

Adaptive evolution of a yeast for palm oil replacement: genotype-phenotype relationships by nanopore sequencing

Supervisory team:

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Host institution: University of Bath

CASE partner: Oxford Nanopore Technologies

Project description:

The main goal of our research is to make evolutionary and genomic tools work for industry and to improve the outcomes of fungal interactions that matter for people. Currently we are working on *Metschnikowia pulcherrima*, a ubiquitous species of yeast that produces high concentrations of an oil with properties similar to those of palm oil. Palm oil is the most commonly produced vegetable oil and is used in a vast range of products including processed foods, cosmetics, cleaning products and biofuels, but palm oil production is environmentally and socially deleterious. *Metschnikowia pulcherrima* could provide a route to a more sustainable alternative to palm oil, but this requires significant advancement of the capabilities of this yeast.

We are using adaptive laboratory evolution to improve the productivity and utility of *Metschnikowia pulcherrima*. The aim of this project is to understand the genetic changes underlying phenotypic changes in *Metschnikowia pulcherrima* when it is subjected to a series of adaptive evolution scenarios. These scenarios are focused on improving the properties of *Metschnikowia pulcherrima* for industrial exploitation, including inhibitor and fungicidal resistance, and ability to thrive in a heterogeneous environment; the scenarios include inhibitor tolerance, temperature, microbial competition, and substrate conversion.

The genetic changes underlying phenotypic changes in fungi are strongly linked to copy number fluctuation, genomic restructuring, and epimutation (a heritable change that affects gene expression without a change in DNA sequence, including base modification). Since such genetic changes are relatively difficult to detect with standard sequencing technology, we will exploit the capacity of nanopore sequencers (e.g. the MinION™) to make very/ultra long reads and to detect base modifications to elucidate the genetic changes in *Metschnikowia pulcherrima* during adaptive evolution. Data-informed mathematical modelling will be used to enhance understanding of evolutionary mechanisms. Although industrial utility is the focus of these adaptive evolution experiments, the evolutionary mechanisms elucidated can additionally be used as a point of comparison to the near relative and emerging pathogen *Candida auris*, the marine pathogenic yeast *Metschnikowia bicuspidata*, and the biocontrol yeast *Metschnikowia fructicola*.

This PhD project will provide broad, multidisciplinary training encompassing yeast biology, fungal genetics, basic molecular biology, nanopore sequencing, bioinformatics, and mathematical modelling

of genetic changes. The project is sponsored by Oxford Nanopore Technologies (ONT). In addition to regular update meetings with ONT staff and technical support from ONT, the studentship will incorporate a placement of at least three months with ONT.