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Identification of GLP1 agonist-related genes in liver and brain transcriptome

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Introduction: Liraglutide, stable GLP-1 analogue is anti-diabetic and obesity medication. Deu to its complex Mechanisms, systems biology-based approach is needed. The current study aimed to identify GLP1 agonist- related genome-wide transcriptomic alterations in liver and brain tissues.

Methods: From GEO database, two mice gene expression datasets were obtained, including liver and brain transcriptomes. Using DESeq2, differential expression analysis was conducted.

Results: Based on uncorrected p-value < 0.01, 383 DEGs between GLP1 agonist and control were obtained in liver gene expression dataset In the case of brain genome-wide transcriptome, 73 genes were altered in GLP1-agonist group. The global GLP agonist-related signatures of liver tissues were not related to those of brain tissue. The liver GLP1 agonist-related genes were estimated to be involved in lipid metabolism, mitochondria function, diabetes, obesity, and vitamin D biological pathways. In the case of the brain GLP1 agonist-related genes, they were involved in CNS development, immune and inflammation, lipid metabolism, diabetes, and RNA splicing pathways. We compared the liver and brain DEGs in GLP1 agonist groups, proposing that SFPQ gene was altered in both two tissues. SFPQ is located in chromosome 1, and is known to be expressed in mainly ovary, brain, uterus, cervix, skin, thyroid, adipose, and prostate tissues.

Conclusion: By using genome-wide transcriptome datasets, we identified several potential GLP1 agonist-related mechanisms. Moreover, we uncover a gene, SFPQ, as the robust GLP1 agonist related genes