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Analysis of the interactions between adiponectin hormone and T-cadherin with bioinformatics methods

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Interaction between adiponectin and T-cadherin provides beneficial cardioprotective and regenerative effects on the cardiovascular system [1–4]. Adiponectin accumulates in the heart, endothelium, and skeletal muscles through interaction with T-cadherin [3]. T-cadherin specifically binds with the hexameric and high-molecular form of adiponectin. However, the details of ligand-receptor interaction between adiponectin and T-cadherin remains poorly characterized [5]. The complex of T-cadherin and adiponectin hexamer is still not crystallized and its structure is unknown.

The aim of the research is analysis of interactions between the T-cadherin receptor and adiponectin using bioinformatics analysis. Adiponectin and T-cadherin sequences were found from BLAST searches against the NCBI's RefSeq database. The multiple alignment of adiponectin and T-cadherin sequences was constructed with MUSCLE and visualized using Jalview. Bioinformatic analysis of adiponectin and T-cadherin sequences was made

using pocketZebra, visualCMAT [6]. Thus, co-evolving residues and positions of probable binding sites were identified for adiponectin: V117, G118, I43, R92, E64, Y189, D187, S200, G199, Q188, Q190, E191 (the numbering for adiponectin will be in accordance with Q15848 sequence) and T-cadherin: K115, V82, A691 (the numbering for T-cadherin will be in accordance with P55290 sequence). It is interesting to note that the mutations of adiponectin at positions 117, 118, 187, 188, 193 influence on T-cadherin binding [5]. We found the same and other positions of binding sites of adiponectin. We believe that our approach is fruitful for receiving new knowledge about the complex of T-cadherin-adiponectin. These probable binding sites could be useful for following molecular modelling of the complex.

The work was partly carried out with the financial support of the President of the Russian Federation (grant MK-3144.2019.7). The bioinformatics research has been partly carried out using the equipment of HPC computing resources at Lomonosov Moscow State University and computing resources of Complex for Simulation and Data Processing for Mega-science Facilities at NRC “Kurchatov Institute” (ministry subvention under agreement RFMEFI62117X0016), http://ckp.nrcki.ru/.

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