

Genetic variation and resistance development in HIV-1 infected patients from Denmark and Greenland

Tina Vasehus Madsen, MSc

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Official opponents: Gitte Kronborg, Alex Lund Laursen, and Jan Albert, Sweden.

Tutors: Jan Gerstoft and Louise Bruun Jørgensen.

Correspondence: Tina Vasehus Madsen, Statens Serum Institut, Department of Virology, Virus Biosafety (BL-3) Laboratory, Artillerivej 5, 2300 Copenhagen S, Denmark.

E-mail: tvm@ssi.dk

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ABSTRACT

The PhD dissertation was carried out at Statens Serum Institut, Department of Virology, and accepted for defence by the Faculty of Health Sciences, University of Copenhagen.

Phylogenetic analyses of HIV-1 gene sequences from Greenland inferred a distinct genetic diversity between viruses from this region and viruses with the same subtype from different geographic regions. The genetic diversity is due to founder effect. Analyses also indicated that even though several introductions of HIV-1 had occurred in Greenland, only a single one caused a circulating epidemic. The majority of the analysed Greenlandic sequences grouped closely together in a phylogenetic cluster. Sequence analyses also showed a high prevalence of resistance mutations (30%) in untreated Greenlandic patients compared to untreated Danish patients (4%). The presence of resistance mutations in untreated patients indicate transmission of resistant virus from treated patients. The analyses cover samples from 1999 to 2004, and in light of the improved treatment options in Greenland it could be interesting to analyse whether the high prevalence of transmitted resistance is still seen in the population.

The second part of the study concerns acquired resistance due to treatment. Sequence analyses and phylogenetic analyses indicated that virus in a highly treated patient can revert to wild type during treatment interruptions. However, the analyses also showed that reinitiation of treatment induced recruitment of resistant virus from the cellular memory.