Position by institution 2

ESR No. 3
Host Institution: KNAW-CBS Fungal Biodiversity Centre, Utrecht
ESR enrolled at: University of Amsterdam

Institute	KNAW-CBS Fungal Biodiversity Centre, Utrecht
Lab	Yeast and Basidiomycete Research Group
Responsible person	Teun Boekhout, PhD
Job title	Early Stage Researcher: PhD thesis on Yeast pathogen diagnostics
Job description	Short description: - Required degree: BSc (Hons) (e.g. U.K./Ireland), MSc, or equivalent in biology, biochemistry, molecular biology, clinical/molecular microbiology or related subject - Preferred qualification and expertise: (Fungal) molecular biology, knowledge in use of molecular-biological databases, advanced bioinformatics knowledge, knowledge on clinical microbiology - Duration: 36 months - Language: English (essential), - Contact: Teun Boekhout, Tel.: + 31 (0)30 2122600; Mail: t.boekhout@cbs.knaw.nl **The Yeast and Basidiomycete Research Group:** Yeasts are among the best-studied eukaryotes on earth due to some very well studied species, such as *Saccharomyces cerevisae* and *Schizosaccharomyces pombe*. This, however, covers only a fraction of the known diversity of yeasts. Our research focuses on: 1. Understanding yeast biodiversity and evolution 2. Mechanism of pathogenicity 3. Innovative diagnostics 4. Fungal biodiversity and ecology **PhD project** Objectives: To develop a robust and reliable yeast identification tool based on comparative genomics analysis of the entire yeast domains, including *Candida, Cryptococcus* and *Malassezia.* ESR3 will address innovative yeast diagnostics with emphasis on species and resistant isolates using the output of bioinformatics comparisons (from WPs 2-3). A clade-specific approach will be followed for the development of an "ALL-yeast" probe, an "ALL-Candida" probe, an "ALL- Cryptococcus" probe, and we will focus on the least inclusive group, the single pathogen species. CBS-KNAW holds a big collection of 10,000 molecularly barcoded (ITS and D1D2) strains that will be used for probe validation. Methodology: WP2 will generate a series of genome domains that will be explored for probe generation using available bioinformatics tools, PrimerSelect software (DNASTAR Lasergene 8). Probe optimisation will be done in collaboration with ESR1 (P1) and PO1 and by extensive testing in the clinical laboratory (P8) using WP2 validated strains, including reliability, sensitivity etc. In collaboration with clinical partners clinical samples will be tested and compared with current methods of clinical yeast identification. Also cell-based assays will be developed. Expected Results: A set of candidate and validated nucleotide domains that are useful for the development of diagnostic probes/primers of pathogenic yeast species and groups thereof. These diagnostic primers will be further validated further in the clinical partner laboratory (P8). **Planned secondment(s):** P4 BIOTECHVANA (2 months; Y1; to learn bioinformatics and databases); OP1 (1 month; Y1; to learn how to mathematically optimize diagnostic probes); P5 UNIABDN (1 month, Y2; to validate candidate probes using animal models); P8 IMU (3 months; Y3; to validate candidate diagnostic markers in a clinical setting). The student will also closely interact with the students at CRG, Biotechvana, QVQ, Bruker and Medical University of Innsbruck.