Abstract

More recently, an oxacillin-resistant mechanism was identified in clinical isolates of methicillin-resistant Staphylococcus aureus (MRSA) that are resistant to linezolid and tigecycline. This mechanism is characterized by a mutation in the 23S rRNA-encoding gene adjacent to the cfr gene, named L3 Tyr158Ser. Linezolid inhibits protein synthesis by interfering with the formation of the 70S initiation complex, thereby preventing the translation of certain key antibiotic target proteins for which aminoglycosides, glycopeptides, daptomycin and tigecycline are effective. L3 Tyr158Ser mutation confers resistance to several antibiotic classes, including aminoglycosides, glycopeptides, daptomycin and tigecycline. The L3 Tyr158Ser mutation was previously detected in methicillin-resistant coagulase-negative staphylococci (CoNS) and demonstrated to be responsible for elevated MIC results for linezolid. The present study evaluated the genetic context of the L3 Tyr158Ser mutation in coagulase-negative staphylococci (CoNS) and clinical isolates of MRSA. Materials and Methods: Isolates were collected between 2007 and 2009 from hospitals in North Liberty, IA, USA. cfr genotyping was performed by Southern blot and hybridization. cfr genotyping was also performed for all isolates using Amplification-refractory mutation system (ARMS) and sequencing. Results: Of the 164 isolates, 22 (13%) were cfr-positive. The cfr mutation was located within the 23S rRNA gene. The cfr sequence was 99% identical to that reported in clone 205. The L3 Tyr158Ser mutation was specifically located in the 23S rRNA gene. All cfr-positive isolates were susceptible to tigecycline and daptomycin. Conclusion: The L3 Tyr158Ser mutation is a novel mechanism of resistance to linezolid and tigecycline in coagulase-negative staphylococci (CoNS) and clinical isolates of MRSA. The L3 Tyr158Ser mutation is located within the 23S rRNA gene and is responsible for elevated MIC results for linezolid and tigecycline.