



**SDI Review Form 1.6**

Journal Name:	<a href="#">British Microbiology Research Journal</a>
Manuscript Number:	2014_BMRJ_13523
Title of the Manuscript:	NOCARDIOPSIS SP. 5 ENDOPHYTIC TO TULSI LEAVES – ISOLATION AND ANTIMICROBIAL ACTIVITY
Type of the Article	Short Communication

**General guideline for Peer Review process:**

This journal's peer review policy states that **NO** manuscript should be rejected only on the basis of '**lack of Novelty**', provided the manuscript is scientifically robust and technically sound.

To know the complete guideline for Peer Review process, reviewers are requested to visit this link:

(<http://www.sciencedomain.org/page.php?id=sdi-general-editorial-policy#Peer-Review-Guideline>)



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**PART 1: Review Comments**

	<b>Reviewer's comment</b>	<b>Author's comment</b> (if agreed with reviewer, correct the manuscript and highlight that part in the manuscript. It is mandatory that authors should write his/her feedback here)
<b><u>Compulsory</u></b> REVISION comments	<p>The authors described the isolation of Nocardiosis sp. And its antimicrobial activities. This manuscript could be considered for publication in BMRJ, but some major revision should be regarded by the authors before the manuscript could be accepted in this journal.</p> <p><b>General Comments:</b></p> <ol style="list-style-type: none"> <li>1) In "Introduction", more information regarding Nocardiosis and its potential in producing bacteriocin needs to be included.</li> <li>2) Provide the colony image, light microscope image of the strain as figure in the manuscript.</li> <li>3) Provide antimicrobial image of strain Nocardiosis no. 5 inhibiting growth of reported pathogens as figures.</li> <li>4) The 16S rRNA gene sequence reported was 1088 bp. This length is not long enough to provide accurate information in genbank blast and phylogenetic tree. Nearly full length sequence of about 1400 bp is needed. Author needs to consider gene cloning of the 16S rRNA gene to obtain the nearly full length.</li> <li>5) The phylogenetic tree needs to be improved. A outgroup is required to stabilize the topological structure of the tree. Genbank accession number should be included for each strain listed in the tree. Symbols such as "&lt;_&gt;" and "&lt;i&gt;" should be deleted from the tree. The tree needs to be reconstructed. Also the resolution and quality of the tree needs to be improved.</li> </ol>	



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<b><u>Minor</u></b> REVISION comments	1) Line 154: Author mentioned using MEGA4 software for construction of phylogenetic tree. But the citation is referring to MEGA5 version. Please clarify which version of MEGA you have used.	
<b><u>Optional/General</u></b> comments		

**Reviewer Details:**

Name:	<b>Anonymous</b>
Department, University & Country	<b>Monash University, Malaysia</b>