Next Generation Sequencing for Genomic Analysis of Cfr(B)-producing Enterococcus faecium Causing Infections in a New Orleans Medical Center

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Abstract

Background: Cfr(B) is a major mechanism for resistance in E. faecium that has spread worldwide and is associated with hospital outbreaks. We previously sequenced four New Orleans E. faecium isolates (strain 18961R, 18203R, 18010R, and 26261R) in the last two years in our hospital system as part of the routine microbiology workflow to identify emerging resistance mechanisms and reduce transmission risk. The Cfr(B) resistance determinant was reported to be present in 6/7 isolates and is a member of the 

Keywords: Enterococcus faecium, enterococcal infection, Next generation sequencing, Cfr, vancomycin

Methods

Bacterial isolation: Ten E. faecium isolates (strain 18961R, 18203R, 18010R, 26261R, 29213S, 18961S, 18010S, 18203S, and 18961S) were isolated from the New Orleans hospital system. In addition, two index isolates (18010R and 18203R) were isolated in this hospital system. This study presents the characterization of these isolates by using Next generation sequencing (NGS)

NGS performed on all isolates of E. faecium for resistance genes (687-bp) and confirmed resistance to vancomycin, cefazolin, azithromycin, trimethoprim, sulfamethoxazole, tetracycline, and minocycline. All isolates were resistant to both vancomycin and tetracycline. The genotypes of these isolates were IVDW 2016

Conclusions

The clinical and laboratory standards Institute (2015). Aminoglycoside resistance was detected in all isolates. Virulence genes were found in all isolates. Transcriptional expression from the tuf and mcr-1 genes were found in the CRP-2 strain from the NGS analysis. The results of the NGS analysis were consistent with published literature on the genetic diversity of E. faecium. The NGS analysis demonstrated that the isolates were closely related and closely related to the previously reported E. faecium isolates from other hospital systems. This information can be used to better understand the transmission and spread of resistance in E. faecium isolates in New Orleans.

References


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Figure 1: Arrangement of pEF and surrounding genes on an 14.4 kb E. faecium genome

Table 1: Antimicrobial susceptibility profile of Cfr(B)-producing E. faecium isolate in the Octave New Orleans hospital system.

Table 2: Virulence and resistance genes detected in Cfr(B)-producing E. faecium isolates by NGS.

Table 3: MLS resistance profile of Cfr(B)-producing E. faecium isolates from the Octave New Orleans hospital system.