Analysis of gene co-expression weighted network identifies specific module related to Parkinson

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Abstract: Genome wide analysis for identifing candidate genes can be one of the important steps in understanding the complex traits or diseases mechanisms. Given the complexity and multifactorial nature of the traits and diseases in most cases, understanding the mechanism of these goals requires a system

biology approach. The system biology has been developed with development of techniques related to this field of science. In this study, we tried to use a network approach for comprehensive analysis of the blood cells of people with Parkinson's disease[1, 2]. The microarray data associated with the blood cells of people with Parkinson's disease were received from the GEO under the format of the GDS2519 dataset. This dataset contains of disease and healthy (control) samples. After performing initial preprocessing, eliminating outlier sample and creating disease and control datasets, the Weighted Gene Correlation Network Analysis (WGCNA) in R-programming language was used to create a co-expression network from these datasets. The Limma package was also used to identify differential expression genes. At the end, different gene clusters were identified using the relevant functions in the WGCNA package[3, 4]. Based on differential expression test and gene overlap computations, the blue, black and yellow module in disease network were proposed as a candidate module for Parkinson's disease. Functional analysis showed that the blue module was involved in metabolism and apoptosis processes, while the black module was involved in target protein binding to ER and membrane. The yellow module was also involved in transcription processes and the translocation between the nucleus and the cytoplasm[5].

Keywords: System biology; WGCNA; Parkinson; Module; blood cell

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