

## Format for ANSWERING REVIEWERS



May 22, 2015

Dear Editor,

Please find enclosed the edited manuscript in Word format (file name:26529-Revised manuscript.docx).

**Title:** Hepatitis C virus genotypes in Myanmar

**Author:** Nan Nwe Win, Tatsuo Kanda, Shingo Nakamoto, Osamu Yokosuka, Hiroshi Shirasawa

**Name of Journal:** *World Journal of Gastroenterology*

**ESPS Manuscript NO:** 26529

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

1 The format has been updated.

2 The revisions have been implemented according to the suggestions of the reviewers:

(1) The comment from reviewer **00030389**

*Response to your Major comment #1: "Page 6, lines 6-16. The authors should discuss the relationships of the prevalence of HCV genotypes in the Yunnan province in China and the immigrant workers from Cambodia and Myanmar to Thailand with those in Myanmar."*

Thank you for your valuable suggestions. We agree with you. According to your suggestions, we revised our manuscript as follows:

On page 6, line 7 - page 7, line 8,

In the Yunnan province in China, where is located in the far southern part of Mainland China bordering Laos, Vietnam, and Myanmar, HCV genotypes 1a, 1b, 3a, 3b, 6a, 6n, and 6u were found in 1.3%, 20%, 24%, 30%, 5%, 11% and 8.8%, respectively, of patients who were co-infected with HCV and HIV<sup>[20,21]</sup>. A similar HCV genotype distribution of intravenous drug users was reported in this area<sup>[22]</sup>. They<sup>[22]</sup> reported that HCV genotype 6 was most common (47%), followed by HCV genotypes 3 (41%) and 1 (12%) in intravenous drug users of the Yunnan province. Lwin et al. reported that HCV genotypes 1a, 3a, 3b, and 6 were found in 9%, 11%, 20%, and 60%, respectively, of patients in Muse where is located adjacent to the Yunnan<sup>[19]</sup>. There seems to be the some association of HCV genotype distribution between Muse in Myanmar and Yunnan province in Mainland China.

In a large number of immigrant workers from Cambodia and Myanmar to Thailand, the predominant HCV genotypes were 1a, 1b, 3a, 3b and 6 (6e, 6f, 6m, 6p and 6r)<sup>[23]</sup>. The seroprevalence of HCV infection in immigrant workers from Cambodia and Myanmar to Thailand was reported to be 2.3% or 1.7%, respectively. HCV genotypes 1a, 1b, 3a, 3b and 6 were 0%, 24%, 16%, 4% and 56%, respectively, in immigrant workers from Cambodia to Thailand, and those were 6.7%, 6.7%, 26.7%, 33.3% and 26.6%, respectively, in immigrant workers from Myanmar to Thailand. Geographic distribution of HCV genotype 6 covered mainly southern

China and the mainland of Southeast Asia, including Vietnam, Laos, Thailand, **Cambodia** and Myanmar<sup>[24-27]</sup>.

*Response to your Major comment #2: "Conclusion. They should mention the options of DAAs treatment for different genotypes and their SVR rates."*

Thank you for your valuable suggestions. We agree with you. According to your suggestions, we revised our manuscript as follows:

On page 7, line 2 from the bottom – page 8, line 12,

## **CONCLUSION**

DAAs are currently available and will be available in the near future to treat patients infected with HCV. In regards to the use of DAAs, the importance of measuring HCV genotypes is increasing and will also increase specifically in Myanmar. **DAAs against HCV could lead to higher SVR rates (90-95%) in patients infected with almost all HCV genotypes other than HCV genotype 3<sup>[9,10,29]</sup>. With current DAAs, HCV genotype 3 is the most difficult-to cure HCV genotype<sup>[29]</sup>. HCV NS5B polymerase nucleotide inhibitor sofosbuvir plus ribavirin for 12 and 24 weeks could lead 61-68% and 94% SVR rates, respectively, in non-cirrhotic treatment-naïve patients with HCV genotype 3<sup>[29]</sup>. Those could lead only 21-34% and 92% SVR rates, respectively, in cirrhotic treatment-naïve patients with HCV genotype 3<sup>[29]</sup>. In treatment-experienced patients, those treatments could lead to less SVR rates<sup>[29]</sup>. In patients with HCV genotype 6, HCV NS5A inhibitor ledipasvir plus sofosbuvir could lead to ~96% SVR rates<sup>[29]</sup>. Most of the data of HCV genotypes were from Yangon and countries other than Myanmar. It is important to determine the prevalence of HCV genotypes in Myanmar.**

*Response to your Major comment #3: "They should discuss the difference of the prevalence of HCV genotypes among the different area in Myanmar."*

Thank you for your valuable suggestions. We agree with you. According to your suggestions, we made a new Figure 1 and Table 1, and revised our manuscript as follows:

On page 5, line 3 from the bottom – last line,

.....PCR products. **Previous reports<sup>[16-19,22,23]</sup> showed the inconsistent data of the prevalence of HCV genotypes among the different area in Myanmar (Table 1), suggesting that this difference may attribute to the regional difference (Figure 1).**

(2) The comment from reviewer **02447117**

*Response to your comment: " In this summary, the authors described the genotype distribution of HCV in Myanmar. They indicated the inconsistent data in previous reports and suggested that this difference may attribute to the regional difference. If so, they should get together the data of previous reports in Table and indicate the regional difference by using the map of Myanmar."*

Thank you for your valuable suggestions. We agree with you. We made a new Figure 1 and Table 1, and revised our manuscript accordingly.

3 The references and typesetting were corrected

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

Sincerely yours,

A handwritten signature in black ink, appearing to read 'Tatsuo Kanda'. The signature is written in a cursive, flowing style with some loops and flourishes.

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