

ESPS Peer-review Report

Name of Journal: World Journal of Biological Chemistry

ESPS Manuscript NO: 8037

Title: The value of a newly sequenced bacterial genome

Reviewer code: 00753131

Science editor: Ma, Ya-Juan

Date sent for review: 2013-12-16 08:32

Date reviewed: 2013-12-16 13:18

CLASSIFICATION	LANGUAGE EVALUATION	RECOMMENDATION	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"/> Existed	<input type="checkbox"/> High priority for publication
<input checked="" type="checkbox"/> Grade C (Good)	<input checked="" type="checkbox"/> Grade C: a great deal of language polishing	<input type="checkbox"/> No records	<input type="checkbox"/> Rejection
<input type="checkbox"/> Grade D (Fair)	<input type="checkbox"/> Grade D: rejected	BPG Search:	<input type="checkbox"/> Minor revision
<input type="checkbox"/> Grade E (Poor)		<input type="checkbox"/> Existed	<input checked="" type="checkbox"/> Major revision
		<input type="checkbox"/> No records	

COMMENTS TO AUTHORS

The manuscript necessitates substantial editing before being considered for a serious review. Apart from grammatical error the manuscript has several sections that are conversational than a part of a serious scientific review. For example, several journals with their current impact factor should not be part of a scientific review in a scientific journal.

ESPS Peer-review Report

Name of Journal: World Journal of Biological Chemistry

ESPS Manuscript NO: 8037

Title: The value of a newly sequenced bacterial genome

Reviewer code: 00289673

Science editor: Ma, Ya-Juan

Date sent for review: 2013-12-16 08:32

Date reviewed: 2013-12-22 00:14

CLASSIFICATION	LANGUAGE EVALUATION	RECOMMENDATION	CONCLUSION
<input type="checkbox"/> Grade A (Excellent)	<input type="checkbox"/> Grade A: Priority Publishing	Google Search:	<input type="checkbox"/> [Y] Accept
<input type="checkbox"/> [Y] Grade B (Very good)	<input type="checkbox"/> [Y] Grade B: minor language polishing	<input type="checkbox"/> [] Existed	<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"/> [] No records	<input type="checkbox"/> [] Rejection
<input type="checkbox"/> Grade D (Fair)	<input type="checkbox"/> Grade D: rejected	BPG Search:	<input type="checkbox"/> [] Minor revision
<input type="checkbox"/> Grade E (Poor)		<input type="checkbox"/> [] Existed	<input type="checkbox"/> [] Major revision
		<input type="checkbox"/> [] No records	

COMMENTS TO AUTHORS

In this short review manuscript the authors discussed the progresses made in sequencing bacterial genomes and the impact of the availability of these genome sequences (as drafts versus completed and well-annotated genomes) on the scientific progress in the field. Specifically, the authors evaluated the impact on antibacterial discoveries and vaccine development. As the authors stated it well in the manuscript, it takes more than the sequencing of a genome to develop vaccines and antibacterial molecules. Understanding the biochemical and physiological mechanisms of gene products will be needed to take full advantage of genome sequences. Although the availability of draft genomes is useful for comparative analysis of limited gene families across many species, it does not provide sufficient information on intergenic regions of the genomes, which are generally rich in repetitive sequences. I would consider this short review as a good contribution to scientific community. Below are some comments to improve the manuscript: 1-The manuscript would be strengthened if the authors include a figure showing the general workflow and steps during sequencing process a bacterial genome (from genomic DNA to full genome sequence). 2-It would be helpful if the authors briefly introduced the main sequencing platforms currently (or will be) available (i.e., Illumina, Ion Proton, SOLiD, Roche 454 sequencing, etc.) with their advantages and limitations in relation to sequencing repetitive sequences and GC or AT contents of bacterial genes (not only intergenic regions). 3-Line 284. What the authors meant by "reality". Please explain. 4-Lines 285-286. Please elaborate on "other factors play a major role in ..." 5-Abstract: The sentence "When no further studies are expected to be performed using a particular bacterial genome, it is more likely that it will be deposited as a draft. Otherwise, the painstaking tasks of improving and finishing the genome (complete data) must be undertaken." would read better as: If no further interests are



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expressed for a particular bacterial genome, it is more likely that the sequencing of its genome will be limited to a draft stage, and the painstaking tasks of completing the sequencing of its genome and annotation will not be undertaken. 6-Line 53. Replace “it discussed” with “it discusses”