Reviewer's report

Title: Type 2 Diabetes Genetic Association Database manually curated for the study design and odds ratio.

Version: 1 Date: 9 September 2010

Reviewer: Wei Yu

Reviewer's report:

This manuscript described a database that collects and deposits the detail information of published genetic associations regarding to type 2 diabetes. Such specialized database will be useful for diabetes disease genomics research community.

• Major Compulsory Revisions
  1. The completeness of the published literature is a key for such databases. The literature in this database was retrieved from Phenopedia of HuGE Navigator which is designed for displaying genetic association summary information by disease. Sometimes Phenopedia is more specific but not sensitive enough to catch all possible literature due to some design limitations. For more sensitive literature search in HuGE Navigator, HuGE Literature Finder should be used. If you search “type 2 diabetes” in Literature Finder and limited it from 2001 to 2009, you will get 3013 articles. Besides, although the collection of genetic association literature in HuGE Navigator is in general very comprehensive, it may miss some articles. Is there any other literature search strategy being used for catching some possible missing articles?

  2. Comparisons with other databases are important to demonstrate the completeness of the database. Although the manuscript made comparisons with other databases, it should be more specific on literature coverage, such as how many overlaps with other db, how many missing, how many unique records in the T2DGAD, etc.

  3. I have a concern about the continuous usefulness of the database if the database only collects the data from 2001 to 2009 without future updating. I am sure it will be obsolete very soon. Is there any updating plan?

• Minor Essential Revisions
  1. Meta-analyses articles usually provide very important summary information about re-synthesis of the data. It should be included in the database. I am sure they should be fitted into the current data format.

  2. I recommend that the data from GWAS published be flagged since it provides more reliable information about association compared to the traditional candidate gene approach, especially in current GWAS era. The same thing is for Meta-analyses publications if included.
Discretionary Revisions

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

**Quality of written English:** Needs some language corrections before being published

**Statistical review:** No, the manuscript does not need to be seen by a statistician.