



## BAISHIDENG PUBLISHING GROUP INC

7901 Stoneridge Drive, Suite 501, Pleasanton, CA 94588, USA

Telephone: +1-925-223-8242

Fax: +1-925-223-8243

E-mail: bpgoffice@wjgnet.com

http://www.wjgnet.com

### PEER-REVIEW REPORT

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

**Manuscript NO:** 32549

**Title:** Naturally occurring mutations in the reverse transcriptase region of hepatitis B virus polymerase from treatment-naïve Korean patients infected with genotype

**Reviewer's code:** 02521748

**Reviewer's country:** Japan

**Science editor:** Yuan Qi

**Date sent for review:** 2017-02-22

**Date reviewed:** 2017-02-25

CLASSIFICATION	LANGUAGE EVALUATION	SCIENTIFIC MISCONDUCT	CONCLUSION
<input type="checkbox"/> Grade A: Excellent	<input type="checkbox"/> Grade A: Priority publishing	Google Search:	<input type="checkbox"/> Accept
<input type="checkbox"/> Grade B: Very good	<input type="checkbox"/> Grade B: Minor language polishing	<input type="checkbox"/> The same title	<input type="checkbox"/> High priority for publication
<input type="checkbox"/> Grade C: Good	<input type="checkbox"/> Grade C: A great deal of language polishing	<input type="checkbox"/> Duplicate publication	<input type="checkbox"/> Rejection
<input type="checkbox"/> Grade D: Fair	<input type="checkbox"/> Grade D: Rejected	<input type="checkbox"/> Plagiarism	<input type="checkbox"/> Minor revision
<input type="checkbox"/> Grade E: Poor		<input type="checkbox"/> No	<input type="checkbox"/> Major revision
		BPG Search:	
		<input type="checkbox"/> The same title	
		<input type="checkbox"/> Duplicate publication	
		<input type="checkbox"/> Plagiarism	
		<input type="checkbox"/> No	

### COMMENTS TO AUTHORS

This is a well-designed and well-written paper reporting the important role of naturally occurring nucleotide analogue resistance mutation of hepatitis B virus genotype 2 in the liver disease progression, particularly in the generation of hepatocellular carcinoma. I believe that this study contributes to deep understandings of the pathogenesis of liver cancer.



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## PEER-REVIEW REPORT

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

**Manuscript NO:** 32549

**Title:** Naturally occurring mutations in the reverse transcriptase region of hepatitis B virus polymerase from treatment-naïve Korean patients infected with genotype

**Reviewer's code:** 03479057

**Reviewer's country:** Tunisia

**Science editor:** Yuan Qi

**Date sent for review:** 2017-02-22

**Date reviewed:** 2017-03-20

CLASSIFICATION	LANGUAGE EVALUATION	SCIENTIFIC MISCONDUCT	CONCLUSION
<input type="checkbox"/> Grade A: Excellent	<input type="checkbox"/> Grade A: Priority publishing	Google Search:	<input type="checkbox"/> Accept
<input checked="" type="checkbox"/> Grade B: Very good	<input checked="" type="checkbox"/> Grade B: Minor language polishing	<input type="checkbox"/> The same title	<input type="checkbox"/> High priority for publication
<input type="checkbox"/> Grade C: Good	<input type="checkbox"/> Grade C: A great deal of language polishing	<input type="checkbox"/> Duplicate publication	<input type="checkbox"/> Rejection
<input type="checkbox"/> Grade D: Fair	<input type="checkbox"/> Grade D: Rejected	<input checked="" type="checkbox"/> No	<input checked="" type="checkbox"/> Minor revision
<input type="checkbox"/> Grade E: Poor		BPG Search:	<input type="checkbox"/> Major revision
		<input type="checkbox"/> The same title	
		<input type="checkbox"/> Duplicate publication	
		<input type="checkbox"/> Plagiarism	
		<input checked="" type="checkbox"/> No	

### COMMENTS TO AUTHORS

The paper represent an accepted population survey and contributes to the literature important information for genetics and viral genomic. Its impact is significant and thus is appropriate for this journal. In this paper the author investigate the occurrence of mutations in the reverse transcriptase region (RT) of HBV polymerase and the aggravation of the pathology in treatment naïve Korean chronic patients infected with G-C2. The paper was clear, easy to follow and thus the conclusion was evident and well justified. However, I would like to mention that, as the progression of liver disease in HBV infection is fostered by active virus replication which in turn is reflected by serum HBV DNA high levels. I wonder if the author can perform an epidemiological investigation of this mutation and the relationship to the HBV viral load in his group of patients (the chronic and the HCC patients too) may be by review their case record and the progression of level of viremia??. Given that the HBV DNA load reflects the physiological outcome of the viral infection and thus aggravation of the infection from



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<http://www.wjgnet.com>

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chronic stage to HCC development it will be interesting to investigate the viral load... I had some difficulties in reading the table 3 and I wonder if the author would be able to present it better with clear version and well organized The article is well written, but there were few errors need correction... I would recommend that the article be accepted with minor revisions if these are satisfactorily done.