The fungal cell wall genome: phylogenetic implications

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Fungi are among the large numbers of organisms belonging to different taxonomic groups, both prokaryotic and eukaryotic, that posses cell walls, and we may conclude that it is precisely the cell wall the structure that best characterizes the kingdom Fungi. The cell wall is the structure that provides the cell its shape, its resistance to the difference in the osmotic pressure between the cytoplasm and the medium, protects it from the aggression of multiple extra-cellular agents, and first comes in contact with solid substrates and other organisms, thus establishing a cross-talk with the environment.

Pioneer methods for the isolation of intact cell fungal walls, and chemical analyses that became more sophisticated each time, and especially the development of sensitive proteomic techniques for the identification of proteins, permitted to elaborate a model of the fungal cell wall as made of two different kinds of components, one consisting of structural microfibrillar polysaccharides, mainly chitin, and the other one made mostly of amorphous polysaccharides and glycoproteins. It was established that both types of components interacted among themselves, as occurs in man-made composites, to provide the cell wall its specific mechanical properties: the first one its resistance to tensions, and the second one its resistance to pressure and to protect the former from fatigue and fracture. These components, joined by covalent and non-covalent bonds give rise to a tri-dimensional coherent structure that conserves its organization through a peculiar process involving a mixture of specific catalytic processes and self-assembly reactions.

Further studies carried out with Ascomycete yeasts, mainly *Saccharomyces cerevisiae*, established their cell walls as representatives of the rest of the fungi, concluding that it is made by the association of the structural polysaccharides (a small amount of chitin and a major amount of β1-3, glucans), with β1-6, glucans and glycoproteins bound either covalently or non-covalently.

With the advent of genomic techniques that provide the possibility to obtain the sequence of full genomes from different fungi, and powerful methods to analyze their phylogeny, it became possible to analyze whether this model truly represents the fungal cell wall, and how the structure and its different components have evolved.

Utilizing all this information it has been possible to analyze the set of genes that play a role in the synthesis of different types of proteins, supposedly associated with the fungal cell wall, or in the synthesis of the *bona fide* components that make it up, study their phylogenetic relationships, and how their possible evolution correlated or not with the accepted trends of fungal evolution. The accumulated evidence indicates that not only there are important differences in the chemical components of the cell walls of the several fungal taxa (as was initially demonstrated by chemical analyses), but allowed to establish the phylogenetic relationships of the enzymes that synthesize them. Analysis of their possible evolution, suggests that apparently this occurred independently in the several taxonomic groups. The final image is that the cell wall of *S. cerevisiae* is far from being a model for the rest of the fungal groups, and that except for their basic architectural features, each one of them posses peculiar types of the cell wall synthetic machinery, composition, and structure, that have been changing and departing from their relatives for a long time in the evolutionary history