

STRUCTURAL AND EXPRESSION ANALYSIS OF THE TRANSCRIPTIONAL FACTOR ENCODING GENE *PACC* OF *PARACOCCIDIOIDES BRASILIENSIS*

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Environmental pH is an important signal for fungi physiology, intervening at the transcriptional regulation of several gene products. In *Aspergillus nidulans*, cellular adaptation to different pH values is achieved through the PacC transcription factor, activated by neutral or basic pH. Homologues to *pacC* genes were isolated from different plant and human pathogenic fungi, being somehow related to their pathogenicity. *Paracoccidioides brasiliensis* (*Pb*) is a dimorphic fungus, endemic in Latin America, which causes a severe systemic mycosis in humans. We have identified in *P. brasiliensis* a homologous gene to *A. nidulans pacC*. *Pb pacC* genomic sequence presents 2397 nucleotides and four putative introns. RT-PCR analyses suggest that the fourth predicted intron, which does not present a stop codon in any possible reading frame, is retained in the mature mRNA. The predicted PacC protein is composed of 706 amino acid residues and shares conserved motifs with the majority of the published homologous sequences. The highest identity is with the skin pathogen *Trichophyton rubrum* PacC (50,2%). Expression analyses of *Pb pacC* gene, after fungal growth in acidic, neutral and alkaline pH, demonstrated that it is transcribed in all conditions assayed. This work identified the first described transcriptional factor gene of *P. brasiliensis*, which may participate in a pH-dependent signaling pathway. Key words: pH adaptation, *pacC*, *Paracoccidioides brasiliensis*.