

August 29th, 2013

Dear the Editor of *World Journal of Gastroenterology*

Please find enclosed the edited manuscript in Word Format (file name: 4602-revision.doc).

Title: Screening of *SLC25A13* mutation in the Thai population

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The manuscript has been improved according to the suggestions of reviewer:

1. Format has been updated
2. Revision has been made according to the suggestions of the reviewers

Reviewer 00070897

(1)... They screened 1537 subjects for a novel pathologic allele p.met1?.... They did not determine the clinical phenotype of these subjects or whether these mutations are clinical pathologic correlation, as the authors mentioned in the manuscript.

Response: The 1537 subjects were from general population; therefore, clinical phenotype for the disease was not applied to.

(2) Required major language polishing

Response: The manuscript was edited by a native English speaker (L.T.J. who is one of the authors)

Reviewer 00291404:

No corrections suggested

Reviewer 00646503

(3) The authors should explain why use a Roman (XIX, I) numeral designation to describe mutations.

Response: The conventional nomenclature of mutations of *SLC15A13* gene has been widely used; therefore, to ensure that the readers would easily follow the story in term of mutation type, we used conventional nomenclature side by side to the standard nomenclature. We now add this explanation into the main text (page 8, line 9-12)

(4) The authors should explain why it was made a division into 5 regions of Thailand. There are perhaps ethnic differences between the areas from which come the blood samples?

Response: Thank you for bringing up this important point. We added explanation for this into the last line of page 6 till line 5 of page 7

“This was to avoid ascertainment bias of study population since we did not know whether or not there was ethnic difference of the *SLC15A13* variants among subpopulation of Thailand. Moreover, Thai people from the Southern part are more ethnically related to Malay descendents and people from Northeastern are more ethnically related to Laotian and Cambodian descendents.”

(5) Why polymorphism IVS11+17C>G and c.1311C>T were not included in Table 2?

Response: Table 2 shows prevalence of pathologic alleles, and the IVS11+17C>G and c.1311C>T polymorphisms were likely benign variants.

(6) In the Results section is not clear what the authors mean to say: “This novel variant is located at the last base of exon 13, likely resulting in a synonymous change, c.C437C.”

Response: This nucleotide change likely to results in a synonymous change; however, its location at the last base of exon 13 may possibly lead to splicing error and therefore additional analysis such as mRNA transcript analysis and/or bioinformatic analysis is required to support the conclusion. This explanation is in the Discussion section. However, to make it clear in the Result section, we have made changes as follow: “This novel variant is located at the last base of a codon and also the last base of exon 13, likely resulting in a synonymous change, c.C437C, suggesting that this variant is likely a rare polymorphism. Calculated donor splice score remained unchanged (0.97), suggesting that this variant is likely a rare polymorphism.”

(7) Required minor language polishing

Response: The manuscript was edited by a native English speaker.

Reviewer 00069066

(8) The conclusion must answer the title of this study.

Response: We have made changes as shown in the Abstract.

(9) Required minor language polishing

Response: The manuscript was edited by a native English speaker.

3. References and typesetting were corrected.

Thank you again for publishing our manuscript in the *World Journal of Gastroenterology*.

Sincerely yours,

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