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Limited Overlap in Transmission Clusters of HIV and HCV Among MSM in the Netherlands

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Abstract #542

Background

Men who have sex with men （MSM） practicing unsafe sex are at risk to become infected with HIV-1 and hepatitis C virus （HCV）. MSM infected with HIV/HCV-coinfection may represent high risk core groups and could be drivers of the HIV-epidemic among MSM.

Methods

MOSAIC: The MSM observational study for acute infection with hepatitis C （MOSAIC） was initiated in 2008 to identify the frequency, clinical consequences and determinants of acquiring acute HCV infection among HIV-infected MSM in the Netherlands.

ATHENA: the AIDS Therapy Evaluation in the Netherlands （ATHENA） cohort is a national observational study that includes anonymized data from （nearly） all HIV-infected patients, followed longitudinally in one of the 27 Dutch HIV treatment centers since January 1996.

In this study, HIV transmission clusters were selected in an HIV subtype B phylogenetic tree consisting of HIV *pol* sequences. Cluster composition was then compared between MSM with or without evidence of HCV-coinfection （antibody/RNA）. In addition, HIV and HCV phylogenies of HIV/HCV-coinfected MSM were compared for MSM that had an HCV *NS5B* sequence available.

Results

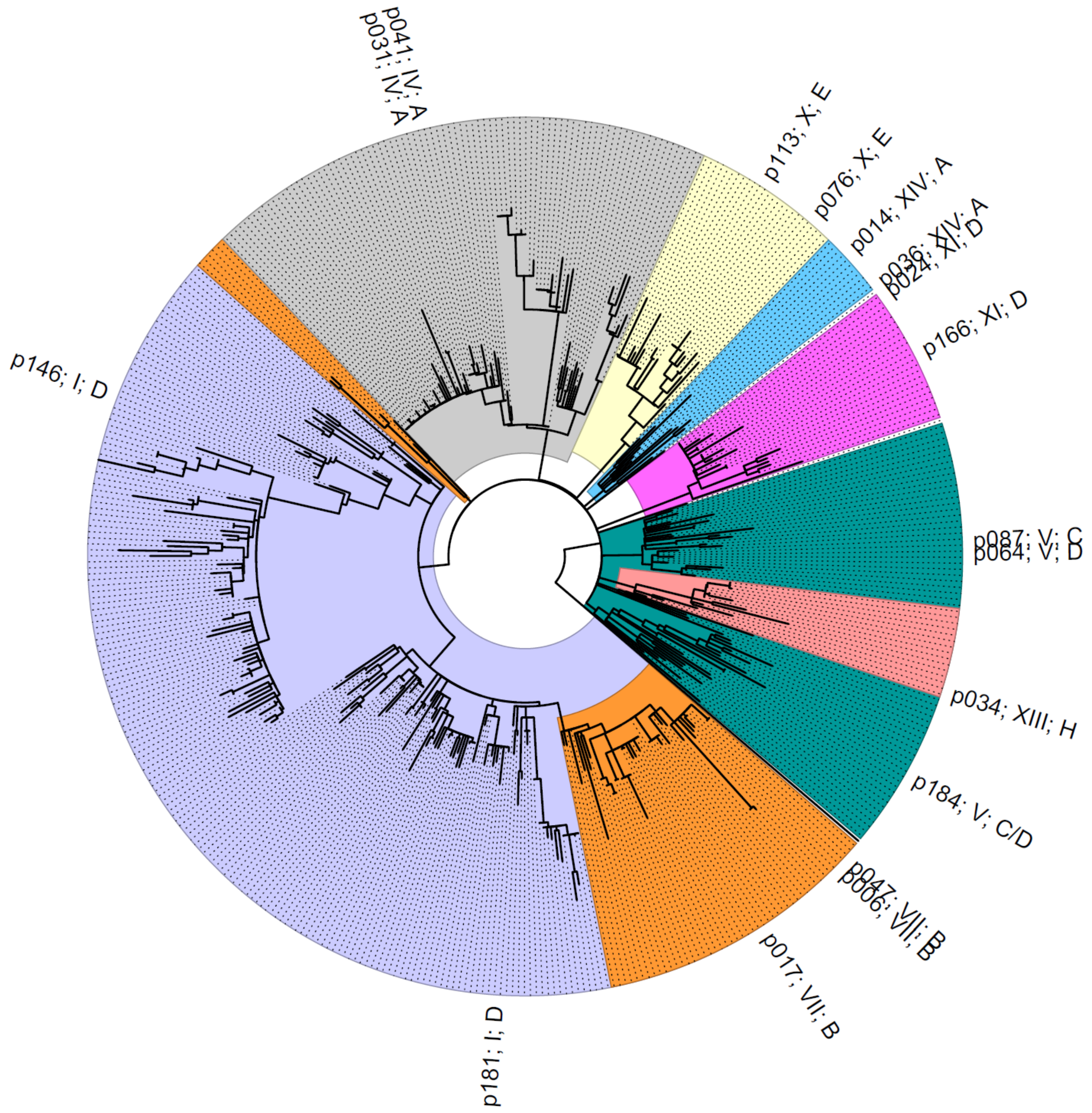

Figure 1: Phylogenetic tree of HIV *pol* sequences of HIV-infected MSM in the Netherlands. At least 2 MSM in each of these 8 identified transmission clusters （named *I-XIV* according to cluster size） showed overlap with HCV *NS5B* tree topology （HCV phylogenetic trees are shown below）.

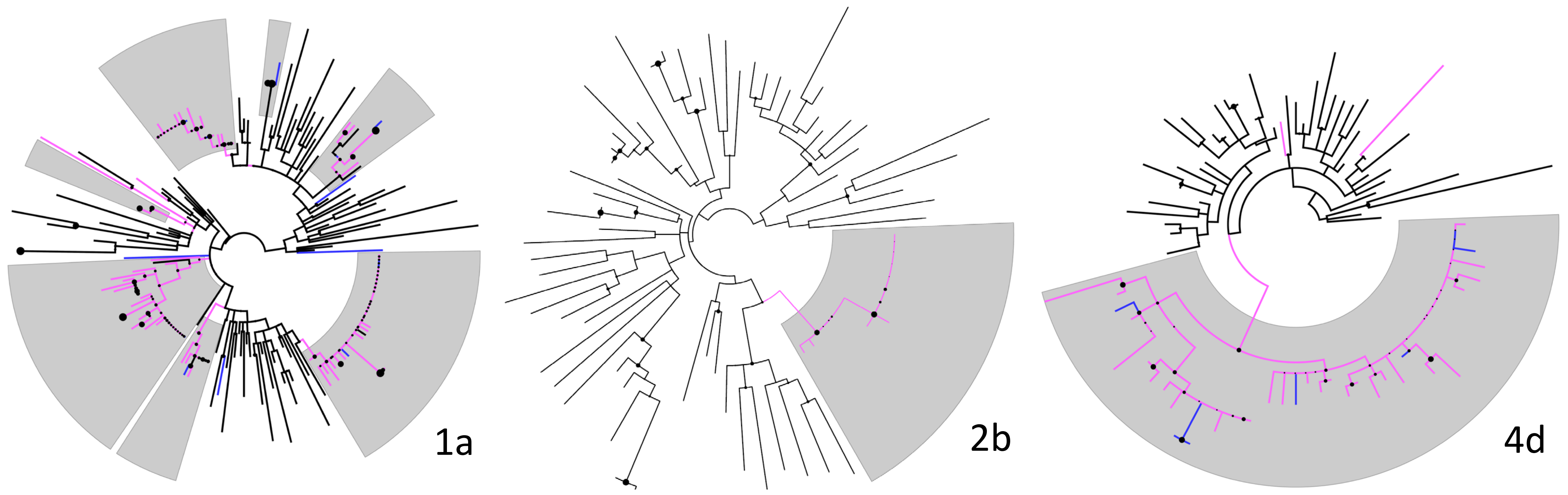

Figure 2: Phylogenetic trees of HCV genotype 1a/2b/4d *NS5B* sequences of 126 HIV/HCV-coinfected MSM. The identified transmission clusters are shaded grey （named A-K according to cluster size）. Study sequences are shown for MSM with and without HIV *pol* sequences available in pink and blue, respectively. Reference sequences are shown in black.

Out of a possible 12,900 HIV-infected MSM included in ATHENA, we included 5,038 MSM with HIV *pol* sequences available, 563 （11%） of whom were （ever） co-infected with HCV. The majority of acute HCV infections were of HCV genotype 1a （59%）, 4d （20%）, and 2b （7%）.

In total, 118 HIV clusters of >10 sequences included 3,084/5,038 （61%） HIV *pol* sequences, and 97/118 （82%） clusters contained ≥1 HCV infection. In only 5/97 （5%） HIV clusters harboring MSM with evidence of HCV infection, the proportion of HCV-infected individuals exceeded 25%; these specific HIV clusters were relatively small.

HCV sequences were obtained from 150 HCV infections among 126 MSM that participated in the MOSAIC study, 21 of whom had ≥1 reinfection. Ultimately, 19/150 （13%） HCV infections showed overlap in HCV and HIV phylogenetic tree topologies.

Conclusion

Our results indicate only limited overlap between the HIV and HCV epidemics among MSM. We found no evidence for high-risk core groups of HIV-infected MSM with elevated risk of HCV infection nor of high risk HIV/HCV-coinfected MSM driving the HIV epidemic.

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