Construction of gene/protein interaction networks for primary myelofibrosis and KEGG pathway-enrichment analysis of molecular compounds

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ABSTRACT. The objective of this study was the development of a gene/protein interaction network for primary myelofibrosis based on gene expression, and the enrichment analysis of KEGG pathways underlying the molecular complexes in this network. To achieve this, genes involved in primary myelofibrosis were selected from the OMIM database. A gene/protein interaction network for primary myelofibrosis was obtained through Cytoscape with the literature mining performed using the Agilent Literature Search plugin. The molecular complexes in the network were detected by ClusterViz plugin and KEGG pathway enrichment of molecular complexes was performed using DAVID online. We found 75 genes associated with primary myelofibrosis in the OMIM database. The gene/protein interaction network of primary myelofibrosis contained 608 nodes, 2086 edges, and
4 molecular complexes with a correlation integral value greater than 4. Molecular complexes involved in KEGG pathways are related to cytokine regulation, immune function regulation, ECM-receptor interaction, focal adhesion, actin cytoskeleton regulation, cell adhesion molecules, and other biological behavior of tumors, which can provide a reliable direction for the treatment of primary myelofibrosis and the bioinformatic foundation for further understanding the molecular mechanisms of this disease.

**Key words:** Gene/protein interaction networks; Primary myelofibrosis; Molecular complexes; KEGG pathway