Metabolic dynamics of starvation induced dormancy in *Saccharomyces cerevisiae*

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Project Goals:

To understand the metabolic mechanism involved in the initiation and departure of starvation induced dormancy in yeast.

Many organisms have adapted evolutionary to dealing with various stresses by entering a state of dormancy. Organisms that enter this dormancy typically make physiological changes that allows them to shut down their metabolism, and become resistant to various environmental perturbations including dessication, pH, and heat stresses. However the specific environmental, metabolic and physiological changes an organism undergoes as it enters and leaves dormancy is not well understood.

Here we use the yeast *Saccharomyces cerevisiae* to address the question of what metabolic changes occur as they enter a starvation induced dormancy. We attempt to answer this question by using gas-chromatography mass-spectrometry (GC-MS) to profile the intracellular and extracellular metabolites present during both log and stationary phase of growth. By combing this data with the genome scale metabolic model of yeast, we are able to follow the extracellular dynamics of metabolic usage and production as they enter log-phase, and transition into stationary phase. Furthermore, by identifying changes in intracellular metabolite concentrations, we are able to identify which metabolic pathways must change as the yeast enter stationary phase.

Our results provide some some suggestions metabolic mechanisms of dominance, which allow for the development of specific hypothesis to test. Answering these questions might allow for the engineering solutions for enhanced dormancy in plants, animals or humans, as well the development of anti-dormancy agents to target deleterious organisms such disease causing bacteria.

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