

Malic Enzyme: A Significant Player in Cardiac Metabolism

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Introduction

The tricarboxylic acid (TCA) cycle plays a central role in energy production in the heart. In addition, it also provides biosynthetic intermediates for many anabolic pathways. Thus, in order to prevent impairment of the TCA cycle, cataplerotic pathways (which deplete TCA cycle intermediates by using them as substrate for biosynthesis of other molecules) need to be balanced with anaplerotic pathways (which increase TCA cycle intermediates by providing entry of substrates at sites other than through acetyl-CoA) so that mitochondrial concentrations of the intermediates remains constant. The existence of this enzyme has been well established in many tissues [1]. There has also been indirect evidence of malic enzyme activity, with the direction of the net flux dependent upon intracellular redox state and/or substrate concentrations [2]. Significant activity of this pathway could confound analysis of ¹³C-NMR spectra. In this report, we provide direct evidence for significant activity of this pathway in isolated perfused rabbit hearts.

Purpose

To determine if ¹³C-NMR spectroscopy can be used to quantitate malic enzyme activity under controlled conditions in the isolated perfused rabbit heart.

Methods

Hearts (n=20) were isolated from New Zealand White male rabbits (1.5-2 kg) and perfused at 37°C in a modified Langendorff preparation. Buffer was a modified Krebs Henseleit solution containing 3% bovine serum albumin, 0.7 mM palmitate, 0.2 mM β-hydroxybutyrate, and 5 mM glucose as metabolic substrates. Insulin was added to the buffer (10 μU/mL) to aid glucose uptake. Perfusion pressure was maintained at 75 mmHg, and a balloon was placed into the left ventricle for continuous monitoring of developed pressures. Following an equilibration period (~30 minutes) for physiological parameters to stabilize, hearts were switched to a buffer containing ¹³C-labeled substrates (2,4-¹³C-β-hydroxybutyrate, U-¹³C-palmitate), and perfused for 2,4,6,8,10,15,30, or 45 minutes. Hearts were rapidly frozen with liquid nitrogen cooled tongs, and extracted using perchloric acid. ¹³C-NMR spectroscopy was performed on the extracts and isotopomer analysis was used to calculate the fractional enrichments of glutamate.

Results

The concentration of the TCA cycle intermediates is below the levels required for isotopomer analysis using ¹³C NMR spectroscopy. Thus, enrichment patterns of glutamate, aspartate and alanine (which are in rapid exchange with α-ketoglutarate, malate and pyruvate respectively, and are present in detectable concentrations) are used to reflect the TCA turnover in isotopomer analysis using ¹³C spectroscopy.

The substrates presented to the heart in the perfusion buffer (2,4-¹³C-β-hydroxybutyrate, U-¹³C-palmitate) will result in the generation of acetyl Co-A that is labeled in the C₂ position, or both the C₁ and C₂ positions. ¹³C-2-acetyl Co-A should not enrich the C₅ of glutamate, and labeling pattern due to 1,2-¹³C-acetyl Co-A should be reflected in the C₅ position of glutamate by the appearance of a doublet. Also, given the introduction of the label only as acetyl Co-A should not result in the enrichment of alanine unless there is anabolic flux from the TCA to pyruvate. The analysis of the obtained spectra revealed the occurrence of a C₅ singlet in glutamate and corresponding ¹³C enrichment in the C₄ position of aspartate and in the C₂ position of alanine. The C₅ singlet of glutamate arises from C₁ enriched acetyl Co-A. Upon review of existing literature and computer simulation models it was concluded that the occurrence of these specific enrichments is due to flux from malate to pyruvate through malic enzyme/PEPCK, which would yield 2-¹³C-pyruvate which is subsequently metabolized to 1-¹³C-acetyl Co-A. The presence of the C₅ singlet was measured against the presence of the C₅ doublet, and the fractional enrichment calculated, to ensure that we were well above the levels of natural abundance.

Conclusions

Under these perfusion conditions, flux through malic enzyme in the rabbit heart was significant; estimated at ≥25% of the total TCA cycle turnover. Traditional estimates of anaplerotic flux (using the ratio of the steady-state ¹³C enrichments in the C₃ (or C₂) and C₄ positions of glutamate) do not reflect this cataplerotic pathway, since anaplerotic flux from aspartate is also labeled. ¹³C NMR spectroscopy can be used to quantitatively measure malic enzyme activity by careful selection of labeled substrates for perfusion along with concomitant observation of the glutamate C₅ singlet, and the subsequent enrichment patterns of alanine and aspartate.

References:

1. Kim, H et al. *Int. J. Biochem. Cell Biol.* 27(11): 1161-7, 1995
2. Sundqvist, K et al. *Biochem. J.* 243(3): 853-7, 1987.

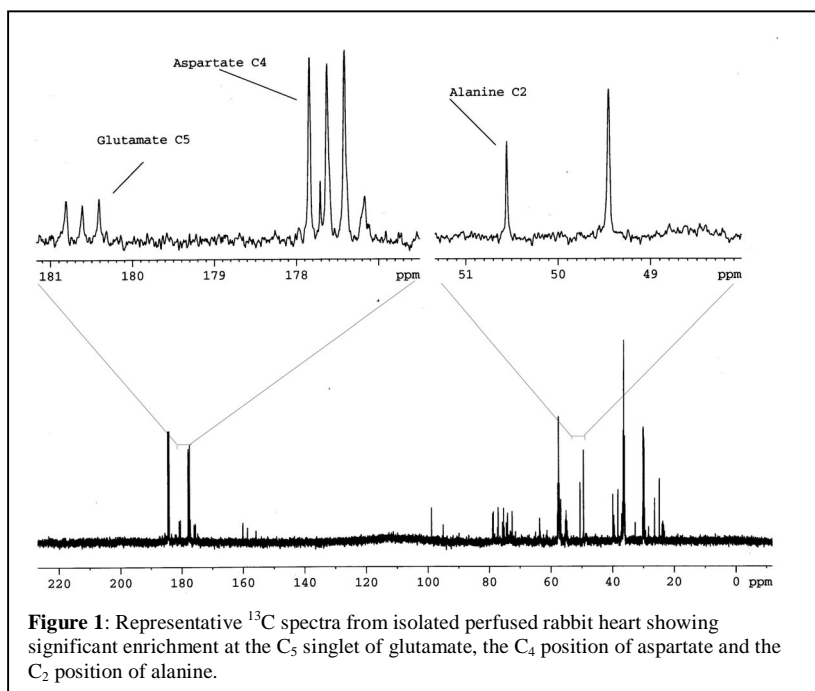


Figure 1: Representative ¹³C spectra from isolated perfused rabbit heart showing significant enrichment at the C₅ singlet of glutamate, the C₄ position of aspartate and the C₂ position of alanine.