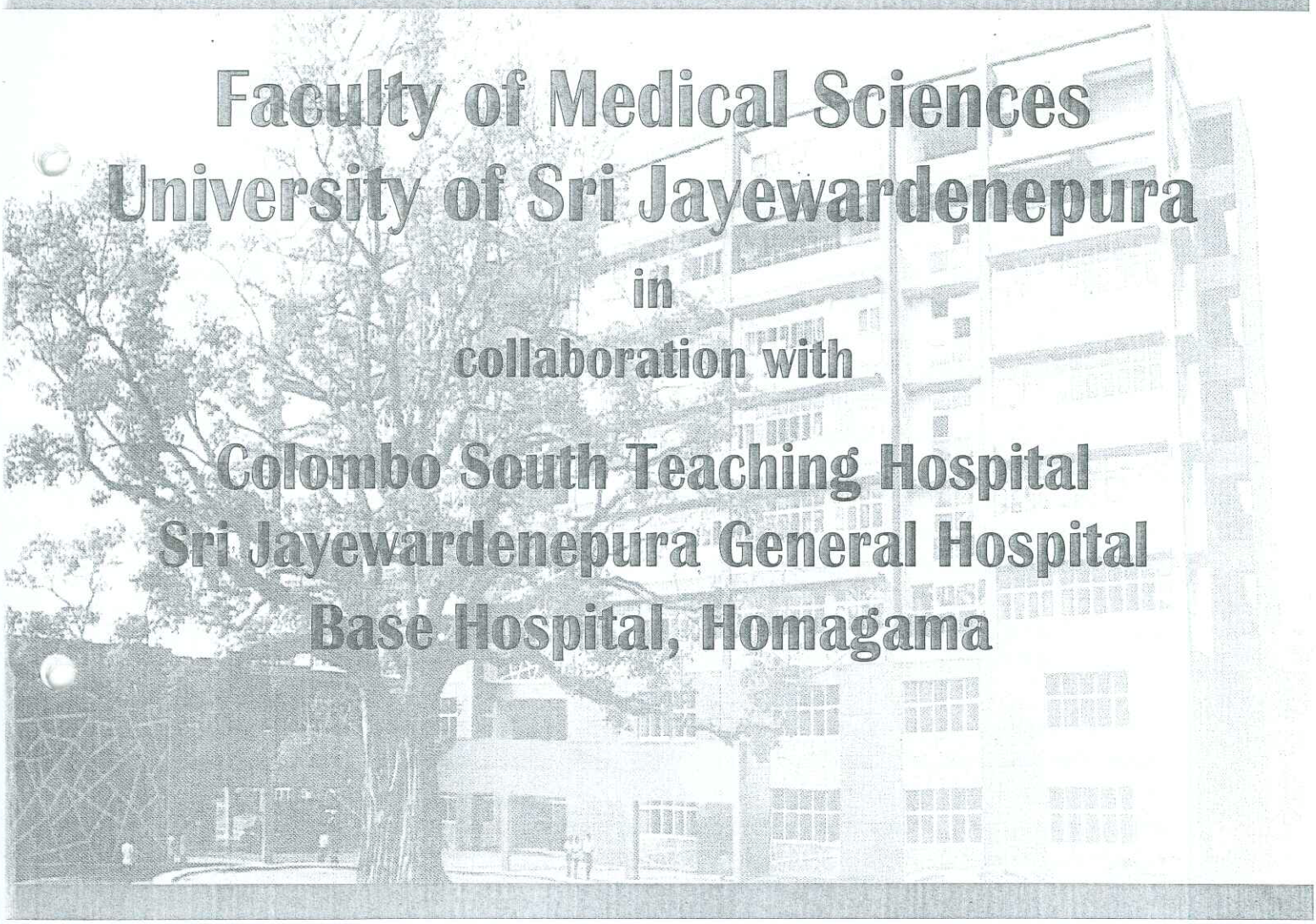
International Conference on Health Sciences 2018



Faculty of Medical Sciences
University of Sri Jayewardenepura

in

collaboration with

Colombo South Teaching Hospital
Sri Jayewardenepura General Hospital
Base Hospital, Homagama

"Beyond Borders Towards Excellence"

Book of Proceedings

7th to 9th October 2018

Waters Edge, Colombo

OP 3

Identification accuracy of oral Candida species from patients with diabetes by phenotypic and molecular methods

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Background: Oral candidiasis in patients with diabetes mellitus has been recognized and reported recently as one of the major oral complications.

Objectives: This study aimed to determine the proportion of different Candida species among patients with diabetes using different phenotypic and molecular based methods and compare the accuracy of both methods.

Methods: Concentrated oral rinse specimens were subjected to culture identification using the germ tube test and sugar assimilation tests. DNA was extracted from concentrated oral rinse specimens and yeast isolates using the glass bead method. Multiplex PCR was carried out using published primers, ITS 4, CA, CT, CG and CP, to identify *C. albicans*, *C. tropicalis*, C. *parapsilosis* and *C. glabrata*. PCR-RFLP with Msp I restriction enzyme was used for species identification.

Results: Of the 250 patients, 142 (56.8 %) were female with a mean age of 60 years. Candida species were confirmed in 204/250 (81.6%) by culture. Culture identified multiple Candida species in 88 patients. Phenotypic identification and PCR-RFLP respectively identified *C. albicans* as the predominant species (66.8%, 68.8%) followed by *C. parapsilosis* (22.8%, 21.6%), *C. tropicalis* (18%, 16%), *C. glabrata* (1.6%, 3.2%) and *C. krusei* (5.6%, 3.6%). The multiplex PCR was positive for Candida species in 89.2 % of patients with *C. albicans* (79.2%) followed by *C. parapsilosis* (35.6%), *C. tropicalis* (31.6%) and *C. glabrata* (5.6%). Considering multiplex PCR as the gold standard, both PCR-RFLP and culture dependent methods had a high, specificity and positive predictive values for *C. albicans* identification. However, poor sensitivity, specificity and PPV values were obtained for non-albicans Candida species.

Conclusions: *C. albicans* was the predominant Candida species among the study population. The conventional culture method has poor specificity in identifying non-albicans Candida species in clinical specimens.

Acknowledgement: This work was supported by the research grant funded by the University of Sri Jayewardenepura (Research Grant No: ASP/06/RE/MED/2014/08), and Medical Research Institute, Sri Lanka (Research Grant No: 2013/33).

OP 4

Sequence based identification of resistance mechanism in *Salmonella typhi* clinical isolates from Northern India

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Background: Surveillance of antimicrobial resistance genes is important for understanding the primary mechanisms and the epidemiology of antimicrobial resistance.

Objectives: To develop pan-genome and core-genome from pathogenic *Salmonella enterica* strains and identify novel multidrug-resistant genes and acquired pathways.