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Track B - Viral resistance testing in clinical trials and practice

## CDB0064 - Prevalence of drug resistance mutations in HIV-1 infected patients failing antiretroviral therapy in Hong Kong

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**Background:** For HIV-1 infected patients experiencing antiretroviral treatment failure genotypic resistance testing (GRT) has become standard of care, guiding clinicians on what antiretroviral regimen to prescribe next. In this study, our goal was to analyze the drug resistance pattern among HIV-1 infected patients at time of treatment failure in Hong Kong.

**Methods:** Between 1993 and 2007, we were able to identify 134 treatment failure patients (TFP) with GRT done at the Integrated Treatment Centre (ITC). Study cases were censored at time of first GRT. The ITC is the largest government outpatient care centre for patients living with HIV in Hong Kong. Resistance was defined as the presence of one or more major mutations as specified by the fall 2007 International AIDS Society - USA Drug Resistance Mutations Group.

**Results:** Overall drug resistance was found in 81/134 (60.4%) TFP. Thirty nine were classified as subtype B, 36 subtype CRF 01AE and 6 other subtypes. Indication for GRT was first treatment failure for 57 (70.4%). Fifty one (63%) were on HAART at time of GRT, 11/51 (22.6%) were previously exposed to mono or dual therapy. Thirty (37%) were on mono or dual therapy at time of GRT. Resistance was found to one antiretroviral drug class 56 (69.1%), 2 classes 22 (27.2%) and 3 classes 3 (3.7%). The drug resistance profile for the NRTI showed the M184V mutation as the most prevalent (58%), followed by TAMs K70R (25.9%), M41L (24.7%), D67N (24.7%), T215Y (21%) and K219Q (14.8%). The most prevalent NNRTI associated mutation was K103N (7.4%). The protease gene mutations L90M was found in 17.3%, followed by M46I (8.6%).

**Conclusions:** In our population not all TFP were found to have antiretroviral drug resistance. A significant proportion of patients with resistance was on or had a history of mono or dual therapy. NRTI associated mutations were the most prevalent.

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