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

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**OBJECTIVE**

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

**RESULTS**

- 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)

**CONCLUSION**

- CRF56_cpx is a complex pattern and is linked to several B/CRF02 and 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