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Bioinformatics analysis of differentially expressed genes in primary osteoporosis

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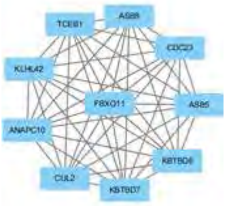
Statement of the Problem: Osteoporosis is a multi-gene related disease; the purpose of this study was to investigate the differentially expressed genes (DEGs) related to the occurrence and development of osteoporosis (OP) as well as screen out potential drug targets.

Methodology & Theoretical Orientation: The microarray data concerns osteoporosis were obtained from GEO database and DEGs were identified by R statistical software. GO and KEGG enrichment analysis, protein-protein interaction (PPI) network analysis, and selection of hub genes were conducted.

Findings: A total of 569 DEGs were screened out, 7 up-regulated and 562 down-regulated. At the same time, GO analysis of DEGs was mainly enriched in processes such as pre-mRNA intronic binding, nuclear body, histone modification and mRNA 3’-end processing, while KEGG analysis mainly involved the ubiquitin mediated proteolysis signal pathway hsa04120. By the calculation of the STRING database, we obtained the PPI network, which is consist of 517 nodes and 363 edges, and the top 10 hub genes (TCEB1, CUL2, KBTBD6, KBTBD7, ASB8, KLHL42, ASB5, FBXO11, ANAPC10, CDC23) of this study were acquired by Cytoscape software.

Conclusion & Significance: The top 10 hub genes might help us understand the pathophysiology of OP, even provide therapeutic targets for the development of drugs. Meanwhile, it might provide some new ideas for funding creative scientific hypotheses of OP.



Biography

Liu has his expertise in the research on the mechanism of osteoporosis, as well as the prevention and treatment of osteoporotic fractures. Especially the role of iron metabolism in the occurrence and development of osteoporosis.

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