



SDI Review Form 1.6

Journal Name:	British Microbiology Research Journal
Manuscript Number:	2014_BMRJ_14627
Title of the Manuscript:	Evaluation of Antibiotic Biosynthetic Potential of Actinomycetes Isolates to Produce Novel Antimicrobial Agents
Type of the Article	Original Research Article

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:

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PART 1: Review Comments

	Reviewer's comment	Author's comment (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)
<u>Compulsory</u> REVISION comments	Section 2.2 Antibacterial assays and Section 3.1 Bioactivity of actinomycete isolates. Why is there no report of the pattern of antibacterial activity? Was there any comparison between diversity of amplicons and antibacterial activity? In the Discussion (lines 246-256) is mention of isolates with antibacterial activity, but lacked amplicons. However, the reverse is not mentioned. Were there any isolates that amplified sequences, but lacked antibacterial activity? Section 3.2 Detection of biosynthetic clusters... the approach chosen does not really detect "clusters", rather just single genes. Section 3.3 Phylogenetic analysis. The results are expected based on the narrow range of isolates selected and sequences amplified. What was the underlying hypothesis? Was it that diverse amplicons might signal production of novel antibiotics? Section 4. Discussion. Lines 274-280. This could add true novelty to the report, as the data might provide a test of the hypothesis that diversity in the amplified gene products reflects novelty in the antibacterial compounds.	



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<u>Minor</u> REVISION comments	(1) What bacteria were screened? (2) Figures 1, 2, and 3 are unnecessary and can be deleted. (3) Lines 118, 129, etc. Delete “biosynthetic gene clusters” as the experimental approach did not detect gene clusters, just individual genes. (4) Figures 4, 5, and 6 are unnecessary as they simply display expected relationships of genes within species. Perhaps, there are instances where the relationship between amplicons does not reflect 16S RNA sequence relationships, perhaps reflecting horizontal gene transmission?	
<u>Optional/General</u> comments	A good deal of effort, but no evidence that the authors thought carefully about the ramifications of the study and its limitations (save those of the PCR amplification).	

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