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Analysis of the local HIV-1 epidemic in Vologda region, Russia: Predominance of CRF03_AB and rapid expansion of URFs

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Objectives

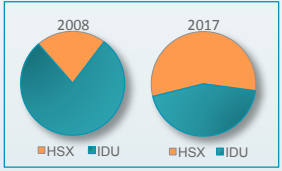
The distribution of HIV-1 subtypes between Russian regions is no uniform. Although sub-subtype A6 is responsible for about 80% of HIV-1 infections in Russia, the CRF03_AB recombinant is widespread in Vologda region (along with Kaliningrad region). At the beginning of the epidemic, this recombinant was responsible for more than 75% HIV-1 cases in the region, primarily due to the rapid growth of infection among injecting drug users (IDUs). In the context of Russia's transition from "IDUs" epidemic to "sexual" epidemic, we can expect the spread of CRF03_AB among other risk groups. Our studies were aimed at studying the current state of the HIV-1 diversity in Vologda region, and reconstruct the spatial-temporal dynamics of the CRF03_AB recombinant.

Methods

Maximum likelihood and Bayesian coalescent-based analyses of time-stamped data were performed on HIV-1 pol sequences generated from PMBC collected from 79 individuals as part of a molecular monitoring in Vologda region during 2016-2018.

Results

In general, sub-subtypes A6 (51.9%) prevailed, followed by CRF03_AB (33%), B (6.3%), URFs (5%) and "other" subtypes. Most of the CRF03_AB sequences belonged to HIV-infected patients from Cherepovets city (n = 52), where this recombinant dominated (48%). The proportion of CRF03_AB among heterosexuals increased from 22% in 2008 to 54% in 2017.



Phylogeography analysis indicated a genetic flow between Cherepovets and Kaliningrad city (BF=15), Ekaterinburg city (BF<10) and Saint-Petersburg city (BF<10), which is consistent with previous epidemiological data. Phylogenetic reconstruction showed that most of CRF03_AB viruses were introduced into the epidemic cluster that appeared in 1999 [1998-2000].

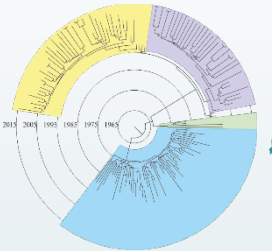


Fig. 1. Bayesian time-scaled maximum clade credibility tree for subtype CRF03_AB sequences that were finally selected in the dataset. Branch lengths are drawn to scale with the concentric circles indicating years. Major significantly supported monophyletic clusters were identified and colored differently.

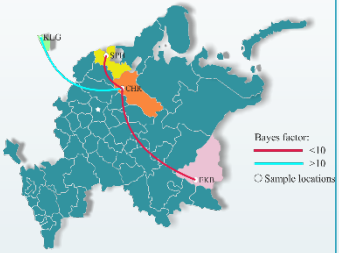


Fig. 2. European part of the map of Russia with migration patterns of the HIV-1 subtype CRF03_AB. Lines between locations indicate migration routes between the HIV-1 CRF03_AB populations and corresponds to the locations state transitions along the branches of the Bayesian MCC tree.

Conclusion

This study provides a new understanding of the HIV-1 epidemic in Vologda region, which is becoming increasingly complex, including due to the emergence of URFs. According to our data, the recombinant CRF03_AB entered the region around 1999, most likely from the Kaliningrad IDUs.

Conclusion

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