HUMAN MHC DIVERSITY AND THE MOLECULAR EPIDEMIOLOGY OF HIV-1 IN SOUTHEAST ASIA

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HIV-1 is one of the most genetically variable viruses ever encountered. However, as described in SE Asia, the inter-clade genetic diversity of HIV-1 may be relatively conserved at the population level. This relative lack of diversity may partially be attributed to the maturity of the epidemic in the region, however social and genetic factors may be operative. This is suggested by the continued dominance of clade E throughout the Greater Mekong Subregion since the simultaneous introduction of subtypes B and E (actually a circulating recombinant form, or CRF, of subtypes A and E) in Thailand. The extensive genetic polymorphism of human MHC (or HLA) may play an important role in shaping the molecular epidemiology of HIV-1. Studies have consistently demonstrated the association of HLA-B*57 and related alleles of the B58 supertype with susceptibility to, and progression of HIV-1 infection among Africans and Caucasians, possibly driven by cytotoxic T-cell activity. Similarly, HLA-A*11, common among ethnic Thais, has been associated with reduced susceptibility to infection. Thus, HLA class I molecules may be 'imprinting' mutations associated with strong immune responses at a population level. The purpose of this presentation/poster will be to describe the parallel diversity of HIV-1 and polymorphism of human MHC, and its significance for the development of an HIV-1 vaccine.


NOVEL GENOTYPING TOOL FOR COMPLEX HIV-1 EPIDEMICS IN SOUTHEAST ASIA


Background: High-resolution HIV-1 genotyping of large sample sets is crucial to define the evolving and dynamic epidemics in Southeast Asia, where subtypes B, C and CRF01_AE, and their recombinants co-circulate. The family of multi-region hybridization assays (MHAs), each with its specific geographic application, combines high-throughput and high-resolution HIV-1 genotyping. MHAbce-v2 was designed to detect most of the strains circulating in Southeast Asia. Here we present the first field test of the assay.

Methods: 180 plasma samples from HIV-1 infected mothers enrolled in a mother-to-child transmission cohort in the Lampang Province, Thailand (1996-1998) were studied. After robotic extraction of viral RNA, amplicons were generated by RT-PCR. In MHAbce-v2, 8 genomic regions of HIV-1 were assessed by real-time PCR using clade-specific fluorescent probes. Non-CRF01_AE strains were confirmed by full-genome sequencing.

Results: 100% of the samples could be typed by MHAbce-v2. 95% of the samples were CRF01_AE. Four samples were subtype B, and 3 were B/CRF01_AE recombinants, each with different genetic structure. One B/C/CRF01_AE recombinant and a possible case of B/CRF01_AE dual infection were observed, their confirmation being underway.
Conclusions: MHAbce-v2 is a sensitive and specific tool, suitable for studying large HIV-1 cohorts in Southeast Asia. Inter-subtype recombinant strains were already present in the mid-90s.

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ON-SITE ASSESSMENT OF QUALITY ASSURANCE (QA) PROGRAMS FOR ANTI-HIV TESTING AMONG 65-HIV TESTING LABORATORIES IN THAILAND

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Background: HIV antibody testing differs from other serological tests because a positive HIV diagnosis can lead to stigmatization. The correct HIV diagnosis can be achieved with very careful use of quality assurance (QA)/quality control (QC). We therefore conducted an on-site assessment to evaluate the effectiveness of QA programs for anti-HIV testing to promote best quality testing for HIV in Thailand with limited financial resources.

Method: Sixty-five HIV testing laboratories were divided into primary testing (63), and reference (2) laboratories, seeking hospital and/or laboratory accreditation under Thai Medical Technologist Standard, ISO 15189, and the US CAP standard, were assessed during 2002-2004.

Results: More than 98% of the inspected laboratories participated (64/65) in at least one EQAS for anti-HIV. We found that HIV testing algorithms used were different and depended upon the laboratory's size and infrastructure. Although EQAS is well-established and most laboratories obtain the correct results, the most common errors and other types of error observed from on-site assessment were caused by implementation of inappropriate QA/QC programs and best practices.

Conclusion: Special considerations for developing countries such as Thailand are testing under non-optimal conditions, best-fit strategy or when test systems fail. Methods to detect and correct mistakes should be employed to avoid the adverse outcomes of HIV misdiagnosis and ensure minimum false diagnostic results.

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