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Integrative analysis of osmoregulation in yeast *Saccharomyces cerevisiae*

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Akademisk avhandling för filosofie doktorsexamen i mikrobiologi, som med tillstånd från Naturvetenskapliga fakulteten kommer att offentligt försvaras Tisdag den 27 Maj 2014 kl. 10.00 i föreläsningssal Carl Kylberg, Institutionen för kemi och molekylärbiologi, Medicinaregatan 7, Göteborg.

ISBN: 978-91-628-9020-9

Abstract

Similar to other unicellular organisms, yeasts frequently encounter environmental stress such as heat shock, osmotic stress, and nutrition limitations, which challenge their growth potential. To survive, all living cells must be able to adapt to changes in their surrounding environment. A set of adaptive responses is triggered that leads to repair of cellular damage in order to overcome these stress conditions. The aim of this thesis is to determine how yeast cells respond to changes in osmolarity and water activity.

Upon hyperosmotic shock, water flows out of the cell, resulting in cell shrinkage, and consequently an increase in the concentrations of all substances present in the cytoplasm. Cells adapt their internal osmolarity by gaining an appropriate cell volume as well as an internal water concentration that is optimal for biochemical processes to recover turgor pressure. Osmoregulation is an active process which is mainly regulated by the High Osmolarity Glycerol (HOG) pathway and controls the cellular water balance.

The HOG pathway is one of the four yeast MAP kinase pathways. It conveys the hyper osmolarity stress stimulus into the cell machinery and instigates appropriate responses, including global readjustment of gene expression, changes in translational capacity, transient cell cycle arrest, and accumulation of the compatible solute glycerol. Together, these processes result in osmoadaptation.

In this thesis I investigated the quantitative characteristics of osmoregulation in the yeast *Saccharomyces cerevisiae*. I applied a combination of traditional molecular approaches and frontline technologies for comprehensive and quantitative measurements, such as high throughput experiments, synthetic biology, single cell analysis and mathematical modeling to understand the interdependence and timeline of different osmoadaptation process.