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► **To cite this version:**

Marie Leoz, Charlotte Charpentier, Constance Delaugerre, Marc Wirden, Veronique Lemée, et al..
Emergence of a New Circulating B/CRF02/G Recombinant Form Spreading in France. CROI, Mar
2016, Atlanta, United States. hal-02264832

HAL Id: hal-02264832

<https://hal-normandie-univ.archives-ouvertes.fr/hal-02264832>

Submitted on 7 Aug 2019

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Emergence of a New Circulating B/CRF02/G Recombinant Form Spreading in France

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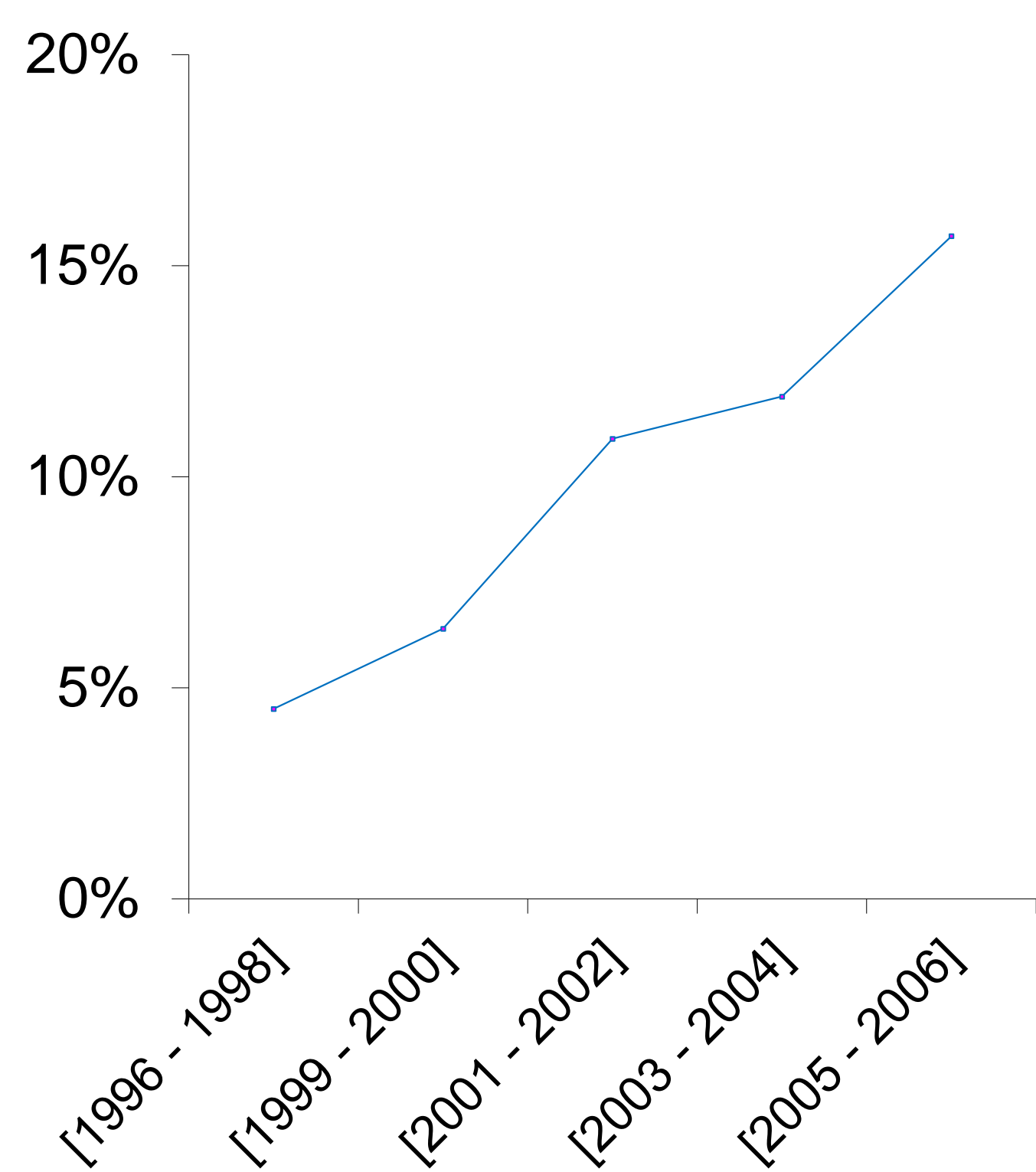
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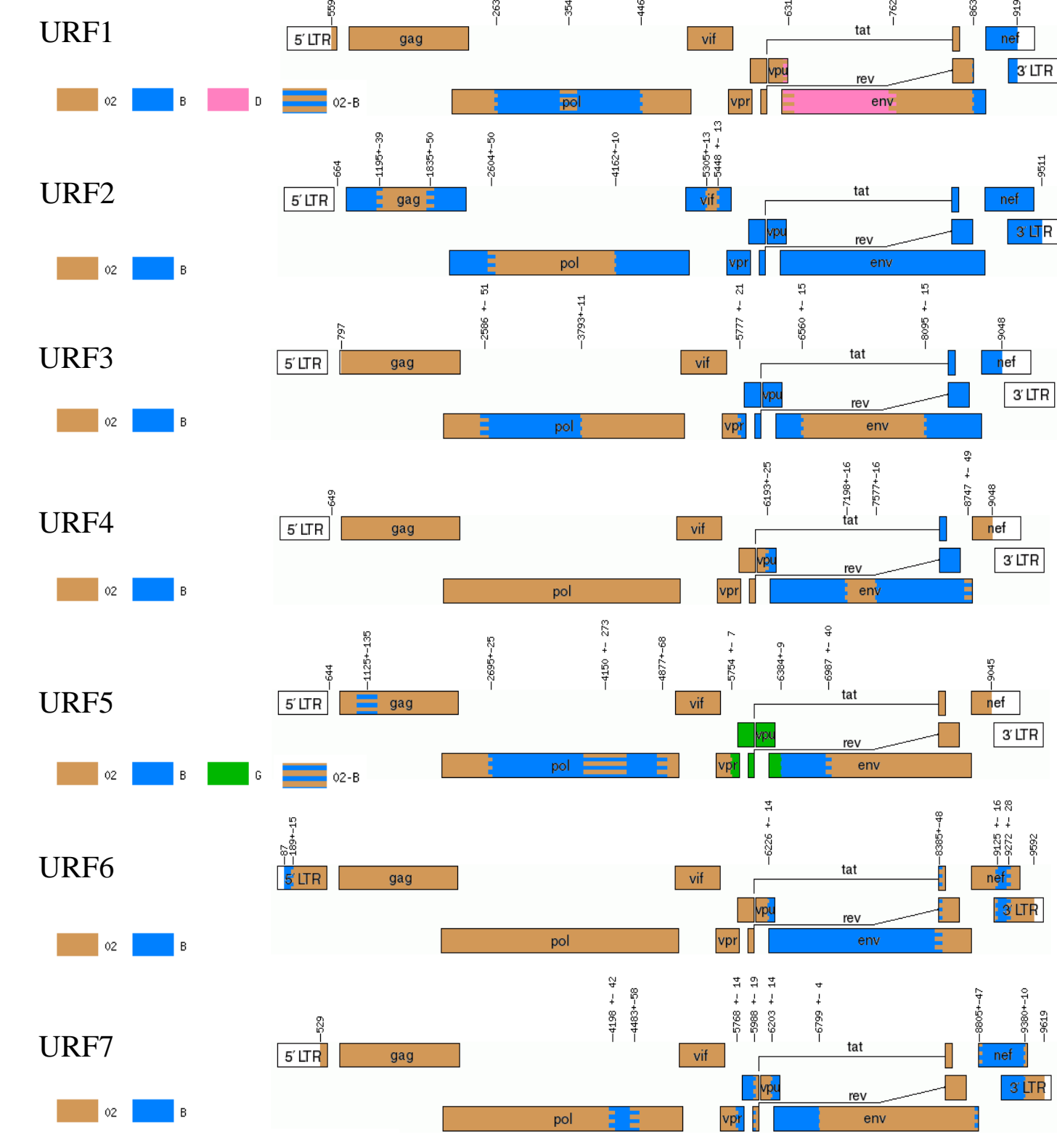
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BACKGROUND

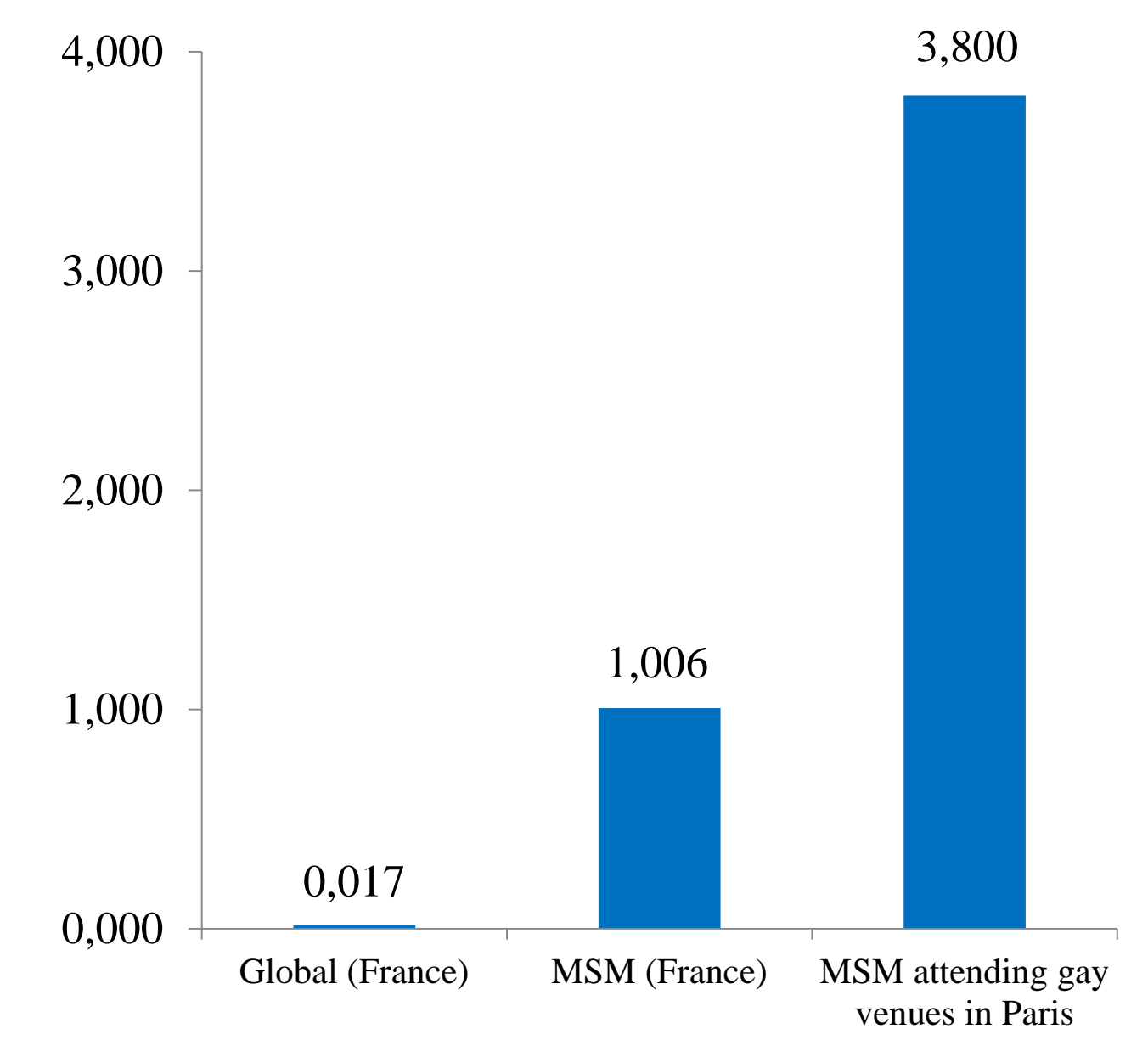


HIV-1 **non-B strains** frequency increases among newly diagnosed **MSM patients** in primary infection in France (Chaix et al., AIDS 2009)



Seven Unique **Recombinant Forms** involving subtype B and CRF02 have been identified in France, six were sampled in MSM patients (Leoz et al., AIDS 2011)

HIV incidence in French MSM in 2008 (new infections per 100 person-years)



Strains close to URF5 have been identified in 3 MSMs living in Paris. The **high prevalence and incidence** in this population (Levu et al., PLOSone 2012) could favor a quick spread of this form.

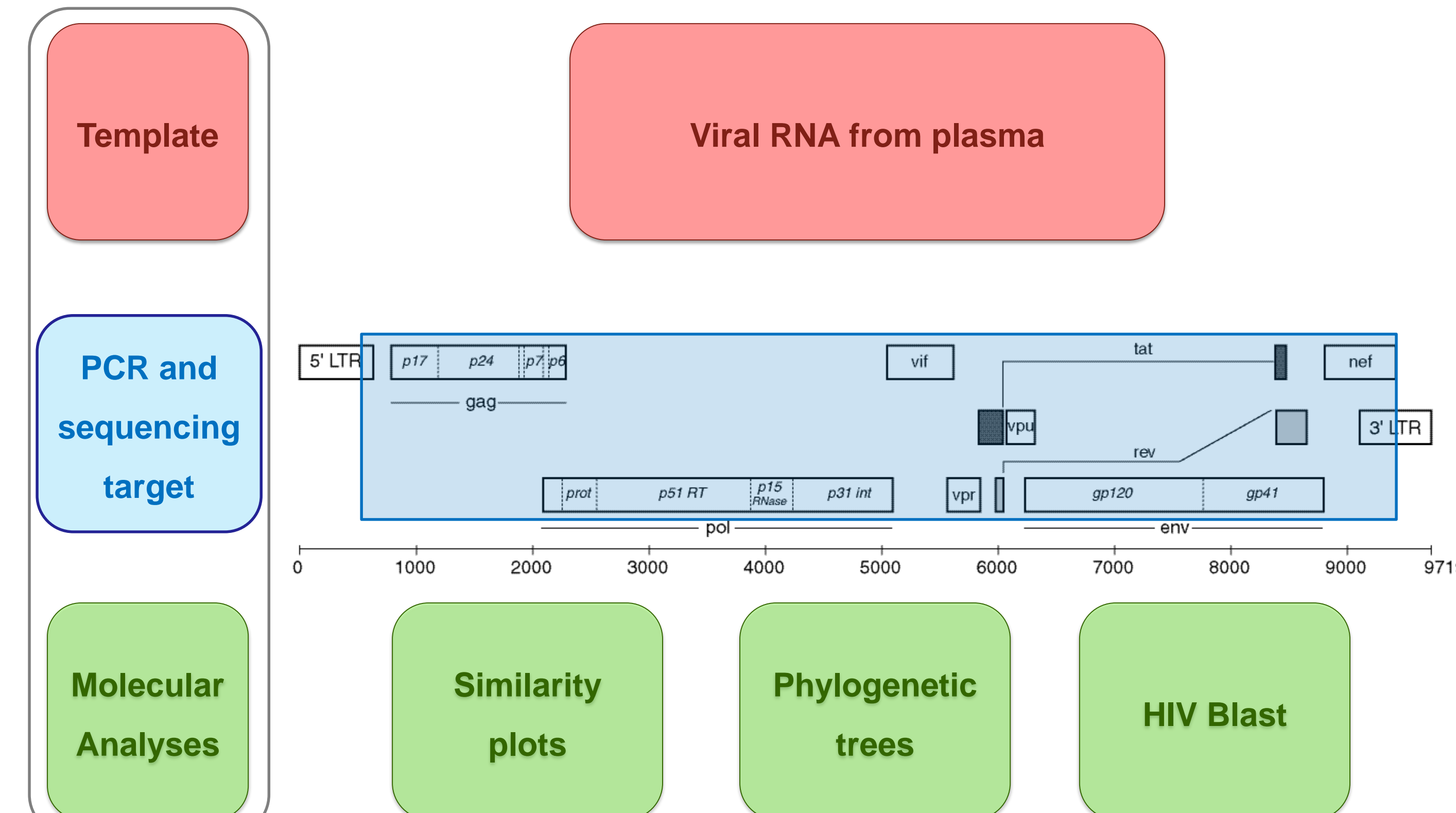
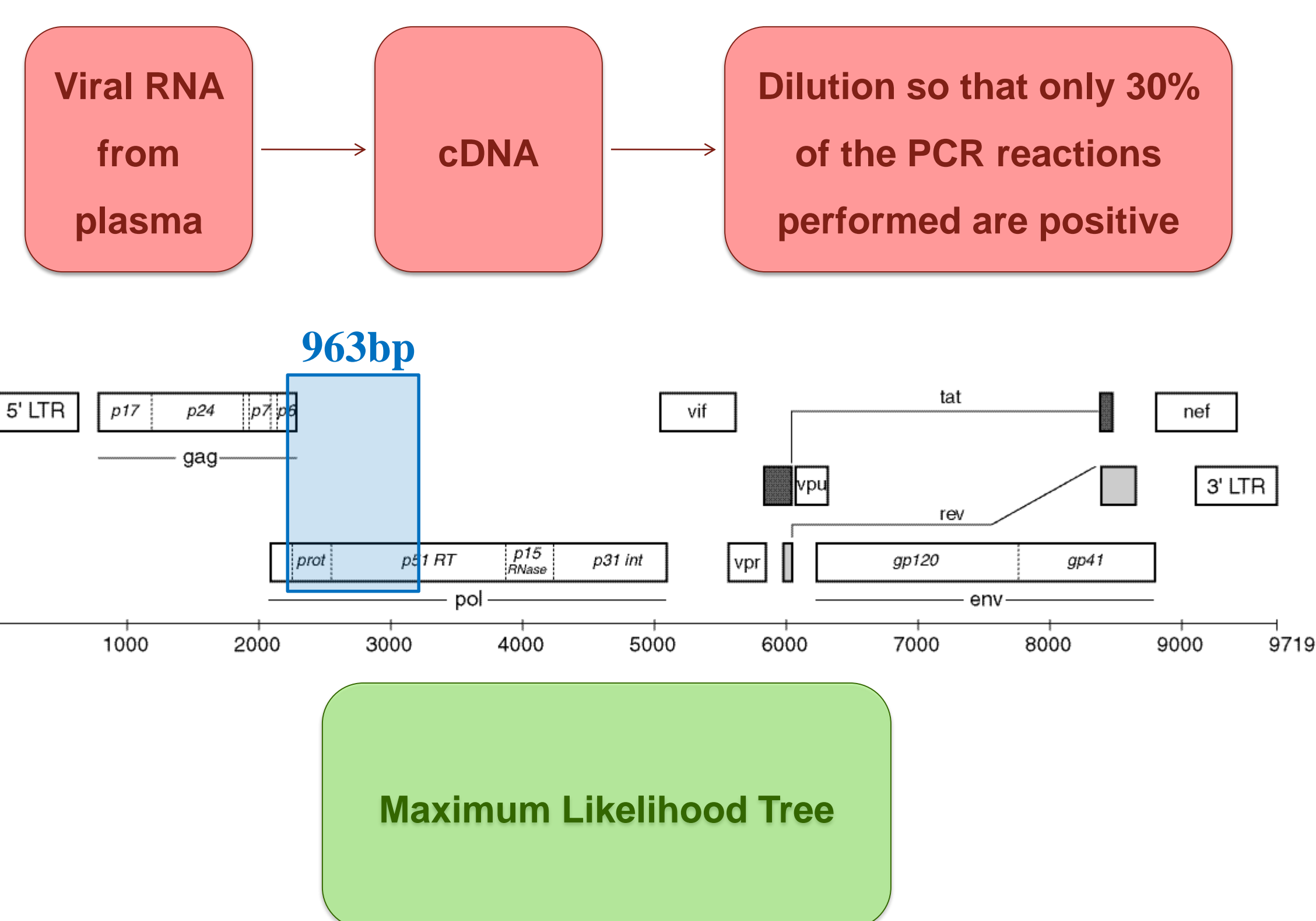
OBJECTIVE

To confirm the **common pattern** of the four strains, characterize the new CRF and explore its **origin**.

METHODS

• Single Genome Amplification, sequencing and quasi-species comparison

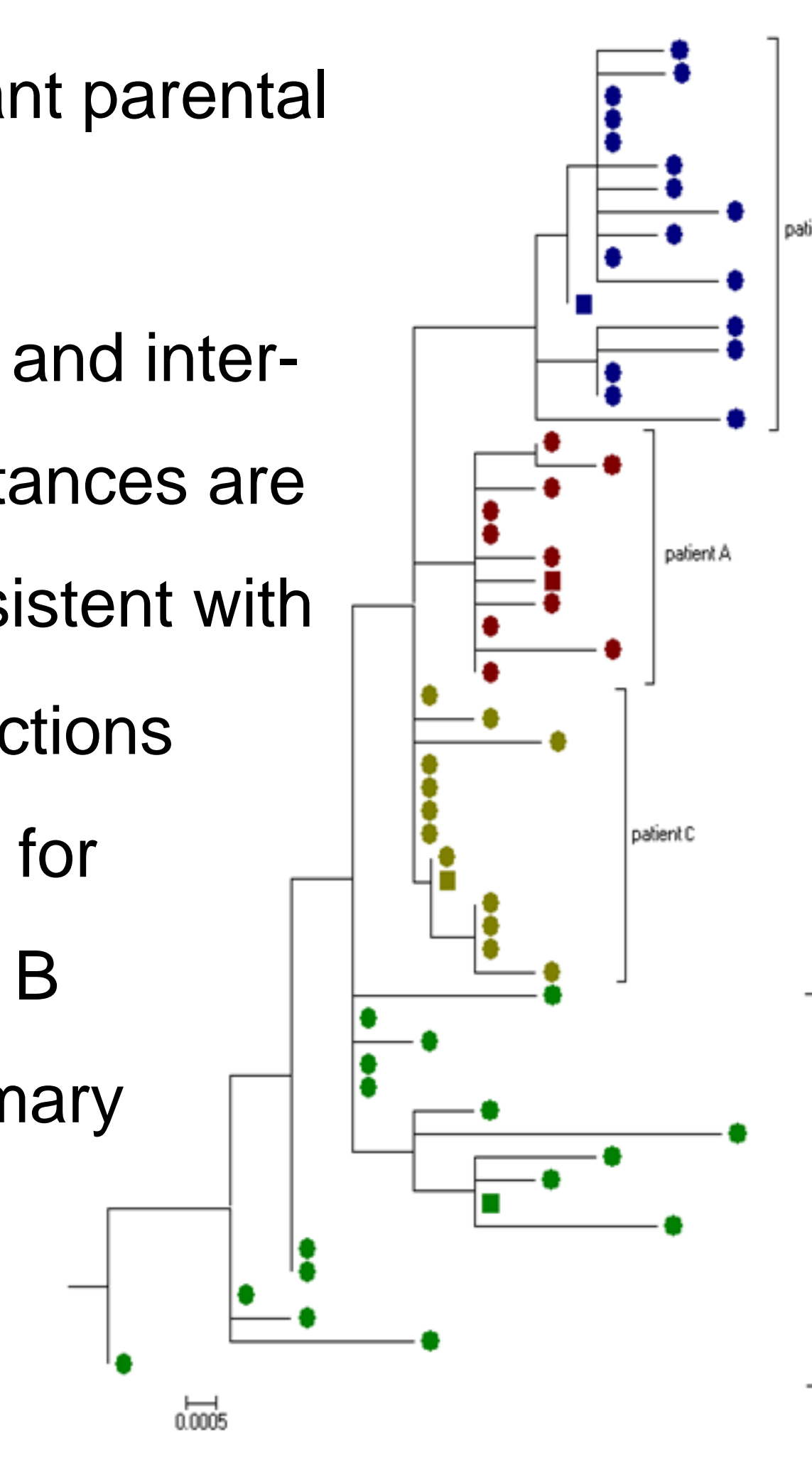
• Near full length amplification, sequencing and phylogenetic analysis



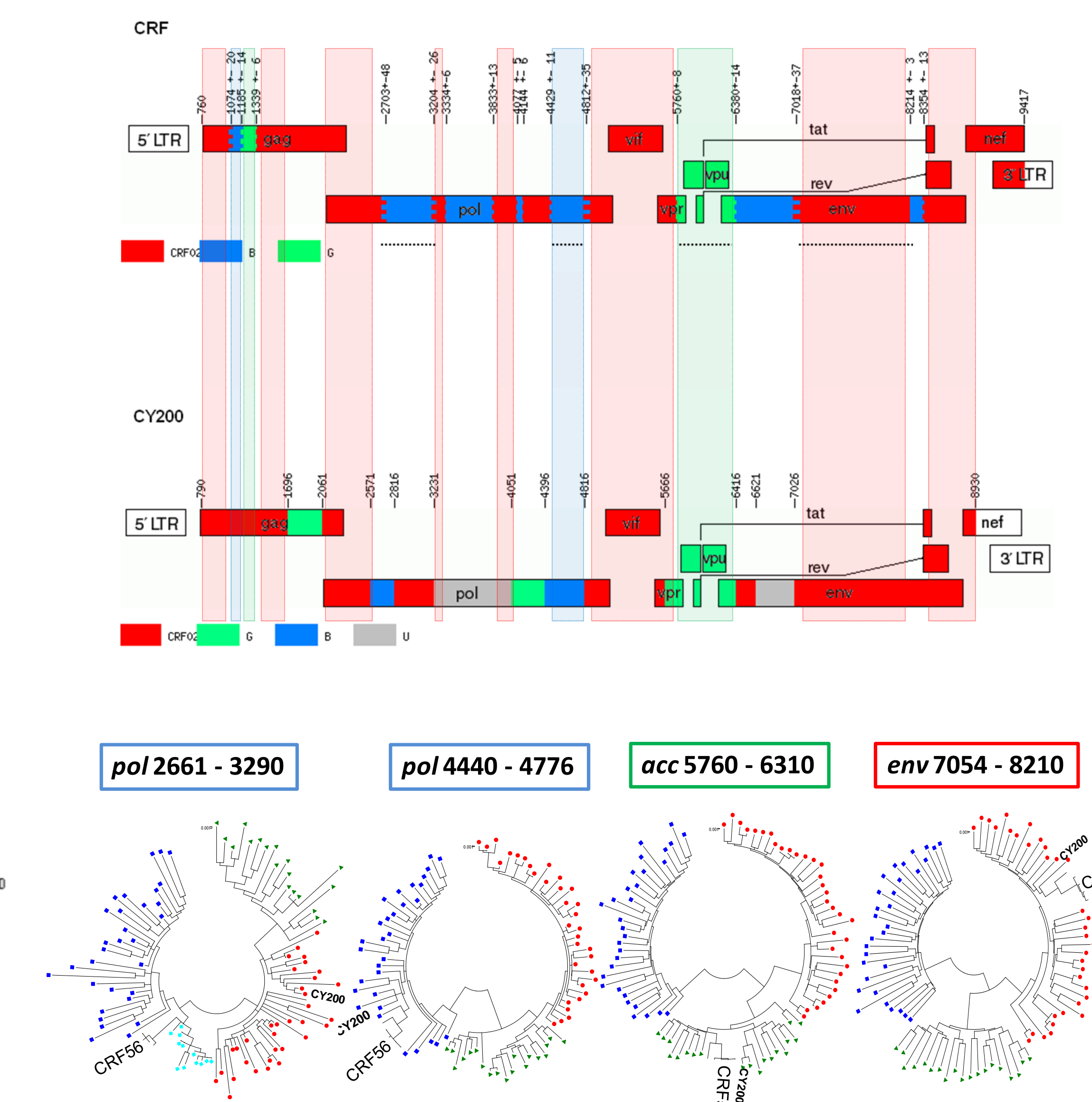
RESULTS

• Single Genome sequencing and quasi-species comparison

• No evidence of non-recombinant parental strains
• The intra- and inter-patient distances are short, consistent with recent infections (confirmed for patients A, B and C; primary infection in 2009 and 2010)



• Near full length sequencing and phylogenetic analysis



• CRF56_cpx is a complex recombinant form of second generation
• CRF56_cpx and CY200 (sampled in a MSM infected in Cyprus in 2007) share 5 breakpoints and cluster together in 12 regions
• In *pol*, CRF56_cpx is also close to twelve B/CRF02 sequences from Greece

CONCLUSION

• CRF56_cpx shows a **complex pattern** and is linked to several B/CRF02 and B/CRF02/G recombinant forms from the **Mediterranean area** : they probably share **common ancestors**

➡ **Growing complexity of HIV-1 molecular epidemiology, at an international scale**

• No parental strains in the samples, short distances between the sequences, all patients MSMs sampled recently, three of them during primary infection

➡ **Recent spread in a high-risk group where high-transmission bursts are frequent**

• Such a context could favor the **quick diffusion** of a highly fit form, as other CRFs that became predominant over their parental strains in other populations

➡ **Need for a surveillance of the spread of this CRF**