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Prediction and validation of potential candidate genes for type II diabetes mellitus using bioinformatics analysis

Pabitra Mohan Behera, Ravindra Kumar and Anshuman Dixit[*]

Computational Biology and Bioinformatics Laboratory, Cancer Biology Group, Institute of Life Sciences, Nalco Square, Bhubaneswar, Odisha 751023, INDIA

*Corresponding author: anshumandixit@gmail.com

Abstract

Diabetes is a metabolic disorder characterized by malfunction of glucose metabolism. It leads to other complications like cardiovascular, peripheral vascular, ocular, neurologic and renal abnormalities etc. WHO estimates that 80 per cent of diabetes deaths occur in low and middle-income countries and projects that such deaths will double between 2016 and 2030. India has more people with type II diabetes (more than 50 million) than any other nation. The genetics of type II diabetes is quite intriguing as interaction of genetic, environmental and demographic factors determines individual's risk for it. Several efforts have been made for identification of new genetic loci in last 15 years. The advent of GWA studies involving several thousands of samples has facilitated this progress. In the current work we extant an integrated bioinformatics analysis featuring genetic information from web resources, Gene Ontology enrichment analysis and protein-protein interaction networks. A global protein-protein interaction network was made using medium-confidence interactions of HIPPIE database. Then this confidence scored and functionally annotated interactions were used for fetching of potential clusters containing genes described in three sets such as 348 type II diabetes genes (set1), 2238 genes associated with highly enriched GO terms (set2) and 1686 genes as hubs in the global network (set3). We propose the genes associated with top clusters are closely associated with type II diabetes and can be validated by pathway and functional analysis. We hope the finding of this study may lead to identification of novel therapeutic strategies.

References

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