

The role of HIV viral load and CD4+ cell count in the prolongation of the QT interval in patients from an HIV outpatient clinic

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Background: QTc Interval prolongation is associated with life-threatening arrhythmias and it has been reported to occur more frequently in the HIV-infected population.

Methods: The data was collected from the charts of a cohort of 135 consecutive HIV-infected patients from our HIV outpatient clinic. QTc interval was corrected to the heart rate using Bazze's formula. The cohort was divided into two groups (prolonged QTc and normal QTc interval). QTc interval was considered prolonged if it was >440 ms in males and >460 ms in females. Multiple variables and potential risk factors were collected including the CD4+ cell count and Viral Load (VL) measurements which were done at the same day or within few days from the time the ECG was done.

Results: 23 patients were found to have prolonged QTc (17%). No significant difference between the groups was observed for any baseline characteristics; however statistically significant differences were observed with regard to the CD4+ cell count and VL. The ROC curves for both CD4 count and VL were obtained to establish cut-off points. The cutoff points for CD4 count and VL were 144 and 17.9×10^3 respectively. Sixteen of 23 subjects (70%) with prolonged QTc had CD4+ cell counts < 144 cells/mm³ as opposed to only 27 of 112 (24%) of subjects with normal QTc interval (OR: 7.20; 95% CI: 2.88 to 19.33; $p < 0.0001$). For VL, 18 of 23 subjects (78%) with prolonged QTc had levels $\geq 17.9 \times 10^3$ copies/ml, whereas 43 of 105 (41%) of patients with normal QTc had VL greater than the cut-off value (OR: 5.19; 95% CI: 1.79 to 15.05; $p = 0.002$). The simultaneous presence of both risk factors increased the OR to 14.74 (95% CI: 3.84 to 56.55; $p < 0.0001$).

Conclusion: Our study confirmed that the risk of QTc prolongation increases with the progression of the HIV infection. Low CD4 cell count and high Viral load could be considered as independent potential risk factors for QT prolongation in HIV patients in the outpatient clinic settings.

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Modelling the between-host evolution of set-point viral load in HIV infection

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Background: The Human Immunodeficiency Virus (HIV) is capable of evolving rapidly and responding to diverse selection pressures. Previous research has generally focused on the responses of HIV to selection within-host, comparatively little has been done on the response between-host selection. Previous work has proposed that the set-point viral load

also evidence for heritability of SPVL from one infection to the next.

Methods: We developed three models to examine the evolution of the SPVL distribution. One modelled change in strain prevalence in discrete generations of infection. Another incorporated continuous time into this framework. The third was extended to include explicit modelling of host dynamics and variable population size. Comparison of the simulated distribution with observed data allowed estimation of parameter values.

Results: All three models demonstrated that SPVL distribution would converge on the optimum relatively rapidly regardless of the initial distribution of genotypes. The discrete generation model provided a robust measure of the amount of variation attributable to nonviral effects and mutation from one individual to the next. The dynamic population model showed the response of the SPVL distribution to host dynamics.

Conclusion: The models described can be used to simulate the response of SPVL to widespread interventions such as circumcision or treatment, or the response to changing demography.

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Large scale HIV survey in Cameroon by mass HIV testing mobile units: Evidence of HIV epidemic hot spot areas and high HIV vulnerability of women over time

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Background: In Africa where the majority of HIV-infected adults do not know their HIV status, the use of HIV testing mobile units offers relevant public health prospects. In order to increase the HIV testing capabilities of voluntary counselling and testing centres, we developed a decentralized, large scale strategy based on bringing the needed services closer to the people, through the use of mobile units.

Methods: The National Public Health Laboratory "Hygiene Mobile" acquired a van (in order to propose voluntary HIV screening) comprising separate compartments for the driver, the medical team, and laboratory facilities. The screening of HIV-specific antibodies in serum samples was carried out using SD Bioline HIV, (Standard Diagnostics) & Determine (Inverness Medical Innovation). Indeterminate or positive samples were immediately retested by the ImmunoComb®II HIV 1 & 2 Bispot /Hexagon HIV. People

diagnosed as HIV-infected were referred to health care centres.

Results: From April 2005 to November 2008, 114 campaigns were organised in Cameroon (average of 277 volunteers tested per day). Out of 31,610 volunteers who received a pre-test counselling, 31,512 (20,330 males; 11,182 females) tested for HIV (acceptance rate of 99.7%). Their average age was 31 years. Amongst those, 31,210 (99.04%) received post-test counselling. The overall HIV prevalence was 6.06% (HIV infection in women significantly increased from 6.7% in 2005 to 9.73% in 2008). The North West region of Cameroon was the most affected with a prevalence of 15.76% in females and 7.27% in males.

Conclusion: HIV testing through mobile units likely constitutes a useful tool to promote large scale up HIV testing in sub-Saharan Africa and should be integrated into national HIV control programmes. Successive campaigns in a given area allow to evidence hot spots of the HIV epidemic, and to follow the variations of HIV prevalence over time.

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Potential impact of a customized peer-facilitators training program on sexual health intervention

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Background: The human immunodeficiency virus/acquired immune deficiency syndrome (HIV/AIDS) epidemic remains of global significance. Targeting the youth in which most new infections occur especially in Nigeria where the second greatest burden of the epidemic lies is pivotal in HIV prevention. The use of peer facilitators to deliver an integrated sexual health intervention on HIV/AIDS and sexually transmitted infections (STI) in this age group is an important prevention strategy. This study aimed to determine the feasibility of developing and implementing a customized training program related to the delivery of an integrated HIV/AIDS and STI risk reduction intervention for peer facilitators and to evaluate its potential impact on their knowledge, attitudes, and perceived competence.

Methods: We developed and delivered a structured training program and materials about HIV/AIDS and STI prevention in a university setting. The training was offered to facilitators who were planned to be involved in a larger project, known as Integrated HIV-STI Risk Reduction Program. A pretest-posttest survey of single group was conducted. Changes in scores before and after the training program in knowledge, attitude, stigma scores and perceived confidence and competence were measured.

Results: Ten potential facilitators participated in the program and completed both the pretest and posttest survey questionnaire. The trainees' median scores in HIV-related and STI knowledge, attitude and stigma scores had significantly increased compared to the baseline (HIV knowledge from 22 to 30.5; STI knowledge from 8 to 22.5; stigma

scores from 5 to 9; attitude from 39 to 57, $p < 0.05$). Upon completion of the program, majority of the trainees (80–100%) believed that they were competent and confident in performing most of the sexual health intervention activities.

Conclusion: This preliminary study suggests that a customized on-site training program on sexual health intervention designed for and delivered to peer-facilitators could significantly improve their knowledge, attitude and confidence to deliver program related to HIV-STI prevention.

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Molecular epidemiology of HIV-1 in newly-diagnosed treatment-naïve patients in Singapore

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Background: The molecular epidemiology of HIV-1 has not been well studied in Singapore. Information on HIV-1 molecular epidemiology obtained from previous studies was either based on a small sample size or on a specific HIV-1 population (seroconverters). In this study we aimed to have a better understanding to HIV-1 molecular epidemiology in newly-diagnosed treatment-naïve patients on the basis of a larger sample size.

Methods: Newly-diagnosed treatment-naïve HIV-1 patients were prospectively, consecutively recruited from the Communicable Disease Centre, Tan Tock Seng Hospital, Singapore. PCR products of pol gene that encompass the entire protease gene and two-third of the reverse transcriptase (RT) gene were amplified based on PBMC-associated viruses using an inhouse method. Direct sequencing was used to sequence the pol gene PCR products. The pol sequences were used for phylogenetic analysis and for genotypic analysis of drug resistance.

Results: One hundred fifty-one patients were analyzed in this study. Of whom 92% (n = 139) were men, 49.7% (n = 75) were men who have sex with men (MSM), and 49% (n = 74) were heterosexuals. Five HIV-1 subtype/CRF were identified, including CRF01_AE (n = 94, 62.3%), subtype B (n = 53, 35.1%), CRF33_01B (n = 3, 2%), and one each of CRF34_01B and CRF07_BC. MSM accounted for 35.1% (n = 33) of the CRF01_AE infections and 77.4% (n = 41) of the subtype B infections. Phylogenetic analysis showed that 55.3% (n = 52) of 01_AE sequences were clustered in each of 8 clusters and 73.6% (n = 39) of subtype B sequences were clustered in each of 5 clusters; in addition, MSM was more common in one of the clusters compared to heterosexuals in both 01_AE clusters (55.7% vs. 37.7%, OR 11.9, 95% CI 3.9-36.7) and subtype B clusters (87.8% vs. 25%, OR 21.6, 95% CI 4.6-101.5). There was no any known drug-resistant mutation was detected by direct sequencing.

Conclusion: CRF01_AE and subtype B remain the primary etiology for HIV-1 infections in Singapore. The high extent of clustering of MSM suggests active transmission of HIV-1 in this specific population, and therefore, more effective