Reviewer’s report

Title: Association of adipocyte genes with ASP expression: a microarray analysis of subcutaneous and omental adipose tissue in morbidly obese subjects

Version: 3 Date: 6 May 2009

Reviewer: Corneliu Henegar

Reviewer’s report:

Major Compulsory Revisions

I am sorry to say that none of the major methodological concerns, regarding in particular the microarray data analysis, have been addressed by the authors. The main points that have not been adequately addressed or not even considered at all in some cases are the following:

1. First, the functional analysis of the gene expression profiles (i.e. that aims identifying pathways significantly enriched in genes showing significant differential expression in between the compared tissues or conditions) remains as biased as it initially was. The arbitrary manual selection of the pathways the authors hypothesized to be related to metabolism and inflammation in LAT and HAT subjects does not guarantee any significant overrepresentation (i.e. gene enrichment) of these pathways in the analyzed conditions, and therefore it cannot support in any way the relevance of these pathways for the explored context.

2. Secondly, I made a number of suggestions related to the analysis of co-expression relations in between gene expression profiles in microarray data based on the well recognized standard procedures in this field. In particular I suggested the authors apply one of the techniques proposed by Zhang B. and Horwath S. in order to estimate gene expression correlations from microarray data and to filter out a maximum amount of spurious correlations that are so frequent in gene expression datasets, especially when they are obtained by using very small number of subjects. Unfortunately the authors did not considered the suggestion I made and offered no explanation whatsoever for doing so. As a consequence, the relevance of the results presenting correlations between gene expression profiles based on microarray data cannot be guaranteed in any way and should not be accepted as such.

3. Third, I must say that the excuses provided by the authors for not realizing additional morphological or functional studies of the analyzed tissues are absolutely not acceptable. In particular I don’t understand which “ethical issues” have prevented the authors of analyzing the important amount of biological material that is usually obtained during bariatric or gynecologic procedures, material that usually ends by being disposed at the end of these procedures. Also the argument that the microarray studies needed an important amount of biological material, thus preventing further morphological studies of the samples
obtained during the surgical procedures, cannot be accepted. In fact the current technologies available for amplifying genetic material, RNA in this case, are mature enough these days to be able to work properly with only several micrograms of tissue that can be obtained for example through a simple needle biopsy performed on subcutaneous adipose tissue. Therefore I really see no reason why the surgical procedures couldn’t provide enough material for performing both the microarray and the morphological studies of these tissues, other than a conscious decision of the authors of not performing such morphological studies.

**Level of interest:** An article of limited interest

**Quality of written English:** Acceptable

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

**Declaration of competing interests:**

I declare that I have no competing interests.