



University of Cyprus
Department of Biological
Sciences

Ph.D. Thesis Defense

Student Presentation

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This seminar is open to the public via Zoom

<https://ucy.zoom.us/j/64452439484?pwd=RWhyUFVocTFieVJxZzZhZHFSU54Zz09>

Cicek Topcu

Thesis Supervisor: Prof. Leondios Kostrikis

“A COMPREHENSIVE MOLECULAR EPIDEMIOLOGICAL ANALYSIS OF HIV-1 IN CYPRUS: UNRAVELING THE COMPLEXITY OF TRANSMISSION DYNAMICS, TRANSMITTED DRUG RESISTANCE, AND NOVEL CIRCULATING RECOMBINANT FORMS”

The human immunodeficiency virus type 1 (HIV-1) epidemic has been a major public health threat on a global scale since the early 1980s. Despite the introduction of combination antiretroviral therapy (cART), the incidence of new HIV-1 infections has continued to rise to this day. Thus, with the continuous transmission of HIV-1 and the lack of a cure, it is imperative for molecular epidemiological studies to be performed, in order to monitor the infection and ultimately be able to control the spread of this virus. This thesis provides a comprehensive molecular epidemiological analysis of the HIV-1 infection in Cyprus, through examining 305 HIV-1 sequences collected between March 9, 2017, and October 14, 2021. Employing advanced statistical and bioinformatic techniques, the research delved deeply into understanding the transmission dynamics of the HIV-1 epidemic in Cyprus, as well as monitoring of HIV-1 genetic diversity and surveillance of transmitted drug resistance. The characterization of Cyprus's HIV-1 epidemic revealed a diverse landscape, comprising 21 HIV-1 group M pure subtypes and circulating recombinant forms (CRFs), alongside numerous uncharacterized recombinant strains. Subtypes A1 and B emerged as the most prevalent strains, followed by CRF02_AG. The findings of the thesis also revealed high levels of transmitted drug resistance (TDR) patterns, raising concerns for the efficacy of cART. The demographic profile of individuals involved in HIV-1 transmission underscored the disproportionate burden borne by young to middle-aged Cypriot males, particularly those in the MSM community, who reported being infected in Cyprus. Assessment of the spatiotemporal evolutionary dynamics illustrated the global interconnectedness of HIV-1

transmission networks, implicating five continents in the dissemination of strains within Cyprus; Europe, Africa, Asia, North America, and Oceania. The thesis also included the development and evaluation of novel methodologies, HIV-1 pol RT-PCR and near-full-length HIV-1 genome RT-PCR assays, and the implementation of state-of-the-art visualization analytics for near-real-time detection of cohorts at substantial risk of HIV-1 infection, which were instrumental in addressing the HIV-1 epidemic. Additionally, the identification and characterization of five novel HIV-1 CRFs, CRF91_cpx, CRF129_56G, CRF130_A1B, CRF131_A1B, and CRF138_cpx, and two unique recombinant forms (URFs) underscore the dynamic nature of HIV-1 evolution in Cyprus. Overall, this thesis advances comprehension of the HIV-1 epidemic in Cyprus and highlights the importance of understanding HIV-1 transmission dynamics through continuous surveillance efforts. Furthermore, this work emphasizes the critical role of innovative methodologies and technologies in addressing the challenges posed by HIV-1 transmission globally, laying the groundwork for targeted public health interventions aimed at curbing its spread and improving patient outcomes.