DTU Library

Can we find common evolutionary patterns and trade-offs in yeast? Automated and high throughput solutions

Torres Montero, Pablo; Feist, Adam M.; Martinez, José Luis

Link back to DTU Orbit

Can we find common evolutionary patterns and trade-offs in yeast? Automated and high throughput solutions

Pablo Torres-Montero, Adam M. Feist, José L. Martínez.

The primary objective of this project is to investigate a crucial question in the field of life science: does microbial evolution exhibit convergence in adapting to challenging and rapidly changing environments? Additionally, there is a practical aspect to consider: if convergent evolutionary strategies exist among microbial species, do they entail similar trade-offs associated with the acquired traits? Discovering such symmetry could enable the development of accurate predictive models and facilitate the assessment of gain/loss patterns in cell factory design for bio-based production processes. By efficiently predicting potential losses, we can effectively engineer yeast cell factories to acquire advantageous novel traits.

To address these fundamental questions, the project will employ adaptive laboratory evolution (ALE) using a diverse set of yeast strains commonly utilized in both fundamental research and industrial production. This selection encompasses a wide range of species across the phylogenetic tree, ranging from "ancient" genera like *Yarrowia* to more "recent" ones such as *Pichia, Debaryomyces, Ogataea, Kluyveromyces,* and *Saccharomyces.*

The chosen strains will undergo adaptive laboratory evolution in response to various stressors present in industrial production setups, including high temperatures, high/low pH levels, high salinity/osmolarity, fermentation inhibitors, and oxygen-limited environments. Throughout the ALE process, the evolved strains will be sequenced at different time points to gain insights into the genetic changes occurring during adaptation. This comprehensive approach, combined with thorough physiological and multi-omic profiling, will facilitate an extensive comparative analysis across species. The integration of automation and high-throughput methodologies is a keystone component for this project, as this approach has the potential to increase the efficiency and scope of the experimental processes, leading to the acceleration of the adaptation, screening, and characterization, and significantly enhancing the scalability and reliability of the study, enabling us to uncover broader trends and patterns in microbial evolution.

The goal is to identify common patterns in the evolution strategies employed by different species to cope with the same type of stress. Additionally, the comparative analysis will explore whether there is a correlation between species in terms of trade-offs associated with the newly acquired traits. The findings from this project have the potential to greatly enhance the productivity and efficiency of yeast cell factories, with significant implications for various industries.