first line and second line HAART based treatment. In resource-poor settings such as Mozambique the lack of adequate infrastructure, high costs of viral load tests and the availability of salvage treatment has hindered the intended objective of monitoring HIV treatment, suggesting an important concern regarding the development of drug resistance. The general aim of this study was to evaluate natural occurring polymorphisms and resistance-associated mutations in the gp41 region of HIV-1 isolates from Mozambique. The study included 78 patients naive to ARV treatment and 28 patients failing first line regimen, recruited from the Alto Mae Health Centre in Maputo. The gp41 gene from 103 patients was sequenced and resistance associated mutations for Enfuvirtide were screened. Subtype analysis revealed that 93% sequences were classified as subtype C, 2% as subtype G, 1% as subtype A1, and the other 4% as mosaic recombinant forms. No Enfuvirtide resistance associated mutations in HR1 of gp41 were detected. The major polymorphisms in the HR1 were: N42S, L54M, A67T, and V72I. This study suggests that this new class of antiviral drug may be effective as a salvage therapy in patients failing first line regimens in Mozambique. However further phenotypic studies are required to determine the clinical relevance of these polymorphisms detected in this study.

A4 The transmission dynamics over ten years of human immunodeficiency virus type 1 in Vietnam

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The HIV epidemic in Vietnam is evolving from a concentrated epidemic in men who inject drugs and female sex workers to sub-epidemics of men who have sex with men and to the general population. Understanding the infection dynamics and the temporal and geographical trends in transmission events in the population are crucial for national HIV control and prevention strategies. In collaboration with two largest primary and referral hospitals for HIV treatment in Ho Chi Minh City and Ha Noi, we have conducted cohort studies of over 1,000 patients on antiretroviral therapy (ART) and have access to approximately 800 HIV polymerase sequences from ART-naïve patients collected over a 10-year period from 2004 to 2014. The first-line ART cohorts includes 220 patients initiating ART in Ho Chi Minh City from 2005 to 2007 and 650 patients initiating ART in Hanoi from 2011 to 2015. The median age was 36 years and 70% were male. Median CD4 cell count was 90 cells/mm^3 and the median HIV RNA level was 5.2 log10 copies/mL. The second-line ART cohort enrolled 330 patients who failed first-line ART and were switched to second-line ART from 2006 to 2011. We propose to perform phylogenetic analyses including molecular clock calculations to investigate HIV evolution, HIV transmission dynamics, and trends over 10 years in Vietnam. HIV transmission dynamics includes the pattern of transmission, transmission of drug resistant strains, drug-resistance mutational pathways, and rapidity of viral spread.

A5 Peripheral blood cells contribute to HIV-1 viremia induced by romidepsin

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Anti-retroviral therapy (ART) suppresses viral replication and restores immune function in HIV patients. However, cessation of treatment results in viral rebound from persistent proviruses in latently infected cells. A recent clinical trial investigated the ability of the latency-reversing agent romidepsin to increase HIV-1 transcription as part of an approach to clear persistent proviruses. The administration of romidepsin once weekly for three consecutive weeks to individuals on suppressive ART revealed quantifiable increases of intracellular and plasma HIV-1 RNA in 5 of 6 participants which coincided with the romidepsin infusions. However, the origin of the romidepsin-induced plasma HIV-1 RNA is unknown. To address this, we compared intracellular HIV-1 DNA and RNA sequences from peripheral blood CD4+ T cells to HIV-1 RNA sequences obtained from the plasma during romidepsin treatment. CD4+ T-cells were obtained at baseline, following the second and third romidepsin infusion, and 10 weeks after the final romidepsin treatment. Plasma was collected 24 and 72 h following each romidepsin infusion. Single-genome sequencing of the env region was used to genetically characterize the virus from intracellular proviral DNA, the transcribed intracellular HIV-1 RNA as well as the plasma RNA pool and MEGA 6.0 was used to perform phylogenetic analysis. The intracellular HIV-1 DNA and RNA sequences obtained during romidepsin therapy contained a mean of 13.5% and 36% defective sequences, respectively. However, 8% defective sequences were found in plasma-derived HIV-1 RNA. Plasma-derived RNA and intracellular HIV-1 DNA and RNA sequences intermingled throughout the phylogenetic tree. In one participant, we identified one plasma-derived HIV-1 RNA sequence identical to, and another highly similar (>99.7%) to, intracellular HIV-1 DNA sequences. Another participant had 16 plasma-derived HIV-1 RNA sequences that were >99.7% similar to intracellular HIV-1 RNA or DNA sequences. One of these plasma sequences was identical to both intracellular RNA and DNA sequences. The plasma-derived HIV-1 RNA sequences in this participant also contained three large clonal populations. Our findings demonstrate that romidepsin induced transcription from proviruses in peripheral blood cells, which contributed to viremia in patients on suppressive ART. Intermingling of plasma-derived HIV-1 RNA sequences with intracellular HIV-1 RNA and DNA sequences indicates activation of multiple infected cells. In one participant the clonal plasma HIV-1 RNA sequences indicated that a subset of transcriptionally activated proviruses contributed to the majority of viremia. Therefore, HIV-infected cells in the blood are important reservoirs of HIV-1 during effective therapy and harbor proviruses capable of contributing to viremia during romidepsin therapy.

A6 Persistence and transmission of H7N9 influenza virus in Guangdong, China 2013–2015: implications for live poultry market intervention

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The increasing spread of H7N9 influenza virus and its potential for human-to-human transmission pose a heavy burden to global public health. Since the novel avian influenza A H7N9