Protein-protein interaction network analysis of osteoarthritis-related differentially expressed genes

Y.C. Zhu[1]*, B.Y. Deng[1]*, L.G. Zhang[1], P. Xu[3], X.P. Du[3], Q.G. Zhang[1] and B. Yang[2]

[1]Department of Orthopedics, Shanghai Tenth People's Hospital,
Tongji University School of Medicine, Shanghai, China
[2]Shanghai Health Bureau of Health Supervision, Shanghai, China
[3]Qidong Hospital of TCM, Jiangsu, China

*These authors contributed equally to this study.
Corresponding authors: B. Yang / Q.G. Zhang
E-mail: yangbo45789@gmail.com / zhangqinggang25642@gmail.com

ABSTRACT. The purpose of this study was to identify genes and pathways for osteoarthritis (OA) diagnosis and therapy. We downloaded the gene expression profile of OA from Gene Expression Omnibus (GEO) database including 10 early OA, 9 late OA, and 5 normal control samples. Next, we screened differentially expressed genes (DEGs) between early- and late-stage OA samples comparing with healthy control samples. Then, the Search Tool for the Retrieval of Interacting Genes/Proteins (STRING) software was used to construct protein-protein interaction (PPI) network, which was to predict the proteins that may interact with DEGs. The Gene Ontology (GO)-enrichment method was used to analyze the function of genes in the PPI networks. Meanwhile network module analysis was performed using Cytoscape. A total of 24 and 29 DEGs were identified for the early and late OA, respectively. *TAC1* showed the highest degree in the PPI network.

Functional annotation of the *TAC1* network module indicated that this gene is associated with the G protein-coupled signal transduction pathway. In summary, *TAC1*, together with G protein-coupled receptors, appear to play a role in the biogenesis and progress of OA. Further analysis of this gene and pathway could therefore provide a potential target for the diagnosis and treatment of OA.

Key words: Osteoarthritis; Differentially expressed gene; Protein-protein interaction network