COMPARATIVE BIOINFORMATIC ANALYSIS OF HUMAN AND LABORATORY ANIMAL AEROBIC RESPIRATION ENZYMES

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Aerobic respiration is one of the key cellular processes, and is fundamental to understanding how biological activity has shaped the history of our planet. Most enzymes involved in the respiratory chain are multi-subunit complexes encoded by both nuclear and mitochondrial DNA. Thus, the regulation of respiration is necessarily a highly coordinated process that must orchestrate the production, assembly, and function of mitochondria to meet the energy needs of the organism. The purpose of this study is to identify the enzymes involved in the process of aerobic respiration and to determine the homology of amino acid and nucleotide sequences of the enzymes in the series: the pulmonary freshwater mollusk *Biomphalaria glabrata – Rattus norvegicus – homo sapiens*.

The amino acid and nucleotide sequences of the following twenty enzymes of aerobic respiration served as material for the study: Acetyl-CoA transporter-1 (EC:2.8.3.8), Isocitrate dehydrogenase-1, NADPH-soluble (EC:1.1.1.1.42), Mitochondrial creatine kinase-2 (EC:2.7.3. 2), Mitochondrial cytochrome oxidase, subunit VIa (EC:7.1.1.9), Mitochondrial cytochrome oxidase, subunit Va (EC:7.1.1.9), Mitochondrial acetyl-CoA synthetase-2 (EC:6. 2.1.1.1), Mitochondrial NADPH dehydrogenase (EC:7.1.1.2), Mitochondrial cytochrome c-1 (EC:7.1.1.8), Mitochondrial aconitase-2 (EC:4.2.1.1. 3), Mitochondrial ubiquinone cytochrome *c* reductase (EC:7.1.1.1.8), Mitochondrial isocetrate dehydrogenase-3 (EC:1.1.1.1. 41), Mitochondrial flavoprotein, polypeptide beta (EC:1.1.1.5.3), Mitochondrial aspartate aminotransferase-2 (EC:2.6.1.1.1), Mitochondrial proton carrier (EC:7.1.1.1), Mitochondrial malate dehydrogenase-2 (EC:1.1.1.1.37), Mitochondrial isovaleryl-CoA-dehydrogenase (EC:1.3.8.4), Mitochondrial pantothenate kinase-4 (EC:2.7. 1.33), Mitochondrial aminotransferase-2 (EC:2.6.1.42), Methionine B sulfoxide reductase (EC:1.8.4.6), Mitochondrial pyruvate dehydrogenase kinase-4 (EC:2.7.11.2).

All investigated enzymes were found both in higher mammals (*homo sapiens* and *rattus norvegicus*) and in the pulmonary freshwater mollusk *Biomphalaria glabrata*, which belongs to the family *Planorbidae*, as well as *Planorbarius corneus*, inhabiting water bodies in the territory of the Republic of Belarus.

Comparative-bioinformatics analysis revealed that the homology of enzymes in mollusk relative to humans for amino acid sequences ranged from 32.89% to 82.28% and for nucleotide sequences from 32.06% to 83.37%. The highest values are characteristic of enzymes: Mitochondrial NADPH dehydrogenase (82.28%), Isocitrate dehydrogenase-1, NADPH-soluble (79.22%), Mitochondrial aconitase-2 (77.38%), Mitochondrial flavoprotein, polypeptide beta (71.5%), Mitochondrial aspartate aminotransferase-2 (68.49%), Mitochondrial isovaleryl-CoA dehydrogenase (68.42%) and Mitochondrial malate dehydrogenase-2 (67.39%). The lowest values are characteristic of the enzymes: Mitochondrial proton carrier (33.67%) and Mitochondrial acetyl-CoA synthetase-2 (32.89%). The values of the other enzymes are at an average level in the range of 40.4%-60.08%. On comparative analysis of human and rat enzymes, the percentage of homology for amino acid sequences is in the range of 77.32%-96.41% and for nucleotide sequences 65.98%-96.38%, which is a high indicator of homology.

Thus, our study has provided new insights into the long-standing debate on the origin and evolution of enzymes involved in aerobic respiration. Such flexibility of respiration allows organisms to survive in different environments. The presence of all enzymes and their high level of homology in laboratory animals proves that they have a common origin.