

## ABSTRACT

### Genetic Variability of *C. albicans* at Oral Mucosa in Regulation Levels of Diabetes Mellitus Diseases

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*C. albicans* infections were found in 80% of the Diabetes Mellitus (DM) population. This is because the ethiopathogenesis underlying this infection is complicated, involving both immunity and molecular pathways, while the molecular pathway of this infection remains to be fully understood. The objectives of this study were to comprehend the ethiopathogenesis of *C. albicans* infection in the oral cavity of DM patients at a molecular level by observing the existence of SAP1 and SAP3 genes, and to comprehend the genetic variability of *C. albicans* isolated in Surabaya. The result of a phenogram analysis described that *C. albicans* colonizing the oral mucosa of well-regulated DM patients had the tendency to be of close genetic relationship (with a genetic distance of 0.762) to that of poorly-regulated DM patients. With reference to regulation levels, the existence of SAP3 gene *C. albicans* in DM patients showed an average score in non-DM patients of  $11512.86 \pm 1348.26$ , lower than that of well-regulated DM patients of  $10319.53 \pm 9028.21$  and poorly-regulated DM patients of  $14793.86 \pm 8851.28$ . In this study, of all *C. albicans* samples taken from well-regulated DM patients, poorly-regulated DM patients and non-DM patients, more than 75% were serotype A and the remaining were serotype B. The existence of serotype B in poorly-regulated DM patients was higher than that in other groups. IL-1 $\beta$  and TNF- $\alpha$  in poorly-regulated DM patients were significantly different ( $p < 0.005$ ) from those in other groups, while well-regulated DM patients had no significant difference from non-DM patients in terms of IL-1 $\beta$  and TNF- $\alpha$ . It can be concluded that the isolated existence of SAP3 genes *C. albicans* in Surabaya was correlated by the level of regulation of DM patients. A correlation was found between genetic variability and *C. albicans* virulence and the level of regulation in DM patients. Virulence was not only determined by serotype, such as that suggested by antecedent theory, but also correlated by the existence of SAP3 genes. Thereby, the result of this study can be employed as a basis for a diagnostic determination with a more accurate concept of *C. albicans* infection in the oral mucosa of DM patients.

**Keywords:** Diabetes Mellitus, *C. albicans* infections, Secretory Aspartyl Proteinases (SAP), genetic variability and cytokine