



ACADEMIC EXAMS
AT THE FACULTY OF MEDICINE OF THE UNIVERSITY OF LISBON
INSTITUTE OF ADVANCED TRAINING

Masters:

Emerging Infectious Diseases (3rd Edition)

Name of Student:

Vânia Cristina Viriato Oliveira

Subject of Thesis:

Genetic Diversity and Analysis of Susceptibility of the Human Immunodeficiency Virus to Anti-Retrovirals in Cape Verde.

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Mark:

Very Good

Jury:

President: Professor Francisco Antunes (FMUL)

Orientator: Professor Emília Valadas (FMUL)

Co- Orientator: Professor Nuno Taveira (ISCSEM)

Jury Members: Professor Saraiva da Cunha (FMUC)



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ABSTRACT

The spread of the HIV/AIDS infection in Cape Verde in 2005 was below 1%, although more than 50% of these cases were already at the AIDS stage. A group of 148 HIV-infected patients started to be treated with antiretroviral drugs already in 2005. The blood samples analysed in this work were taken from this population, considering both the cases of patients undergoing antiretroviral therapy and patients that never followed such therapy.

Therefore, the main objectives steering this thesis were: to characterize both the HIV-1 and HIV-2 genetic diversity and origin in Cape Verde; to determine the genetic variability of antiretroviral resistant HIV-1; to identify the types of resistance mutations for both treated and untreated HIV-1 patients.

The regions PR and RT in the *pol* gene, as well as the region C2V3C3 in the *env* gene, were sequenced for 27 patients with HIV-1 where: 17 were following a given therapy, six were not following any therapy. That information was not available in the case of the remaining four patients. Sequences for the C2V3C3 region in the *env* gene were also obtained for 14 HIV-2 patients.

The analysis of the sequences showed large phylogenetic heterogeneity of HIV-1 in Cape Verde. The G subtype was present in 13 sequences (48%). The B, F1 and CRF02_AG subtypes have occurred in two sequences each (7%). The C subtype has occurred in one sequence (4%). Six viruses were recombinant subtypes or CRFs (22%). The genotypic classification was not possible in two sequences (7%). Upon analysis of both the PR and RT the following mutations were detected for untreated patients: IPs resistance mutations (minor mutations L10I and A71V), NRTIS (M41L) and NNRTIs (K103N and Y318YF). In the case of treated patients the following mutations were detected: IPs resistance mutations (minor mutations L10I/V and V11I), NRTIS (K65R, T69d) and NNRTIs (K103N and Y181C).

The phylogenetic analysis of HIV-2 sequences revealed that all of them belong to group A. Sequences 05HANCV29 and 05HANCV36 have strong genetic homology with the reference virus HIV2ROD.

Keywords: Cape Verde, HIV-1, HIV-2, HIV-1 genotypes, natural polymorphisms, resistance mutations.