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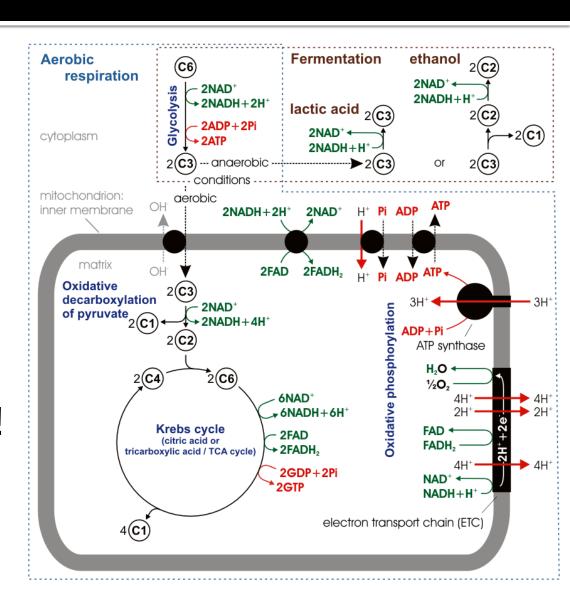
# (Kreb's, Citric Acid, TCA) Cycle

## Objectives

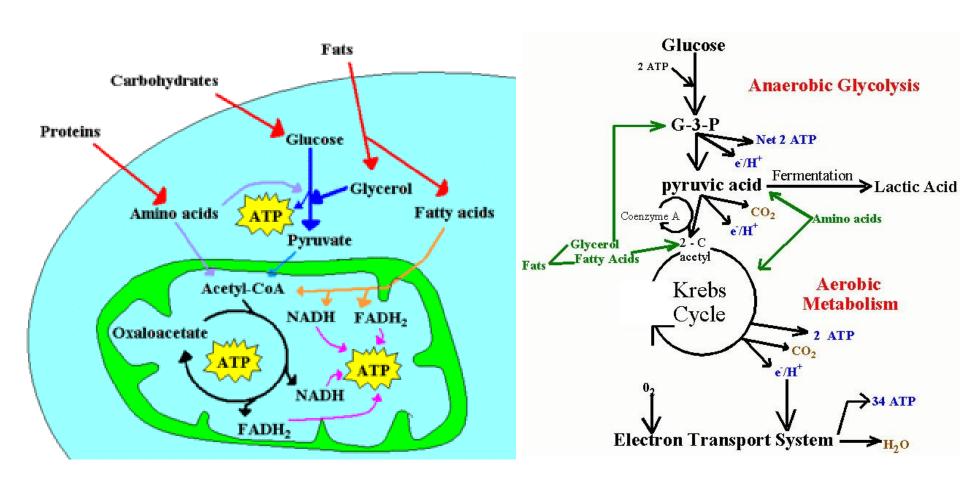
- Why do we need it?
- Location & where is it in the picture?
- Electron (energy) carrying molecules
- Components
- Enzymes & cofactors
- Regulation
- Intermediates & anaplerotic reactions

### Why do we need it?

- A route to make
  ATP eventually
  (most ATP is generated through oxidative phosphorylation)
- There is no life without TCA cycle!



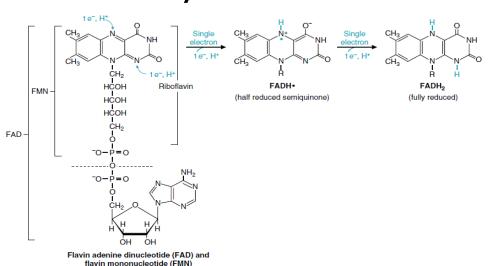
### How does it fit?



## Electron (energy) Carrying Molecules (NAD+, FAD)

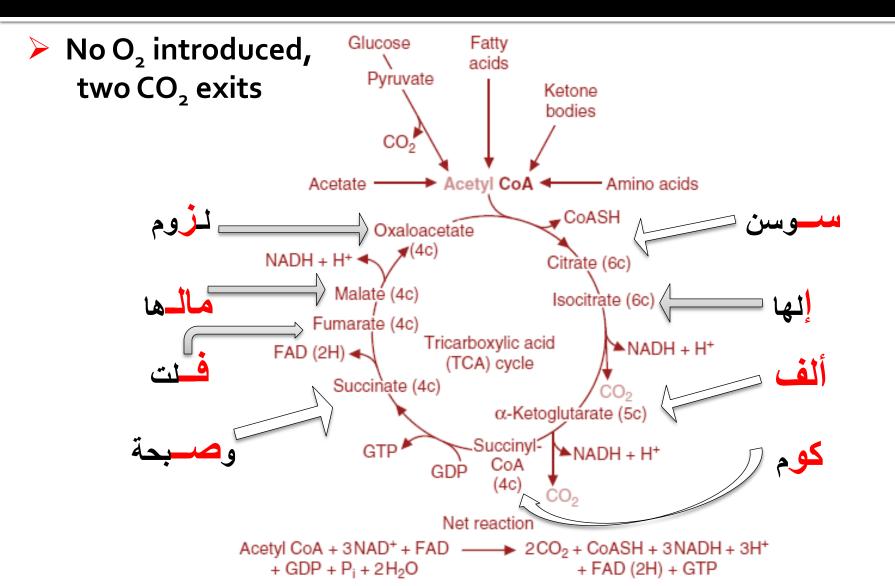
#### > FAD

- Single electrons (H•), different sources
- Succinate to fumarate, lipoate to lipoate disulfide in α-KG
- FAD must remain tightly, sometimes covalently, attached to its enzyme
- > E° for enzyme-bound FAD varies



- NAD
- Pair of electrons (H-), same source
- Alcohols to ketones by malate dehydrogenase & isocitrate dehydrogenase
- NADH plays a regulatory role in balancing energy metabolism

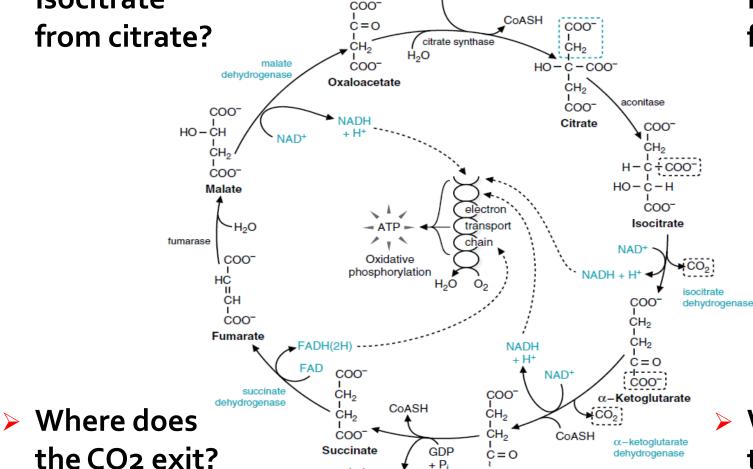
### Components & stepwise reactions



## Does Acetyl-CoA exit as 2 CO2?

CH<sub>2</sub>C SC<sub>0</sub>A Acetyl CoA

Why to make **Isocitrate** from citrate?



C = 0

SCoA

Succinyl CoA

succinate

thiokinase

**GTP** 

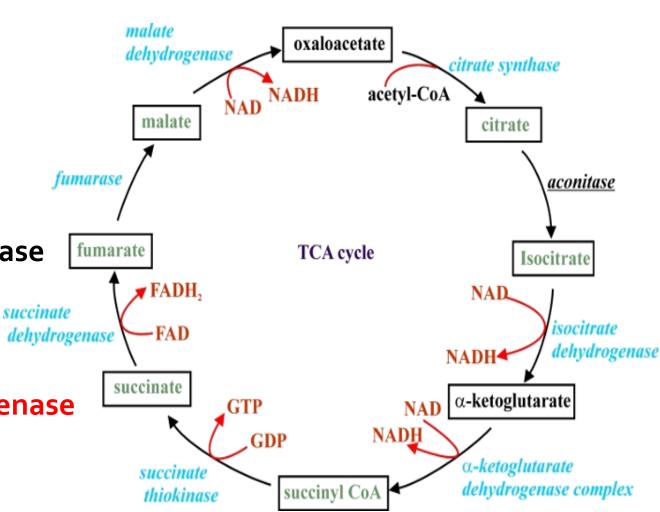
Why to make **Isocitrate** from citrate?

> Where does the CO2 exit?

dehydrogenase

## **Enzymes of the TCA Cycle**

- Citrate cynthase
- Aconitase
- Isocitrate dehydrogenase
- α-ketoglutarate dehydrogenase
- Succinate thiokinase
- Succinate dehydrogenase
- Fumarase
- Malate dehydrogenase



## Formation and Oxidation of Isocitrate

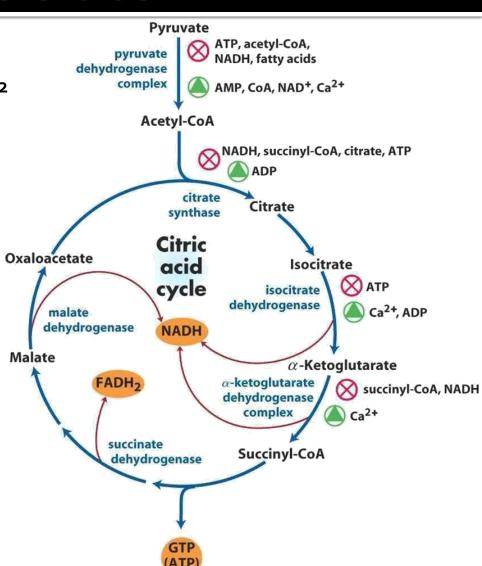
- Oxidative decarboxylation, CO<sub>2</sub>
- 3° to 2° alcohol

Control at the committed step of glycolysis

Fructose 6 - phosphate

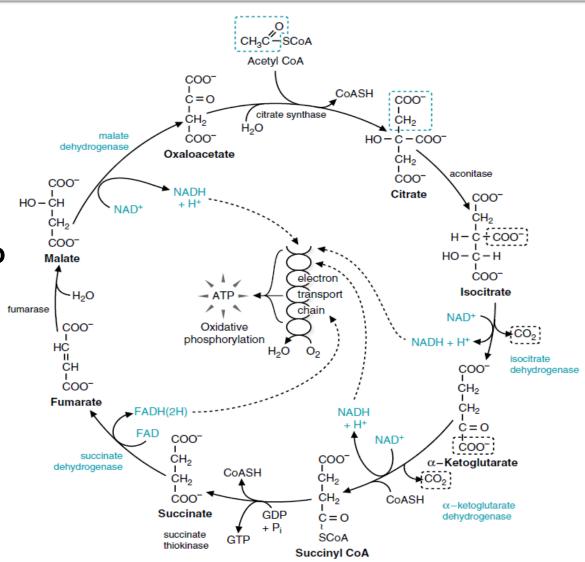
Phosphofructokinase
Activated by F-2,6 - BP
Activated by AMP
Inhibited by ATP and citrate

Fructose 1,6 - bisphosphate



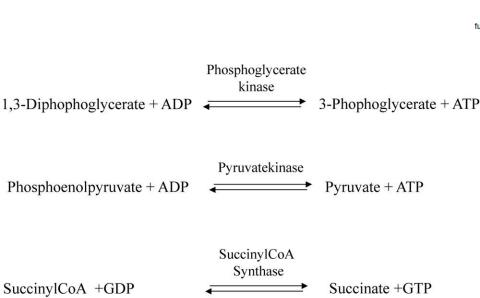
## α-Ketoglutarate to Succinyl CoA

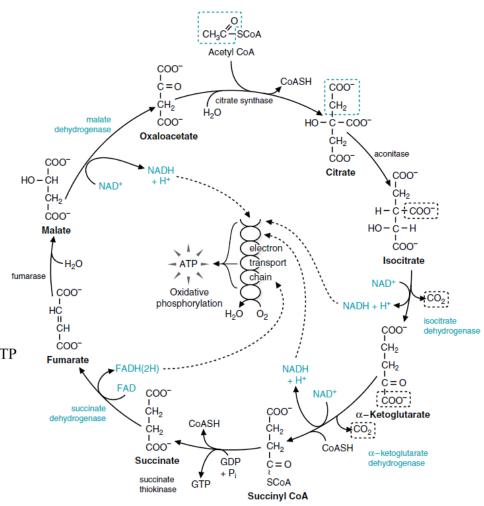
- Oxidative decarboxylation
- Thiamine pyrophosphate, lipoic acid, and FAD
- Keto group oxidized to acid, CoA-SH, succinyl CoA
- Energy conserved as NADH, thioester bond



#### **Generation of GTP**

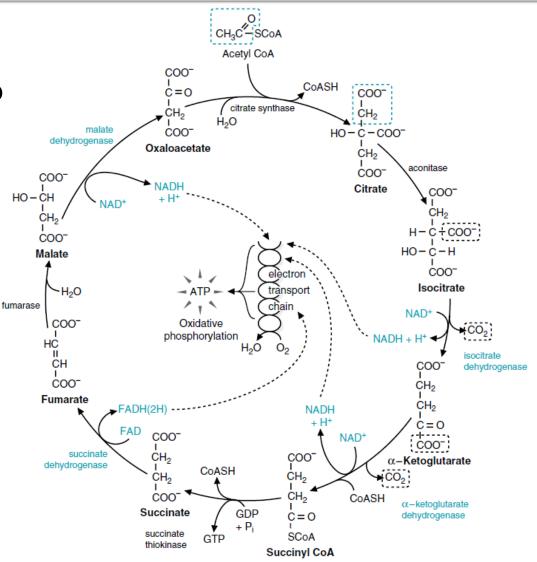
Succinyl CoA thioester bond, succinate thiokinase, substrate level phosphorylation





## Oxidation of Succinate to Oxaloacetate

- Oxidation of succinate to fumarate, succinate dehydrogenase, FAD
- ➤ Fumarase, OH + H<sup>+</sup> from water, fumarate to malate
- Alcohol group of malate oxidized to a keto group, NADH



#### CoA

- Forms a thioester bond, CoASH & an acyl group (e.g., acetyl CoA, succinyl CoA)
- Sulfur vs. oxygen (carbon can be activated, -13kcal, GTP, keeps the reaction going)

A

CH<sub>3</sub> - C' ~ SCoA

Acetyl CoA

CH<sub>2</sub>

Citrate

Synthase

OAA

HS-CoA

C-O
CH<sub>2</sub>

CH<sub>2</sub>

CC

Citrate

A. CoASH Forms thioesters with acyl groups (-CR) Phosphopantetheine - Pantothenic acid C=0 $NH_2$ 2-O3PO

Adenosine 3',5'-bisphosphate

## α-Ketoacid Dehydrogenase Complexes (TLCFN)

δ COO-

γ CH<sub>2</sub>

α-Ketoglutarate

COO

Succinyl CoA

CoASH

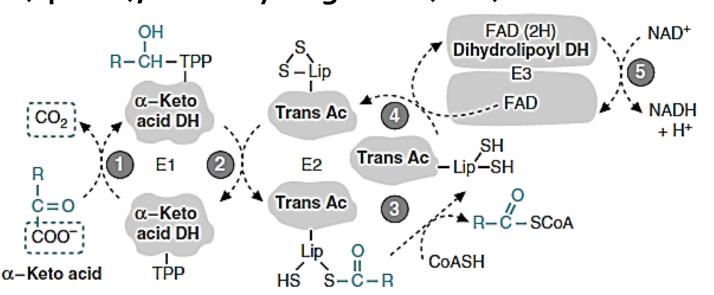
Thiamine-(P)(P)

α-ketoglutarate

Lipoate

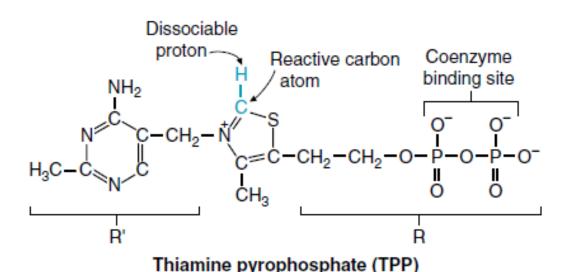
- (α-ketoglutarate, pyruvate, and branched chain α-keto acid) dehydrogenase complexes
- ► Huge enzyme complexes, multiple subunits of 3 different enzymes (no loss of energy, substrates for E2 and E3 remain bound → higher rate)

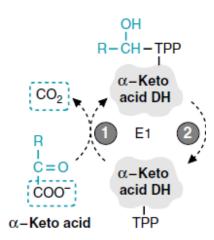
E1, E2, & E3 are a decarboxylase (TPP), a transacylase (lipoate), & a dehydrogenase (FAD)



## Thiamine Pyrophosphate

ightharpoonup Thiamine deficiency, α-ketoglutarate, pyruvate, & branched chain α-keto acids accumulate in the blood



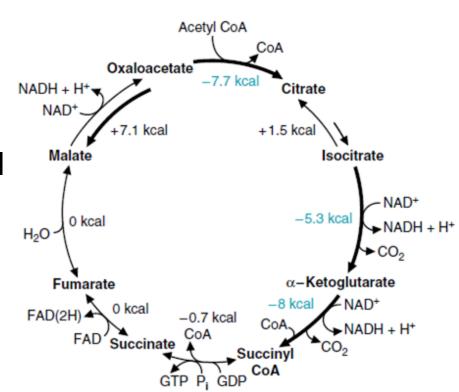


## Bioenergitics of the TCA Cycle

- Like all pathways, overall net ΔG (-228 kcal/mole), not 100%
- NADH, FAD(H2), and GTP (10ATP), 207 Kcal, 90%
- Three reactions have large (-ve) values
- Physiologically irreversible, low products
- Aconitase (+ΔG), maintains 20 times of citrate/Isocitrate, Acetyl CoA in cytosol for fatty acid and cholesterol synthesis
- Malate DH (+ΔG), favors malate over oxaloacetate, fasting, liver, substrate for gluconeogenesis

```
kcal/mole

3 NADH: 3 × 53 = 159
1 FAD(2H) = 41
1 GTP = 7
Sum = 207
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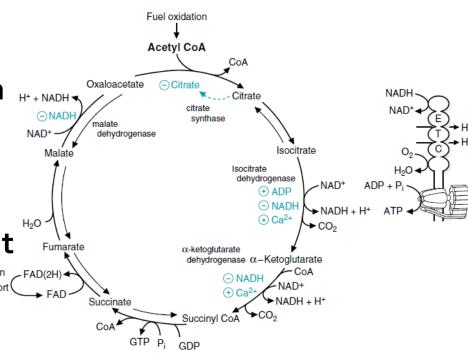


## Regulation of the TCA Cycle

- Correspond to ETC (ATP/ADP)
- Two major messengers (feedback): (a) phosphorylation state of adenines, (b) the reduction state of NAD
- Adenine nucleotides pool and NAD pool are relatively constant

#### Citrate Synthase

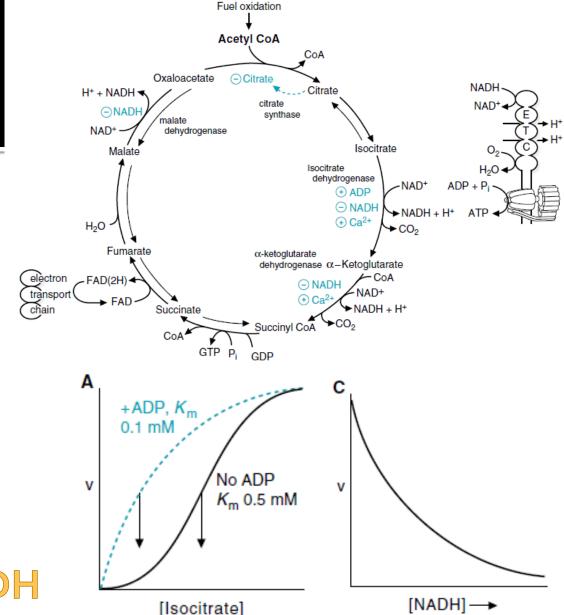
- The first step, no allosteric regulation
- Rate regulated by oxaloacetate & citrate (inhibitor)
- Malate-oxaloacetate equilibrium has [] < K<sub>m</sub>, NADH/NAD<sup>+</sup> (acetyl-CoA will be used for ketone bodies)



## Isocitrate DH

- Best regulation at ratelimiting step (Isocitrate DH)
- Allosterically: activated (ADP, Ca<sup>+2</sup>)
- Inhibition (NADH)
- No ADP vs. ADP (K<sub>m</sub> less), a small change in ADP, great effect

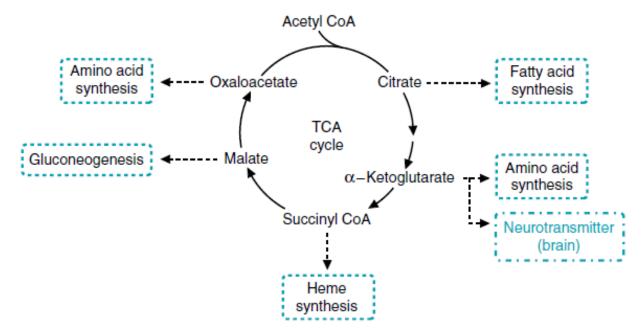
#### α-Ketoglutarate DH



- Inhibited by NADH and succinyl CoA, GTP
- Activated by Ca<sup>+2</sup>, muscle contraction

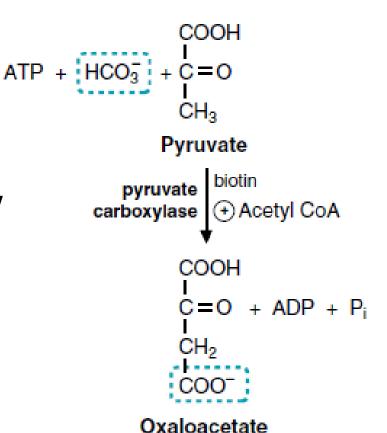
## TCA Cycle Intermediates

Intermediates are Precursors for Biosynthetic Pathways (citrate, acetyl CoA, fatty acid synthesis, liver) (fasting, malate, gluconeogenesis, liver) (Succinyl CoA, heme biosynthesis, bone marrow) (α-ketoglutarate, glutamate, GABA, a neurotransmitter, brain) (α-ketoglutarate, glutamine, skeletal muscle to other tissues for protein synthesis)



### **Anaplerotic Reactions**

- Pathways or reactions that replenish the intermediates of the TCA cycle
- Pyruvate Carboxylase is a major anaplerotic enzyme (requires biotin)
- Found in many tissues, liver, kidneys, brain, adipocytes, and fibroblasts
- Very high conc. In liver and kidney (gluconeogenic pathway)
- Activated (acetyl CoA)



## Other Anaplerotic Routes (Amino Acid Degradation)

