

Draft Genome Sequence of Yarrowia lipolytica NRRL Y-64008, an Oleaginous Yeast Capable of Growing on Lignocellulosic Hydrolysates

Background/Objective

The oleaginous yeast *Yarrowia lipolytica* NRRL Y-64008 is a promising host for high-titer production of fatty acid-derived biofuels and chemicals due to its ability to grow in the presence of organic acids at low pH and produce lipids from lignocellulosic hydrolysates. Interesting phenotypes observed for this strain include the ability to utilize plant-based sugars and to grow on undetoxified biomass hydrolysates.

Approach

Leveraging PacBio sequencing, we sequenced the genome of *Y. lipolytica* NRRL Y-64008 to further investigate its physiology and metabolism to produce biofuels and bioproducts.

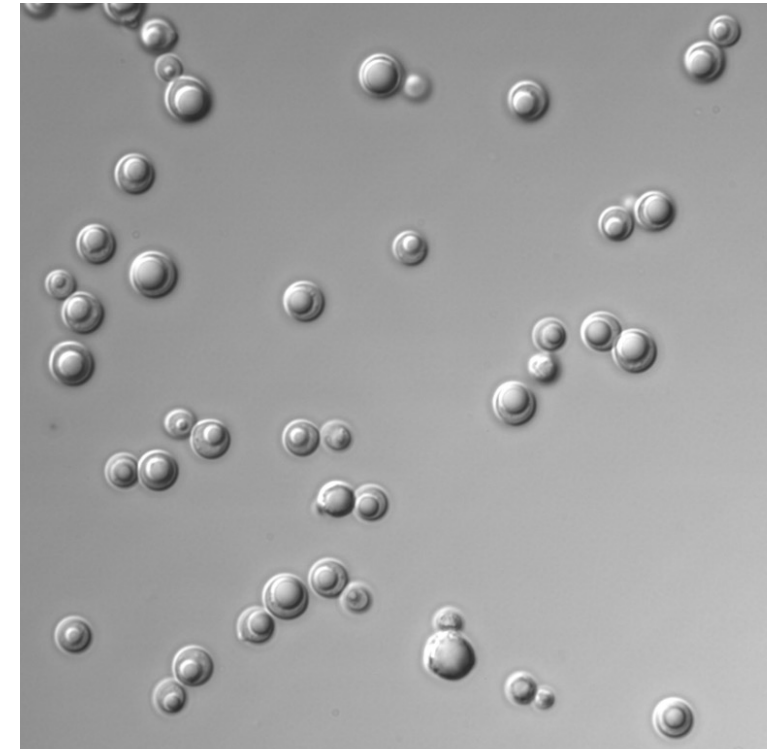
Results

- The 20.5 Mb genome assembly was composed of 6 contigs ($N_{50} = 3$ Mb) with a GC content of 49.04%.
- The Joint Genome Institute Annotation process predicted 6,577 protein-coding genes.

Significance/Impacts

The annotated genome sequence of *Y. lipolytica* NRRL Y-64008 will aid in its development for producing lipids and lipid-based products from organic acids and lignocellulosic hydrolysates.

Jagtap et al. 2023. "Draft Genome Sequence of *Yarrowia lipolytica* NRRL Y-64008, an Oleaginous Yeast Capable of Growing on Lignocellulosic Hydrolysates." *Microbiology Resource Announcements*. DOI: 10.1128/MRA.00435-23.



***Yarrowia lipolytica* NRRL Y-64008 cells in differential interference contrast (DIC) microscopy.**