

Academic City University College, Accra, Ghana
Society for Multidisciplinary & Advanced Research Techniques (SMART)
Trinity University, Lagos, Nigeria
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IEEE Computer Society Area Six

33rd ECOWAS iSTEAMS ETech Multidisciplinary Conference (ECOWAS-ETech)

Incidence, Characterization And Virulence Profiling Of Clinical *Candida* Species Isolated From Primary Health Centres In Oyo Town.

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Abstract

Candida species are normal commensals of the female lower reproductive tract and other anatomical sites such as the auditory cavity, oral cavity, digestive tract and the skin. There is therefore need to continuously carry out surveillance studies on the risk factors associated with *Candida* infections. The aim of this study was to determine the phenotypic and genotypic antifungal resistance as well as the virulence profiles of the clinical *Candida* species within Oyo Town. A systematic random sampling technique was used to select one hundred and twenty one (121) apparently healthy females aged between 18 and 40 outpatients attending selected Primary Health Centers (PHCs) in three Local Government Areas within Oyo metropolis (Oyo East, Oyo West and Atiba), Oyo State, Nigeria. High Vaginal Swab (HVS) and Ear Swab (ES) samples were collected from each of the women. The samples were streaked directly on Saboraud Dextrose Agar plates and *Candida* spp. were identified using CHROM Agar. The isolated *Candida* spp. were phenotypically screened for virulence factors and susceptibility to antifungal agents. The virulence and antifungal resistance genes of isolates that produced the virulence phenotypes were determined using Real-time Polymerase Chain Reaction. A total of 136 *Candida* spp. were obtained from the samples: Eighty-four (84) *Candida* spp. were obtained from HVS (49 *Candida albicans*, 14 *Candida krusei*, 11 *Candida glabrata*, and 10 *Candida tropicalis*) and 52 *Candida* spp. were isolated from the ES (26 *Candida albicans*, 13 *Candida glabrata*, 7 *Candida tropicalis* and 6 *Candida krusei*). *Candida albicans* strains isolated from the HVS and ES were highly positive to haemolysis (24.5%, 38.7%), lipase activity (55.1%, 38.7%), phospholipase activity (20.4%, 20.1%) and biofilm formation (10.8%, 3.1%). The antifungal assay revealed that 43.5% *Candida albicans* and 79.7% non-*Candida albicans* spp. were resistant to nystatin and fluconazole. *Candida albicans* OEOA5 produced azole resistance gene (*CDR1*) at 300 bp while *Candida albicans* ATAF21 and OEOA5 produced multi-drug resistance gene (*MDR*) at 190 bp. The *Candida* species were phenotypically positive to the tested virulence factors. They produced azole and multi-drug resistance genes. Isolate OEOA 5 was molecularly identified as *Candida albicans* with accession number MK530515 while Isolates ATOO 14 was molecularly identified as *Pichia kudriavzevii* with accession number KX273822. Continuous surveillance studies must therefore be carried out to monitor associated risk factors of *Candida* infections (such as washing of the vagina or ear with soap, misuse of antibiotics, and use of public toilets) as well as antifungal resistance among clinical *Candida* species.

Keywords: *Candida* species, Antifungal agents, Resistance, Virulence genes, Clinical specimens.

Proceedings Citation Format

Fashogbon, R.O., Popoola, B.M., Adefioye, O. & Atinuke, Olanbiwoninu, A.A. (2022): Production and Characterization of laccase and silver Nanolaccase from *S. commune* and their application as Antibacterial and Wastewater Treatment Agents. Proceedings of the 33rd ECOWAS iSTEAMS Emerging Technologies, Scientific, Business, Social Innovations & Cyber Space Ecosystem Multidisciplinary Conference. University of Ghana/Academic City University College, Ghana. 29th Sept – 1st Oct, 2022. Pp 99. www.isteam.net/ecowasetech2022. dx.doi.org/10.22624/AIMS-/ECOWASETECH2022P17
