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Genomic Modeling of an Outbreak of Multidrug Resistant *Shigella sonnei*, California, USA, 2023–2024

Appendix

Methods

We sequenced all isolates on an Illumina MiSeq using v2 300 cycle chemistry in a paired end, 2x150bp configuration. All raw sequence data fastq files were assembled using SPAdes v 1.1, and genotyping was performed using sonneityping in mykrobe v 0.12.1 (*1*,*2*). To determine the presence of antibiotic gene resistance, gene annotation was performed using ResFinder with database v 4.11.1 and AMRFinder Plus v 3.11.20 (*3*–*5*). Using these databases, we did not identify resistance genes unique to the cases of bacteremia. Genes for the specific antimicrobial classes that help to predict resistance were: cephalosporins (*blaCTX-M-15*), tetracyclines (*tet(A)*), aminoglycosides (*aph (6)-Id*, *aph(3")-Ib, aadA1),* trimethoprim (*drfA1*), and quinolones (*qnrS1*)." Variant calling was performed using snippy v 4.6.0 using reference genome NC_007384.1 (*5*). BEAST2 xml parameters, and R code for generating trees can be found in this github respository www.github.com/tjlloyd/ShigellaMASCOT.

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