

Discovery of novel metabolic pathways in the yeast *Candida intermedia* (30/60 ECTS)



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Supervisor: Cecilia Geijer (cecilia.geijer@chalmers.se)

Division of Industrial Biotechnology at the Department of Biology and Biological Engineering, Chalmers University of Technology

<http://www.chalmers.se/en/departments/bio/research/industrial-biotechnology/>

Background: A future biobased society relies on the development of potent industrial microorganisms that can convert all the different sugars from agricultural, forestry and industrial waste streams into fuels, chemicals and materials. To be able to tailor these microorganisms for the job ahead, we first need a far better understanding of the proteins responsible for uptake (sugar transporters) and conversion (enzymes) of biotechnologically important sugars, including pentoses, disaccharides and oligomers. In yeast, genes that encode proteins for sugar metabolism in some instances group together in the genome and form so called **metabolic gene clusters**. Such clusters are excellent starting points to elucidate the physiological roles of sugar transporters and catalytic enzymes and to discover new metabolic pathways. We have discovered a very interesting metabolic gene cluster in the yeast species *Candida intermedia*, which we hypothesize is important for the yeast's ability to use lactose.

Thus, the aim of the master thesis project is to determine the physiological role of this metabolic gene cluster. The work will include cloning and genome editing in *C. intermedia* to delete both individual genes and the whole gene cluster, and to characterize the mutants using growth and enzymatic assays. We are also very interested to understand the transcriptional regulation of the cluster, which can be determined using qPCR.

The project will include learning and using various methods:

- Molecular biology techniques (PCR, qPCR, cloning, gene deletions, DNA amplification and purification)
- Microbiology techniques (culturing of cells using shake flasks and bioreactors, transformations, OD measurements, microscopy, phenotypic characterization etc)
- Biochemical techniques (HPLC, enzymatic assays etc)