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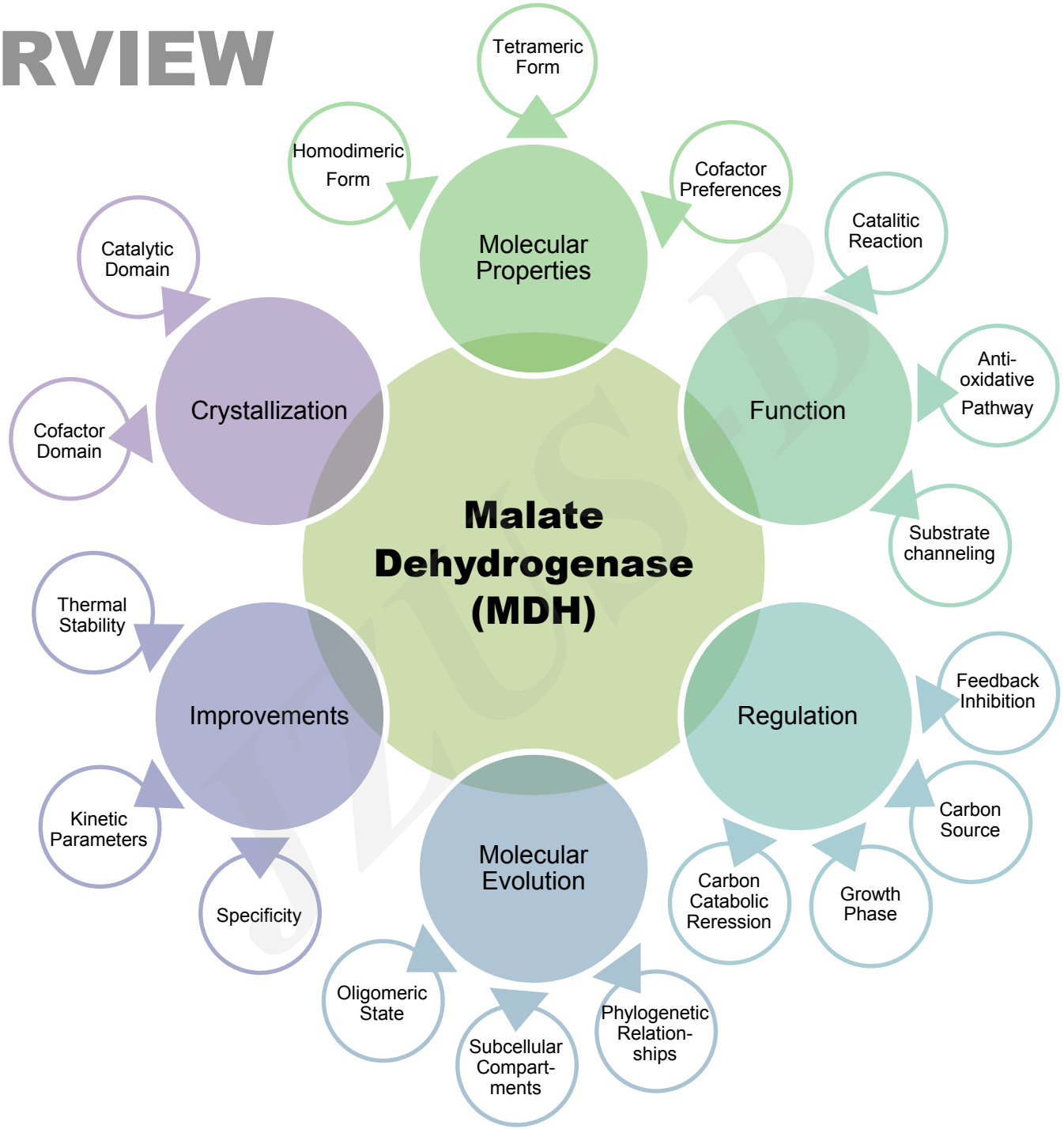
Function, kinetic properties, crystallization, and regulation of microbial malate dehydrogenase

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Key words: Malate dehydrogenase, carbon metabolism, tricarboxylic acid cycle

OVERVIEW


Malate Dehydrogenase (MDH)
Molecular Properties
Tetrameric Form
Homodimeric Form
Cofactor Preferences
Function
Catalitic Reaction
Anti-oxidative Pathway
Substrate channeling
Regulation
Feedback Inhibition
Carbon Source
Growth Phase
Carbon Catabolic Reression
Molecular Evolution
Phylogenetic Relation-ships
Subcellular Compart-ments
Oligomeric State
Improvements
Specificity
Kinetic Parameters
Thermal Stability
Crystallization
Cofactor Domain
Catalytic Domain

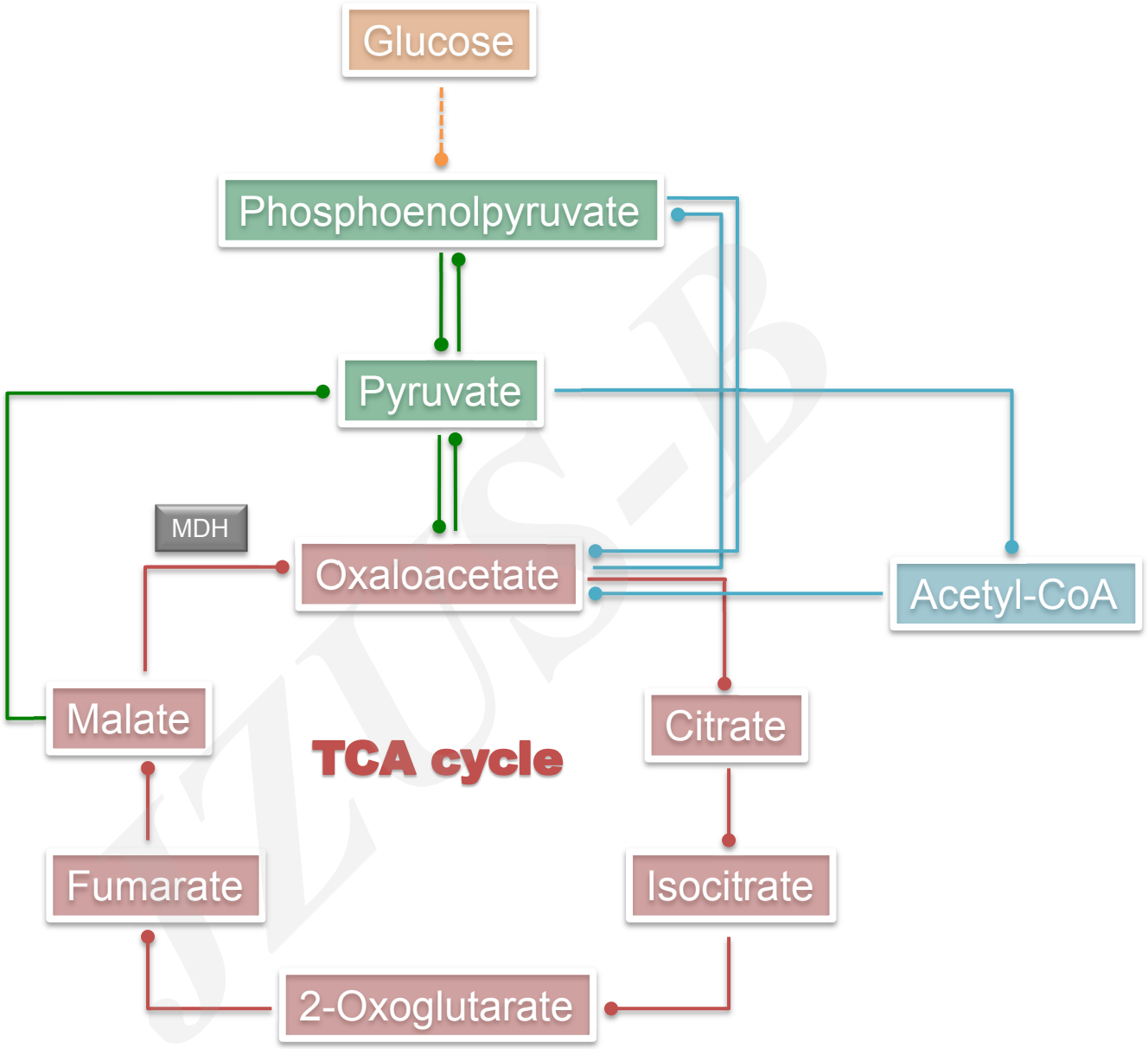


Figure shows phosphoenolpyruvate-pyruvate-oxaloacetate (PEP-Pyr-OAA) node (including pyruvate shunt), and tricarboxylic acid (TCA) cycle. These metabolic pathways are closely interconnected to malate dehydrogenase (MDH) enzyme catalysis.

MAIN FEATURES

- Malate dehydrogenase (MDH) carries out the interconversion between malate and oxaloacetate employing either NAD^+ or $NADP^+$ as a cofactor.
- MDH is part of the TCA cycle, the most important metabolic pathway for supplying ATP to aerobic organisms.
- It has been reported different affinities and specificities for substrate and cofactor among MDH enzymes of different microorganisms and celular compartiments.
- Its tertiary structure is widely conserved. In contrast to this, its amino acid sequence is poorly conserved making difficult to elucidate its molecular evolution.
- Being an ubiquitous enzyme, its subject to different mechanisms of regulation as activity inhibition and carbon catabolic repression.

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