Supplemental Digital Content 1

Table. Characteristics of the HIV-1 strains related to groups O, N and P, used in the study.

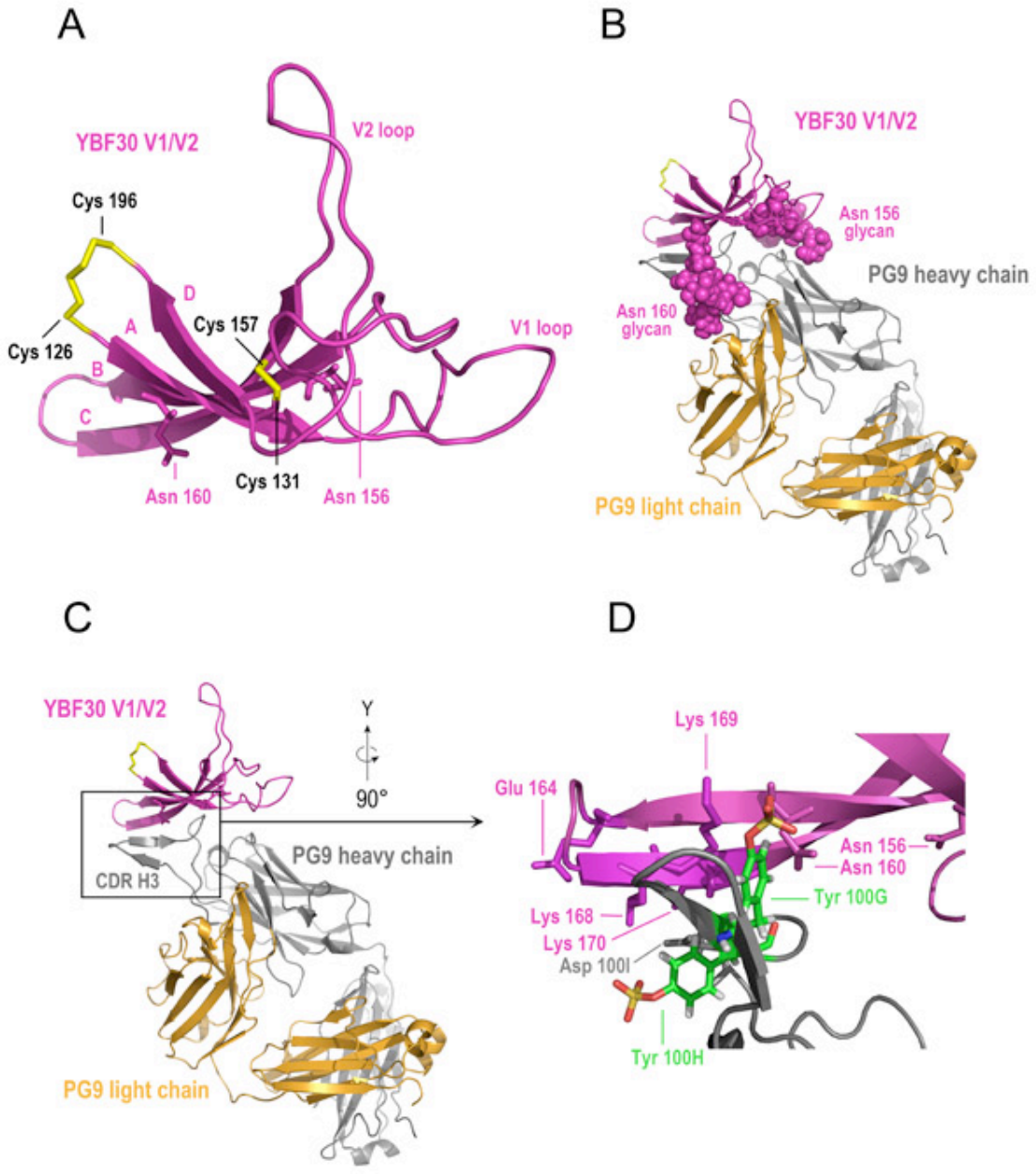
Code	Group (Clade[1])	Isolation from	Clinical stage at time of isolation	CD4+ T-cell count (/mm^3) at time of isolation	Nb of passages	Study of origin
BCF02	O (A)	PBMC	AIDS	19	≥ 2	Roques et al (30)
BCF03	O (A)	PBMC	Symptomless	97	≥ 2	Roques et al (30)
RBF125	O (B)	plasma	*NA*	*NA*	0	Depatureaux et al (38)[4]
RBF189	O (A)	plasma	AIDS	*NA*	2	Depatureaux et al (38)[4]
YBF16	O (C)	PBMC	AIDS	*NA*	≥ 2	Roques et al (30)
YBF35	O (U[2])	PBMC	AIDS	*NA*	≥ 2	Roques et al (30)
YBF37	O (U[2])	PBMC	pulmonary tuberculosis	*NA*	≥ 2	Roques et al (30)
YBF38	O (A)	PBMC	pulmonary tuberculosis	*NA*	≥ 2	Roques et al (30)
YBF39	O (A)	PBMC	AIDS	*NA*	≥ 2	Roques et al (30)
RBF168	P	PBMC	Symptomless	268	0	Plantier et al (23)
YBF30	N	PBMC	AIDS	*NA*	≥ 2	Simon et al (24)
RBF208	M-O Rec.[3]	plasma	AIDS	6	0	Vessière et al (28)

[1] Defined by the phylogenetic analysis of the Pr-RT region of the *pol* gene and at least the gp41 region of the *env* gene.
[2] Unclassified.
[3] Recombinant strain : HIV-O clade A (*pol* gene) / HIV-M subtype (*env* gene)
[4] Unpublished, patients identified in France through the RES-O network (38).

NA: not available

Supplemental Digital Content 2

Three-dimensional model of the V1/V2 domain from gp120 of the YBF30 strain of HIV-1 complexed with PG9 neutralizing antibody.



Legend. (A) Ribbon diagram of YBF30 V1/V2 loop showing the four anti-parallel β-strands (labelled A, B, C, D) forming the core domain. Side-chains of the two asparagines (Asn 156 and Asn 160) bearing the N-linked glycan chains (not shown for clarity) are shown as sticks. The two disulfide bonds of YBF30 V1/V2 are colored yellow. (B) and (C) 3D model of the V1/V2 domain of YBF30 complexed with PG9. Glycan chains of YBF30 V1/V2 which form major interactions with PG9, are represented as CPK (panel B). In panel C, glycan chains were not shown to emphasize the additional interaction formed between strand C of YBF30 with the complementarity determining region H3 of PG9 (boxed area). The heavy and light chains of PG9 are colored grey and orange, respectively. (D) Close up view of the main region of interaction of PG9 with YBF30 V1/V2 domain without the glycan chains. The complex was slightly rotated along the Y-axis so as to highlight interacting residues. Side-chains of cationic lysines of YBF30 (Lys 168, Lys 169 and Lys 170) forming electrostatic interactions with negatively charged residues of PG9 including sulphated tyrosines Tyr 100G, Tyr 100H as well as Asp 100I are represented by sticks. Glu 164 in the turn linking strand B to strand C in YBF30 is also shown. This amino acid is believed to play an important role in the sensitivity of V1/V2 loop of various HIV-1 strains to PG9. The figure was prepared with Pymol (www.pymol.org).

Structural modeling. Based on the sequence homology of YBF30 with CAP45, we used the recently defined structure of the V1/V2 domain of HIV-1 gp120 in complex with PG9 to model the structure of the YBF30 V1/V2-PG9 complex. In a first step of our modeling strategy, we generated a 3D model of the V1/V2 loop of YBF30 gp120 by comparative modeling using the SwissModel server at Expasy (www.expasy.ch) and the structure of V1/V2 loop from CAP45 (3U4E PDB code) complexed with PG9 Fab as template. Because the glycan moiety of YBF30 V1/V2 loop could not be included in the modeling procedure, we extracted the two N-linked glycans from CAP45 V1/V2 and grafted them on the

corresponding asparagines (Asn 156 and Asn160) of YBF30 V1/V2. A quick energy minimization was performed to relieve any steric constraints within the model. However the two glycan chains were held fixed to avoid modifications of their conformations, since they form the major site of interaction of V1/V2 with PG9. Quality of the YBF30 V1/V2 model was found to be satisfactory as assessed by various tools including Anolea and Gromos. Finally, the model of YBF30 V1/V2 complexed to PG9 was obtained by superimposing individual components of the complex onto the CAP 45 V1/V2-PG9 complex. The whole structure was energy-minimized without any constraints on the protein moiety of YBF30 V1/V2 while fixing all other atoms by 500 steps of conjugate gradient algorithm using Discover (InsightII software, Accelrys Inc).