A20 The search for replication-competent HIV during effective therapy

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Current antiretroviral therapies for HIV-1 are not curative because a small number of CD4+ T-cells remain infected with a latent, replication-competent provirus that contributes to viral rebound after the cessation of therapy. Several approaches to purge persistent HIV-1 reservoirs are in the beginning phases of clinical trials. To ensure future curative therapies target replication-competent HIV-1 proviruses for eradication, a thorough understanding of the distribution of replication-competent HIV-1 within T-cell subsets and how activation and proliferation of these cells contribute to the maintenance of the replication-competent HIV-1 reservoir is required. This study will employ a full-length single-proviral sequencing assay based on Next Generation Sequencing (NGS) techniques to sequence the entire HIV-1 genome of proviruses isolated from CD4+ T-cell subsets (central, transitional, and effector) sorted from peripheral blood and lymphoid tissue after 5–15 years of suppressive therapy from two groups of participants (1) three participants who initiated therapy during acute/early infection and (2) three participants who initiated therapy during chronic infection. Replication-competent proviruses will be identified by the absence of deletions and APOBEC3G induced hypermutation. The infection rates of replication-competent proviruses located in specific cell populations between participants will be compared along with the frequencies of replication-competent proviruses between different T-cell populations and within tissue-derived cells from these participants. This important study will allow us to determine whether specific cellular compartments harbour replication-competent HIV-1 and will provide valuable information for future curative HIV-1 clinical trials.

A21 HIV-1 sub-subtype F1 outbreak among MSM in Belgium

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HIV-1 non-B subtype infections have been observed in Belgium since the 1980s. However, subtype B predominates amongst men having sex with men (MSM), whereas other subtypes are mainly associated with sub-Saharan African migrants and heterosexual risk behavior. In the last decade, subtype F1 diagnoses have increased substantially in Belgium, representing 9% of newly diagnosed and therapy-naïve HIV-1 patients linked to care in 2014. In the present study, the Belgian subtype F1 epidemic has been characterized within a global context, where F1 is responsible for <1% of HIV-1 infections. The Belgian AIDS Reference Laboratories collected HIV-1 pol sequences from patients linked to care and sub-subtype F1 was verified using Rega v3 and COMET v1.0 subtyping tools. Concordant F1 sequences were retained from 293 patients, who were diagnosed with HIV-1 between 1988 and 2015. The number of F1 diagnoses increased from three in 2001–2 to 83 in 2013–4. Seventy-seven percent were men, with 52% homosexual, 15% bisexual, and 15% heterosexual contact as the probable transmission route (18% not registered). Belgium was the probable country of infection for 54% of the patients, whereas for 38% this information was not registered. A reference dataset from countries with a high burden of F1 infections or with a potential role in the global origin of sub-subtype F1 was collected from public and private databases and the phylogeny was reconstructed using RAxML and BEAST. These analyses indicate that 190 Belgian F1 sequences, 97% from men, and 72% with homosexual/bisexual risk behavior (17% not registered), belong to a monophyletic group with two sub-clades. Together with a Spanish clade, the Belgian clade is embedded in the Brazilian subtype F1 diversity and probably emerged after single or two migration events from South-America with one dead-end lineage (2 strains) and one actively spreading cluster (188 strains). This study reconstructed the structure of the local HIV-1 F1 epidemic and showed that onward transmission of subtype F1 occurs extensively among MSM. It illustrates the introduction and dissemination of strains in one geographically restricted risk group in which the subtype was previously absent.

A22 Increase in the numbers of HIV-1 non-B subtypes and potential recombinant forms circulating among Slovenian MSM in recent years

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In Slovenia, as in many Western countries, subtype B is still a predominant HIV-1 subtype and was historically correlated with the epidemic among men who have sex with men (MSM). In recent years, several reports demonstrating an increasing prevalence of non-B subtypes have been published. The majority of infections with non-B subtypes were linked to the heterosexual mode of transmission in previous Slovenian studies, thus the aim of this study was to investigate whether non-B subtypes are also becoming more prevalent among MSM in Slovenia. Between the years 2000 and 2014, a total of 520 people were diagnosed with HIV-1 infection in Slovenia. During the