Reviewer's report

**Title:** Gene Regulatory Network reveals Oxidative Stress as the Underlying Molecular Mechanism of Type 2 Diabetes and Hypertension

**Version:** 1  **Date:** 26 April 2010

**Reviewer:** shipra agrawal

**Reviewer's report:**

**Major comments:**

Paper presented by Jesmin et al looks promising. I have some suggestions to improve the basic structure of this paper:

1. Paper targets on differential expression pattern of all the genes from T2D-specific datasets. T2D is a complex genetic disorder and the gene expression will vary because of several other core genetic and physiological changes. Authors should first focus on differential expression pattern of reported T2D, obesity and hypertension candidate genes to generate a primary core layer. Further they can relate to the genes, which are getting altered due to the transcriptional alteration of primary layer.

2. Authors have mined the literature to find the genes. They should give the statistics that how many genes are actually reported to have the genetic association with t2d, obesity etc. They should make available the entire data information for further review. T2D-Db is an available resource for T2D candidate genes. It also includes candidates for obesity and other risk factors. Please refer the database for your list.

3. The study could propose a hypothetical model for the co regulation of the inflammatory diseases by studying the key hubs regulations, their interactions and associations, which was not reported previously. Such information can be used for discovering novel drug targets for risk factors and other inflammatory processes leading to T2D development.

**Minor points for methods section:**

- The AliBaba text mining tool used in initial gene pool collection (stage 1), searches only the pubmed abstracts. In the stage 1 gene pool collection, the study should have possibly looked for other literature databases and tried their literature mining with additional text mining tools and compared it with AliBaba in order to prevent loosing information if any.

- The stage 3 filtering step has not been elaborated regarding the number of expression datasets used for validation, statistical applications or criteria used to filter their genes.

- Since T2D is a complex genetic disease, I would suggest that develop PPI networks centric to reported candidates. Please investigate the stastically validated network for identifying novel links describing pathophysiology,
inflammation etc.

**Level of interest:** An article of importance in its field

**Quality of written English:** Acceptable

**Statistical review:** Yes, but I do not feel adequately qualified to assess the statistics.

**Declaration of competing interests:**

I declare that I have no competing interests