Reviewer’s report

Title: An epidemiological and molecular study regarding the spread of vancomycin-resistant Enterococcus faecium in a teaching hospital in Bogotá, Colombia 2016

Version: 1  Date: 20 Jul 2018

Reviewer: Laurence Armand

Reviewer’s report:

The authors have correctly answered all my requirements except those concerning the epidemiological analysis. This analysis is still unclear.

The authors should add an epidemiological curve to visualize in which room(s) the 16 patients involved in the outbreak were located and when VRE colonization/infection occurred.

Second, the authors used the TPS algorithm already published (ref 26). The methodology and results are written more clearly in this latter article that I needed to read to better understand the methodology. This methodology cannot be fully transposed to the present manuscript because, in the case of the outbreak of P. aeruginosa, a WGS and SNPs analysis was performed and the evolution of the number of SNPs was taken into account in the temporality of the transmission. In the VRE outbreak, the molecular profile could only determine if strains are indistinguishable or not. Thus, the arrows indicating the direction of transmission from criterion 4 (Figure 5, part b) are not suitable. Only the colour of the profile is required and the arrows must be removed.

Figure 5 is not clear because units do not appear. It is not clear where the patients were located when they were suspected of transmission. All arrows describing the way of transmission are black and some patients appear to be located in several wards.

In addition, patients belonging to the same unit in Table 2 are not those connected by arrows in Figure 5.

Figure 5 would be clearer with the legend in the figure as for the quoted article (26)

From figure 5, we understand that P4 transmitted to P7 and P14 his strain but in the text (L290) the authors wrote that P4 was "exposed" to P7 and P14?

The authors discuss in the result section the possible ways of transmission from P2 to P7 and from P12 to P13 whereas the strain has not been typed or does not belong to the same genomic profile (L291-298). It has no interest.

Other comments:

L88: Rate instead of percentage
L123: VRE has not become less pathogenic but has caused fewer infections.

L133-143: These data are results, not methods.

L321: The authors should add that some VRE clones are less disseminating than others. It is known that some clonal complexes like CC17 are more epidemiogenic than others.

Are the methods appropriate and well described?
If not, please specify what is required in your comments to the authors.

No

Does the work include the necessary controls?
If not, please specify which controls are required in your comments to the authors.

Unable to assess

Are the conclusions drawn adequately supported by the data shown?
If not, please explain in your comments to the authors.

Yes

Are you able to assess any statistics in the manuscript or would you recommend an additional statistical review?
If an additional statistical review is recommended, please specify what aspects require further assessment in your comments to the editors.

Not relevant to this manuscript

Quality of written English
Please indicate the quality of language in the manuscript:

Needs some language corrections before being published

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