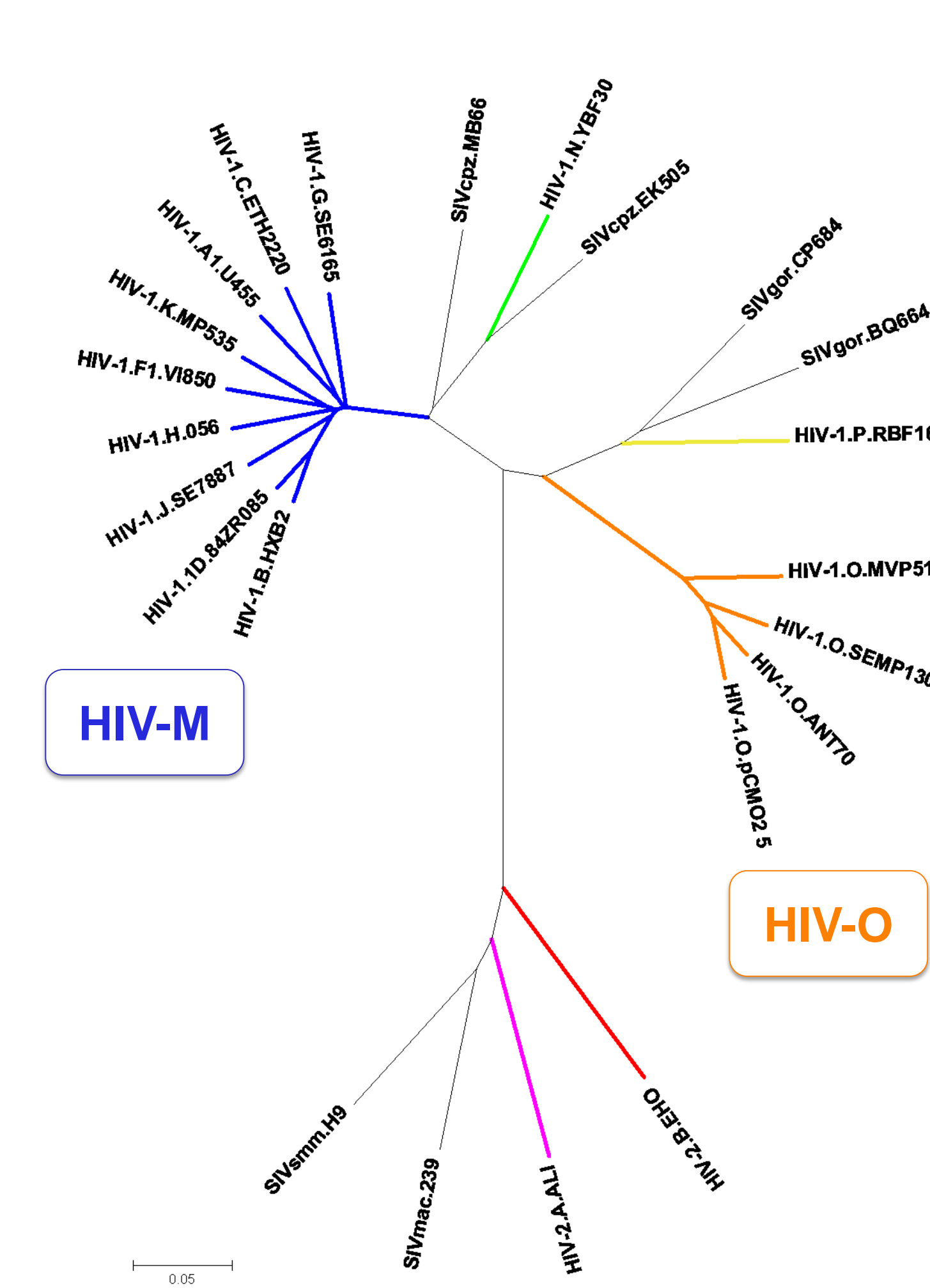
New Insights into HIV-1 Group O Diversity

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

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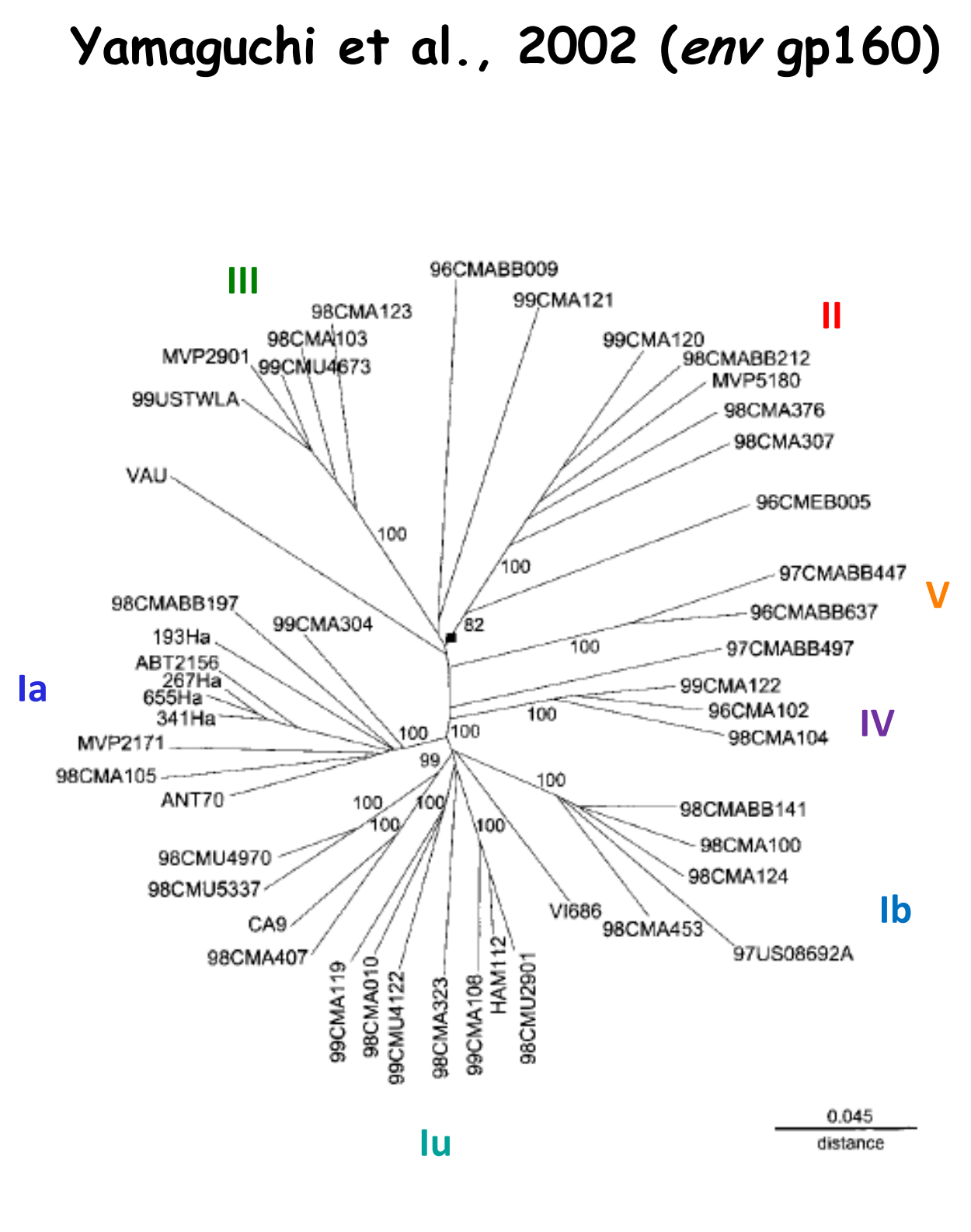
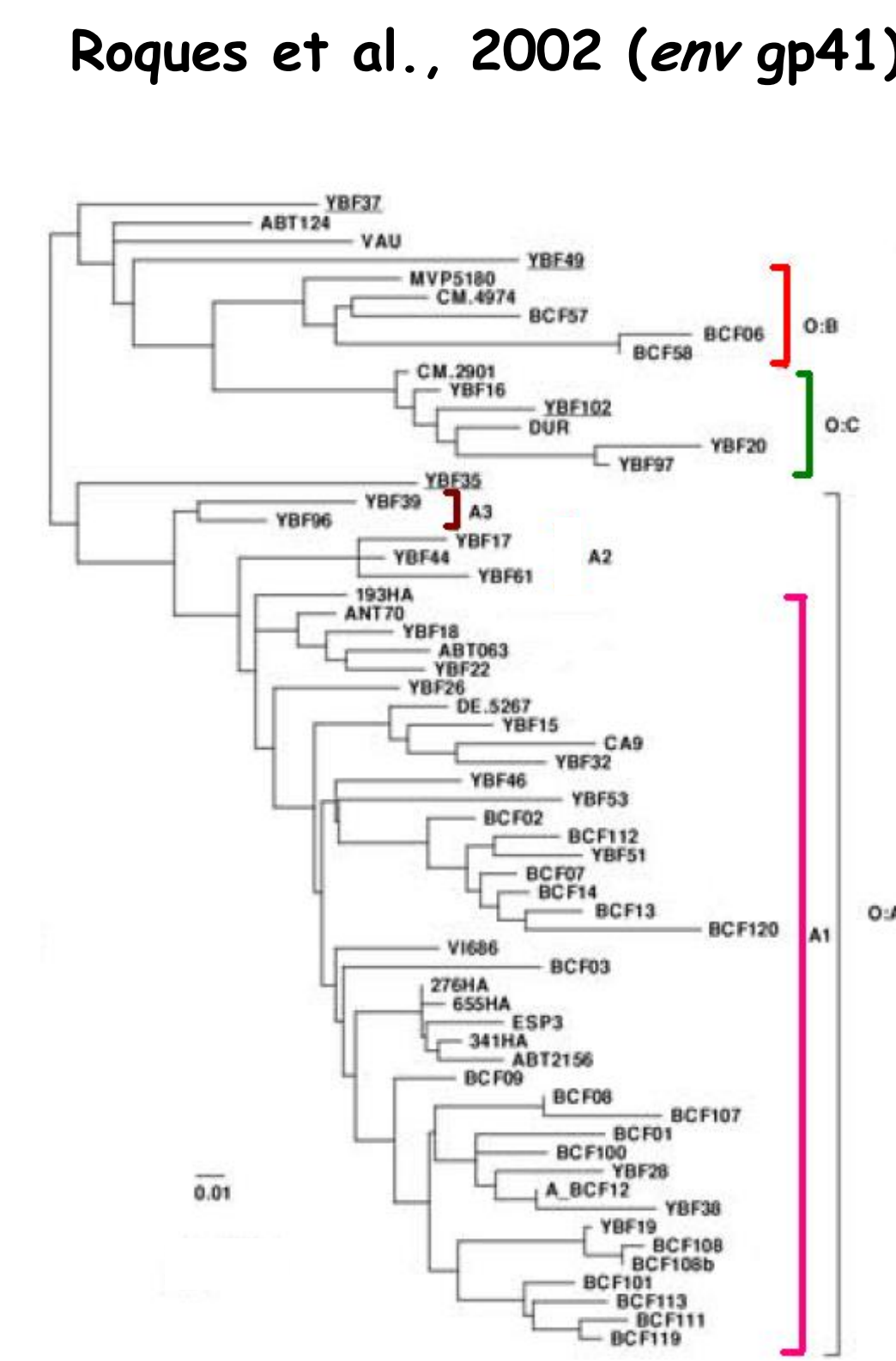
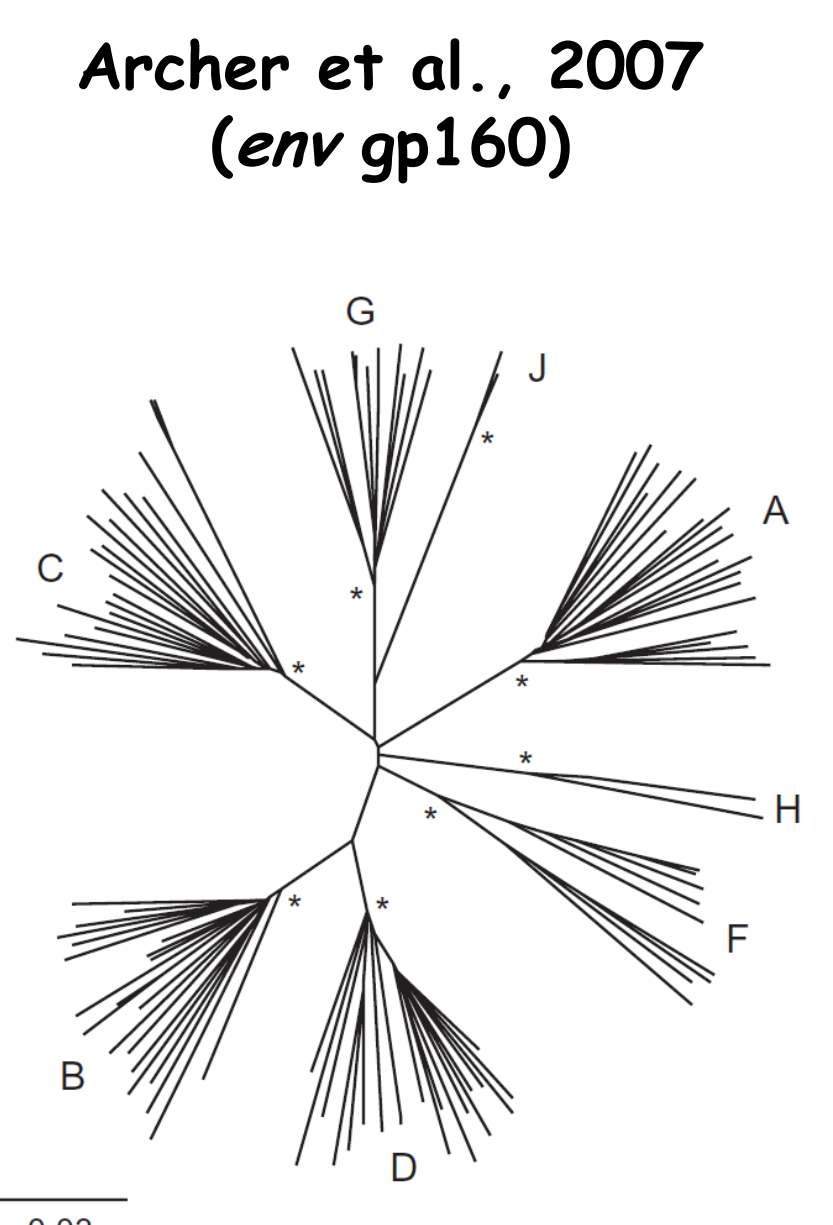
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BACKGROUND



HIV-M

HIV-O



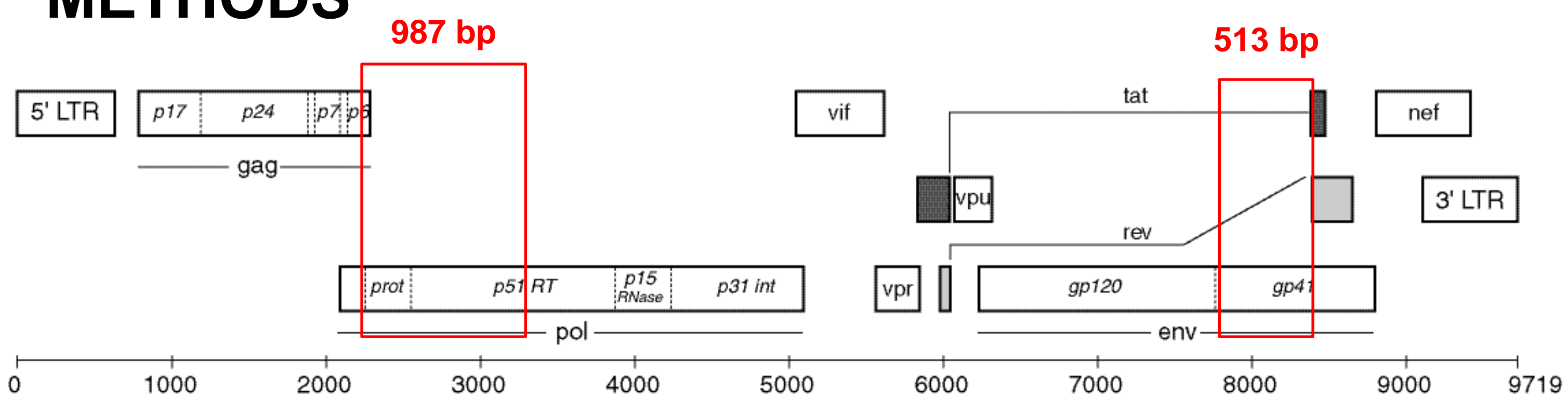
HIV type 1 group M (HIV-M) became pandemic and strain exportations followed by founder effects led to the definition of nine subtypes.

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.

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.

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

Sequenced in 231 patient samples

112 + 125

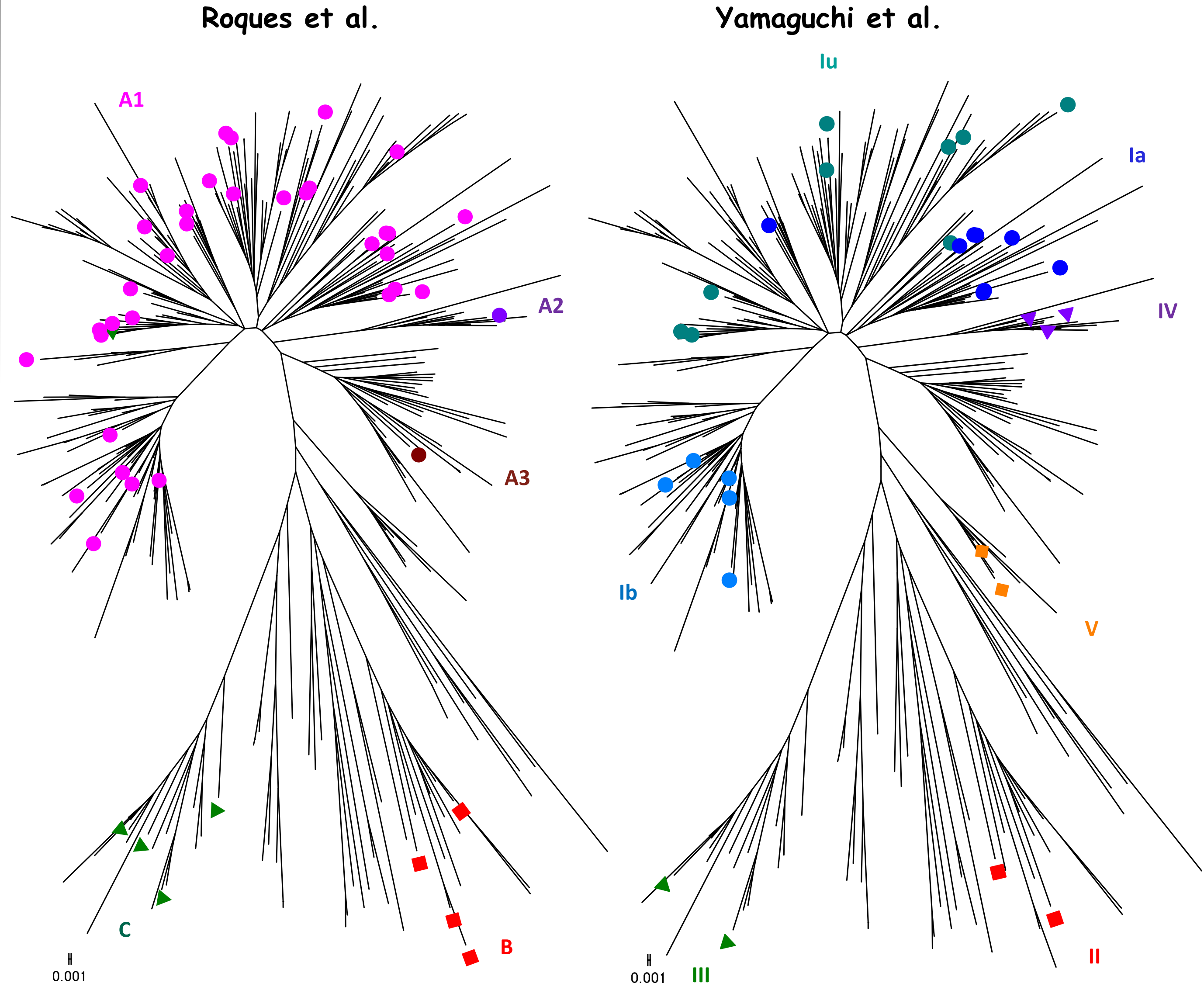
104 + 123



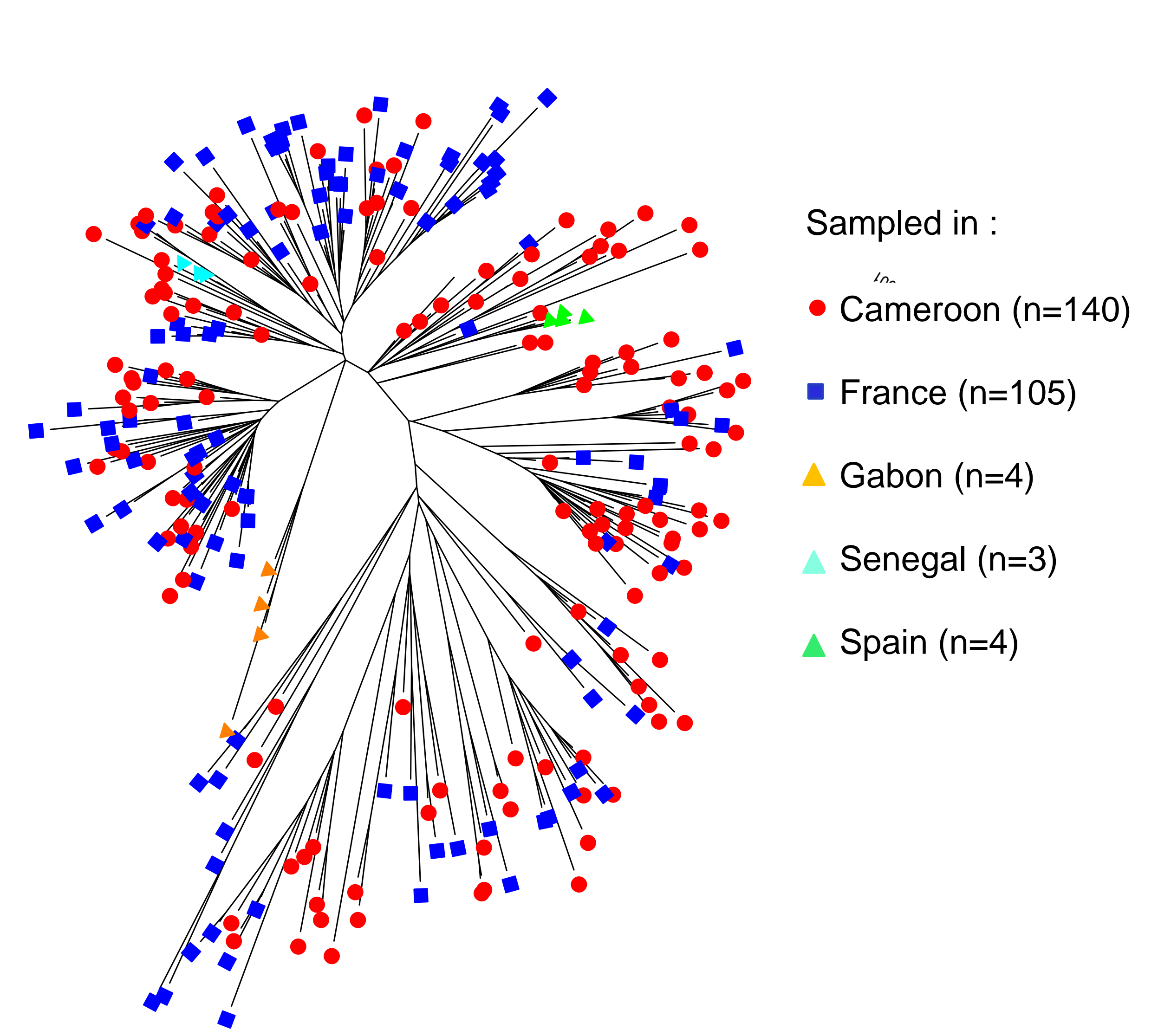
Maximum Likelihood Trees inferred from these sequences plus those available in the HIV database and classified in the nomenclature systems proposed before

RESULTS

Nomenclature comparison (env gp41)
 297 sequences (231+58 from HIV database)



Phylogeographic distribution (pol/pr-RT)
 269 sequences (241+28 from HIV database)



Sampled in :
 Cameroon (n=140)
 France (n=105)
 Gabon (n=4)
 Senegal (n=3)
 Spain (n=4)

	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%)						
Roques	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%)
	Yamaguchi	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.

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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