



**HAL**  
open science

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

Marie Leoz, Charlotte Charpentier, Constance Delaugerre, Marc Wirden,  
Veronique Lemée, Jean-Christophe Plantier

► **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://normandie-univ.hal.science/hal-02264832v1>**

Submitted on 7 Aug 2019

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.





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

Marie Leoz<sup>1,2,3</sup>, Charlotte Charpentier<sup>4</sup>, Constance Delaugerre<sup>5</sup>, Marc Wirden<sup>6</sup>, Véronique Lemée<sup>1</sup>, Jean-Christophe Plantier<sup>1,2</sup>

<sup>1</sup>Laboratoire associé au CNR du VIH, hôpital Ch.Nicolle, CHU de Rouen, France, <sup>2</sup>GRAM EA2656, Faculté de Médecine-Pharmacie, Université de Rouen, France,

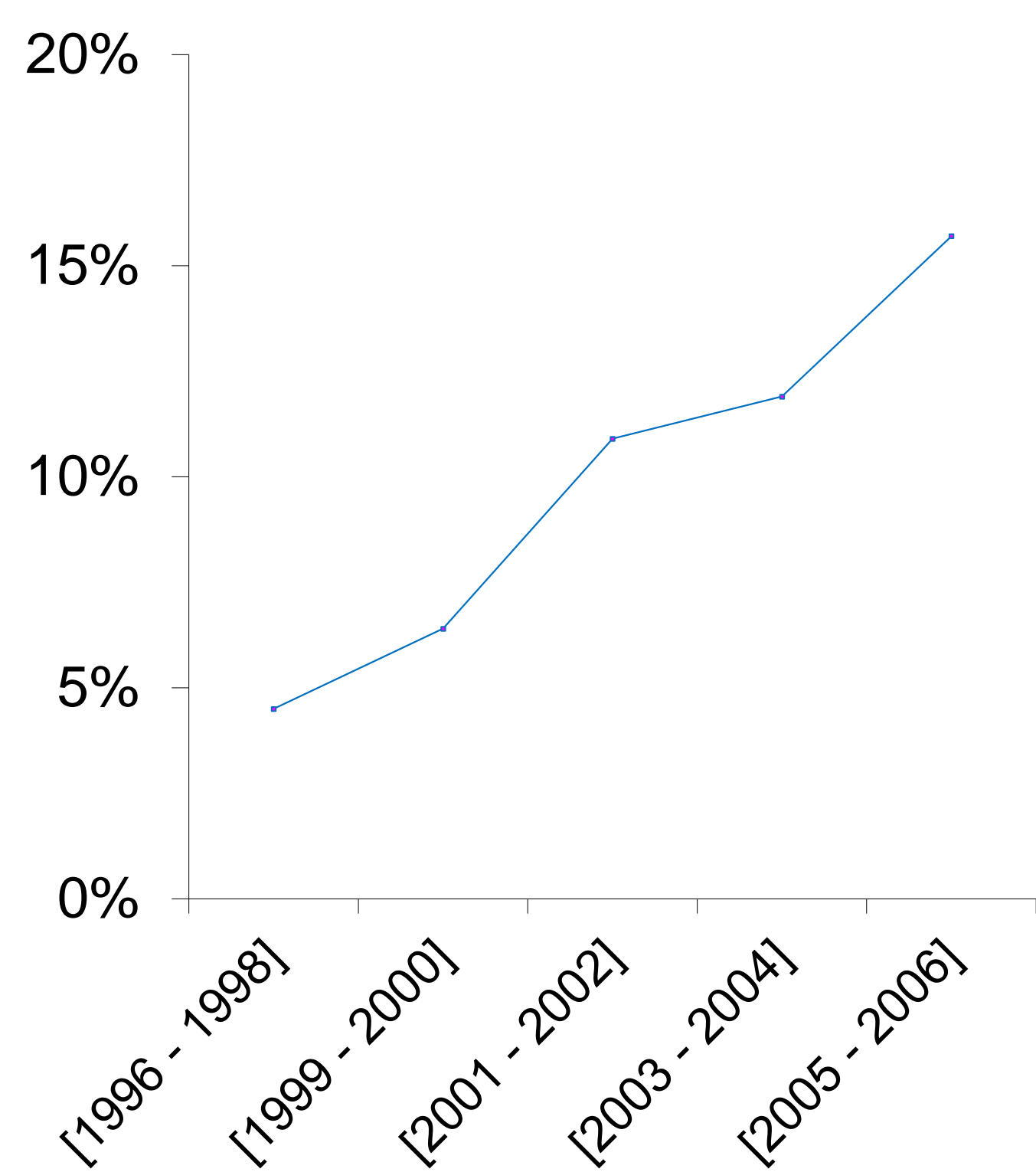
<sup>3</sup>COREVIH Haute-Normandie, Rouen, France <sup>4</sup>AP-HP, Groupe Hospitalier Bichat Claude Bernard, Service de Virologie, Paris, France,

<sup>5</sup>AP-HP, Groupe Hospitalier Saint Louis, Service de Virologie, Paris, France, <sup>6</sup>AP-HP, Groupe Hospitalier Pitié Salpêtrière, Service de Virologie, Paris, France

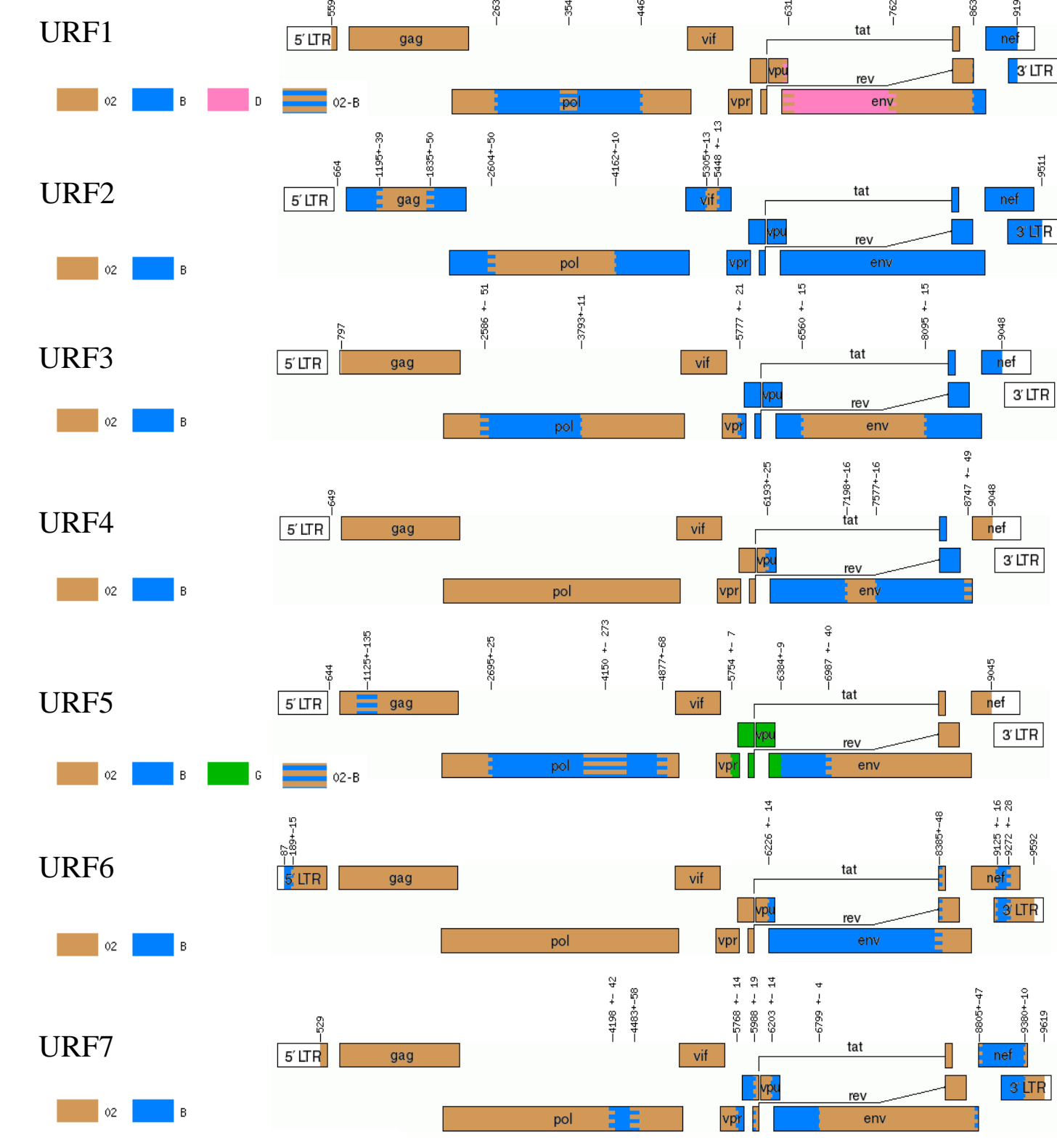
**CONTACT**  
Jean-Christophe PLANTIER  
  
Laboratoire de Virologie  
CHU Charles Nicolle  
1, rue Germont  
76000 Rouen  
  
[Jean-christophe.plantier@univ-rouen.fr](mailto:Jean-christophe.plantier@univ-rouen.fr)



## BACKGROUND

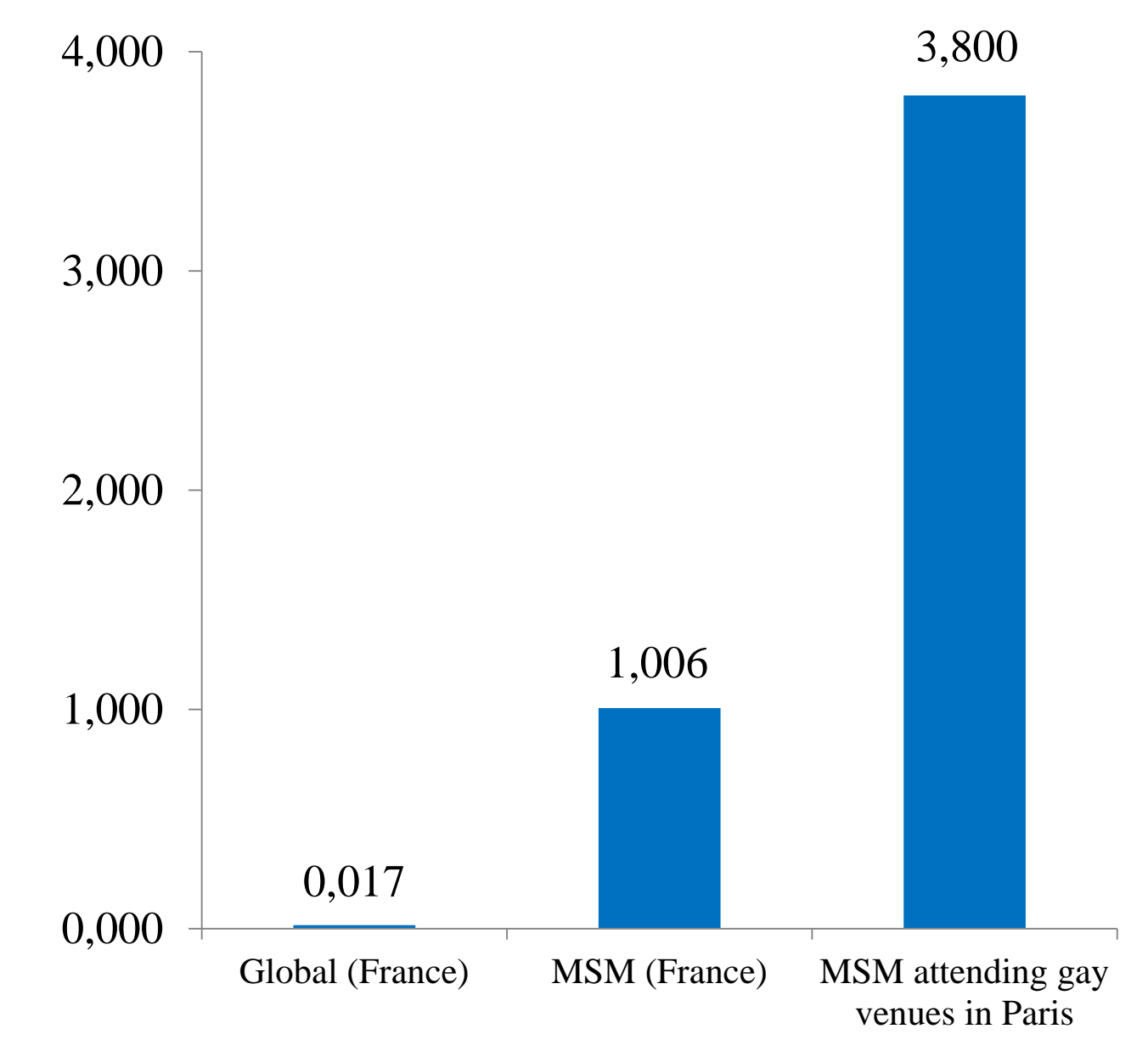


HIV-1 **non-B strains** frequency increases among newly diagnosed **MSM patients** in primary infection in France (Chaix et al., AIDS 2009)



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.

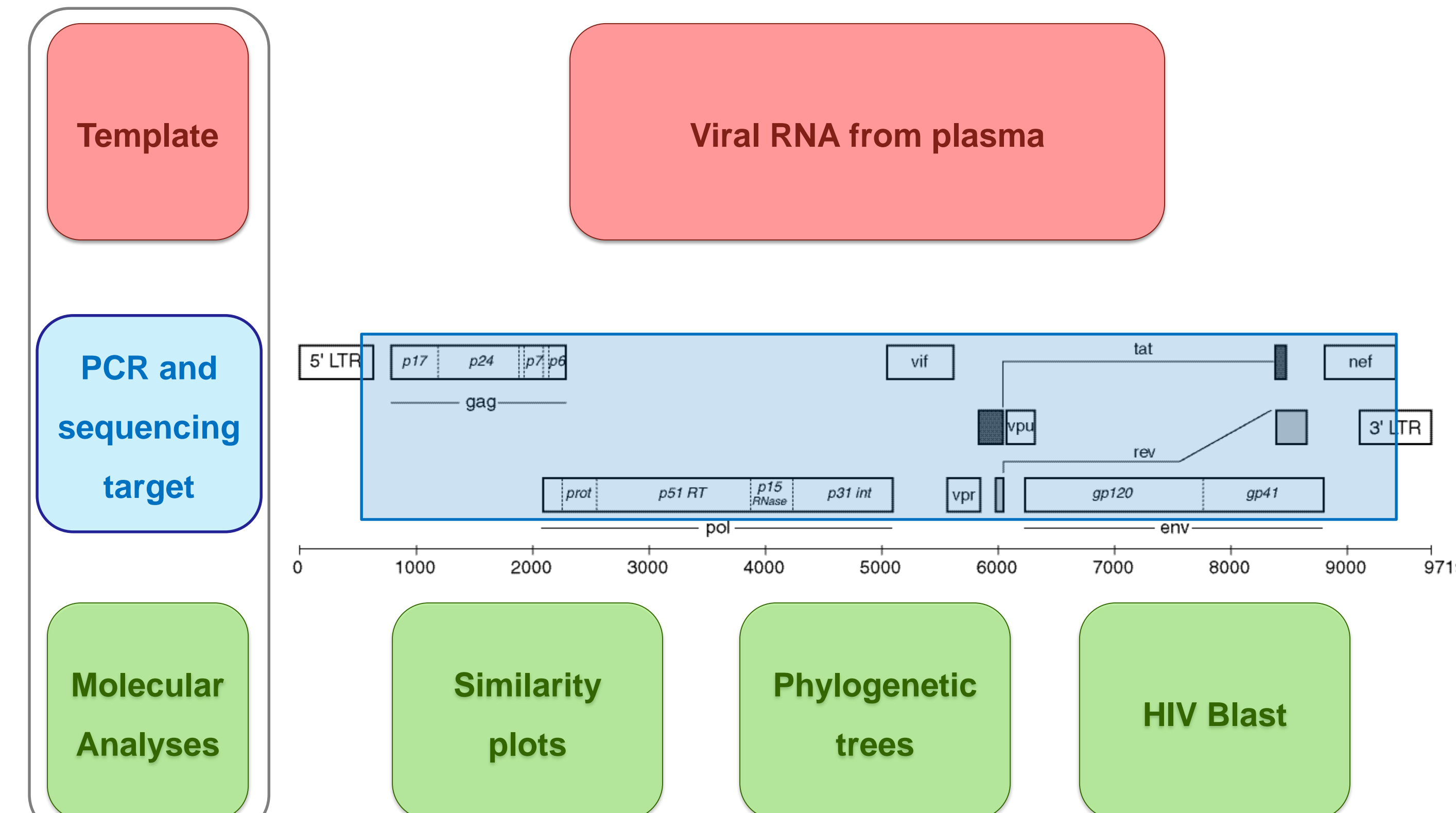
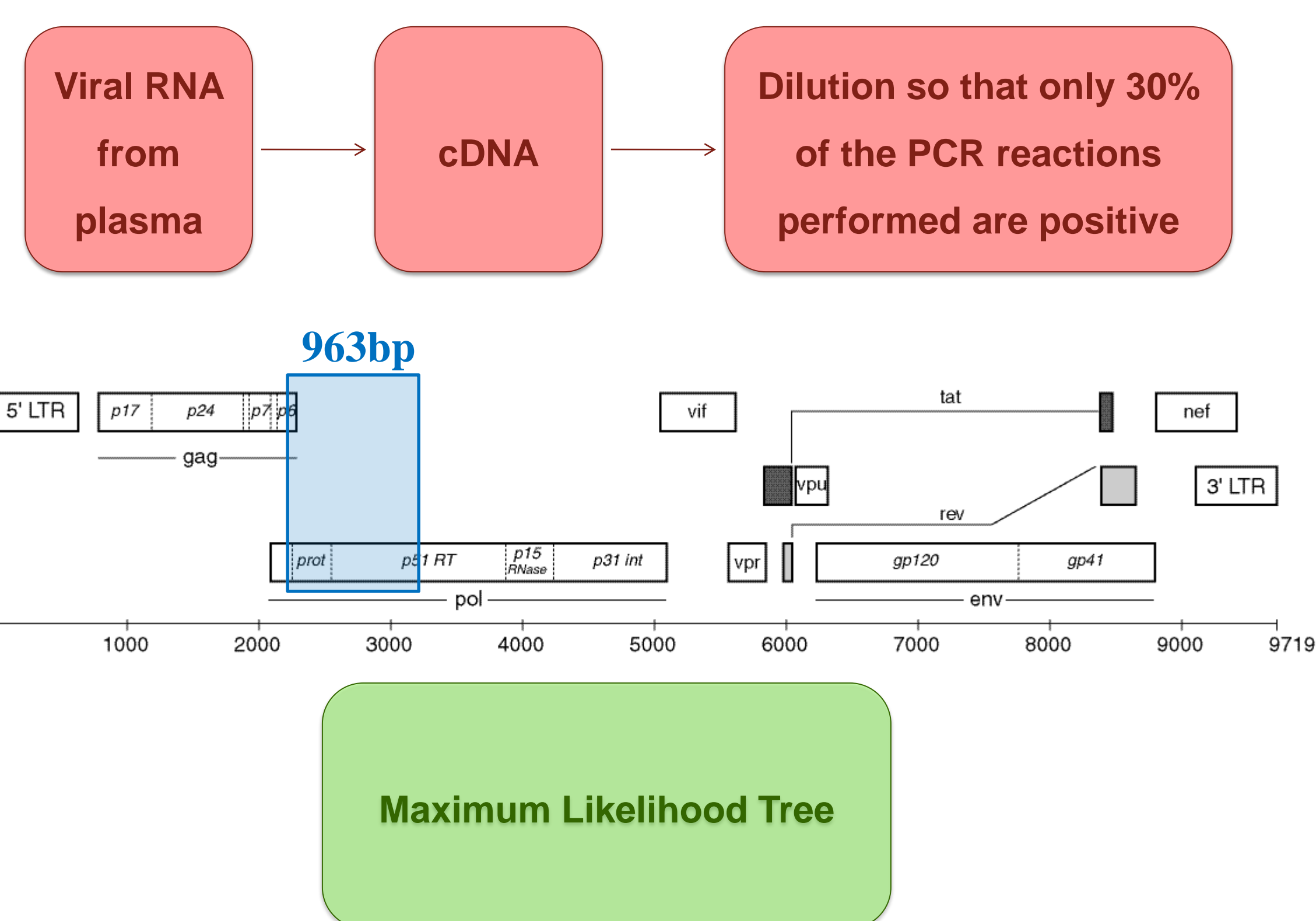
## OBJECTIVE

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

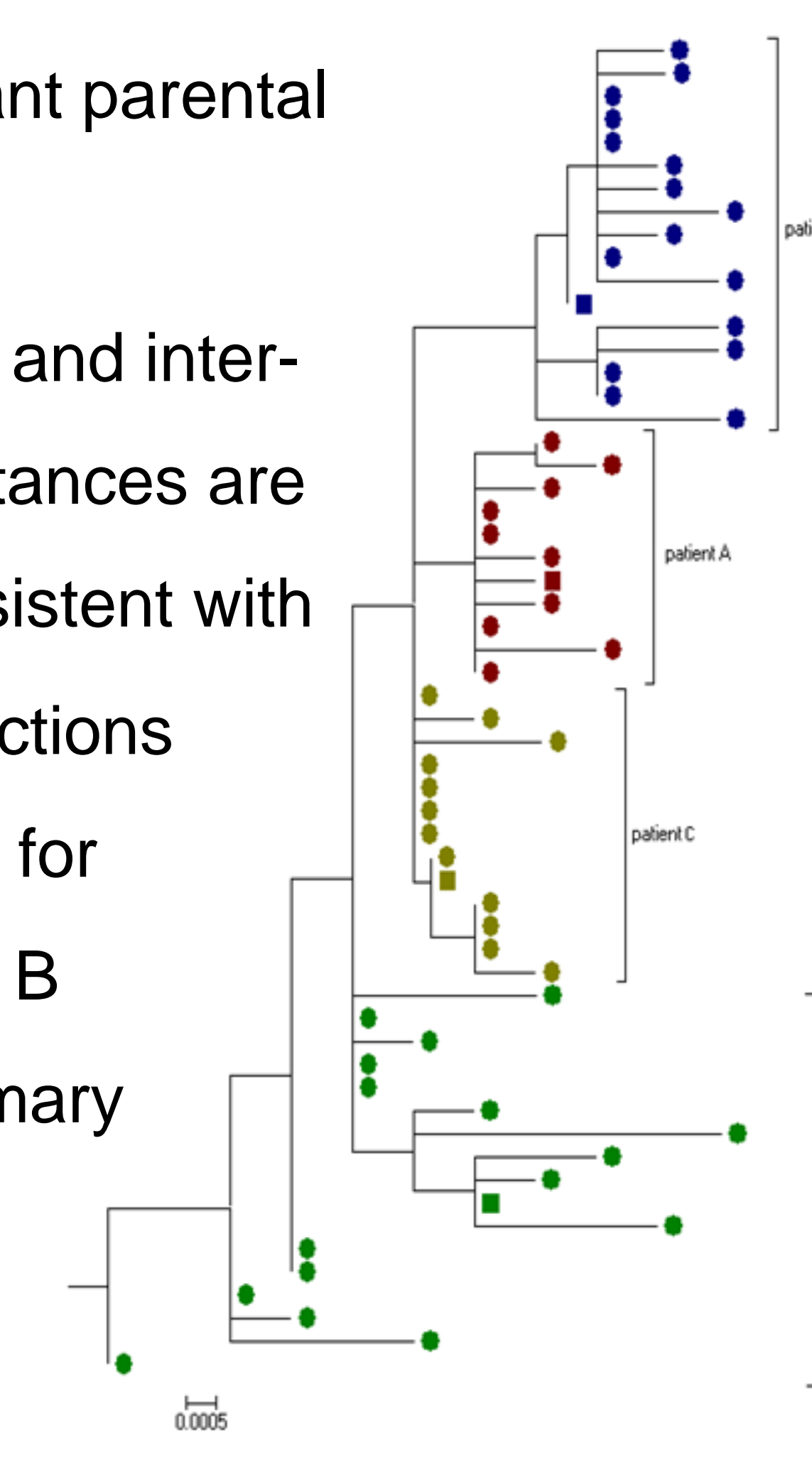
• Near full length amplification, sequencing and phylogenetic analysis



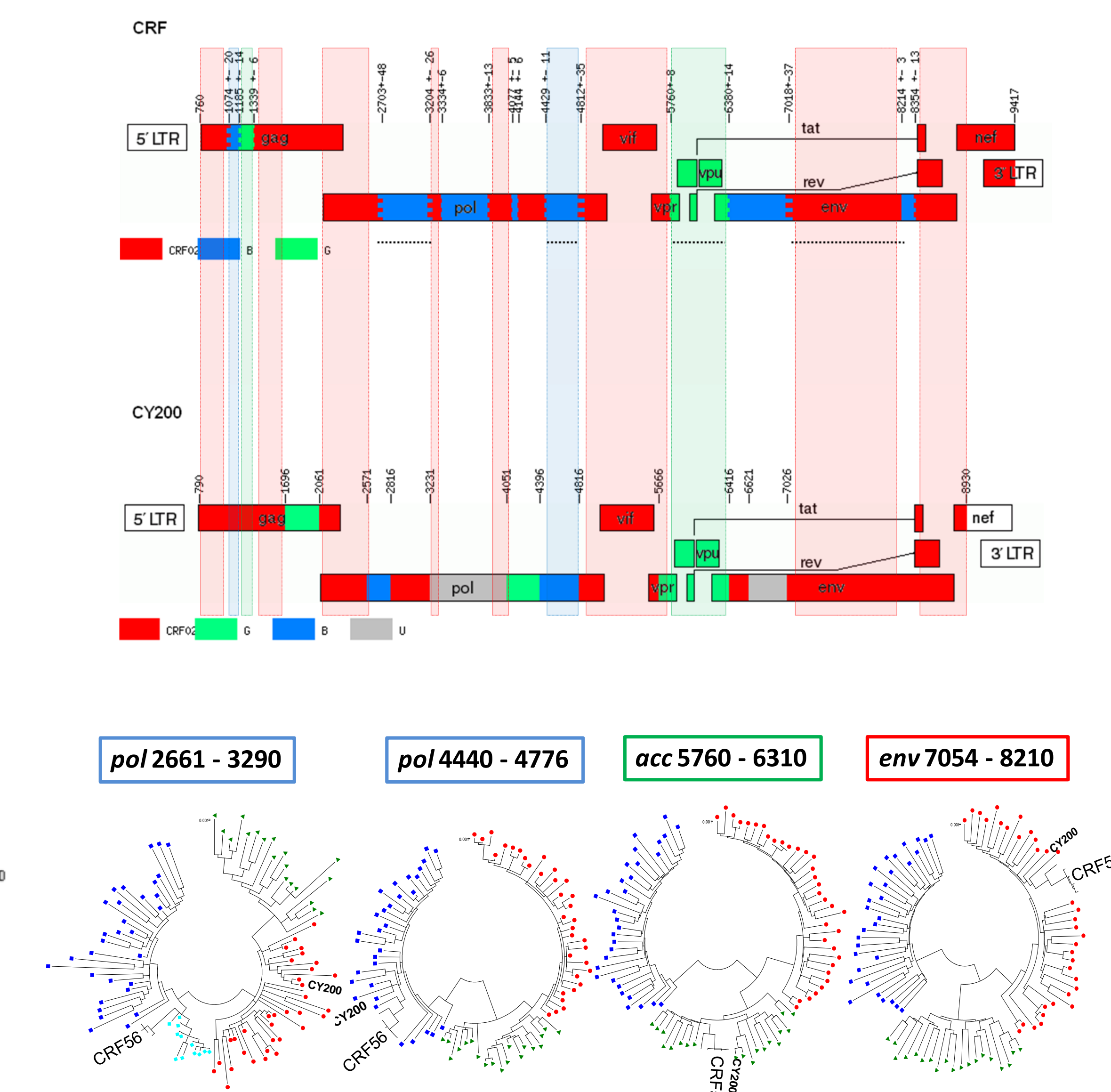
## RESULTS

• 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**