Reviewer’s report

Title: Single nucleotide polymorphisms associated with postoperative inadequate analgesia after single-port VATS in Chinese population

Version: 1 Date: 05 Dec 2019

Reviewer: Daisuke Nishizawa

Reviewer's report:

To Authors:

The authors aimed to evaluate the association of common SNPs among aforementioned genes with the inadequate analgesia after single-port VATS, resulting in the outcomes that they identified SNPs in SCN9A, SCN10A, and SCN11A play a role in the postoperative inadequate analgesia after single-port VATS. These descriptions may seem to be important and benignant, in that the results of the current study may be utilized as predictors for forecasting postoperative analgesic effect for patients receiving this type of surgery. However, there seem to be several minor concerns in this manuscript. The paper will be improved when the authors revise them according to the following comments:

[Minor point]

Overall:
It seems that some English sentences are poor. For example, "This result was consistent with previous reported" should be changed to "This result was consistent with previous reports". The authors should check and edit the entire manuscript again.

Abstract:
The latter "S" letter in the "SNPS" should be lowercase. [Line 38]

Background and Table S1:
The authors explained how genes, known to be involved in systems related to pain perception and modulation based on evidence in the literature, were selected in the present study. However, it seems that the rs2952768 SNP, which was selected in the present study (Table S1), is not related to the 13 genes described and is not related to the UGT2B7 gene. The authors should explain more about this SNP.

Methods:
It is recommended that the authors describe the total number of patients recruited in the Methods section (Patient characteristics).

Results and Table 4:
The authors describe that "Significant associations between genetic mutations and postoperative inadequate analgesia were detected in nine SNPs among six genes (ESR1, P2RY12, SCN11A, SCN10A, SCN9A, and TAOK3) by the logistic regression (see Table 4)." However, only six SNPs seem to show significant associations (P-Value unadjusted < 0.05) according to Table 4. The authors should correct it. [Line 249-251]
Results and Table 4:
The authors describe that "After adjusting for potential confounders, four SNPs remained significant: rs33985936 (SCN11A), rs11709492 (SCN11A), rs6795970 (SCN10A), and 3312G>T (SCN9A)." However, five SNPs seem to show significant associations (P-Value adjusted < 0.05) including rs9340799 (ESR1) according to Table 4. The authors should correct it. [Line 251-253]

Discussion:
If rs9340799 (ESR1) SNP actually shows significant association (P-Value adjusted < 0.05) as well as other four SNPs (rs11709492, rs33985936, rs6795970, and 3312G>T), the authors should discuss the rs9340799 (ESR1) SNP in addition to the other four SNPs.

Table 1, Table 4, Table S1:
The name of the genes should be italicized.

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.

Unable to assess

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?
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

Quality of written English
Please indicate the quality of language in the manuscript:

Needs some language corrections before being published

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