

Review Form 1.6

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| Journal Name: | Asian Journal of Orthopaedic Research |
| Manuscript Number: | Ms_AJORR_94491 |
| Title of the Manuscript: | Molecular Detection of Bone sialoprotein-binding protein (bbp) Genes among Clinical Isolates of Methicillin Resistant Staphylococcus aureus from Hospitalized Orthopedic Wound Patients |
| 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:

(<https://www.journalajorr.com/index.php/AJORR/editorial-policy>)

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) |
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| Compulsory REVISION comments | Figure 1 is not found in this manuscript. It is bad and can't review the basic important data with clear presentation. In result and discussion, there were two different MRSA detection rate. The first one was MRSA overall detection rate which was 40% (21.55%in post-surgical wound sample+19.5% in fracture wound sample) and the second one was MRSA Strained accounted 34.8% comprising 15.8%post-surgical wound and 19%fractured wound samples. The questions are that why MRSA detection rate was categorized two types and also what are the significance of the two detection rate in this study. The researcher mentioned only the 10 samples phenotypic MRSA strains for PCR analysis <i>mecA</i> gene and <i>bbp</i> gene. In this step, how these 10 MRSA samples were selected to proceed <i>mecA</i> gene and <i>bbp</i> gene? Are these samples randomly selected or not? This was not mentioned in Method in which technical steps of bacterial isolation, identification and DNA extraction of <i>mecA</i> gene and <i>bbp</i> gene were overwhelmed. | |
| Minor REVISION comments | Spelling errors in page5 [instead of 'contrast' it is written 'contract'] | |
| Optional/General comments | The data expression of this study is incomplete as figure 1 is missing. The graphs of figure 2 were not complete and it should be more informative and precise. Although this is a descriptive study, it was confused on seeing the two different types of MRSA detection rate and not clear how to reaching to the results on extraction of <i>mecA</i> gene and <i>bbp</i> gene on 10 samples. | |

PART 2:

| | 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) |
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| Are there ethical issues in this manuscript? | (If yes, Kindly please write down the ethical issues here in details) | |

Reviewer Details:

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