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ESPS PEER-REVIEW REPORT

Name of journal: World Journal of Gastroenterology
ESPS manuscript NO: 32537
Title: Genetic Evolution of the HCV NS5A Region in CHC-1 Patients Who Are Non Responders to Two or More Treatments and Its Relationship with the Response to New Treatment
Reviewer's code: 00052887
Reviewer's country: Greece
Science editor: Ya-Juan Ma
Date sent for review: 2017-01-14 10:58
Date reviewed: 2017-01-15 03:15

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

COMMENTS TO AUTHORS

Dear authors, I found your idea and your results very interested, yet some crucial information remains unclear from the abstract that you have sent. 1. In which patients did you check for mutations, how did you choose them/ 2. Were patients chosen from all groups of therapy ? 3. Which DAA's did you choose to treat patients?

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ESPS PEER-REVIEW REPORT

Name of journal: World Journal of Gastroenterology
ESPS manuscript NO: 32537
Title: Genetic Evolution of the HCV NS5A Region in CHC-1 Patients Who Are Non Responders to Two or More Treatments and Its Relationship with the Response to New Treatment
Reviewer's code: 00070056
Reviewer's country: China
Science editor: Ya-Juan Ma
Date sent for review: 2017-01-14 10:58
Date reviewed: 2017-01-18 00:52

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

COMMENTS TO AUTHORS

This manuscript mainly explores the change of sequences within HCV NS5A region which includes PKR binding domain (PKRBD) and the interferon-sensitivity-determining region (ISDR). And researchers also studied the correlation between genomic difference and response of antiviral treatments. However, several defect exist in this manuscript so that I would recommend this manuscript to process a major revision before considering to be published on the World Journal of Gastroenterology. Reasons are listed as follow: 1. The language and sentence pattern of this manuscript should be polished to become more accessible, many sentence and paragraph should be simplified. The word "evolution" in the title of this manuscript is inappropriate, for this research just evaluated the significance of mutation number in the antiviral treatment, it hadn't evaluated evolution and progression in cohort's genome. In addition, some errors and confusing expression are presented in the article. For example, page 7 (part of RT-PCR and direct sequencing), is it proper that viral RNA was extracted from 300 mL serum? (maybe the volume of serum is 300 μl). Page 8 (the

same part), the second-round PCR product was resuspended in 20 mL and 2-5mL of it was sequenced, please check whether these numbers are regular. 2. Following points haven't been illustrated well: 2.1 The method to select 72 patients. 2.2 in page 14，"we conclude that viral variability increases when the PKRBD and ISDR regions present ≥2 mutations.", the base mutations not always induce the phenotype of virus. 2.3 The critical value of baseline viral load is 600000 IU/mL，why and how to choose this cut-off value? 2.4 In Discussion, authors should discuss the potential reasons about high viral load tends to possess more mutation numbers. 2.5 Page 11, the diagnostic value of number of mutations within PKRBD and ISDR would be better to be presented in the form of ROC curves.

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ESPS PEER-REVIEW REPORT

Name of journal: World Journal of Gastroenterology
ESPS manuscript NO: 32537
Title: Genetic Evolution of the HCV NS5A Region in CHC-1 Patients Who Are Non Responders to Two or More Treatments and Its Relationship with the Response to New Treatment
Reviewer's code: 03293797
Reviewer's country: Taiwan
Science editor: Ya-Juan Ma
Date sent for review: 2017-01-14 10:58
Date reviewed: 2017-02-01 15:49

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

COMMENTS TO AUTHORS

This manuscript is a single center, retrospective observational study of genetic evolution of HCV genotype I in patients who received antiviral therapies, but were non-responders to prior therapies . The major strength of this manuscript are its relevance to contemporary practice. It could be applied to clinical judgement of therapeutic strategies in non-responder who received novel DAAs.