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8226 Regency Drive, Pleasanton, CA 94588, United States
Telephone: +1-925-223-8242 Fax: +1-925-223-8243
E-mail: bpgoffice@wjgnet.com http://www.wjgnet.com

ESPS Peer-review Report
Name of Journal: World Journal of Gastroenterology
ESPS Manuscript NO: 8429
Title: Early viral kinetics during HCV genotype 6 treatment according to IL28B polymorphisms
Reviewer code: 00012513
Science editor: Su-Xin Gou
Date sent for review: 2014-01-06 09:58
Date reviewed: 2014-01-06 14:17

CLASSIFICATION	LANGUAGE EVALUATION	RECOMMENDATION	CONCLUSION
[ ] Grade A (Excellent)	[ ] Grade A: Priority Publishing	Google Search:	[ ] Accept
[ ] Grade B (Very good)	[Y] Grade B: minor language polishing	[ ] Existed	[ ] High priority for publication
[Y] Grade C (Good)	[ ] Grade C: a great deal of language polishing	[ ] No records	[ ]Rejection
[ ] Grade D (Fair)	[ ] Grade D: rejected	BPG Search:	[ ] Minor revision
[ ] Grade E (Poor)		[ ] Existed	[Y] Major revision
		[ ] No records	

COMMENTS TO AUTHORS

The manuscript : "Early viral kinetics During treatment HCV genotype 6 According To IL28B polymorphisms" submitted by Srunthron Akkarathamrongsin , is well-crafted and clearly presents the results, in addition the conclusions adequately fit the data obtained in the study.. However, the whole studio is based on the genotype of IL28. And this fact represents a severe methodological limitation. In this sense, it is very surprising and risky the use of a double PCR to establish a genomic SNP when there are well validated method based on real-time PCR with FRET or Taqman probes, even cheaper than the viral load determinations. In fact, the method used for this process has significant limitations , indicated below, which must be clarified in order to consider the publication of this studio . 1) The method is not clearly explained, there is not any indication of criterion of differentiation between different CC , CT and TT genotypes. It is not understood as a simple process of two PCR reactions without specific probes or RFLP can distinguish between these polymorphisms probes. What do you expect to see in the agarose gels at 2% to distinguish between CC , CT or TT? . Perhaps direct sequencing is used?. However this is just indicated in the summary not in the manuscript. If this is the method, methodogical data must be included, because they are not in the manuscript, and some figures must be provided. Moreover, Why a nested PCR is needed for a genomic sequencing?. It claims strongly our attention the not use of a real time method such as the commented to compare the method used in the manuscript. 2) Although the correct correlation with a validated method indicated no documentary evidence of this correlation is provided or only a figure showing the different patterns of genotypes obtained by the proposed method. It should provide clear documentation of the process of validation of the method with examples to check

unambiguity System setting polymorphisms 3) It is highly risky to conduct a study of genomic material by a double PCR process due to the high probability of contamination. For this motive, the authors must provide evidence of the controls used to ensure the absence of contamination and related risks should be indicated in the manuscript. 4) When and because plasma DNA or PBMC DNA were used? , these two alternatives results really surprising, when it is usual the use of ADN of EDTA whole blood . MINNORS COMMENTS : 1 - Currently it is already accepted the existence of seven HCV genotypes

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ESPS Peer-review Report
Name of Journal: World Journal of Gastroenterology
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Title: Early viral kinetics during HCV genotype 6 treatment according to IL28B polymorphisms
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Science editor: Su-Xin Gou
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CLASSIFICATION	LANGUAGE EVALUATION	RECOMMENDATION	CONCLUSION
[ ] Grade A (Excellent)	[Y] Grade A: Priority Publishing	Google Search:	[Y] Accept
[ ] Grade B (Very good)	[ ] Grade B: minor language polishing	[ ] Existed	[ ] High priority for publication
[Y] Grade C (Good)	[ ] Grade C: a great deal of language polishing	[ ] No records	[ ]Rejection
[ ] Grade D (Fair)	[ ] Grade D: rejected	BPG Search:	[ ] Minor revision
[ ] Grade E (Poor)		[ ] Existed	[ ] Major revision
		[ ] No records	

COMMENTS TO AUTHORS
Please provide exact numbers of patients with non-CC genotypes. They appear to be very small which may affect the conclusions. Also I am unsure as to the exact counselling benefit for patients since SVR rates are the same with the difference being mainly in RVR rates. I believe that the conclusion needs to change to reflect that though there is a difference in RVR and very early viral decline a meaningful change in final SVR was not observed.