Reviewer’s report

Title: Effect of GRM7 Polymorphisms on The Development of Noise-Induced Hearing Loss in Chinese Han workers: A Nested Case-Control Study

Version: 0 Date: 30 Oct 2017

Reviewer: Daniela Zanetti

Reviewer’s report:

Comments to the Author

The authors present an interesting study about the effect of metabolic glutamate receptor7 gene polymorphisms (GRM7) on the susceptibility to noise-induced hearing loss (NIHL). The results suggest that the CC genotype of rs1485175 in GRM7 may reduce the susceptibility of individuals to NIHL in Chinese Han population.

The analysis is generally well-conceived and executed, and the paper is well written and easy to follow. However, the sample size for the association analyses is very limited (292 cases and 584 controls) and the study needs of additional analysis in order to validate the results.

Major comment.

¥ pag 9 The continuous variables were implemented tests of normality and all of them were not in accordance with normal distribution, hence they were expressed by the median (range) and the differences between groups were analysed by Wilcoxon rank sum test.

Did the authors consider to rank-transform the variables to normality? The authors could use the rtransfom function in R and after that, rerun all the analysis and compare the results.

¥ Considering the 10 years of follow-up (January 1, 2006 - December 31, 2015) it would be interesting to run time-to-even association analysis (Cox’s proportional hazards model) in order to analyze the association of the incidences events during the 10 years of follow-up.

¥ The authors need to clarify the threshold for Bonferroni correction. After adjusting for multiple testing, considering the numbers of SNPs (5), the authors should use 0.01 as p-value threshold (0.05/5).

Minor comments:

¥ Abstract: The background section is actually an aims section. The author should summarize important results outlined by others in the same field, critically evaluating existing knowledge. They should also identify gaps that this paper is intended to fill.
The authors should revise carefully the language, for example:

Pag 2: Bcakground
Pag 8: locis

In Table 2, MAF and genotype data comes from NCBI dbSNP and 1000 Genomes Browser (CHB). It would be interesting to provide the same information using their dataset of Chinese Han population.

Are the methods appropriate and well described?
If not, please specify what is required in your comments to the authors.

Yes

Does the work include the necessary controls?
If not, please specify which controls are required in your comments to the authors.

Yes

Are the conclusions drawn adequately supported by the data shown?
If not, please explain in your comments to the authors.

Yes

Are you able to assess any statistics in the manuscript or would you recommend an additional statistical review?
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I am able to assess the statistics

Quality of written English
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