Comparing Whole-Genome Sequencing with Sanger Sequencing for spa Typing of Methicillin-Resistant Staphylococcus aureus

spa typing of methicillin-resistant Staphylococcus aureus (MRSA) has traditionally been done by PCR amplification and Sanger sequencing of the spa repeat region. At Hvidovre Hospital, Denmark, whole-genome sequencing (WGS) of all MRSA isolates has been performed routinely since January 2013, and an in-house analysis pipeline determines the spa type. Due to national surveillance, all MRSA isolates are sent to Statens Serum Institut, where the spa type is determined by PCR and Sanger sequencing. The purpose of this study was to evaluate the reliability of the spa types obtained by 150-bp paired-end Illumina WGS. MRSA isolates from new MRSA patients in 2013 (n = 699) in the capital region of Denmark were included. We found a 97% agreement between spa types obtained by the two methods. All isolates achieved a spa type by both methods. Nineteen isolates differed in spa types by the two methods, in most cases due to the lack of 24-bp repeats in the whole-genome-sequenced isolates. These related but incorrect spa types should have no consequence in outbreak investigations, since all epidemiologically linked isolates, regardless of spa type, will be included in the single nucleotide polymorphism (SNP) analysis. This will reveal the close relatedness of the spa types. In conclusion, our data show that WGS is a reliable method to determine the spa type of MRSA.