TRANSCRIPTION FACTORS INVOLVED IN THE CELL WALL BIOSYNTHESIS OF *C. ALBICANS*

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Candida albicans is a polymorphic fungus that colonizes the human gastrointestinal tracts as a commensal in healthy humans. However, it is able to produce deep-rooted infections in patients suffering cancer, organ-transplantation and other immunocompromising conditions. During these interactions *C. albicans* establishes contact with host cells through its cell wall, which is the outermost fungal structure.

The fungal cell wall determines the shape of the fungal cell and protects the protoplast against physical, osmotic and oxidative damage. The *C. albicans* cell wall is mainly composed of β-glucans (β- 1,3 and β-1,6-glucan), chitin and mannoproteins. These three components are dispersed throughout the cell wall, although mannoproteins are mostly concentrated on the outer surface. Mannoproteins represent 30-40% of the total cell wall and determine the surface properties, enabling *C. albicans* cells to interact with and adhere to host tissues. Mannoproteins can be bound to the cell wall components by different kind of linkages: (I) Hydrogen bonds and/or hydrophobic interactions; (II) Disulphide-bridges and (III) covalently bound mannoproteins. *C. albicans*, as an opportunistic pathogen, must be able to adapt its growth to a range of environmental changes. For these adaptations, *C. albicans* should modulate in a coordinate way the expression of many genes. In *C. albicans*, many of the MAP (mitogen-activated protein) kinase pathway components are important for virulence and morphological transition. For this reason the knowledge of the role of the transcriptional factors should help us to understand the interaction between *C. albicans* and host tissues, a process where the cell wall plays an important role. So, studies concerning cell wall regulation are becoming more important each time.

The determination of the complete genomic sequence of *C. albicans* has allowed the *in silico* identification of 70 potential $Zn(II)_2C_6$ transcription factors. One of these factors, CaCwt1, shows a high homology with *Saccharomyces cerevisiae* Rds2p. *Scrds2* mutants are hypersensitive to calcofluor white, a drug interfering the correct cell wall assembly. As its orthologous in *S. cerevisiae*, CaCwt1p transcriptional factor seems to be involved in cell wall architecture. Several transcription factors (Cas5p, Ace2p, Efg1p, Bcr1p…) play a role in the regulation of the cell wall components biosynthesis and assembly.

Little it is know so far about transcription regulation of cell wall genes; however, the knowledge of these transcriptional regulators has opened new insights into *C. albicans* cell wall structure regulation. Characterization of unknown transcription factors and studies concerning their interactions and mechanisms of action will provide new evidences about regulatory networks controlling cell wall composition and assembly of the cell wall components of the pathogenic fungus *C. albicans*.