

# *Near-Complete Genome Sequence of *Lipomyces tetrasporous* NRRL Y-64009, an Oleaginous Yeast Capable of Growing on Lignocellulosic Hydrolysates*

## *Background/Objective*

- *L. tetrasporous* is an oleaginous yeast capable of detoxifying inhibitors, withstanding low pH levels, and using plant-based sugars.
- It has a remarkable potential for achieving rapid and high lipid accumulation when using undetoxified lignocellulosic hydrolysates. This yeast has been considered an attractive host for industrial-scale lipid production.
- Investigation of its physiology and metabolism to produce biofuels and bioproducts is limited by the lack of genome sequence efforts.

## *Approach*

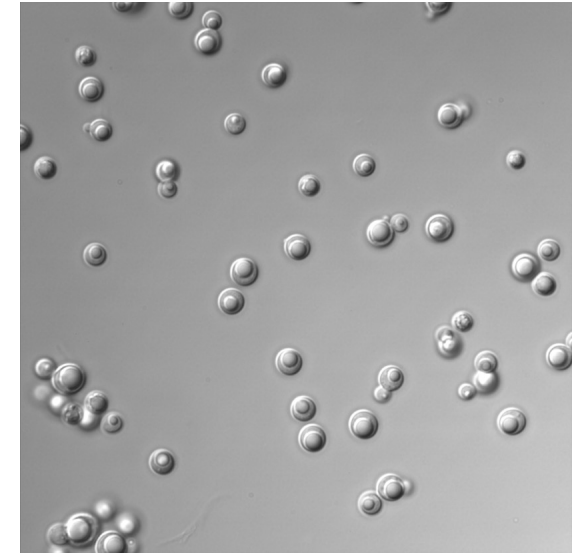
Here, we sequenced the genome and transcriptome of *L. tetrasporous* NRRL Y-64009, leveraging PacBio sequencing.

## *Results*

- The 20.78-Mb genome assembly was composed of 18 contigs ( $N_{50} = 5$  Mb), a GC content of 48.12%.
- The Joint Genome Institute Annotation pipeline predicted 8,004 protein-coding genes.

## *Significance/Impacts*

The annotated genome sequence of *L. tetrasporous* will aid future genetic and genomic studies for producing lipids and lipid-based bioproducts from lignocellulosic hydrolysates.



***Lipomyces tetrasporous* NRRL Y-64009 cells in differential interference contrast (DIC) microscopy.**