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From: XXX YYY<xxx@yyy.zzz>

Sent: Mon, Sep 2, 2013 at 5:32 PM

To: Managing Editor

Subject: Request for final decision for manuscript number
2013_BMRJ_5533

I was asked to make a final decision on this manuscript. This manuscript has been through two sets of peer reviews and the authors have made the requested changes. However, I agree with the third reviewer who rejected the paper during the first review and did not review the manuscript again after changes had been made.

Here are my reasons for rejecting this paper.

1. There is nothing new, novel or original in this study. The only thing that might be of interest is the percent of healthy people who are carrying presumptive methicillin-resistant *S. aureus*. (But that is not discussed in the text or compared to other studies in the discussion).
2. There is no concrete evidence that all 69 isolates obtained were even *S. aureus*. Classifying strains by Bergey's manual is not infallible and confirmation by sequencing of the 16S rDNA gene should have been done.
3. Only one strain per positive human carrier were isolated. If this study was really to study the diversity than more strains should have been obtained from the positive samples. Does each person only carry one strain of *S. aureus*?
4. Plasmids were only obtained from 24 of the 51 methicillin-resistant strains so there statement that "Plasmid profile analysis in conjunction with the antibiotic resistance typing is valuable in the epidemiological investigation of methicillin-resistant *Staphylococcus aureus* (MRSA)" holds for less than 50% of the strains. Sequence analysis of CRISPR regions would be a little more valuable as more than 60% of *Staphylococci* tested have one or more CRISPR regions. To be really valuable a technique needs to be chosen that will work on all isolates - even RAPD typing would be preferable.
5. Aside from the fact that less than 50% carried plasmids - how were the plasmid profiles valuable? There was no correlation with plasmid size or restriction profile with the antibiotic resistances determined.

6. There is very little discussion and how this data compares to previous studies.
6. There are inconsistencies in the text as well as spelling and grammatical mistakes.

Editor's Details:

Alexandra H Smith

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Note: Modification was done in this document ONLY to hide the email id.