A person is standing on a rocky mountain peak in the foreground, looking out over a vast, golden-hued sea of clouds. In the background, there are dark, rugged mountains with patches of snow under a clear sky. The scene is captured during the golden hour, with warm light illuminating the clouds.

Journal Club

Valentin Marteau

31.05.2022

Article

A non-canonical tricarboxylic acid cycle underlies cellular identity

<https://doi.org/10.1038/s41586-022-04475-w>

Received: 19 February 2021

Accepted: 26 January 2022

Published online: 9 March 2022



Check for updates

Paige K. Arnold^{1,2,6}, Benjamin T. Jackson^{1,2,6}, Katrina I. Paras^{1,3}, Julia S. Brunner¹, Madeleine L. Hart⁴, Oliver J. Newsom⁴, Sydney P. Alibeckoff⁴, Jennifer Endress^{1,3}, Esther Drill⁵, Lucas B. Sullivan⁴ & Lydia W. S. Finley^{1✉}

¹Cell Biology Program, Memorial Sloan Kettering Cancer Center, New York, NY, USA. ²Louis V. Gerstner Jr. Graduate School of Biomedical Sciences, New York, NY, USA. ³Weill Cornell Graduate School of Medical Sciences, Cornell University, New York, NY, USA. ⁴Human Biology Division, Fred Hutchinson Cancer Research Center, Seattle, WA, USA. ⁵Department of Epidemiology and Biostatistics, Memorial Sloan Kettering Cancer Center, New York, NY, USA. ⁶These authors contributed equally: Paige K. Arnold, Benjamin T. Jackson. ✉e-mail: finleyl@mskcc.org

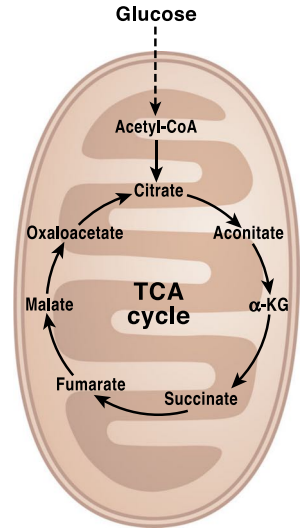
Aim

Tricarboxylic acid (TCA) cycle:

- Central hub of cellular metabolism important for both energy production and biosynthesis
- Series of chemical reactions to release stored energy through the oxidation of acetyl-CoA derived from carbohydrates, fats, and proteins
- Mammalian cells display diversity in TCA-cycle activity

→ **How is this diversity achieved?**

→ **Is the TCA cycle critical for establishing cell fate?**

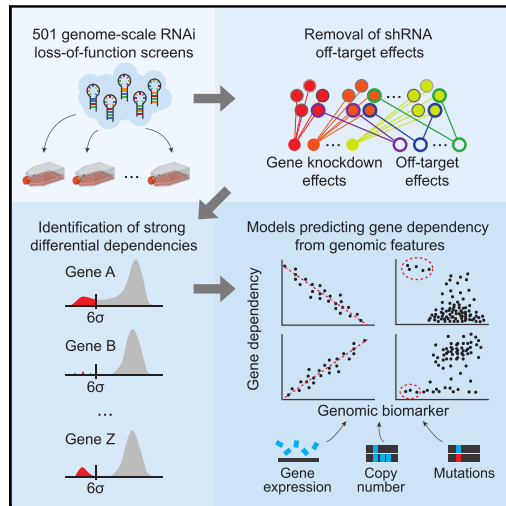


Martínez-Reyes & Chandel; *Nat. Commun.* (2020)

DepMap project

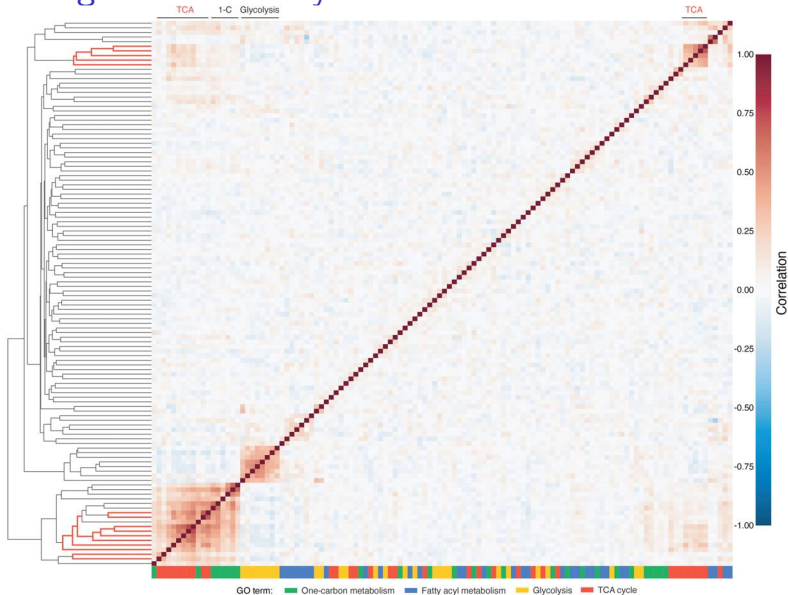


- **Project goal:** Systematic identification of cancer dependencies
- Genome-scale loss-of-function screens performed in diverse human cancer cell lines
- Dependency score: Function of both the magnitude of the differential dependency and its prevalence in cell line collection

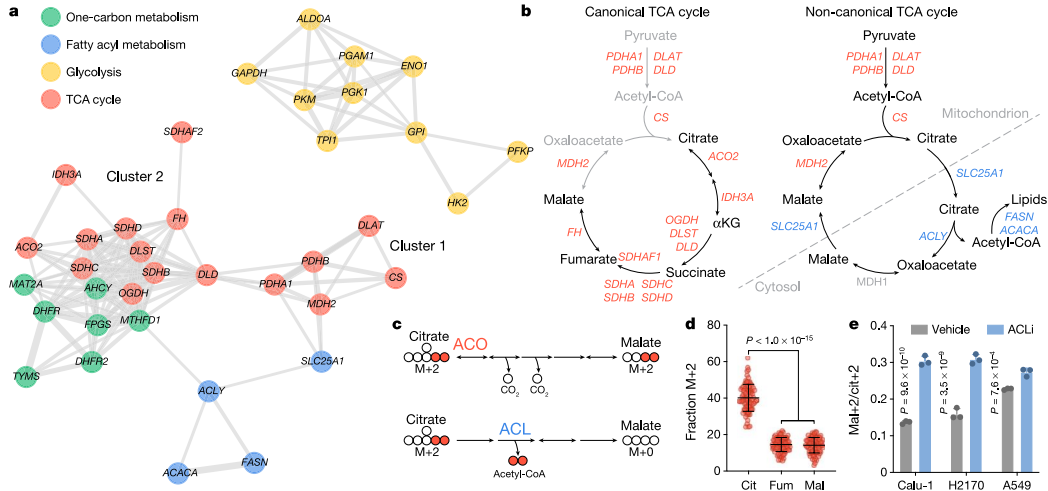


Tsherniak et al. *Cell* (2017)

Metabolic gene essentiality correlations across cancer cell lines



Two modes of TCA cycle metabolism



ACO: aconitase; ACL: ATP citrate lyase

Two modes of TCA cycle metabolism

- a**
- One-carbon metabolism
 - Fatty acyl metabolism
 - Glycolysis



b

Canonical TCA cycle

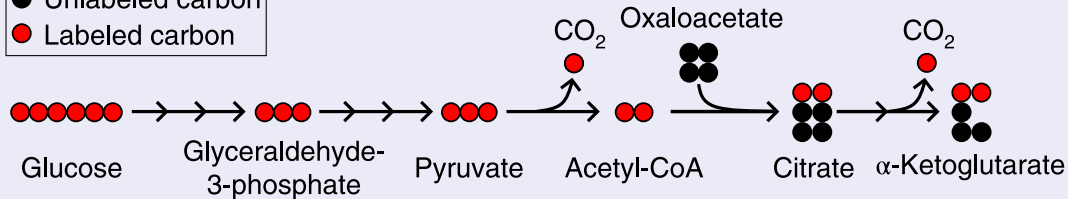
Pyruvate
PDHA1 PDHB
DLAT DLD

Non-canonical TCA cycle

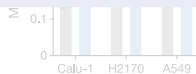
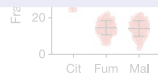
Pyruvate
PDHA1 PDHB
DLAT DLD

Stable isotope tracing:

- Unlabeled carbon
- Labeled carbon

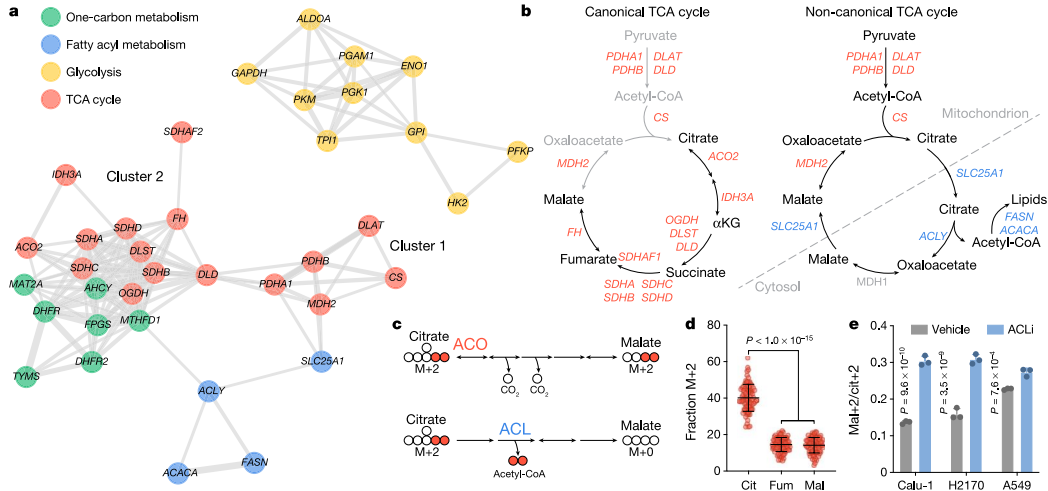


Llufrio, Cho & Patti; *Nature Protocols* (2019)



ACO: aconitase; ACL: ATP citrate lyase

Two modes of TCA cycle metabolism



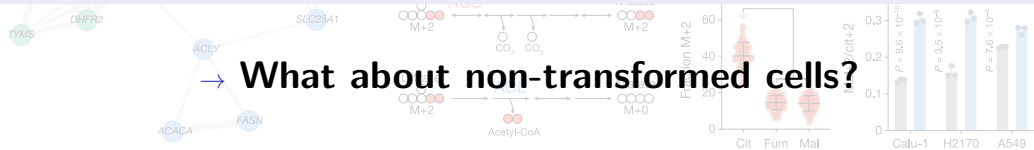
ACO: aconitase; ACL: ATP citrate lyase

Two modes of TCA cycle metabolism

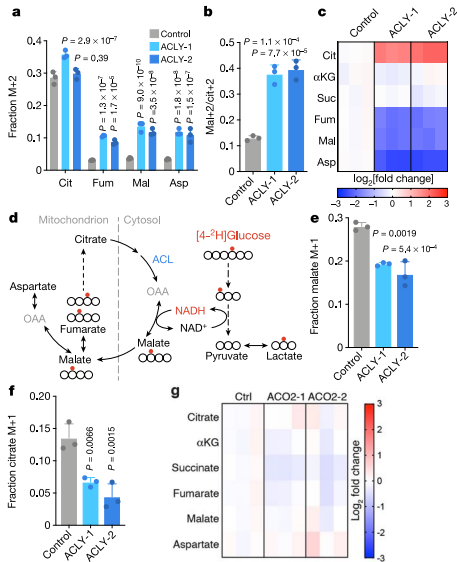


Main points:

- Mapping gene cluster onto TCA cycle suggest clear division up-/downstream of citrate
- Hypothesis:** ACL may support metabolic demands by forming a non-canonical TCA cycle, capable of continuous oxaloacetate regeneration for citrate production
- ^{13}C labelled $\frac{\text{malate}}{\text{citrate}}$ ratio to monitor canonical vs. non-canonical TCA cycle activity

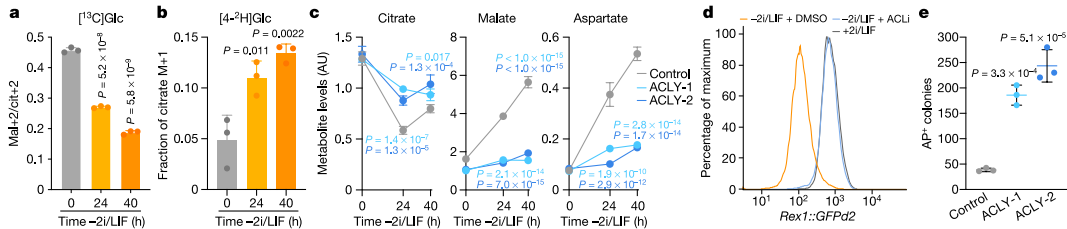


Embryonic stem (ES) cells engage a non-canonical TCA cycle



- ES cell line with genetic disruption of Acly and Aco2
 - Acly mutation substantially alters levels of TCA cycle metabolites associated with cytosolic citrate processing
- Does a portion of the TCA cycle flow through ACL?
- Deuterated $[4-^2\text{H}]$ glucose tracing
 - Cytosolic malate is recycled back into the mitochondria for citrate regeneration

Exit from pluripotency requires ACL

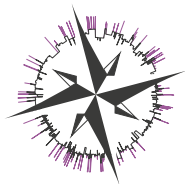


- TCA cycle switch after pluripotency exit
- Differentiated cells rely on the non-canonical TCA cycle to maintain TCA cycle intermediates
- TCA cycle configuration plays a role in facilitating cell state transitions

Summary

- Combining isotope tracing with genetic manipulation of Acly and Aco2 provide direct evidence of a non-canonical TCA cycle with differential activity across cell states
- **Main advantages:**
 - Retain rather than combust reduced carbon and regenerate cytosolic NAD^+ required to sustain glycolysis
 - Non-canonical TCA cycle maintains oxaloacetate regeneration by circumventing several TCA cycle steps which minimizes mitochondrial NADH production
- Starting hypothesis based on genetic co-essentiality mapping database **DepMap**

Cancer Dependency Map



dependency map
Consortium

- **Project goal:** Systematic identification of genetic and pharmacologic cancer dependencies and the biomarkers that predict them

Genetic screens

Genome-wide
loss-of-function
screens
(Achilles)

Cellular models

Molecular characterization
of existing and
new cell lines
(CCLE/CCLF)

Drug sensitivity

Single and pooled cell
line compound
screens
(PRISM, CTRP)

Predictive modeling

Computational models
of vulnerabilities
(CDS)

CANCER DEPENDENCY MAP



Genetic
targets



Therapeutic
leads



Patient
stratification

Cancer Dependency Map

- Achilles project 22Q2 release: 17,387 genes were screened in 1086 cell lines
- **R** Bioconductor package: "depmap"
- **Python** PyPI package: "depmap-downloader"

