Molecular Characterization of *Saccharomyces cerevisiae* Extracellular Matrix and Yeast Response to Different Sizes of Hyaluronan

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Yeast, *Saccharomyces cerevisiae*, presents itself as the best studied eukaryotic model, with the possibility to modify its genetic information with highly advanced molecular techniques. This microorganism displays a high degree of similarity and conservation of processes with higher eukaryotes. Several fundamental mechanisms such as cell cycle regulation, DNA replication, recombination and repair were first uncovered in this microorganism. From areas as cancer to neurological diseases, as Parkinson, yeast has provided vital information.

Different kinds of diseases in humans are connected to the Extracellular Matrix (ECM), like fibrosis and scleroderma. Therefore, the study of ECM components function as well as its regulation has been receiving lots of attention. Several of these, such as the structural molecule Hyaluronic Acid (HA) and diffusible growth factors, have the capacity to signal and redirect the behavior of the surrounding cells. HA has the ability to give different signal inputs depending solely on its size and concentration.

Yeast is a unicellular eukaryotic with the remarkable capacity to live as individual, small aggregates and colonies. Within a colony, yeast cells live or die according to their relative position, being able to differentiate into hyphae, as well as pseudohyphae, and stalks. All these accomplished through the communication between the cells within the colony, which are embedded on a yet uncharacterized ECM.

Besides ECM tridimensional structure aspect, none is known regarding its composition and organization. So an efficient method for the extraction, analysis and identification of *S. cerevisiae* ECM components, proteins and sugars, in colonies is currently in the last phase of implementation. The knowledge of the main constituents of the ECM will be a milestone in the establishment of this microbe as a model organism for ECM-related processes.

Yeast doesn’t present the necessary enzymes and receptors to produce a response from HA. As yeast lacks the capacity to produce, degrade or “understand” the HA molecules, it is an excellent model for the manipulation of all aspects regarding the eukaryotic transduction of information from HA. The heterologous expression of HA receptors in yeast (CD44 and HMMR),the effect of this glycosaminoglycan on the main pathways, HOG, PKC or TOR, as well as changes in duplication time, chronological aging or life span, are also currently underway.

The main asset of our work resides on the use of a simpler and better understood model, the yeast, for the study of HA effects on eukaryotic cells, and how the information is transduced.

The characterization of yeast own ECM, and the understanding of the HA effect on this microorganism could lead yeast to a privileged position as a model organism for the study of ECM-related pathologies.