# One bioinformatics pipeline for genomic characterisation of *Candida* sp. clinical strains

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*Candida* sp. are the most common cause of fungal infections [1]. The increase of *Candida* antifungal resistance to the most widely used antifungals is alarming, given persistent infections are common and may be left untreated [2]. Genomic surveillance of *Candida* isolates allows for the investigation of the biology, ecology, phylogenomics and epidemiology of these pathogens. Importantly, the genomic characterisation of *Candida* isolates provides accurate species identification, monitoring of antifungal resistance, and the surveillance of the emergence of novel pathogens, which are crucial for appropriate diagnostic and treatment [3].

On the other hand, as eukaryotic unicellular organisms, *Candida* sp. present specific genomic characteristics that distinguish them from the most commonly studied genomes, i.e., bacteria and human. In this way, many of the open-source bioinformatic tools becomes inappropriate to tackle fungal genomes as needed, which hinders this type of analyses and delays their application to the clinical setting. Furthermore, Oxford Nanopore Technologies have been presented as an easy-to-use sequencing methodology in the clinical setting [4], but ONT-dedicated bioinformatic pipelines aiming to analyse and extract useful information from fungal genomes collected during infection are still lacking.

In this work, we have addressed this issue, and propose a bioinformatics pipeline to conduct isolates identification and variant analysis of fungal species with clinical relevance, starting with raw data from MinION sequencing of whole genomes of ten *Candida* sp. isolates from vaginal, oral and blood samples. Our results show the importance of genomic surveillance for the accurate identification of pathogens and understanding the adaptability of isolates to particular niches. Future work involves Illumina sequencing of these genomes for hybrid assembly/read correction and improvement of our analysis pipeline.

[1] doi: 10.1101/cshperspect.a019778
[2] doi: 10.1093/ofid/ofy358
[3] doi: 10.1038/s41426-018-0045-x
[4] https://nanoporetech.com/applications/clinical-research (last accessed 20210407)

# Genomic characterisation of

# *Candida albicans* clinical isolates

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