# TRANSCRIPTIONAL CONTROL OF *PGA55*, A GENE PREDICTED TO CODE A UNIQUE GPI-PROTEIN IN *CANDIDA ALBICANS*

Carol Kobori da Fonseca[1], Fabrício Freitas Fernandes[1], Paulo Sérgio Rodrigues Coelho[1].

[1]Departamento de Biologia Celular e Molecular e Bioagentes Patogênicos. Faculdade de Medicina de Ribeirão Preto - Universidade de São Paulo, Ribeirão Preto - SP, Brazil.

In fungi the glycosylphosphatidylinositol - anchored proteins perform functions such as cell to cell and cell to host tissue adhesion, cell wall biogenesis and remodelling. We have studied 12 *PGA* genes predicted to code unique GPI-proteins in *Candida albicans*. *PGA55* encodes a 1,176 residue protein with an N-teminal secretion signal, a C-terminal omega site for GPI attachment and a middle domain rich in serine/threonine. The recent assembly of the *C. albicans* diploid genome revealed two *PGA55* alleles differing 684 bp in their ORF size. Northern analysis revealed two *PGA55* transcripts that according to their sizes are presumably expressed from the two individual alleles. Efg1 is a trancription factor that positively regulates the dimorphic transition from yeast to filamentous form. Interestingly, in *EFG1* mutant the expression of the larger *PGA55* transcript is decreased and the expression of the smaller one is increased. We also observed that yeast cells growing at the mid-log phase shows a peak in *PGA55* transcription. Since *PGA55* does not have homologs we believe that it may play a unique role on *C. albicans* comensalism or pathogenesis.

**Key words:** *Candida albicans,* morphogenesis, GPI-protein, *PGA55*
**Acknowledgements:** FAPESP, FAEPA.