cent) were successfully genotyped: HIV-1 subtype C was the most prevalent (97 per cent), followed by subtype A1 (1.2 per cent), mosaic recombinant forms (1.2 per cent), subtype G (0.5 per cent), and subtype D (0.2 per cent). Over 60 per cent of the children had at least one mutation associated to drug resistance to NRTI/NNRTI. As expected a high frequency of mutations to NNRT (52.9 per cent) in comparison to NRTIs (11.4 per cent) due to the low genetic barrier of this class of drugs was observed. For NNRTI, K103N, Y181C, E138A, and G190A were most common whereas for the NRTI, M184V was the most common. Maternal prophylaxis with HAART was significantly ($P < 0.05$, OR 2.41) associated with the emergence of drug resistance mutation to NRTI in HIV infected children. In conclusion, the high level of transmitted-resistant viruses observed in this study suggests that political strategies to enhance the level of adherence in maternal HAART should be taken into account. This is an important consideration due to the fact that Mozambique recently implemented the integrated PMTCT option B+ approach. Low adherence in such a treatment context may undermine de efficacy of first-line option in the country. Continuing surveillance studies among HIV infected children remains critical to monitor the impact of PMTCT strategies. Furthermore, current results highlight the need to reinforce adherence counseling with appropriate follow up.

A17 Transmitted drug-resistant mutations among recently infected HIV-1 patients in Israel, 2000–2014

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Transmitted drug-resistant mutations (TDRM) may hamper successful anti-HIV-1 therapy and impact future control of the HIV-1 epidemic. Recently infected, therapy-naïve individuals are best suited for surveillance of TDRM. Here, we investigated the prevalence of HIV-1 mutations in a sample of recently infected HIV-1 patients diagnosed between 2000 and 2014 in Israel. Historical samples from eighty recently infected patients were subjected to ABI-based sequencing (ABS) and MiSeq next-generation sequencing (NGS). DeepChek-HIV software was used to analyze the results. Most patients were males (80 per cent) and men who have sex with men were the major risk group (58.8 per cent). Overall, TDRM was detected in 8.8 per cent of patients by ABS and 31.3 per cent by NGS, ranging from 2.7 or 24.3 per cent, respectively, in 2000–2007 to 13.9 or 37.2 per cent, respectively, in 2008–2014. All ABS-detected TDRM were identified by NGS. The prevalence of TDRM impacting protease inhibitors, nucleoside reverse transcriptase inhibitors and nonnucleoside reverse transcriptase inhibitors was 0, 3.8, and 5 per cent, respectively, for ABS analyses and 11.3, 26.2, 7.5 per cent, respectively, for NGS analyses. Patients with NGS detected TDRM had significantly lower viral load (4.9 vs. 5.7 median log copies/ml, $P < 0.05$) and higher number of low-prevalence non-synonymous reverse transcriptase (RT) mutations compared to those without NGS-detected TDRM. None had integrase resistance mutations. The most abundant, albeit, minor-frequency RT TDRM were the K65R and D67N, while K103N, M184V, and T215S were observed at high frequency. Minor TDRM did not persist in later samples and did not hinder successful treatment. NGS can substitute ABS for surveillance of TDRM. Although rates of HIV-1 protease and RT TDRM in Israel are high and continue to increase from 2000 to 2014, minor TDRM do not become major species or interfere with therapy. The need for ongoing surveillance of low-frequency TDRM should be revisited in a larger study.

A18 HIV-1 genetic diversity and drug resistance in Haiti

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HIV-1 subtype B appears to be the most genetically diverse AIDS virus in Haiti. However, there have been few phylogenetic analyses on circulating drug-resistant HIV-1 strains. The primary objective of this study is to analyze the patterns of genetic diversity of HIV-1 in Haiti and describe the molecular epidemiology of HIV-1 drug resistance (HIV-DR) in the population. HIV-1 genotyping was performed for HIV-positive patients who were either initiating or failing antiretroviral therapy from 2005 to 2010. The Stanford University Database (http://hivdb.stanford.edu/hiv) was used to analyze the protease-RT sequences for mutations associated with resistance to antiretroviral drugs. In the context of this course, the pol gene sequences obtained from these patients will be pooled in a database and used to perform the phylogenetic analyses. This study will provide a global view of HIV-1 genetic diversity and drug resistance strains circulating and transmitted within the country. Phylogenetic analysis of HIV-DR strains is absolutely necessary to monitor HIV-DR strain evolution, and will also contribute to strengthening the implementation of public health strategies to prevent and address the emergence of HIV-DR in Haiti.

A19 The impact of HIV-1 on the evolution of *Mycobacterium tuberculosis*

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HIV significantly affects the immunological environment during tuberculosis co-infection, and therefore may influence the selective landscape upon which *M. tuberculosis* evolves. To test this hypothesis, whole-genome sequences were determined for 169 South African *M. tuberculosis* strains from HIV-1 co-infected and uninfected individuals and analysed using two Bayesian codon-model based selection analysis approaches: FUBAR which was used to detect persistent positive and negative selection (selection respectively favouring and disfavouring nonsynonymous substitutions); and MEDS which was used to detect episodic directional selection specifically favouring