PEER-REVIEW REPORT

Name of journal: World Journal of Gastroenterology

Manuscript NO: 49124

Title: Exploring the hepatitis C virus genome using single molecule real-time sequencing

Reviewer's code: 01548565

Reviewer's country: China

Science editor: Jia-Ping Yan

Reviewer accepted review: 2019-05-19 01:32

Reviewer performed review: 2019-05-20 08:40

Review time: 1 Day and 7 Hours

SCIENTIFIC QUALITY	LANGUAGE QUALITY	CONCLUSION	PEER-REVIEWER STATEMENTS
[ ] Grade A: Excellent	[Y] Grade A: Priority publishing	[ ] Accept (High priority)	Peer-Review:
[Y] Grade B: Very good	[ ] Grade B: Minor language polishing	[Y] Accept (General priority)	[Y] Anonymous
[ ] Grade C: Good			[ ] Onymous
[ ] Grade D: Fair	[ ] Grade C: A great deal of language polishing	[ ] Minor revision	Peer-reviewer's expertise on the topic of the manuscript:
[ ] Grade E: Do not publish	[ ] Grade D: Rejection	[ ] Major revision	[Y] Advanced
		[ ] Rejection	[ ] General
			[ ] No expertise
			Conflicts-of-Interest:
			[ ] Yes
			[Y] No

SPECIFIC COMMENTS TO AUTHORS

SMRT sequencing can directly demonstrate linkage of nucleotide changes over a span of more than 20 kbp, and thus can be applied to directly examine the haplotypes of viruses or bacteria whose genome structures are changing in real time. As the result, SMRT sequencing has been applied in various studies of viral genomes including

determination of the full-length contiguous genome sequence of hepatitis C virus (HCV), targeted deep sequencing of the HCV NS5A gene, and assessment of heterogeneity among viral populations. Recently, the emergence of multi-drug resistant HCV viruses has become a significant clinical issue and has been also demonstrated using SMRT sequencing. In this review , the author introduce the novel third-generation(SMRT sequencing) PacBio RSII/Sequel systems, compare them with conventional next-generation sequencers, and summarize previous studies in which SMRT sequencing technology has been applied for hepatitis C virus genome analysis. In addition, another long-read sequencing platform, nanopore sequencing technology were introduced, and discuss the advantages, limitations and future perspectives in using these third-generation sequencers for HCV genome analysis. As the results, the conclusion is accept.

INITIAL REVIEW OF THE MANUSCRIPT

Google Search:

[   ] The same title

[   ] Duplicate publication

[   ] Plagiarism

[Y] No

BPG Search:

[   ] The same title

[   ] Duplicate publication

[   ] Plagiarism

[Y] No

PEER-REVIEW REPORT

Name of journal: World Journal of Gastroenterology

Manuscript NO: 49124

Title: Exploring the hepatitis C virus genome using single molecule real-time sequencing

Reviewer's code: 02937551

Reviewer's country: China

Science editor: Jia-Ping Yan

Reviewer accepted review: 2019-05-17 07:15

Reviewer performed review: 2019-05-28 07:59

Review time: 11 Days

SCIENTIFIC QUALITY	LANGUAGE QUALITY	CONCLUSION	PEER-REVIEWER STATEMENTS
[Y] Grade A: Excellent	[ ] Grade A: Priority publishing	[ ] Accept (High priority)	Peer-Review:
[ ] Grade B: Very good	[Y] Grade B: Minor language polishing	[Y] Accept (General priority)	[Y] Anonymous
[ ] Grade C: Good			[ ] Onymous
[ ] Grade D: Fair	[ ] Grade C: A great deal of language polishing	[ ] Minor revision	Peer-reviewer's expertise on the topic of the manuscript:
[ ] Grade E: Do not publish	[ ] Grade D: Rejection	[ ] Major revision	[Y] Advanced
		[ ] Rejection	[ ] General
			[ ] No expertise
			Conflicts-of-Interest:
			[ ] Yes
			[Y] No

SPECIFIC COMMENTS TO AUTHORS

This review shows that PacBio RS II platform combined with circular consensus sequencing (CCS) can reliably provide data for full-length HCV genome sequencing analysis, especially to detect resistance-associated substitution (RAS) for DAA treatment failure.

INITIAL REVIEW OF THE MANUSCRIPT

Google Search:

[   ] The same title

[   ] Duplicate publication

[   ] Plagiarism

[Y] No

BPG Search:

[   ] The same title

[   ] Duplicate publication

[   ] Plagiarism

[Y] No