

The Contribution of Angola to the Early Spread of the HIV-1 Epidemic

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Background and Objectives

Understanding how, when and why the HIV-1 virus adapted to the human population and become pandemic is crucial to prevent its propagation and the establishment of other potential future viral pandemics. It is known that the HIV-1 group M epidemic started in Kinshasa, Democratic Republic of Congo (DRC), and soon spread across the Congo river to Brazzaville located in Republic of Congo (RC), and further to Lubumbashi and Mbuji-Mayi (DRC), around 1930s (~1937 [95% Bayesian Credible Interval: 1919-1957])¹.

Angola borders and has long-term links with DRC and RC as well as high levels of HIV-1 genetic diversity². Therefore, we aimed to investigate the role of this country in the initial spread of the HIV-1 pandemic.

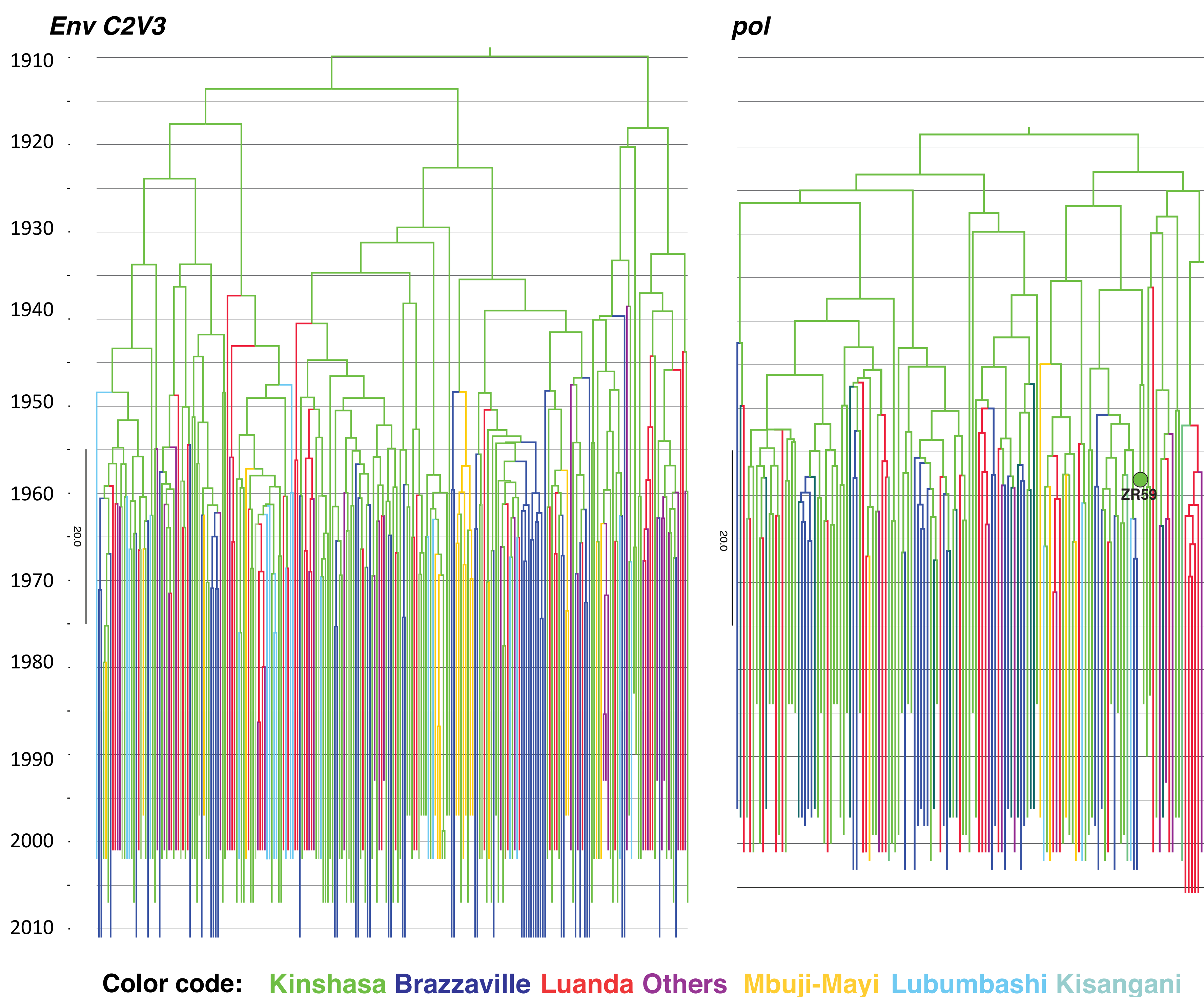
Methods

- ❖ We retrieved *env* C2V3, *pol* sequences and city locations from DRC, RC and Angola from published articles and Los Alamos HIV database.
- ❖ We created three random datasets for *env* and two for *pol* based on time span, geography and viral diversity using Phylogenetic Diversity Analyzer (<http://www.cibiv.at/software/pda/>). Each *env* dataset comprised 148 sequences: 72 from DRC, 36 from RC and 36 from Angola, whereas each *pol* dataset included 134, 50 and 70 sequences, respectively.
- ❖ The overall temporal signal of the datasets was evaluated with Path-O-Gen (<http://tree.bio.ed.ac.uk/software/pathogen/>).
- ❖ A non-reversible phylogeographic model implemented in BEAST³ was used to infer a time-calibrated phylogenetic history. The Bayesian Stochastic Search Variable Selection and robust counting analyses were performed to estimate the most significant pathways of viral dispersal⁴.

Results and Discussion

- ❖ The pandemic originated in Kinshasa (Fig. 1: green color) and the timing of the most recent common ancestor of group M was ~1918 [1900-1937] using *env*, and 1910 [1886-1931] using *pol*, as other studies have shown^{1,5}

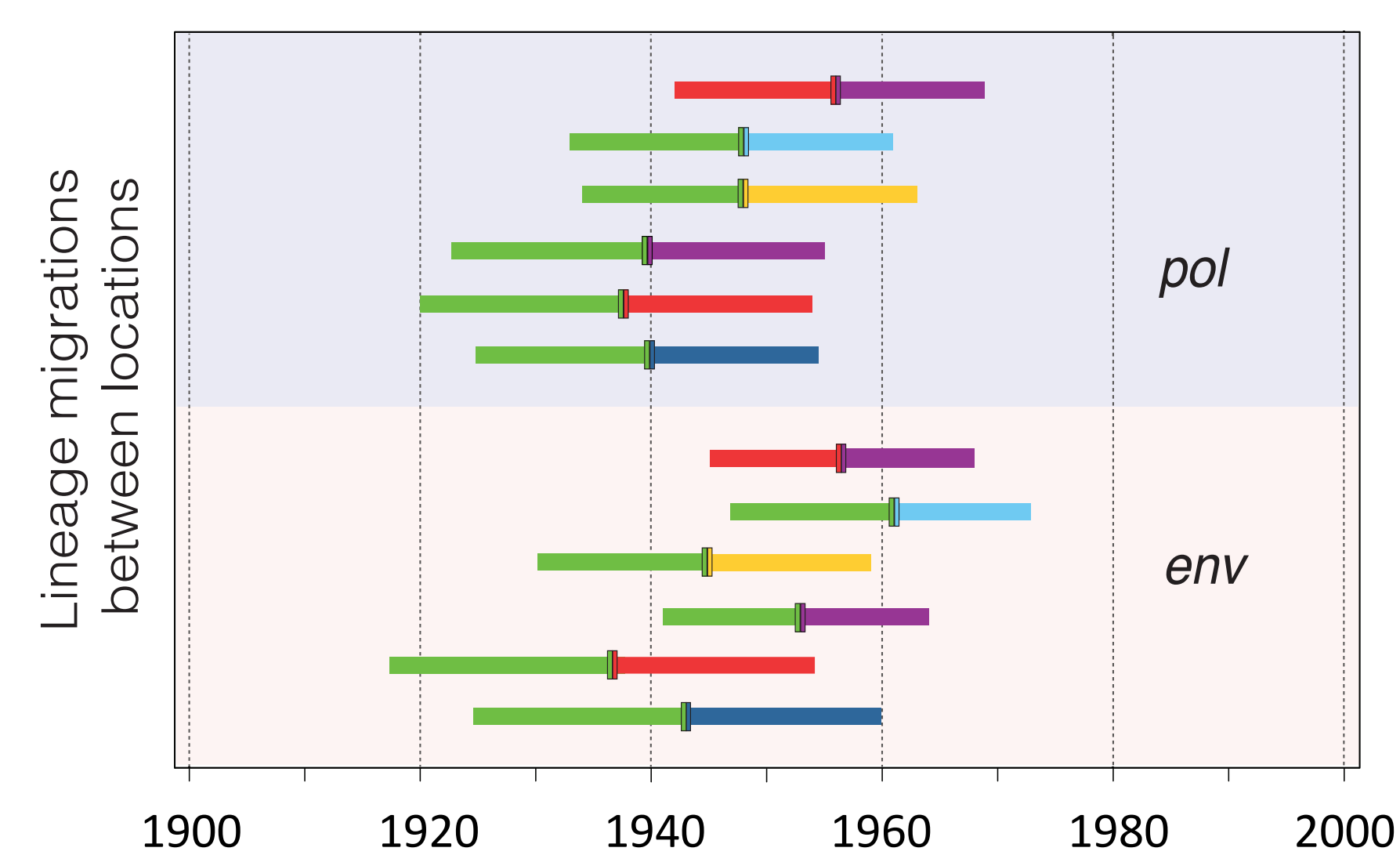
Figure 1: Maximum clade credibility trees of the *env* and *pol* datasets



- ❖ Noteworthy, the earliest HIV-1 introduction to Angola was in ~1936 [1917-1954] using *env* and ~1937 [1920-1954] using *pol*, whereas the earliest introduction to Brazzaville was around 1943 [1925-1960] and ~1940 [1925-1955], respectively (Fig. 1 and Fig. 2).

- ❖ 30% of all HIV-1 migrations out of Kinshasa were directed to Luanda, as many as to Brazzaville. Other significant links with Angola included mainly the province of Cabinda but with fewer migrations.

Figure 2: The earliest dates of significant lineage migrations



The line represents the average timing of the earliest introduction and corresponding BCIs. Color codes in the lines indicate the exporter (left) and the importer (right), according to the direction of the migration.

Conclusions

We show that a large number of initial HIV-1 migrations out of Kinshasa were directed to Angola, occurring as early as to Brazzaville. This study indicates a pivotal role of Angola in the early spread of the HIV-1 epidemic, thus sharing the epicenter with DRC and RC.

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