

Tricarboxylic Acid Cycle and its Role in Energy Production

Edvin Roy^{*}

Department of Applied Sciences, Saimaa University of Applied Sciences, South Karelia, Finland

DESCRIPTION

The Tricarboxylic Acid Cycle, also known as the (TCA cycle) or Krebs cycle, is a central metabolic pathway that occurs in the mitochondria of eukaryotic cells. It serves as a key hub for energy production and the catabolism of carbohydrates, fats, and amino acids. Through a series of enzymatic reactions, the TCA cycle oxidizes acetyl-CoA derived from various fuel sources, generating energy-rich molecules such as Adenosine Triphosphate (ATP), reduced coenzymes, and carbon dioxide. This article delves into the intricacies of the TCA cycle, exploring its significance in cellular metabolism and the production of Adenosine Triphosphate (ATP).

The steps of the tricarboxylic acid cycle

The TCA cycle consists of eight enzymatic reactions that take place sequentially, with each reaction catalyzed by a specific enzyme. The cycle begins with the entry of acetyl-CoA, which is derived from glucose, fatty acids, or amino acids, into the cycle.

Step 1: Formation of Citrate Acetyl-CoA combines with oxaloacetate, forming citrate through the enzyme citrate synthase. This step also releases coenzyme A (CoA).

Step 2: Isomerization aconitase catalyzes the isomerization of citrate into isocitrate.

Step 3: Oxidative decarboxylation isocitrate is oxidatively decarboxylated by isocitrate dehydrogenase, resulting in the formation of alpha-ketoglutarate and the reduction of Nicotinamide Adenine Dinucleotide (NAD+) to NADH.

Step 4: Oxidative decarboxylation alpha-ketoglutarate is further oxidatively decarboxylated by alpha-ketoglutarate dehydrogenase, yielding succinyl-CoA, carbon dioxide, and NADH.

Step 5: Substrate-level phosphorylation succinyl-CoA is converted into succinate through the action of succinyl-CoA synthetase. This step leads to the synthesis of one molecule of Guanosine Triphosphate (GTP), which can subsequently be converted to ATP.

Step 6: Dehydrogenation succinate is oxidized to fumarate by succinate dehydrogenase, with the reduction of flavin adenine dinucleotide (FAD) to FADH2.

Step 7: Hydration fumarate is hydrated to form malate, catalyzed by fumarase.

Step 8: Oxidation malate is oxidized to oxaloacetate by malate dehydrogenase, generating NADH.

The role of the tricarboxylic acid cycle in energy production

The primary function of the TCA cycle is to generate energy-rich molecules, including NADH and FADH2, which serve as electron carriers. These reduced coenzymes play a crucial role in oxidative phosphorylation, the final step of cellular respiration, where ATP is synthesized in the electron transport chain.

NADH and FADH2 produced during the TCA cycle donate their electrons to the electron transport chain, leading to the production of ATP through oxidative phosphorylation. This process involves the transfer of electrons through a series of protein complexes, ultimately generating a proton gradient across the mitochondrial membrane. The flow of protons back into the mitochondrial matrix through ATP synthase drives the synthesis of ATP.

Regulation and integration with other metabolic pathways

The TCA cycle is tightly regulated to ensure efficient energy production and metabolic balance within cells. The activity of key enzymes in the cycle is regulated by feedback inhibition, allosteric regulation, and post-translational modifications.

Furthermore, the TCA cycle is interconnected with other metabolic pathways. For example, it receives metabolites from glycolysis, fatty acid oxidation, and amino acid catabolism. Intermediates of the TCA cycle can also be utilized for the synthesis of various biomolecules, such as amino acids and nucleotides.

Citation: Roy E (2023) Tricarboxylic Acid Cycle and its Role in Energy Production. J Mol Pathol Biochem. 4:148.

Copyright: © 2023 Roy E. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Correspondence to: Edvin Roy, Department of Applied Sciences, Saimaa University of Applied Sciences, South Karelia, Finland, E-mail: edvinroy@yahoo.com **Received:** 02-May-2023, Manuscript No. JMPB-23-25148; Editor assigned: 05- May-2023, Pre QC No: JMPB-23-25148 (PQ); Reviewed: 19-May-2023, QC No: JMPB-23-25148; Revised: 26-May-2023, Manuscript No: JMPB-23-25148 (R); Published: 02-Jun-2023, DOI: 10.35248/jmpb.23.4.148

Clinical implications

Dysregulation of the TCA cycle can lead to metabolic disorders and various diseases. Defects in TCA cycle enzymes or disruptions in the availability of intermediates can result in metabolic imbalances and impair energy production. For instance, mutations in genes encoding TCA cycle enzymes are associated with rare genetic disorders such as mitochondrial diseases. Moreover, alterations in TCA cycle activity have been observed in several pathological conditions, including cancer and neurodegenerative diseases. Cancer cells often exhibit metabolic reprogramming, relying on aerobic glycolysis rather than oxidative phosphorylation for energy production. This metabolic shift, known as the Warburg effect, influences tumor growth and provides a potential target for cancer therapeutics. The tricarboxylic acid cycle, a fundamental metabolic pathway, plays a central role in energy production and the catabolism of carbohydrates, fats, and amino acids. Through a series of enzymatic reactions, the TCA cycle generates ATP, reduced coenzymes, and carbon dioxide. It is intricately connected with other metabolic pathways, contributing to cellular metabolism and the synthesis of biomolecules.

Understanding the TCA cycle's functioning and regulation is crucial for unraveling the complexity of cellular metabolism and its implications in health and disease.