ABSTRACT

Background

Human essential hypertension (EH) is a complex, multifactorial disorder with genetic, environmental and demographic factors contributing to its pathogenesis. It was estimated that globally, there will be 1.56 billion people affected by it by the year 2025. It was revealed that multiple interactions exist among multiple genes in pathogenesis of essential hypertension. Epistasis is defined simply as 'interaction with different genes'. The more common polygenic form of essential hypertension is developed as the consequence of epistasis.

Method

The task started with the identification of candidate genes associated with essential hypertension. For this purpose, abstracts published in PubMed database from 01/January/2000 to 01/December/2010 were used. There were 1105 abstracts thus obtained. Out of these abstracts, manual selection of essential hypertension related genes was done. There were 153 such genes identified .As this data sample showed gene name ambiguity it had to be standardized in terms of HGNC standard gene names. For this task, gene synonyms were identified using two databases, Entrez Gene and iHOP. HGNC standard gene set were obtained by using gene prospector knowledgebase and aligning these two data sets, non redundant quality candidate gene set were harvested. Then subset of ten genes was selected based on scoring system by which the gene prospector is adapted. As the next step, gene interaction network was created by using Cytoscape bioinformatics tool. The elimination of second hierarchical level of the network was done thereafter. The ultimate results gave a gene interaction network with first hierarchical level and statistical analysis.

Results and conclusion

This gene interaction network is important in many ways. The finding of genes related to pathogenesis of essential hypertension is an exhausting task because relevant information in the biomedical literature remains hidden in the form of unstructured text. The other problem is that determining disease-related genes requires laborious experiments. Therefore predicting candidate genes before experimental analysis will save time effort and cost as well.