UNIVERSITY OF CYPRUS
DEPARTMENT OF BIOLOGICAL SCIENCES

The Department of Biological Sciences cordially invites you to the thesis defense of the PhD candidate

STAVRIA PANAYIDOU
(Dr. Yiorgos Apidianakis Research Laboratory)

entitled

"INVESTIGATING THE ROLE OF *PSEUDOMONAS AERUGINOSA* METABOLISM IN VIRULENCE"

Abstract

The current worldwide spread of antibiotic resistance demands novel approaches for anti-infective therapy. *Pseudomonas aeruginosa* (*P. aeruginosa*) is a gram-negative bacterium classified among the few priority pathogens urgently requiring new and effective treatments. In this study to identify novel therapeutic targets against *P. aeruginosa*, we focused on virulence-related metabolic genes, which are not essential for the physiological bacterial growth. By assessing 553 metabolic and 95 non-metabolic gene mutants of the *P. aeruginosa* strain PA14 for virulence in *Drosophila melanogaster*, we found 16.5% of the metabolic and 8.5% of the non-metabolic genes to be important for full virulence. Strikingly, most of the selected metabolic and all the non-metabolic mutants grow efficiently in culture or colonize the host like the wild-type strain. Thus, a significant portion of the metabolic mutants, exhibit defects in virulence that cannot be attributed to auxotrophy. The identified metabolic genes belong to 7 central metabolic pathways and their mutants exhibit defects in various virulence properties, as well as in an acute murine lung infection assay.

Moreover, we quantitively assessed the pathogenicity of 18 *P. aeruginosa* and 12 non-*P. aeruginosa* fully sequenced strains in two *Drosophila* infection assays, and six strains were validated in a mouse infection assay. Comparative genomic analysis of all strains shows no correlation between pathogenicity and gene content of different *Pseudomonas* strains. For this reason, we used a transcriptomic approach by which we made a comparison between the transcriptome and the virulence potential of 3 high and 3 low in virulence *P. aeruginosa* strains. We found that *P. aeruginosa* virulence, which to this point remains unpredictably combinatorial at the genome level, may be described at the transcriptome and functional level by conserved core-metabolism modules that control and indicate the virulence of disparate *P. aeruginosa* strains.

Friday, September 13th, 2019 at 14:00
Building FST02, Floor -2, Room B230 (Panepistimioupoli Campus)
The presentation is open to the public.