Physiological and transcriptional characterization of Saccharomyces cerevisiae engineered for production of fatty acid ethyl esters

Saccharomyces cerevisiae has previously been engineered to become a cell factory for the production of fatty acid ethyl esters (FAEEs), molecules suitable for crude diesel replacement. To find new metabolic engineering targets for the improvement of FAEE cell factories, three different FAEE-producing strains of S. cerevisiae, constructed previously, were compared and characterized by quantification of key fluxes and genome-wide transcription analysis. From both the physiological and the transcriptional data, it was indicated that strain CB2I20, with high expression of a heterologous wax ester synthase gene (ws2) and strain BdJ15, containing disruptions of genes DGA1, LRO1, ARE1, ARE2 and POX1, which prevent the conversion of acyl-CoA to sterol esters, triacylglycerides and the degradation to acetyl-CoA, triggered oxidative stress that consequently influenced cellular growth. In the latter strain, stress was possibly triggered by disabling the buffering capacity of lipid droplets in encapsulating toxic fatty acids such as oleic acid. Additionally, it was indicated that there was an increased demand for NADPH required for the reduction steps in fatty acid biosynthesis. In conclusion, our analysis clearly shows that engineering of fatty acid biosynthesis results in transcriptional reprogramming and has a significant effect on overall cellular metabolism.

General information
State: Published
Organisations: Novo Nordisk Foundation Center for Biosustainability, Yeast Cell Factories, Chalmers University of Technology
Contributors: de Jong, B. W., Siewers, V., Nielsen, J.
Number of pages: 9
Publication date: 2016
Peer-reviewed: Yes

Publication information
Journal: Fems Yeast Research
Volume: 16
Issue number: 1
Article number: fov105
ISSN (Print): 1567-1356
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.91 SJR 1.308 SNIP 0.787
Web of Science (2017): Impact factor 2.609
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.51 SJR 1.254 SNIP 0.855
Web of Science (2016): Impact factor 3.299
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.56 SJR 1.196 SNIP 0.741
Web of Science (2015): Impact factor 2.479
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.37 SJR 1.076 SNIP 0.831
Web of Science (2014): Impact factor 2.818
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.5 SJR 1.248 SNIP 0.863
Web of Science (2013): Impact factor 2.436
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.56 SJR 1.192 SNIP 0.841
Web of Science (2012): Impact factor 2.462
ISI indexed (2012): ISI indexed yes