



भारतीय आयुर्विज्ञान अनुसन्धान परिषद, विषाणु इकाई, कोलकाता
ICMR VIRUS UNIT, KOLKATA
(INDIAN COUNCIL OF MEDICAL RESEARCH)
(Under Dept. of Health Research, Ministry of Health & Family Welfare, Govt. of India)
I. D. & B. G. Hospital Campus, General Block No. (GB) - 4, (East Wing), 1st Floor
57, Dr. Suresh Chandra Banerjee Road,
P.O. Box EC-61, Beliaghata, Kolkata - 700 010, INDIA

Dated: 11. 12. 2014

Dear Editor,

Please find enclosed the edited manuscript in Word format (file name: 14221-review .doc).

Title: Current molecular methods for the detection of Hepatitis C virus in high risk group population: a systematic review

Author: Rushna Firdaus, Kallol Saha, Aritra Biswas, Anirban Mukherjee and Provash Chandra Sadhukhan

Name of Journal: *World Journal of Virology*

ESPS Manuscript NO: 14221

As per your advice, we have revised the manuscript and rewrite the portions that were highlighted by crosscheck. As advice by you, we could not do the rechecking by crosscheck as this software is not a freeware and our institute does not subscribe to it. Nevertheless we tried utmost best to do the revision, but certain portions were left as it is such as:

1. the most common screening test for HCV [enzyme immunoassay (EIA)] :
Page 6, this line is a common sentence used in everyday language. Hence we did not change it.
2. Since HCV is a RNA virus, reverse transcription PCR is used to detect viral RNA. [35-37]
The viral genome is 9.6kb long, contains a single open reading frame that is translated to produce a single protein product, which is then further processed to produce functional proteins for viral replication and propagation. [36] At the 5' and 3' ends of the viral RNA are the untranslated region (UTR) that are not translated.
Page 8: This portion contains general description about HCV. This portion is cited properly therefore we did not change these lines.
3. based on the sequence of the core region could reliably identify subtypes as well as major genotypes since the sequence divergence was greater than the divergence of the 5'UTR sequence
Page 8: these lines describes the sequence diversity of HCV genotype, the text has been cited properly, and therefore no change has been made to the text.
4. The quantitation of HCV viral RNA in Cobas Amplicor is performed using the HCV Quantitation Standard. The HCV Quantitation Standard is a non-infectious Armoured RNA construct consists of HCV sequences with identical primer binding sites as the

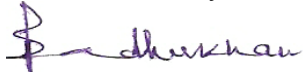
HCV RNA target and a unique probe binding region that allows HCV Quantitation Standard amplicon to be distinguished from HCV target amplicon.

Ans: The above mentioned portion about internal standard of HCV RNA quantitation, and the description is taken from the manufacture's instruction manual, therefore the wording has not been changed, but is it properly cited.

We confirm that there is no conflict of interest amongst authors, if there are any more suggestions please let us know.

Thanking you

Yours sincerely



Provash Chandra Sadhukhan.

Corresponding author

Email-provash2000@gmail.com