# ----- GENERAL INFORMATION -----

DATA TITLE: *Zea mays* KCS enzyme family analysis

DATA ABSTRACT: Characterization of the plant fatty acid elongase (FAE) enzyme system that catalyzes the biosynthesis of very long chain fatty acids has been difficult because of large genetic and biochemical redundancy. Primarily, the first of the four reactions that constitute the FAE system is catalyzed by one of two non-homologous enzymes, the ELONGATION DEFECTIVE LIKEs (ELOs) or 3-ketoacyl-CoA synthases (KCSs). In *Zea mays*, these two enzymes are encoded by 6 and 26 genes, respectively. In this study, we have heterologously expressed the 26 *Zm*KCS proteins in four different *Saccharomyces cerevisiae* strains to gain insight into the function of these putative isozymes. The four *S. cerevisiae* strains were a) a WT strain; b) a strain carrying a deletion of the scelo2 gene; c) a strain carrying a deletion of the scelo3 gene; and d) a strain that carried deletions in both the *scelo2* and *scelo3* genes. Only five of the 26 *Zm*KCS proteins can complement the synthetically lethal *scelo2; scelo3* double mutant. Collectively, this represents 83 experimentally modified yeast strains, plus five control strains.  
  
Data included within this entry are:  
  
1) Growth of cultures of each strain measured as the optical density (OD) 600 nm taken at different times in the growth of each strain. For additional information please see the codebook.  
2) The concentration of different fatty acids produced by each strain. Fatty acids were extracted from lyophilized yeast cell pellets, and methyl esters of fatty acids were analyzed by GC-MS and/or GC-FID; quantification was relative to an internal standard (19 carbon fatty acid) that was spiked into each sample. For additional information please see the codebook.  
3) Transmission electron micrographs of the five yeast strains that are expressing *Zm*KCS proteins, which complement the lethality of the *scelo2; scelo3* double mutant. For additional information please see the codebook.  
4) Cell wall thickness measurements of the five yeast strains that are expressing *Zm*KCS proteins, which complement the lethality of the *scelo2; scelo3* double mutant. For additional information please see the codebook.

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ASSOCIATED PUBLICATIONS:

Associated manuscript publication in progress.

COLLECTION INFORMATION:

Time period(s): August 2015 - June 2021

Location(s): Iowa State University

# ----- FILE DIRECTORY -----

## ----- FILE LIST-----

Growth data ZmKCS Fig S1a.csv - contains growth data for ZmKCS overexpressed in WT

GC data ZmKCS Fig S1b-e.csv - contains fatty acid data for ZmKCS overexpressed in WT

Growth data ZmKCS Fig S2a.csv - contains growth data for ZmKCS overexpressed in scelo2

GC data ZmKCS Fig S2b-e.csv - contains fatty acid data for ZmKCS overexpressed in scelo2

Growth data ZmKCS Fig S3a.csv - contains growth data for ZmKCS overexpressed in scelo3

GC data ZmKCS Fig S3b-e.csv - contains fatty acid data for ZmKCS overexpressed in scelo3

TEM data ZmKCS Fig S4.csv - contains cell wall thickness for ZmKCS complementing strains

GC data ZmKCS Fig 4a-d.csv - contains fatty acid data for ZmKCS complementing strains

Growth data ZmKCS Fig2a.csv - contains growth data for ZmKCS complementing strains

## ----- CODEBOOK -----

DataShare\_CodebookKCScomp.csv - contains variable, measurement, and data description document

# ----- METHODS AND MATERIALS -----

## More details concerning these methods can be found in the Materials and Methods section of the manuscript:

## Growth of yeast strains were monitored by measuring the OD600 of individual cultures using a BioTek microplate reader or manually using a spectrophotometer.

## Fatty acids were extracted from each yeast strain, converted to fatty acid methyl esters, which were analyzed by either GC-MS or GC-FID.

1. Yeast cells were collected by centrifugation and fixed with paraformaldehyde and glutaraldehyde. Following embedding in EPON epoxy resin 50-nm thick microscopic sections were subjected to TEM imaging with a 200kV JEOL JSM 2100 scanning transmission electron microscope.

# ------- SOFTWARE -------

Name: MSD ChemStation

Version: E.02.01.1177

URL: https://www.agilent.com/cs/library/usermanuals/Public/G1701-90066.pdf

Developer: Agilent

Name: JMP Pro 16

Version: 16.0.0

System Requirements: 64 bit OS

URL: www.jmp.com

Developer: SAS Institute Inc.

Name: Microsoft excel

Version: 16.53

System Requirements: [Software requirements for Office 365 for business page](https://products.office.com/en-gb/office-system-requirements?ms.officeurl=systemrequirements&rtc=1)

Developer: Microsoft

Name: Image J

Version: 1.53

System Requirements: Java based

URL: https://imagej.nih.gov/ij/download.html

Developer: Wayne Rasband

Name: Gen5

Version: 3.11.19

URL: <http://www.biotek.com/products/microplate_software/gen5_data_analysis_software.html>

Developer: Agilent

# --- EQUIPMENT -------

Manufacturer: Biotek

Model: Synergy HTX

Embedded Software/Firmware Name: Gen5

Embedded Software/Firmware Version: 3.11.19

Manufacturer: Agilent

Model: 6890 GC

Embedded Software/Firmware Name: MSD Chemstation

Embedded Software/Firmware Version: D.02.00.275

Additional Notes: DB-1ms capillary column (15 m x 0.25 mm x 0.25 µm, Agilent 122-0112).

Manufacturer: Agilent

Model: 7890C GC interfaced to a 5975C mass spectrometer

Embedded Software/Firmware Name: Mass hunter GC/MS software

Embedded Software/Firmware Version: 10.0

Additional Notes: HP-5 ms column (15 m x 0.25 mm i.d. coated with a 0.25 μm film, Agilent Technologies)

Manufacturer: Joel

Model: 200kV JEOL JSM 2100 Transmission Electron Microscope

Embedded Software/Firmware Name: TEMCON

Embedded Software/Firmware Version: 2.16

Additional Notes: Equipped with a GATAN One View 4K camera running GMS 3

# ------- LICENSING -------

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