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ESPS PEER-REVIEW REPORT

Name of journal: World Journal of Virology

ESPS manuscript NO: 16610

Title: Next generation sequencing in clinical virology: discovery of new viruses

Reviewer's code: 00504045

Reviewer's country: China

Science editor: Xue-Mei Gong

Date sent for review: 2015-01-27 20:30

Date reviewed: 2015-01-29 14:37

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 checked="" type="checkbox"/> Grade B: Minor language polishing	<input type="checkbox"/> The same title	<input type="checkbox"/> High priority for publication
<input checked="" type="checkbox"/> Grade C: Good		<input type="checkbox"/> Duplicate publication	
<input type="checkbox"/> Grade D: Fair	<input type="checkbox"/> Grade C: A great deal of language polishing	<input type="checkbox"/> Plagiarism	<input type="checkbox"/> Rejection
<input type="checkbox"/> Grade E: Poor	<input type="checkbox"/> Grade D: Rejected	<input checked="" type="checkbox"/> No	<input type="checkbox"/> Minor revision
		BPG Search:	<input checked="" 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

This manuscript reviewed the evolution of virus discovery and sequencing methods, the current next-generation sequencing(NGS) methodologies and virus enrichment technologies and their applications in the clinical virus discovery. The manuscript was well organized and written. The authors are suggested to include illustrations to demonstrate different NGS and virus enrichment technologies. The manuscript should be improved in grammar. Detailed correction can be found in uploaded revised manuscript.



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ESPS PEER-REVIEW REPORT

Name of journal: World Journal of Virology

ESPS manuscript NO: 16610

Title: Next generation sequencing in clinical virology: discovery of new viruses

Reviewer's code: 00504019

Reviewer's country: China

Science editor: Xue-Mei Gong

Date sent for review: 2015-01-27 20:30

Date reviewed: 2015-02-02 09:42

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 checked="" 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"/> Plagiarism	<input type="checkbox"/> Minor revision
<input type="checkbox"/> Grade E: Poor		<input checked="" 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 checked="" type="checkbox"/> No	

COMMENTS TO AUTHORS

Some errors need correct: 1. Severe Acute Respiratory Syndrome (SARS), should be abbreviated at the first time; 2. Change "and having significant experimental basis" to "and need significant experimental basis"; 3. Change "Additionally, repeated passaging of the virus to obtain high titer is suggested to change the population of virus being sought" to "Additionally, repeated passaging of the virus to obtain high titer is believed could change the population of virus being sought"; 4. Change "The limitations of sequence dependent techniques encouraged the investigators to resort to 'metagenomics'," to "The limitations of sequence dependent techniques prompted the investigators to resort to 'metagenomics'"; 5. Change "Alternatively, in an another study" to "Alternatively, in another study"; 6. Change "here are numerous application pf NGS" to "here are numerous application of NGS";



ESPS PEER-REVIEW REPORT

Name of journal: World Journal of Virology

ESPS manuscript NO: 16610

Title: Next generation sequencing in clinical virology: discovery of new viruses

Reviewer’s code: 00646291

Reviewer’s country: United Kingdom

Science editor: Xue-Mei Gong

Date sent for review: 2015-01-27 20:30

Date reviewed: 2015-02-10 18:48

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 checked="" type="checkbox"/> Grade B: Minor language polishing	<input type="checkbox"/> The same title	<input type="checkbox"/> High priority for publication
<input checked="" type="checkbox"/> Grade C: Good		<input type="checkbox"/> Duplicate publication	
<input type="checkbox"/> Grade D: Fair	<input type="checkbox"/> Grade C: A great deal of language polishing	<input type="checkbox"/> Plagiarism	<input type="checkbox"/> Rejection
<input type="checkbox"/> Grade E: Poor	<input type="checkbox"/> Grade D: Rejected	<input checked="" type="checkbox"/> No	<input checked="" type="checkbox"/> Minor revision
		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

Major comments ? In the section entitled EVOLUTION OF VIRUS DISCOVERY TECHNIQUES insert a Table indicating similarities and differences, and advantages and disadvantages between the different virus discovery techniques ? In the section entitled EVOLUTION OF SEQUENCING TECHNOLOGIES insert a diagram indicating the added features at each stage of the different generations of sequence technologies. ? In the section entitled SAMPLE PREPARATION FOR VIRAL METAGENOMICS & DISCOVERY a brief description of AIAPA, VIDISCA, RCA, TUViD-VM instead of merely listing the viruses discovered using each one of these methodological approaches would benefit the review. ? In the section entitled “BIOINFORMATICS CHALLENGES ASSOCIATED WITH NGS add a Table indicating the bioinformatics challenges and the action that have been taken or have been proposed to overcome them. Minor comments ? Page 4: “and also in their prevention” replace with “in prevention of viral infections” ? Page 4: By the late-1950s, it was generally believed that most of the human pathogenic viruses “have” replace with “had” ? Page 4: Delete (;) after rapid ? Page 6: replace “virus(s)” with “virus(es)” ? Page 6: Rephrase the sentence “Virus isolate(s) were then purified from the cells or cell supernatant using density gradient and



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other high speed centrifugal techniques, followed by structural characterization of viral particles, antigens, nucleic acids, through different biophysical and biochemical methods" ? Page 7: replace "a technique that do not" with "a technique that does not" ? Page 7: The sentence "Metagenomic involve direct unbiased amplification of total genetic material present in a given sample, without culturing the organisms, that are otherwise genetically too diverse to be detected by degenerate or consensus PCR, their cloning and sequencing" does not make sense. ? Page 12: replace "the scientific literature is very less as compared to Roche 454" with "the scientific literature is limited compared to Roche 454" ? Page 16: replace "a novel viruses" with "a novel virus" ? Page 16: rephrase the sentence: "that were designed not anneal to ribosomal RNA" ? Page 17: replace "numerous application pf NGS" with "numerous applications of NGS" ? Page 19: the sentence at the top of the page is not complete ? The references 13, 79 and 94 should be formatted in a similar way as the rest of the references.