Comparative Analysis of Glyoxylate Cycle Key Enzyme Isocitrate Lyase from Organisms of Different Systematic Groups

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Abstract—Isocitrate lyase and malate synthase are the key enzymes of glyoxylate cycle that represents the most important stage on the pathway of conversion of fatty acids to carbohydrates. Until now, induction of enzymes of this metabolic pathway was considered to take place only in cells of prokaryotes, plants, fungi, and nematodes in response to arising demands in carbohydrates. However, the isocitrate lyase activities have been detected in the liver of food-starved rats in our previous work and in pupas of the butterfly *Papilio machaon* in the present study. The enzymes from both studied objects were purified to homogeneous condition. The main kinetic and physicochemical properties of isocitrate lyase were studied. Organisms of evolutionary distant taxa—mammal, insect, and plant—were chosen for comparative analysis of properties of the studied enzyme. A substantial similarity of kinetic and physicochemical properties of plant and animal isocitrate leases has been found. At the same time, the absence of specific for prokaryotic, plant, and nematode isocitrate lyase nucleotide sequences has been established in mRNA from liver of starved rats and swallowtail pupa. These results are completely confirmed by analysis of the complete genome sequences of the mouse, Drosophila, and human. The obtained data raise the question about the pathway of evolution of genes of the glyoxylate cycle key enzymes.