Reviewer’s report

Title: RIPK1 Polymorphisms Alter the Susceptibility to Cervical Cancer among the Uyghur population in China

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Reviewer: Li Shi

Reviewer's report:

The authors selected five SNPs in RIPK1 gene to investigate its association with cervical cancer (CC) among the Uyghur population. The present study would provide some new information of these SNP variations' role in CC in Uyghur population firstly worldwide. However, both the method and the results session were not clear enough.

My comments are as followed:

The material and methods session

a. What are the diagnose specification of CC and the specification of four clinical stages? How to recruit health controls?

b. In this study, MassARRAY was used for SNP genotyping. The information on how to make the genotyping results reliable should be provided.

c. The authors did not describe which type of logistic regression was used in the study, and also the covariates analyzed.

d. The P value should be corrected using Bonferronior or FDR to improve the results reliability.

The results session

a. The study enrolled a modest population size (840 subjects) including 342 cervical cancer patients, however, 130 patients (38% of cervical cancer patients) were lack of clinical stage information which maybe influence the final analysis results.

b. In method session, it indicated that the candidate SNPs with a MAF larger than 0.05 were selected, however, rs3736724 MAF was less than 0.05 both in case and control group in Uygur. This could bring the final analysis bias.
c. In line 15 and line 17, the authors describe the association results for rs2726724, however it is rs3736724 in both table and method session. Please check it.

d. Allelic and genotypic frequencies of the SNPs should be exhibited in table 5 to make the statistical results be evaluated.

e. As the authors mentioned in the manuscript, age is an important risk factor for development of cancer, thus age should be considered as a covariates in the logistic regression analysis. And why 43 years old be selected as the demarcation?

The introduction and discussion session

a. The authors declared "genetic variants of RIPK1 may alter the ability of gene bind substance, activate transcription and induce apoptosis". Proof needs to be provided to support this point.

b. The results showed a relationship between SNPs in RIPK1 and cervical cancer. Though the underlying mechanism of the polymorphisms in cervical cancer is still unclear, the authors should discuss the possible role of the SNPs in combination with the function of RIPK1 in cervical cancer development.

c. There is discrepancy of the SNPs’ role between study of Yao et al and this study. The authors explain that this might be because of the biologic difference to the role of RIPK1 polymorphisms. What is the biologic difference of polymorphisms of RIPK1?

d. Some references were not accordance with the description in the manuscript. Such as Line 42 "Chao et al" in introduction session, Line 20 "Yao et al" in discussion session.

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

No

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

No

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

No
Are you able to assess any statistics in the manuscript or would you recommend an additional statistical review?
If an additional statistical review is recommended, please specify what aspects require further assessment in your comments to the editors.

I am able to assess the statistics

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