Transcriptional regulation of cancer-related target proteins based on microRNAs

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We previously obtained 60 cancer-related target proteins from cancer-related protein-disease network based on OMIM database. Generally, the target proteins can be controlled by transcriptional and translational levels. By using microRNAs (miRNAs), we regulate two different ways at the transcriptional level. One is mRNA control of the target proteins and the other is transcription factor control of the target genes. We acquired miRNA information from miRTarBase, TargetScan, Mir2diseasebase, and TransmiR DB sites. Of 60 proteins, 48 proteins have 150 miRNAs for mRNA control. We also acquired transcription factor information from CONSITE and P-Match sites. Of 60 proteins, 53 proteins have 50 transcription factors (TFs) that bind to 300 bp upstream regions of their genes. For highly reliable miRNA information, we constructed tripartite network for mRNA control and tetrapartite network for transcription factor control, respectively. Tripartite network contained 48 target proteins, 150 miRNAs, and 114 diseases as three different nodes and 627 links. Tetrapartite network contained 38 target proteins, 23 TFs, 336 miRNAs, and 79 diseases as four different nodes and 1,513 links. We filtered highly useful miRNA information by using hub concept of the networks and suggested target proteins, core TFs, and miRNAs for regulation of diseases. These results provide insight that controls disease at the transcriptional level.

▣ Key words: Cancer | Disease network | Transcription factor | MicroRNA

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