

Esophageal cancer: insight into protein network and identification of proteins related to this cancer using bioinformatics tools

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Abstract: Esophageal cancer (EC) is one of the common cancers and is one of the important cause of cancer death in the world. Hence, it seems that this cancer has significant effects on global health. This disease can be divided into two major classes: (1) Esophageal Adenocarcinoma Cancer (EAC) which is rapidly increased in Western countries, and (2) Esophageal Squamous Cell Carcinoma Cancer (ESCC) that incidences in developing countries. Despite numerous studies showing that several environmental factors are main causes of EC incidence, nevertheless, some of the molecular factors and biochemical mechanisms *viz.* mutations, tumor suppressor genes, protein-protein interactions and gene expression, play a key role in causing ESCC and also EAC. With this in mind, the main objective of the current work was detection of protein-protein interactions and also introduce the key proteins which have an important role in the control of esophageal cancer. For this purpose, we firstly considered NCBI and GEO databases and after that, we detected 32 general genes, which all of them had positive effects on the control of this cancer. Finally, in order to find the key protein(s), the protein network was investigated. Our findings revealed that three proteins namely *LYN Proto-Oncogene (LYN)*, *5'-Nucleotidase Ecto (NT5E)* and *Mesenchymal Epithelial Transition (MET)* had the key roles in the control of EC disease. Consequently, our results confirmed the important role of some of the proteins involved in the control of esophageal cancer, suggesting that these proteins may be a useful target for future researches and cancer therapy.

Keywords: Esophageal cancer; protein-protein interaction; systems biology; target therapy