Reviewer's report

Title: Association between polymorphic glutathione S-transferase (GST) genes, their combination and interaction with tobacco smoke and prostate cancer risk: A case-control study

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Reviewer: Rama Mittal

Reviewer's report:

The research article by Lavender et al. demonstrates the role of GST gene polymorphism in PCa susceptibility in men of African descent. Authors have used advanced statistical methods like Multifactor Dimensionality Reduction (MDR) analysis which may be effective for finding interactive/combined effect of different genes polymorphism in small sample size. However, there are some questions to be addressed

Major Compulsory Revisions

1. PCa Sample size seems a bit low as the incidence rate of PCa was higher in SC in 2008 (Cancer Statistics 2008). Therefore, can MDR analysis justify the low sample size of PCa. Moreover, the sample size is low for LR analysis too

2. As the figures indicated in the study clearly show that 22% of PCa cases had PSA value <4 ng/ml. Is there a possibility that some of the controls with PSA less than 4 ng/ml may have PCa.? The authors should refer to paper of Lobe and Catalona. (2006)

3. The data in table 2 shows significant difference between case and control in African ancestry. During LR. Did the authors consider correction for this admixture?

4. As stated in the abstract that advanced statistical methods were used like MDR analysis and hierarchical entropy graphs. Hence data related to hierarchy/ admixture in the subjects, should be provided in a graphical/tabular form for more transparency and understanding

Minor Essential Revisions

1. Result section can be grouped in different subheadings to ease the understanding for the readers.

2. The title of the article does not seem to be appropriate/ confusing, as the study did not demonstrate a significant interaction between smoking and GST gene polymorphisms. Therefore, authors may consider changing the title of the article.

3. It would be idle considering comparing the present data with studies of other population for more lucidity.

Discretionary Revisions

1. GSTM3 3 base pair deletion polymorphism in Intron 6 is another important
maker which could have been considered for study using these advanced statistical methods.

2. There are too many references cited. Try reducing the numbers.