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Constructing comprehensive map of molecules implicated in obesity to identify drug targets

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Obesity is a global pandemic affecting over 1.5 billion people despite the containment measures by health care agencies and governments. The pathophysiology is complex and it is closely associated with disorders such as Diabetes Mellitus Type 2 and coronary heart diseases. We have constructed a comprehensive map of all the molecules (genes, proteins, and metabolites) reported to be implicated in obesity. We used an integrated approach combining public resources and databases, deep curation strategy as well as automated text mining systems to screen over 80,863 abstracts and more than 1000 research articles, in order to construct this molecular map. The system establishes relationships between nodes using quantitative scores in an objective and user friendly manner. It has been designed using Cell Designer (version 4.1). In addition to this, we have also developed new text mining software using programming techniques in Perl to design this system. The obesity molecular map comprises of 803 nodes and 976 edges including 509 proteins, 115 genes, 1 ion, 3 drugs, 3 degraded molecules, 62 complexes, 23 RNA molecules, 83 simple molecules, 3 phenotypes and 1 unknown molecule. Our map shows an "I-shaped structure" with a highly connected central component comprising of nodes such as Leptin, Insulin etc. The central region connects on either sides to the top and bottom ends. The map is divided into modules which are occupied by densely connected nodes termed as hubs. The topological properties, gene ontology analysis and generation of random networks were also conducted. This map is distinct from pathways reported in available databases and public resources. The obesity molecular map paves the way to understand the pathophysiology of obesity and identify not only drug targets but also off-targets for existing drugs.

Biography

Kamal Rawal has obtained his Ph.D. as well as post graduation in bioinformatics from Center for Computational biology and Bioinformatics, Jawahar Lal Nehru University. During his Ph.D., he has worked on identification and characterization of genome wide analysis of mobile genetic elements and their insertion sites through computational techniques. He has developed several automated systems to analyze genomes, generate networks of important genes involved in various human diseases and establishing involvements of signals in genetic machinery such as transcription and retro transposition. He was a research fellow of DBT (2001-2002) and Indian Council of Medical Research (2003-2006). He has been awarded travel grants from Genetic Information Research Institute California, USA, Council for Scientific and Industrial Research, and DST to enable his research objectives. He has developed several bioinformatics and clinical IT tools in the area of machine learning.

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