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Uncovering Anti-Hypertensive Obesity Targets and Mechanisms of Metformin, an Anti-Diabetic Medication

Authors : Lu Yang, Keng Po Lai

Abstract : Metformin, a well-known clinical drug against diabetes, is found with potential anti-diabetic and anti-obese benefits, as reported in increasing evidences. However, the current clinical and experimental investigations are not to reveal the detailed mechanisms of metformin-anti-obesity/hypertension. We have used the bioinformatics strategy, including network pharmacology and molecular docking methodology, to uncover the key targets and pathways of bioactive compounds against clinical disorders, such as cancers, coronavirus disease. Thus, in this report, the in-silico approach was utilized to identify the hug targets, pharmacological function, and mechanism of metformin against obesity and hypertension. The networking analysis identified 154 differentially expressed genes of obesity and hypertension, 21 interaction genes, and 6 hug genes of metformin treating hypertensive obesity. As a result, the molecular docking findings indicated the potent binding capability of metformin with the key proteins, including interleukin 6 (IL-6) and chemokine (C-C motif) Ligand 2 (CCL2), in hypertensive obesity. The metformin-exerted anti-hypertensive obesity action involved in metabolic regulation, inflammatory reaction. And the anti-hypertensive obesity mechanisms of metformin were revealed, including regulation of inflammatory and immunological signaling pathways for metabolic homeostasis in tissue and microenvironmental melioration in blood pressure. In conclusion, our identified findings with bioinformatics analysis have demonstrated the detailed hug and pharmacological targets, biological functions, and signaling pathways of metformin treating hypertensive obesity.

Keywords : metformin, obesity, hypertension, bioinformatics findings
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