Reconstruction of intercellular signaling network in mouse immune system

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Abstract: In the immune system, various types of molecules, cells, and organs interact with each other in response to internal and external stimuli, hence the function of such a system depends on the coordination activity of the components of a network and communications between them. Due to existence of complex communications between immune cells and their high similarity to communications of social network, the immune system can be considered as a multi-layer social network [1][2]. In these networks, communications between the different types of immune cells are carried out through secretory molecules and their cognate receptors. Cytokines molecules are secreted by immune cells in response to invasive agents and in mammals shaped the cellular organization of CNS. These molecules also play a very important role in regulating of cellular communications and normal function of a tissue. Disruptions in regulating of cytokines is associated with the incidence of neuroinflammation diseases and pathogenesis of skin inflammatory diseases [3][4]. Reconstruction of such a complex network can be a way to provide a better understanding of cytokines' function. In this study, gene expression data and receptor-ligand interaction data were used to reconstruct the immune network in mouse. Cytokine-receptor interactions data were gathered using related articles and also public protein-protein interaction databases such as iRefWeb and IntAct. The gene expression microarray dataset of primary immune cells which related to part of the Immunological Genome Project (ImmGen) was extracted from the GEO database with GSE15907 accession number and was analyzed. After analyzing the expression data, the expressed genes associated with cytokines and their receptors were selected among all expressed genes in the expression dataset. Finally, the intercellular signaling network of immune system was reconstructed based on those expressed genes and curated interactions dataset. Analysis of topological properties of the network such as centrality, degree of nodes, degree distribution and etc, by cytoscape software was done. The results of the network analysis were indicated that some of the interactions are general and exist among all types of immune cells, and in contrast, some interactions are specific for a type of cell.

Keywords: Intercellular signaling; Cytokines; Network reconstruction; Immune system

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