Genotypic Evaluation of a Collection of Cfr-producing Staphylococcal Clinical Isolates from the SENTRY Antimicrobial Surveillance Program

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ABSTRACT

Overall, mutations in the 23S rRNA were not detected among CoNS, except in isolate 3147 with a 23S rRNA mutation at position 27805 (G2576T). In contrast, alterations in the L3 and L4 proteins were commonly observed in CoNS. Cfr-producing S. aureus demonstrated whole-genome amplification of cfr alleles.

RESULTS

• Only 19 of 7630 (0.2%) staphylococcal clinical strains carried cfr, detected during a five year period of the SENTRY Program. Within 2006 – 2010, Cfr-positive strains were commonly observed, except in isolates 2907 and 2174 USA 2009 426 >128 2-I ST186 NA SEPI426A C2534T H146Q/V154L/A157R 71_72insG.

• All cfr-carrying S. epidermidis were associated with CC2 and 50.0% of the strains belonged to spa type 2, except for one isolate from Belgium.

REFERENCES


