



PEER-REVIEW REPORT

Name of journal: World Journal of Clinical Cases

Manuscript NO: 63840

Title: Clinical metagenomic sequencing for rapid diagnosis of pneumonia and meningitis caused by Chlamydia psittaci

Reviewer's code: 05929462

Position: Peer Reviewer

Academic degree: PhD

Professional title: Research Assistant Professor

Reviewer's Country/Territory: China

Author's Country/Territory: China

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Reviewer chosen by: Ya-Juan Ma

Reviewer accepted review: 2021-03-19 02:06

Reviewer performed review: 2021-03-21 03:04

Review time: 2 Days

Scientific quality	<input checked="" type="checkbox"/> Grade A: Excellent [] Grade B: Very good [] Grade C: Good [] Grade D: Fair [] Grade E: Do not publish
Language quality	<input checked="" type="checkbox"/> Grade A: Priority publishing [] Grade B: Minor language polishing [] Grade C: A great deal of language polishing [] Grade D: Rejection
Conclusion	<input checked="" type="checkbox"/> Accept (High priority) [] Accept (General priority) [] Minor revision [] Major revision [] Rejection
Re-review	[] Yes <input checked="" type="checkbox"/> No
Peer-reviewer statements	Peer-Review: <input checked="" type="checkbox"/> Anonymous [] Onymous Conflicts-of-Interest: [] Yes <input checked="" type="checkbox"/> No



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SPECIFIC COMMENTS TO AUTHORS

The manuscript "Clinical Metagenomic Sequencing for Rapid Diagnosis of Pneumonia and Meningitis caused by *Chlamydia psittaci*" by Yin et al. reports a diagnosis method, metagenomics next generation sequencing (mNGS), for rapidly determining pathogens in clinical human samples, including bronchoalveolar lavage fluid and cerebrospinal fluid. It is interesting to see bacterial species other than those typical meningitis-causing bacteria identified in CSF. My major concern is that because *C. psittaci* was detected along with *S. pneumoniae*, using mNGS in the CSF of the patient with meningitis. It is known that *S. pneumoniae* can cause meningitis and induce inflammation that disrupts the blood-brain barrier. The authors should be more careful to make a conclusion on meningitis caused by *Chlamydia psittaci*. Minor comments --lines 115-116, the softwares used for quality control of the sequencing reads. --lines 118-120, which method was used to assign the filtered reads to the microbial genome database?