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ESR No. 12
Host Institution: University of Ghent, Belgium
ESR enrolled at: University of Ghent, Belgium

Institute	University of Ghent, Belgium
Lab	Laboratory for Bacteriology Research
Responsible person	Mario Vaneechoutte
Job title	Early Stage Researcher: PhD thesis on molecular ecology and microbiology of <i>Candida vaginitis</i>
Job description	<p>Short description:</p> <ul style="list-style-type: none"> - Required degree: BSc (Hons) (e.g. U.K./Ireland), MSc in biology, biochemistry or equivalent - Preferred qualification and expertise: molecular biology, use of molecular-biological databases, bioinformatics - Duration: 36 months - Language: English (essential), - Contact: Mario Vaneechoutte, Tel.: +32 9 332 3692; Mail: Mario.Vaneechoutte@UGent.be <p>The Laboratory for Bacteriology Research: The Laboratory for Bacteriology Research (LBR) is part of the department Clinical Chemistry of the Faculty of Medicine & Health Sciences at Ghent University, Belgium. It is located at the campus of the Ghent University Hospital, a 1000-bed university hospital. The research of the lab is focused on rapid, easy-to-apply and cheap molecular approaches for the detection, identification and quantification of bacteria and fungi in diverse clinical samples and on approaches for species identification and strain genotyping of cultured microbes. (Reverse transcription) quantitative PCR and melting curve analysis are currently the techniques that are mostly used, in combination with RAPD, FISH and sporadic deep sequencing of DNA and mRNA. Besides application in microbial diagnostics, this expertise has lead to the description of new species and genera and to the characterization of microbial communities (oral and vaginal), with a focus on chronic infection problems, such as airway infection in cystic fibrosis and bacterial vaginosis. The lab hosts one postdoc (bacteriophage therapy), six PhDs (one working on detection of fungi in clinical samples) and one technician.</p> <p>PhD project Objectives: 1. Elucidation of host-pathogen interactions in vaginal samples of women with <i>Candida vaginitis</i> (acute and recurring) as compared to women without vaginitis. Methodology: Dual RNA-sequencing of vaginal samples of women with and without <i>Candida albicans</i> vaginitis: isolation of RNA from vaginal samples, quality control of RNA, reverse transcription PCR, deep sequencing, mapping of mRNAs against human and <i>Candida</i> genomes. Vaginal sampling will be done by using e-swabs (standard procedure). RNA-extraction will be carried out in collaboration with P6 (Jena, Germany). RNA-sequencing will be carried out in collaboration with P1 (Barcelona, Spain). Data analysis will be performed in collaboration with P1 (Barcelona, Spain) and P4 (Valencia, Spain). Expected Results: Identification of virulence factors up-regulated in <i>C. albicans</i> and of the immune response of the host. Candidate genes will be developed into prototype diagnostic tools.</p> 2. Validation of diagnostic tools developed by other partners, using clinical samples collected in the hospital and from general practitioners. Validation will be carried out in collaboration with P8 (Innsbruck, Austria). <p>Planned secondment(s): P6: RNA-extraction and sample processing: 1 month P1 and P4: RNA-sequencing and bio-informatic analysis, integration of in vivo data into bioinformatics pipeline: 3 months P8: clinical validation: 1 month</p>